

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **DSTLIMQLLR**

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

Match to Query 33792: 1499.832708 from(750.923630,2+) rtinseconds(2966) index(59252)

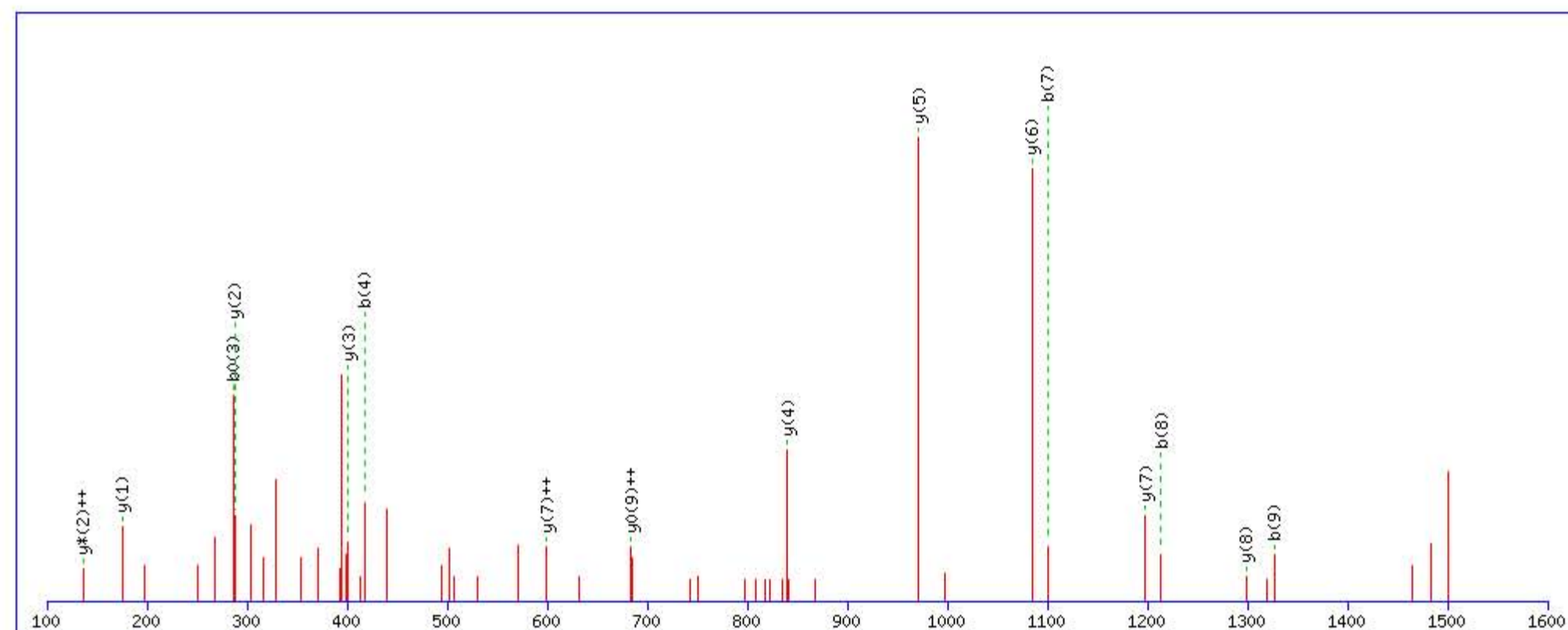
Title: Locus:1.1.1.1645.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1499.820374

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

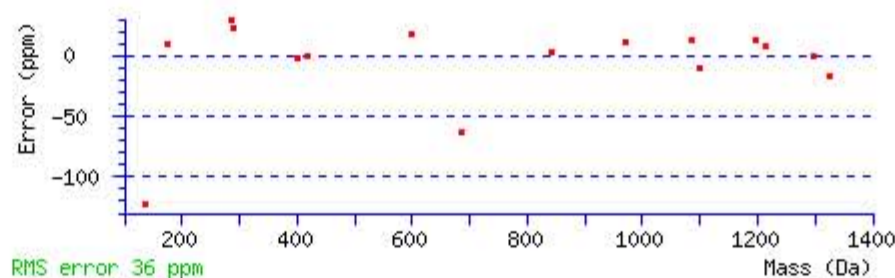
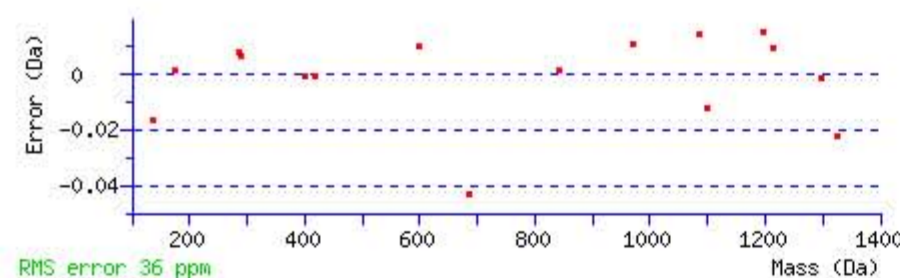
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 47 Expect: 0.00033

Matches : 16/82 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	116.034219	58.520748			98.023654	49.515465	D							10
2	203.066247	102.036761			185.055682	93.031479	S	1385.800726	693.404001	1368.774177	684.890726	1367.790161	684.398718	9
3	304.113926	152.560601			286.103361	143.555319	T	1298.768698	649.887987	1281.742149	641.374712	1280.758133	640.882704	8
4	417.197990	209.102633			399.187425	200.097351	L	1197.721019	599.364147	1180.694470	590.850873			7
5	530.282054	265.644665			512.271489	256.639383	I	1084.636955	542.822115	1067.610406	534.308841			6
6	661.322539	331.164908			643.311974	322.159625	M	971.552891	486.280083	954.526342	477.766809			5
7	1100.547865	550.777571	1083.521316	542.264296	1082.537300	541.772288	Q	840.512406	420.759841	823.485857	412.246566			4
8	1213.631929	607.319602	1196.605380	598.806328	1195.621364	598.314320	L	401.287080	201.147178	384.260531	192.633903			3
9	1326.715993	663.861634	1309.689444	655.348360	1308.705428	654.856352	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 **DSTLIMQLLR**

(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	1499.820374	0.012334	DSTLIMQLLR
22.0	1499.819489	0.013219	SLSLVDNEIELLR
18.8	1499.830719	0.001989	EEIVDKTRLIER
17.9	1499.824203	0.008505	MNKLGTRLVPAER
8.5	1499.830719	0.001989	IEALSSKVQQLER
7.8	1499.819504	0.013204	KTLLVEDILGDER
6.9	1499.820847	0.011861	AFIKNSSLTVHQR
6.9	1499.832062	0.000646	AFSQRASLSIHKR
6.7	1499.820374	0.012334	MVQALTELLR
6.4	1499.814316	0.018392	QQGKAFQRAR

MASCOT **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 33746: 1497.724332 from(500.248720,3+) rtinseconds(1438) index(49079)

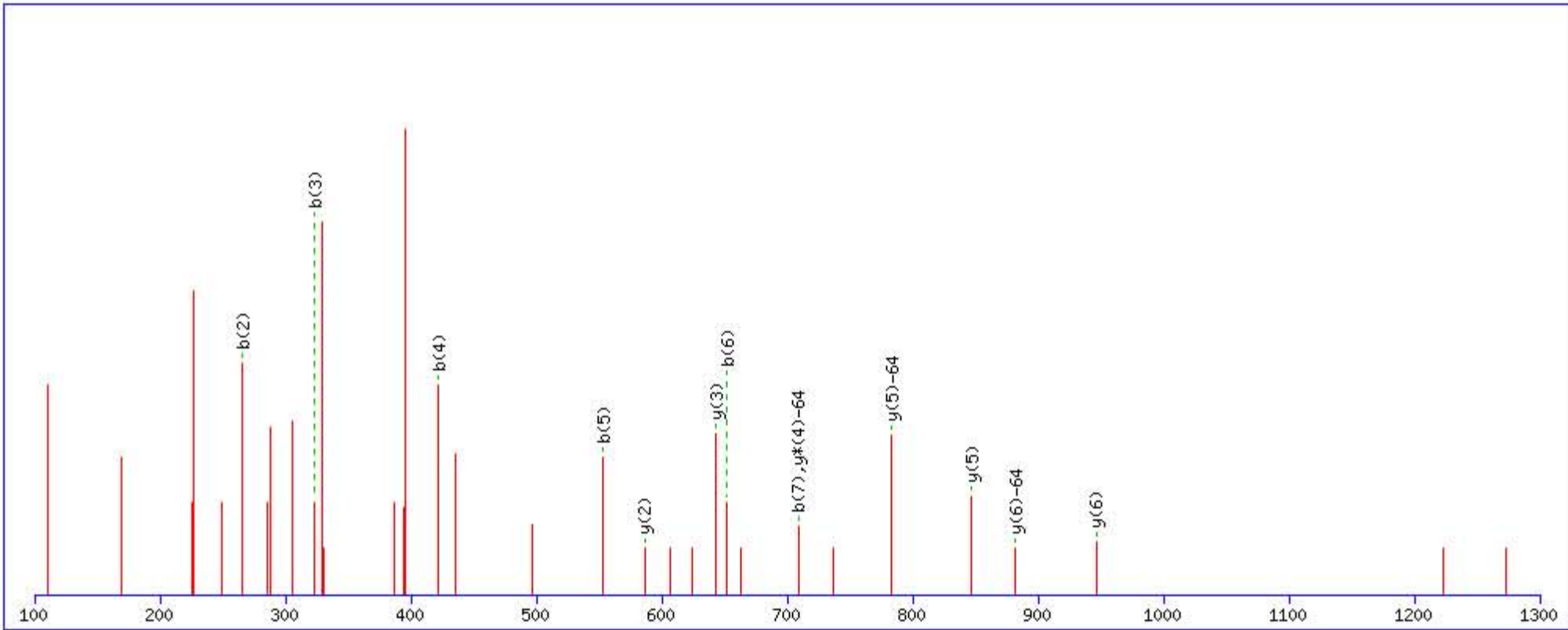
Title: Locus:1.1.1.1116.15 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1497.725464

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

Variable modifications:

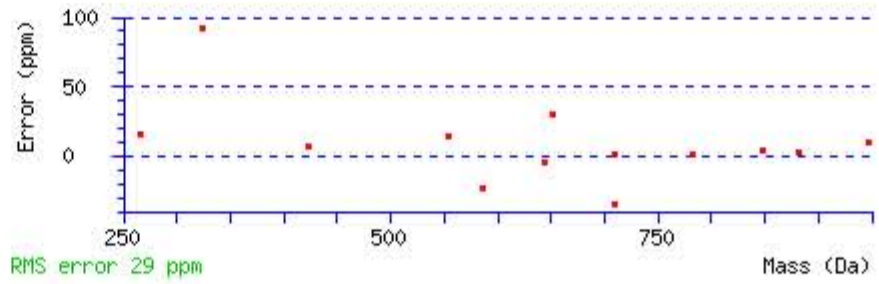
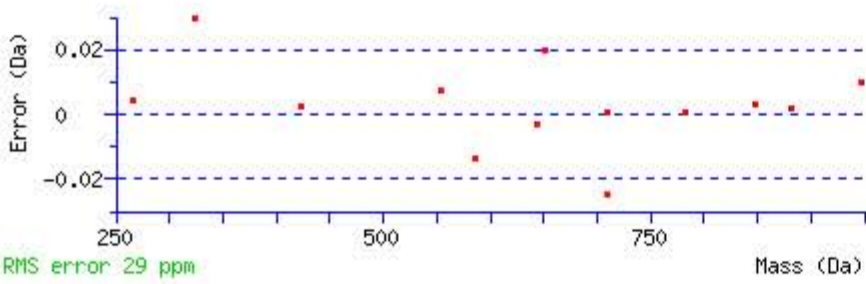
M8 : Oxidation (M), with neutral losses 0.000000 (shown in table), 63.998285

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 31 Expect: 0.011

Matches : 13/118 fragment ions using 24 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	1361.673813	681.340545	1344.647264	672.827270	10
3	323.146230	162.076753	306.119681	153.563478	G	1233.615235	617.311256	1216.588686	608.797981	9
4	422.214644	211.610960	405.188095	203.097685	V	1176.593771	588.800524	1159.567222	580.287249	8
5	553.255129	277.131203	536.228580	268.617928	M	1077.525357	539.266317	1060.498808	530.753042	7
6	652.323543	326.665410	635.296994	318.152135	V	946.484872	473.746074	929.458323	465.232800	6
7	709.345007	355.176142	692.318458	346.662867	G	847.416458	424.211867	830.389909	415.698593	5
8	856.380407	428.693842	839.353858	420.180567	M	790.394994	395.701135	773.368445	387.187861	4
9	913.401871	457.204574	896.375322	448.691299	G	643.359594	322.183435	626.333045	313.670161	3
10	1352.627197	676.817237	1335.600648	668.303962	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
31.2	1497.725464	-0.001132	HQGVMVGMGQK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **DSYVGDEAQS**K

Found in **ACTA_HUMAN**, Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1

Match to Query 34165: 1508.680588 from(755.347570,2+) rtinseconds(1545) index(33589)

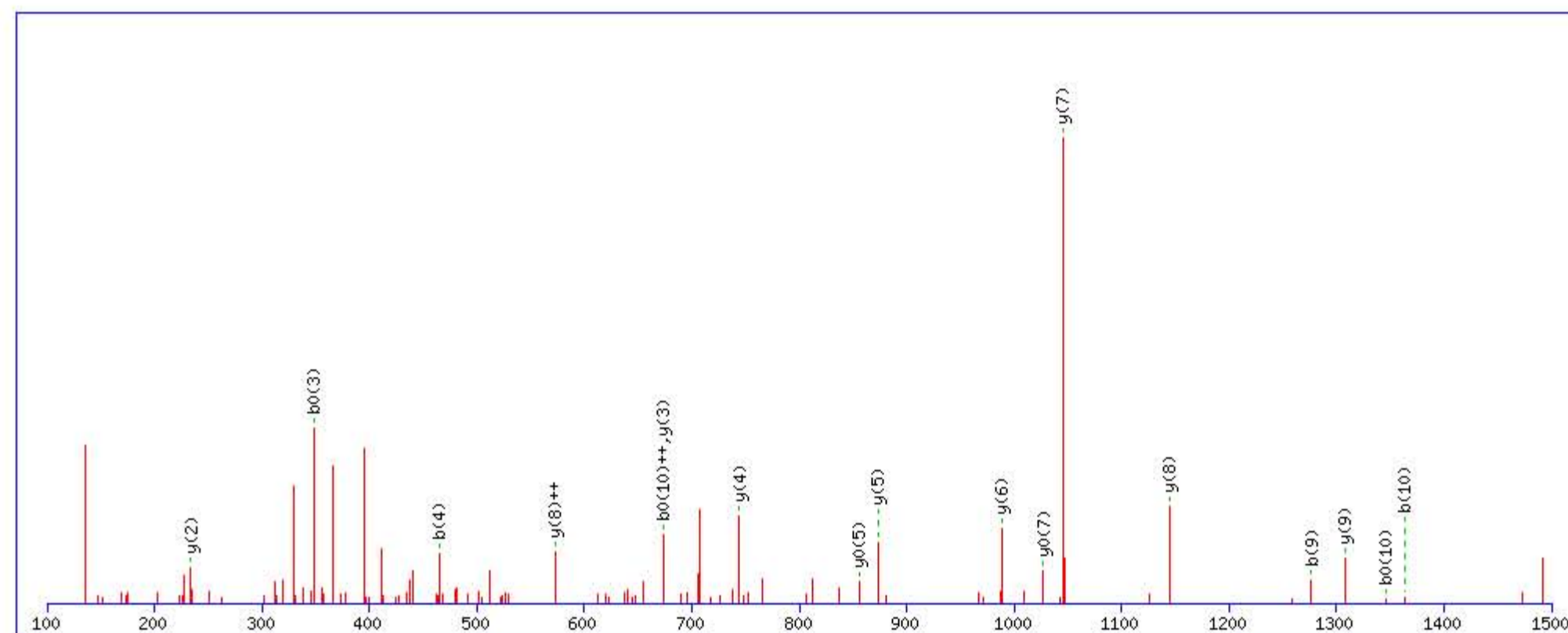
Title: Locus:1.1.1.2957.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1508.681702

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

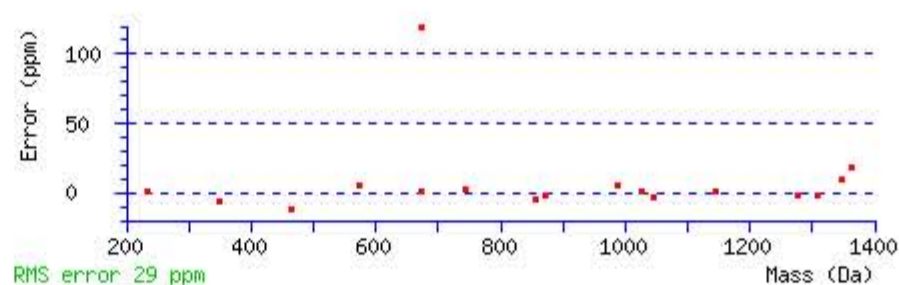
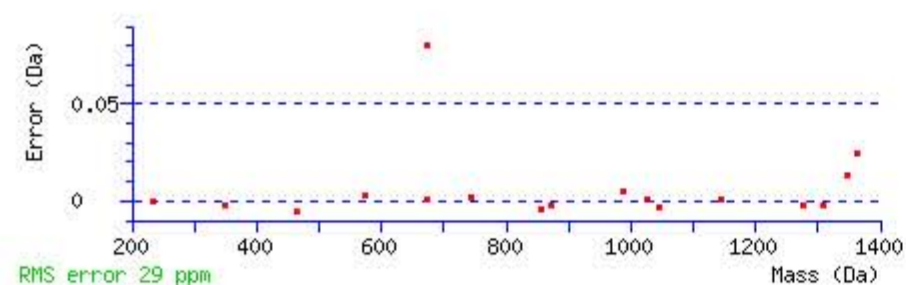
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 53 Expect: 5.6e-005

Matches : 17/102 fragment ions using 28 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.034219	58.520748			98.023654	49.515465	D							11
2	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 **DSYVGDEAQS**K

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.7	1508.681702	-0.001114	DSYVGDEAQS K
7.5	1508.690277	-0.009689	GGRGGMGGSDRGGF NK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SYELPDGQVITIGNER**

Found in **ACTA_HUMAN**, Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1

Match to Query 49230: 2101.062372 from(701.361400,3+) rtinseconds(2611) index(40232)

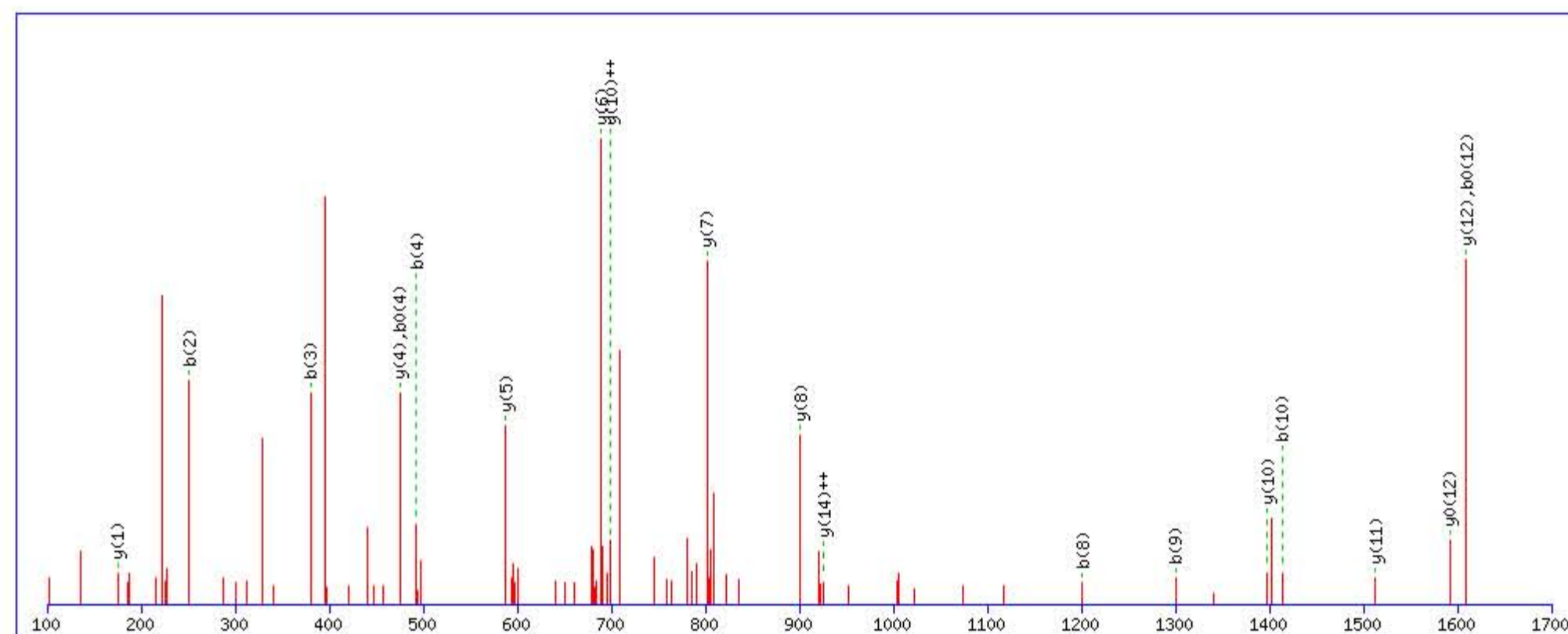
Title: Locus:1.1.1.3328.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2101.051376

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

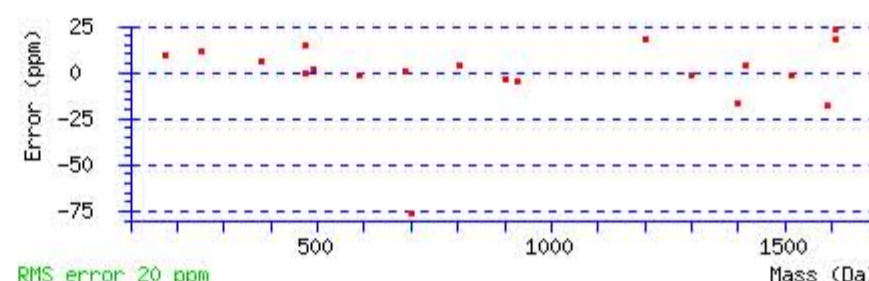
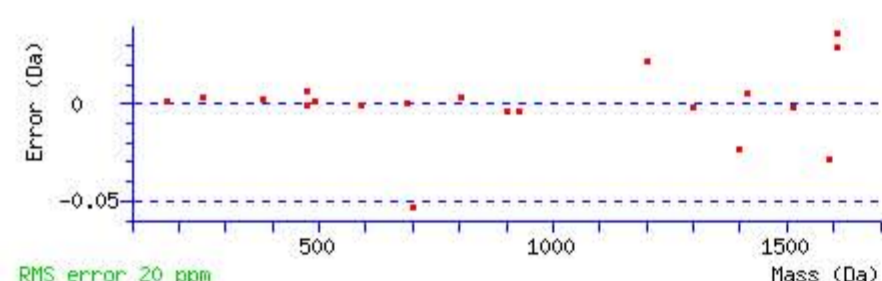
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 55 Expect: 3.1e-005

Matches : 20/164 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							16
2	251.102633	126.054954			233.092068	117.049672	Y	2015.026640	1008.016958	1998.000091	999.503683	1997.016075	999.011675	15
3	380.145226	190.576251			362.134661	181.570969	E	1851.963311	926.485294	1834.936762	917.972019	1833.952746	917.480011	14
4	493.229290	247.118283			475.218725	238.113001	L	1722.920718	861.963997	1705.894169	853.450722	1704.910153	852.958714	13
5	590.282054	295.644665			572.271489	286.639383	P	1609.836654	805.421965	1592.810105	796.908691	1591.826089	796.416682	12
6	705.308997	353.158137			687.298432	344.152854	D	1512.783890	756.895583	1495.757341	748.382309	1494.773325	747.890300	11
7	762.330461	381.668869			744.319896	372.663586	G	1397.756947	699.382111	1380.730398	690.868837	1379.746382	690.376829	10
8	1201.555787	601.281532	1184.529238	592.768257	1183.545222	592.276249	Q	1340.735483	670.871379	1323.708934	662.358105	1322.724918	661.866097	9
9	1300.624201	650.815739	1283.597652	642.302464	1282.613636	641.810456	V	901.510157	451.258716	884.483608	442.745442	883.499592	442.253434	8
10	1413.708265	707.357771	1396.681716	698.844496	1395.697700	698.352488	I	802.441743	401.724509	785.415194	393.211235	784.431178	392.719227	7
11	1514.755944	757.881610	1497.729395	749.368336	1496.745379	748.876328	T	689.357679	345.182478	672.331130	336.669203	671.347114	336.177195	6
12	1627.840008	814.423642	1610.813459	805.910368	1609.829443	805.418359	I	588.310000	294.658638	571.283451	286.145363	570.299435	285.653355	5
13	1684.861472	842.934374	1667.834923	834.421099	1666.850907	833.929091	G	475.225936	238.116606	458.199387	229.603331	457.215371	229.111323	4
14	1798.904399	899.955837	1781.877850	891.442563	1780.893834	890.950555	N	418.204472	209.605874	401.177923	201.092600	400.193907	200.600592	3
15	1927.946992	964.477134	1910.920443	955.963860	1909.936427	955.471851	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
16							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [SYELPDGQVITIGNER](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.3	2101.051376	0.010996	SYELPDGQVITIGNER
7.2	2101.047363	0.015009	IMGGNSILHSAADSVTSAVQK

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 23313: 1200.592788 from(601.303670,2+) rtinseconds(1485) index(33178)

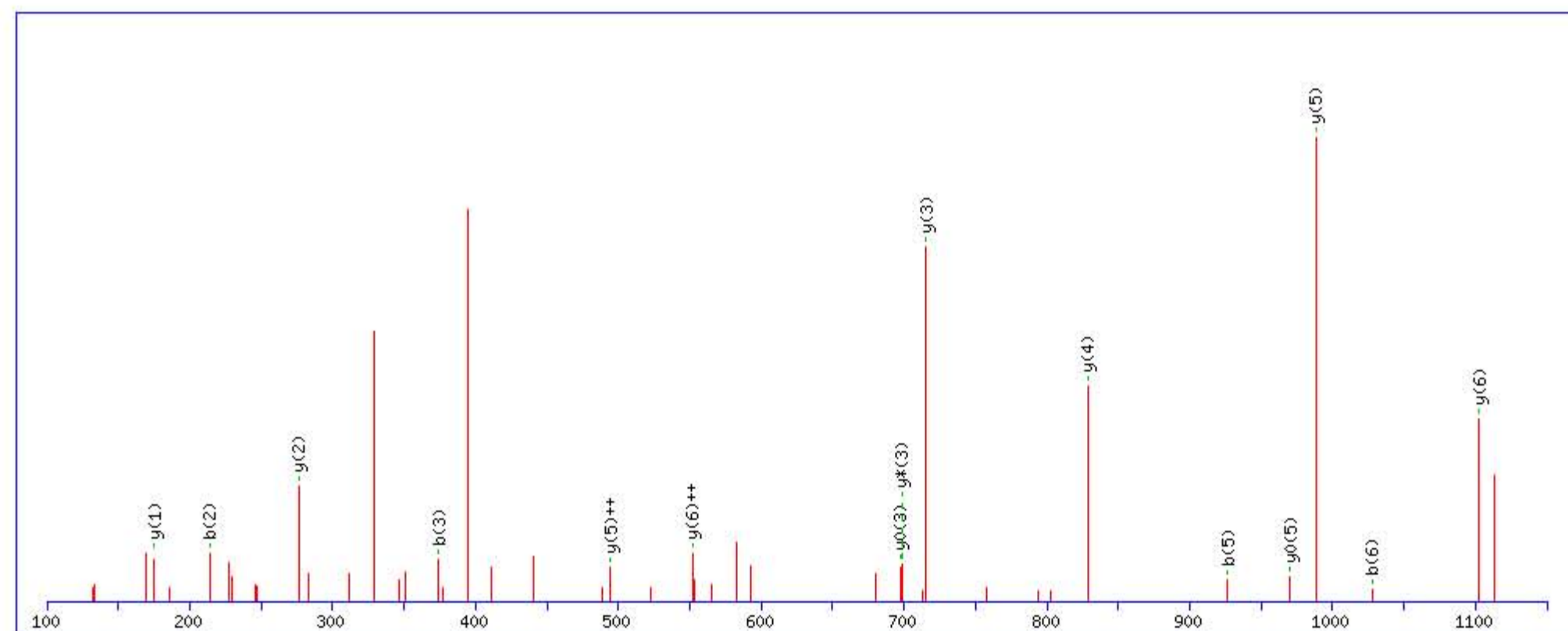
Title: Locus:1.1.1.2936.8 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1200.610733

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

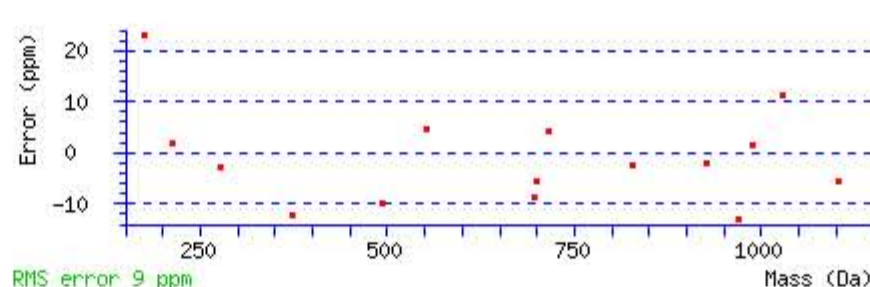
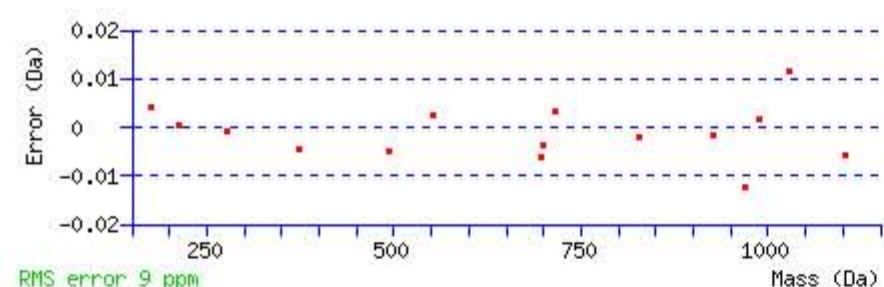
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 39 Expect: 0.00065

Matches : 15/58 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							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
38.7	1200.610733	-0.017945	VNCLQTR
4.4	1200.603333	-0.010545	GRIAEPSVCGR
3.0	1200.592087	0.000701	QEATNATR
2.9	1200.592102	0.000686	QSVGENTR
2.0	1200.603333	-0.010545	SQEGRGTR
0.1	1200.610733	-0.017945	QCNVITR

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

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 29030: 1364.745432 from(455.922420,3+) rtinseconds(1846) index(4828)

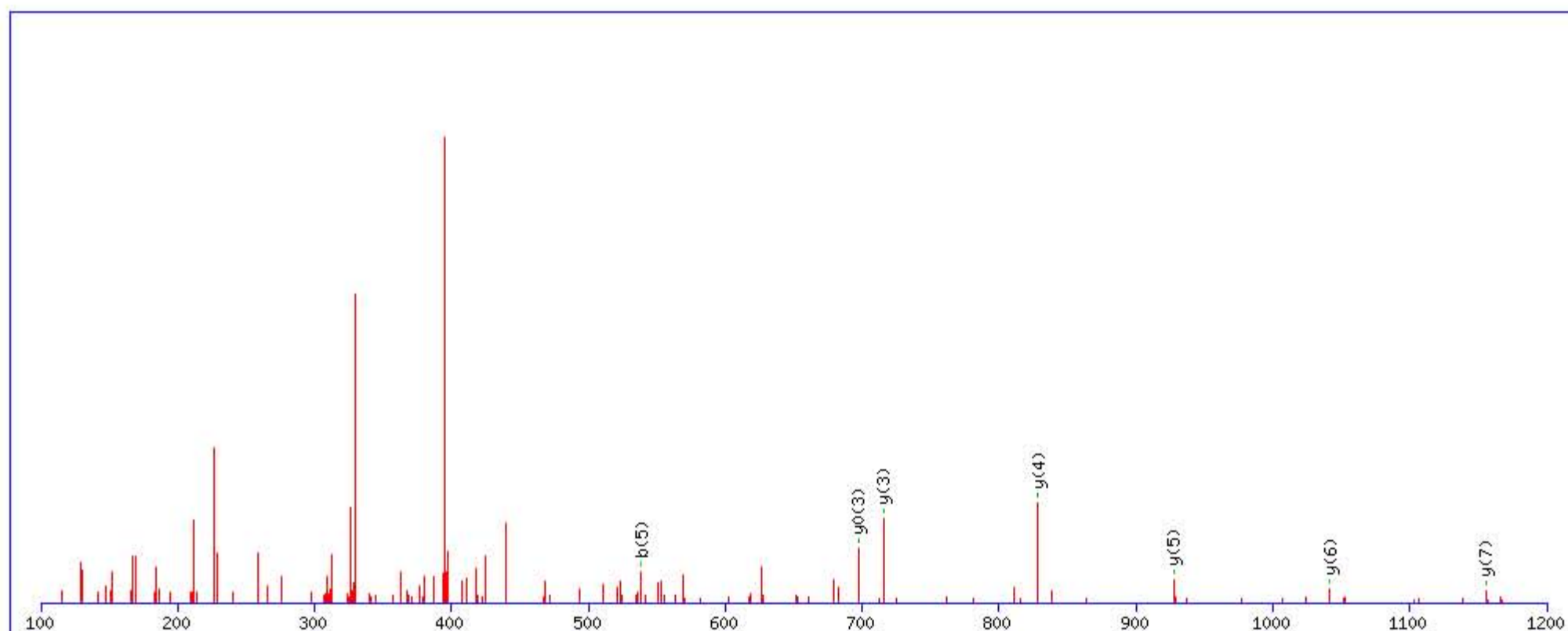
Title: Locus:1.1.1.1452.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1364.748581

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

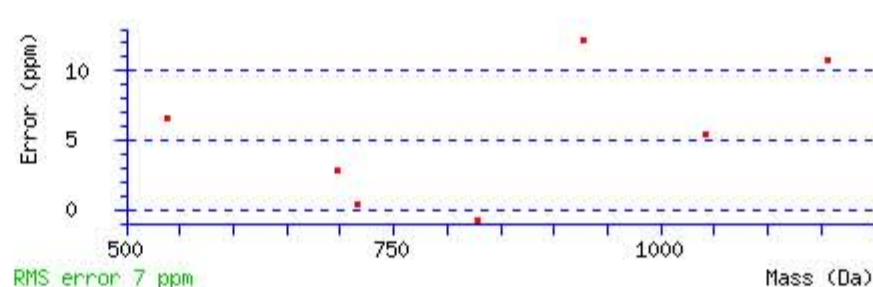
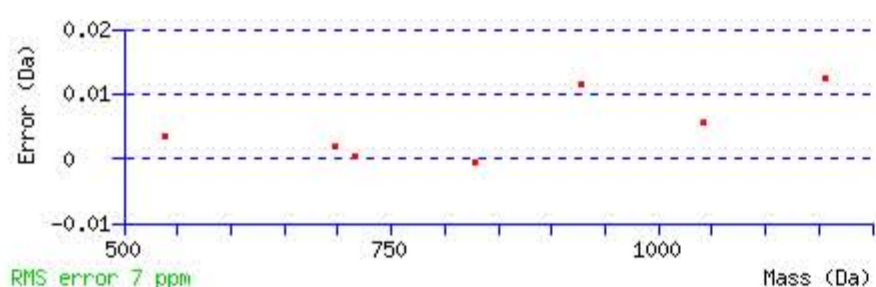
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.024

Matches : 7/76 fragment ions using 11 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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
26.4	1364.748581	-0.003149	LPNNVLQEK
8.5	1364.759827	-0.014395	QTSSLIHR
0.2	1364.745239	0.000193	KVVSWIDVYTR

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 32669: 1456.720928 from(729.367740,2+) rtinseconds(1934) index(5503)

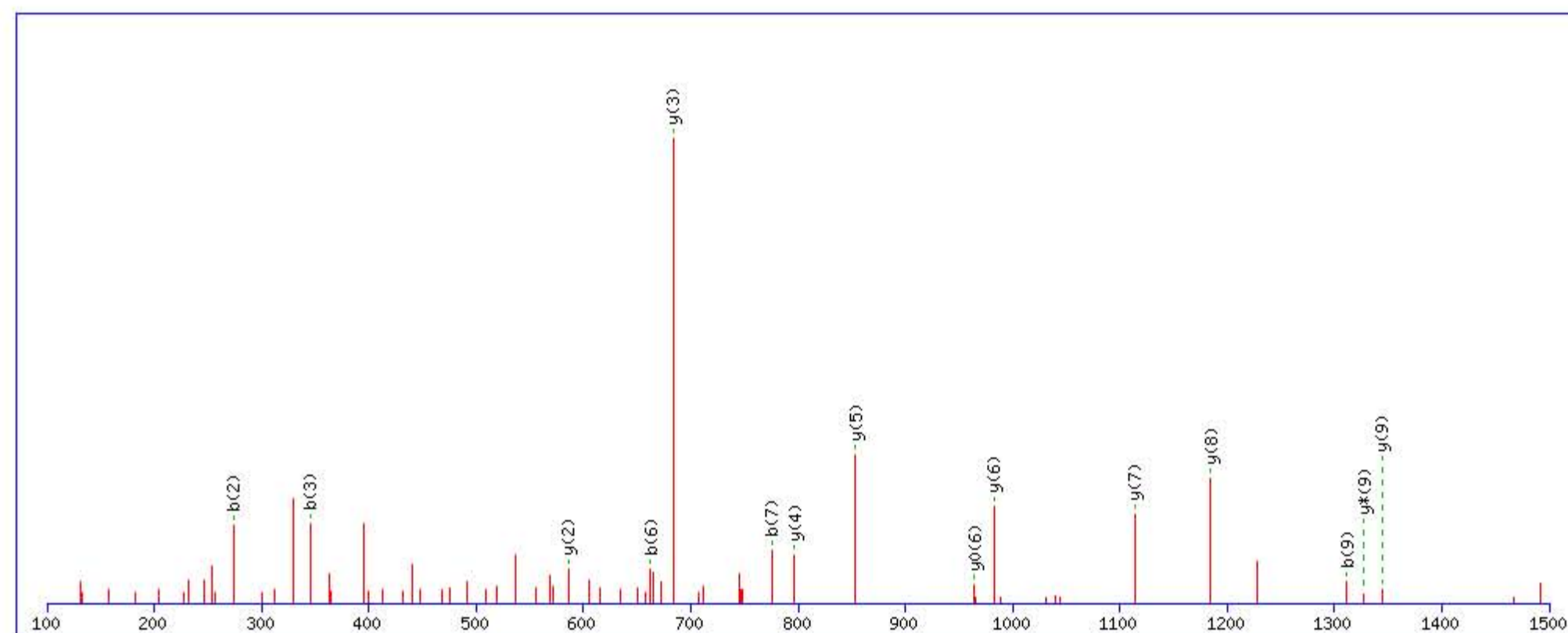
Title: Locus:1.1.1.1482.24 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1456.724030

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

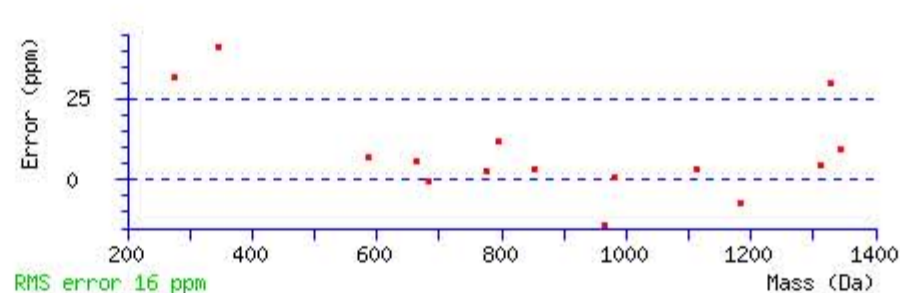
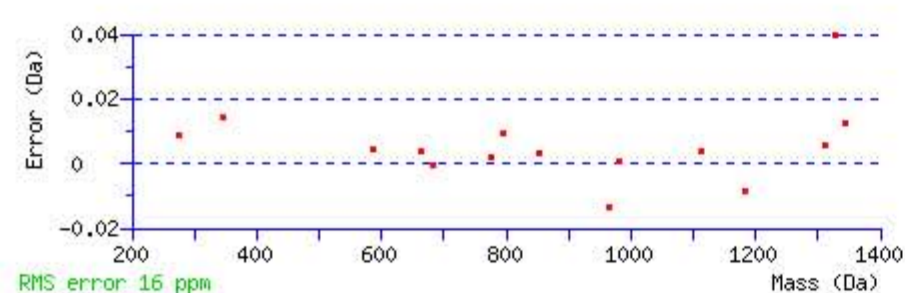
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 56 Expect: 5.2e-005

Matches : 15/74 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							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
56.1	1456.724030	-0.003102	ICAMEGLPQK
15.8	1456.740921	-0.019993	ATVPAGEGVSLEEAK
6.7	1456.742279	-0.021351	LSGSHSQGVAYPVR
4.5	1456.742279	-0.021351	RDGAGGWTPLVSNK
4.0	1456.738434	-0.017506	LFPNTSDPQK
2.0	1456.723145	-0.002217	QQTLEAEEAK
0.6	1456.734390	-0.013462	QDQISASELR
0.5	1456.723160	-0.002232	NQEILDDTAK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **FTDSENVQER**

Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

Match to Query 40311: 1694.744068 from(848.379310,2+) rtinseconds(1574) index(3370)

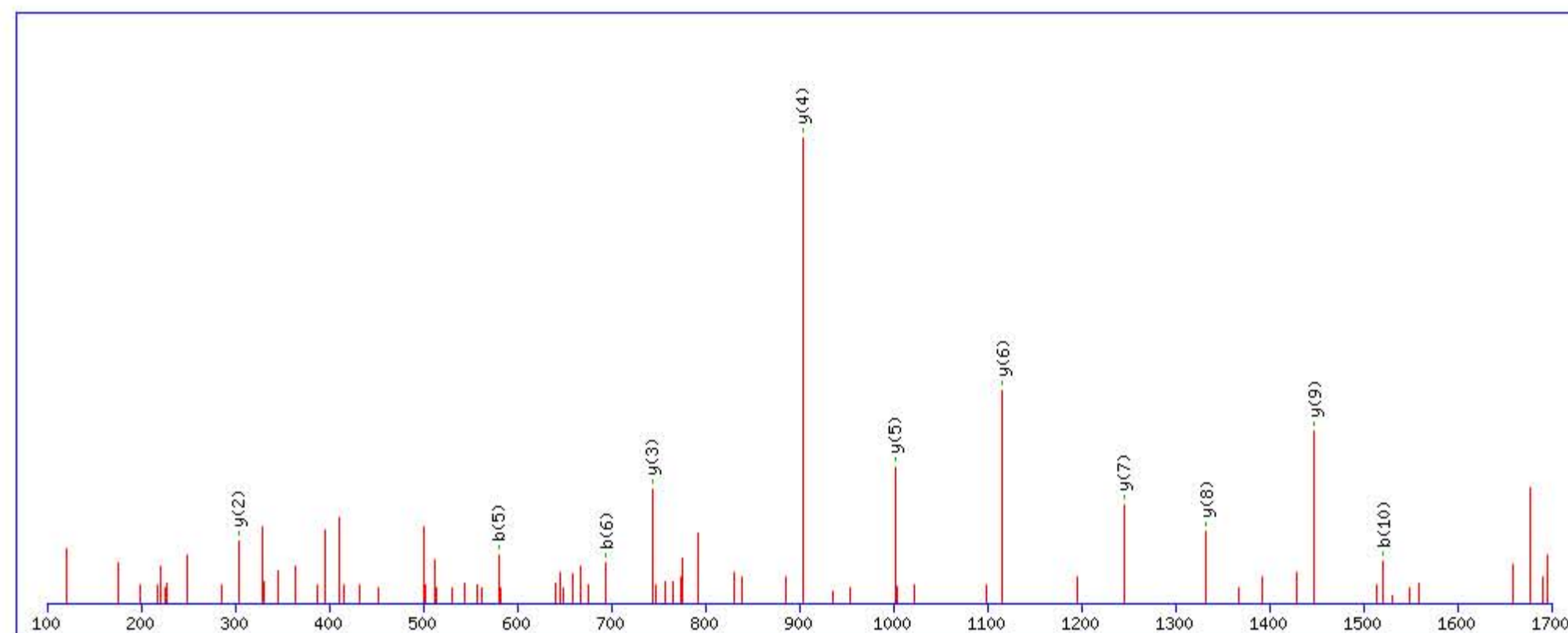
Title: Locus:1.1.1.1357.15 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1694.739243

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

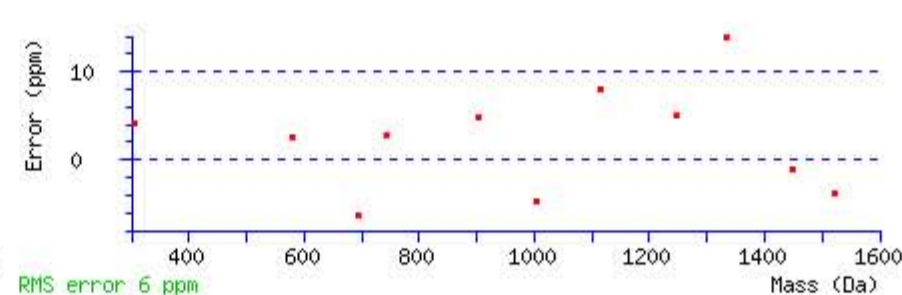
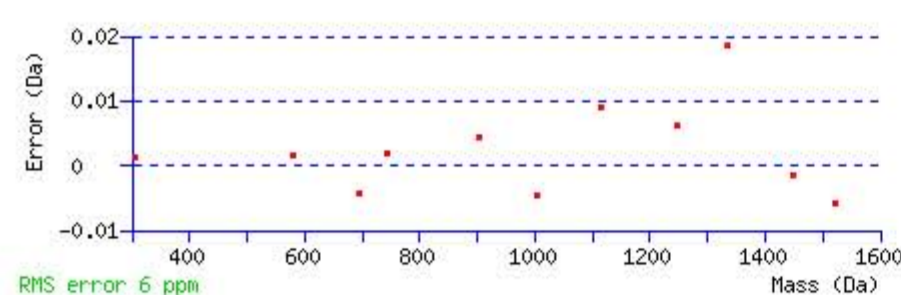
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 63 Expect: 7.2e-006

Matches : 11/106 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	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 **FTDSENVQER**

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

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
63.4	1694.739243	0.004825	FTDSENVQER
12.3	1694.768219	-0.024151	EQSVDCRAGLEFER

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 45629: 1954.968096 from(489.749300,4+) rtinseconds(1350) index(1871)

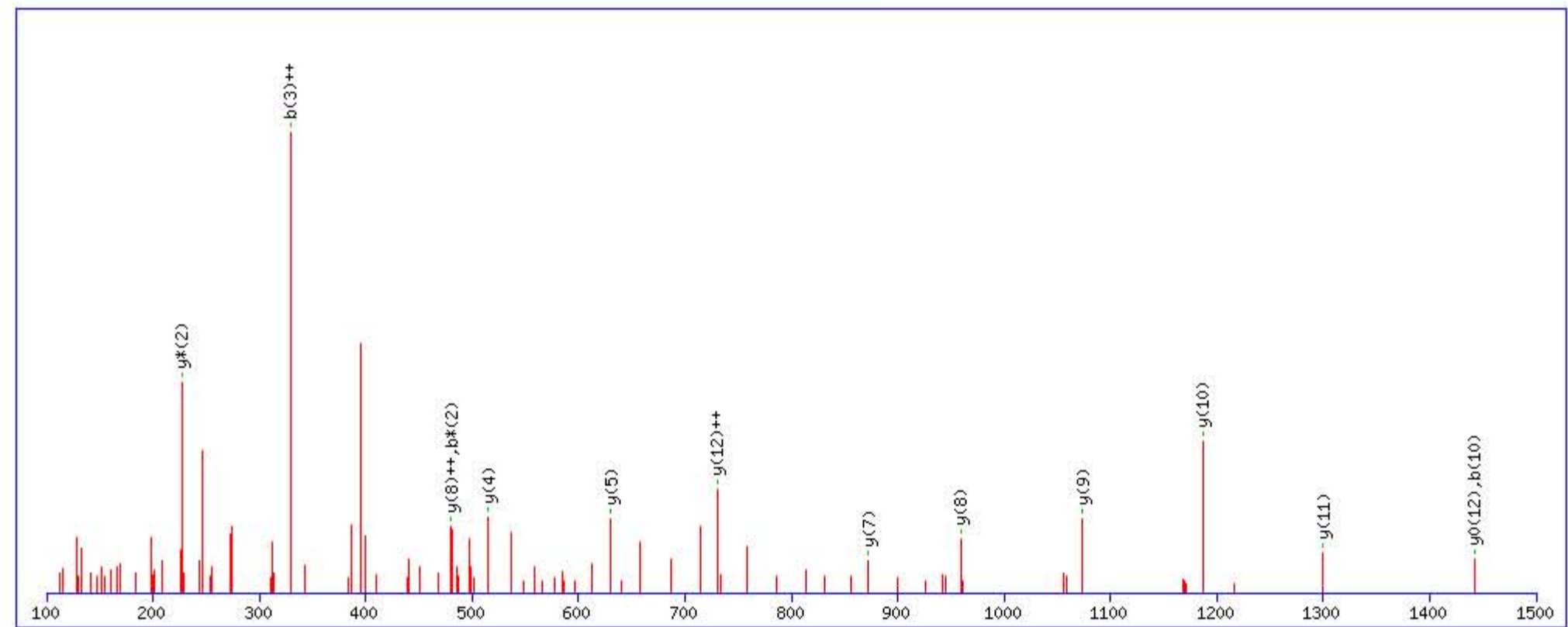
Title: Locus:1.1.1.1279.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1954.971680

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

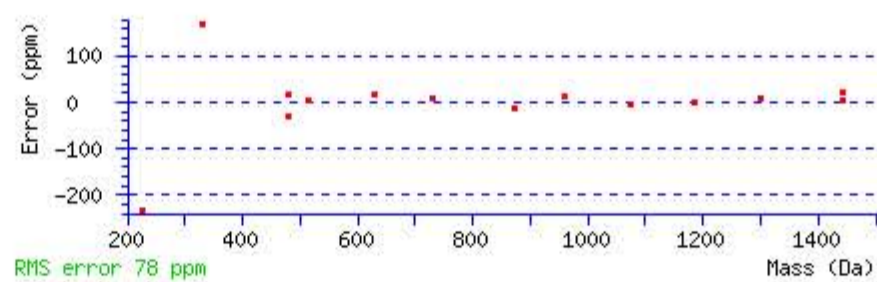
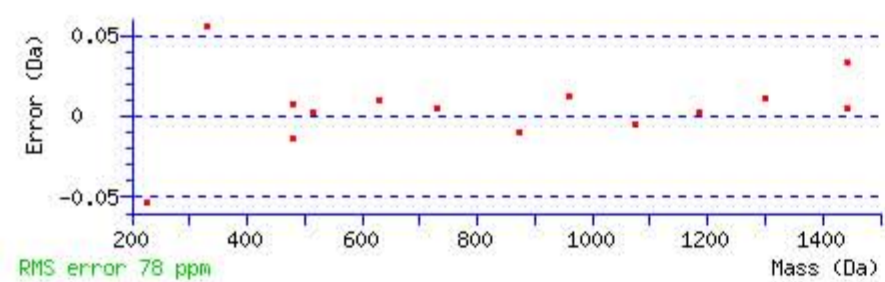
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 60 Expect: 4.1e-006

Matches : 14/136 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	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
60.0	1954.971680	-0.003584	GQCIINSNKDDRPK
2.5	1954.953094	0.015002	KDDRTGTGILSVFGMQAR

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

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 51769: 2235.979722 from(746.333850,3+) rtinseconds(1443) index(2476)

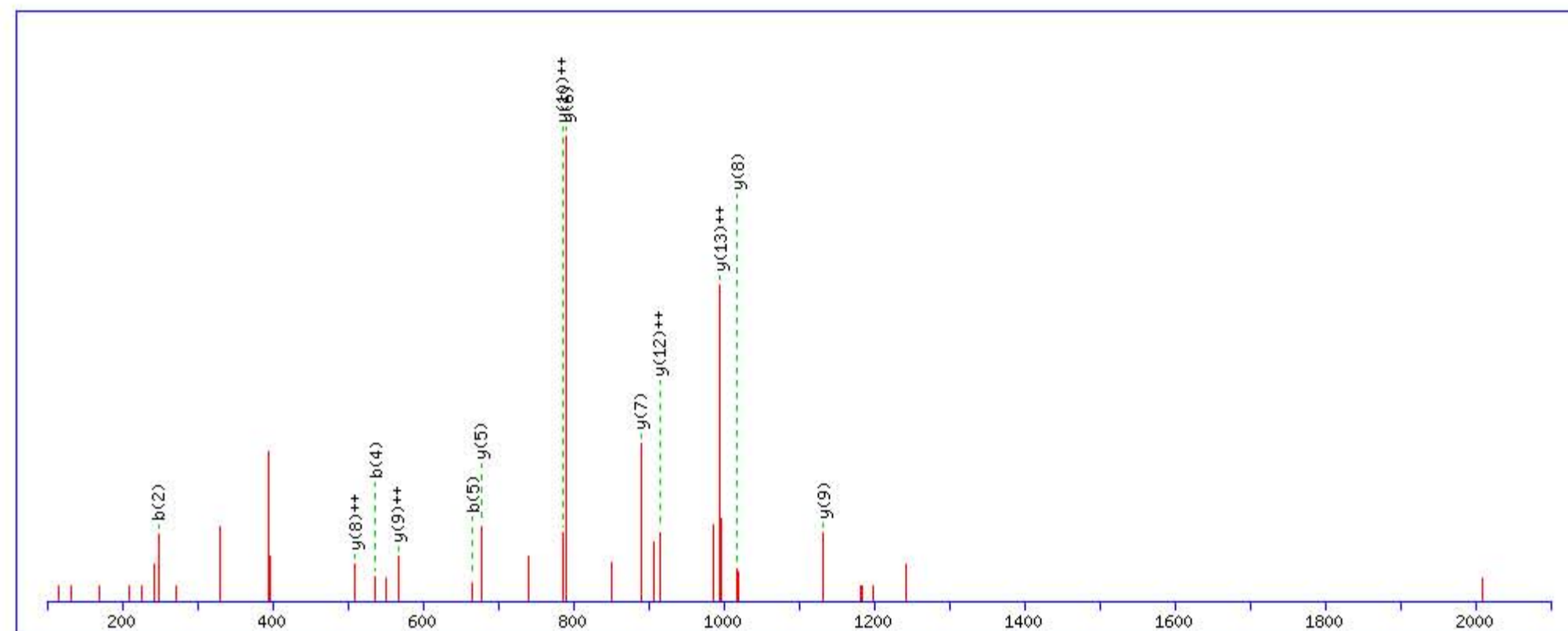
Title: Locus:1.1.1.1311.24 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2235.985703

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

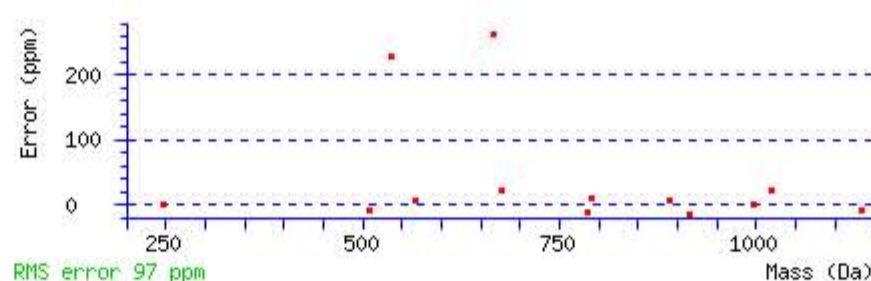
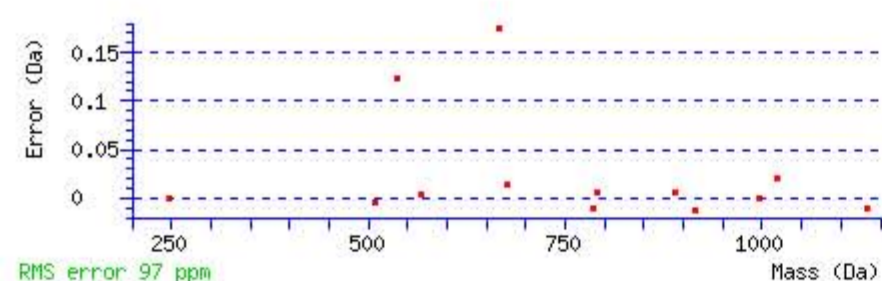
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 32 Expect: 0.0033

Matches : 13/156 fragment ions using 23 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							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
31.7	2235.985703	-0.005981	SCCEEQNKVNCLQTR
8.1	2235.985703	-0.005981	SCCEEQNKVNCLQTR

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 26443: 1312.609468 from(657.312010,2+) rtinseconds(1174) index(1044)

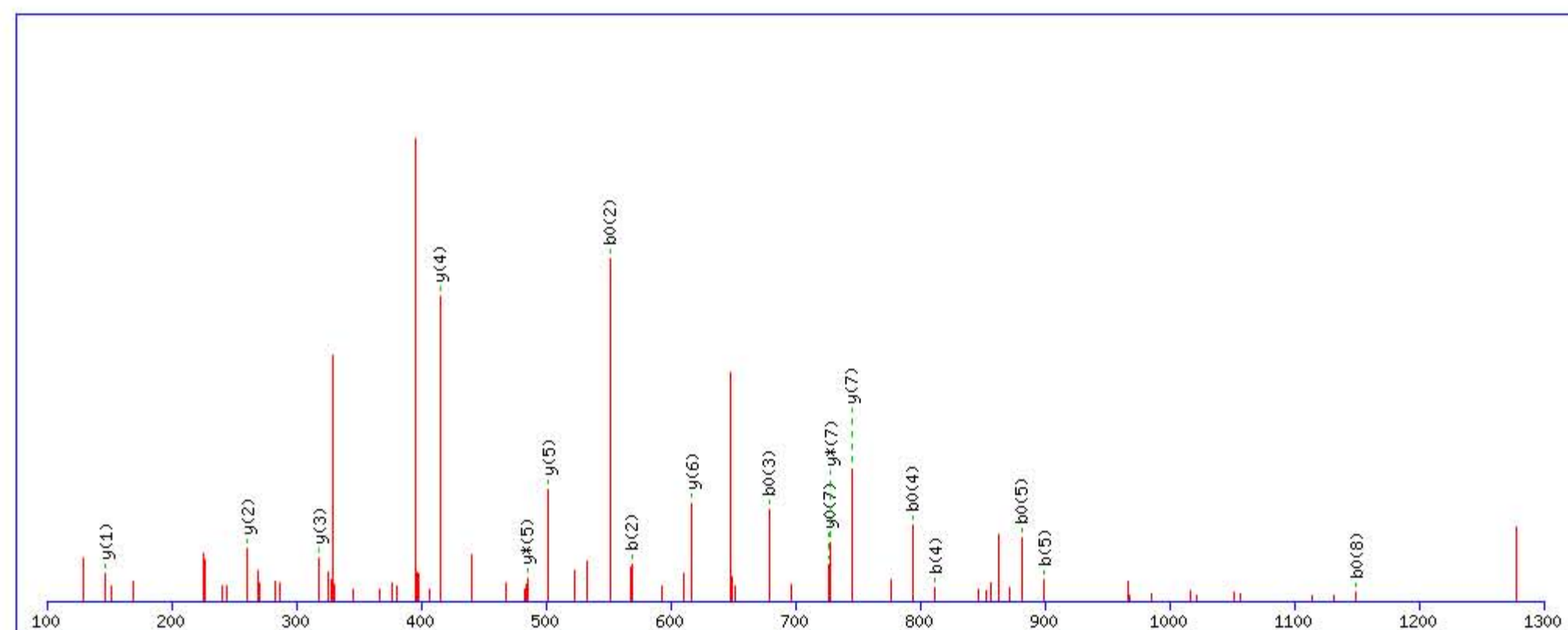
Title: Locus:1.1.1.1217.17 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1312.608139

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

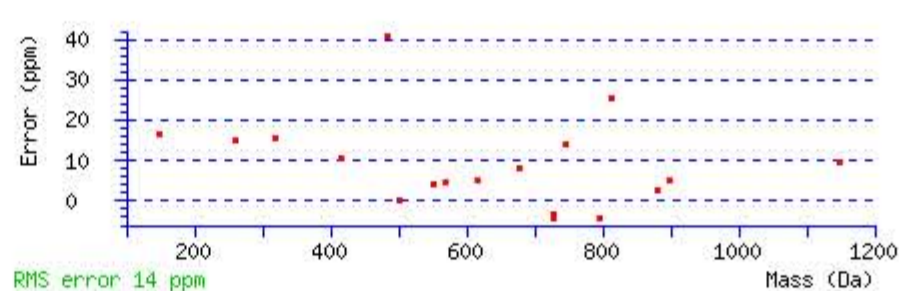
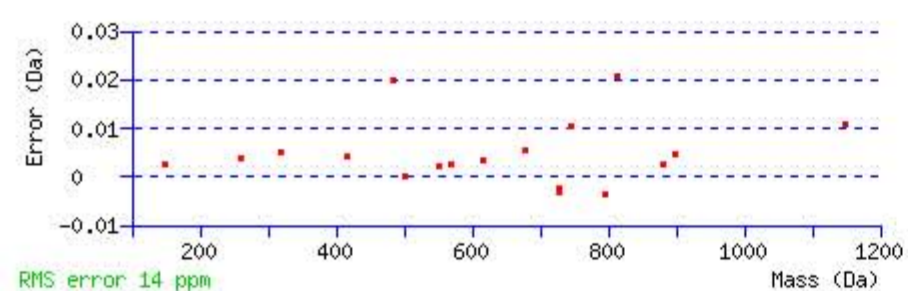
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 35 Expect: 0.0032

Matches : 18/86 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	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
35.1	1312.608139	0.001329	EQQDSPGNK
28.6	1312.608139	0.001329	EQQDSPGNK
8.8	1312.625900	-0.016432	QEAVHTDSLEGK
3.0	1312.596863	0.012605	SKLEEMYEER
0.3	1312.601624	0.007844	CGECGKAFTRK

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

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 38122: 1622.831528 from(812.423040,2+) rtinseconds(1606) index(66496)

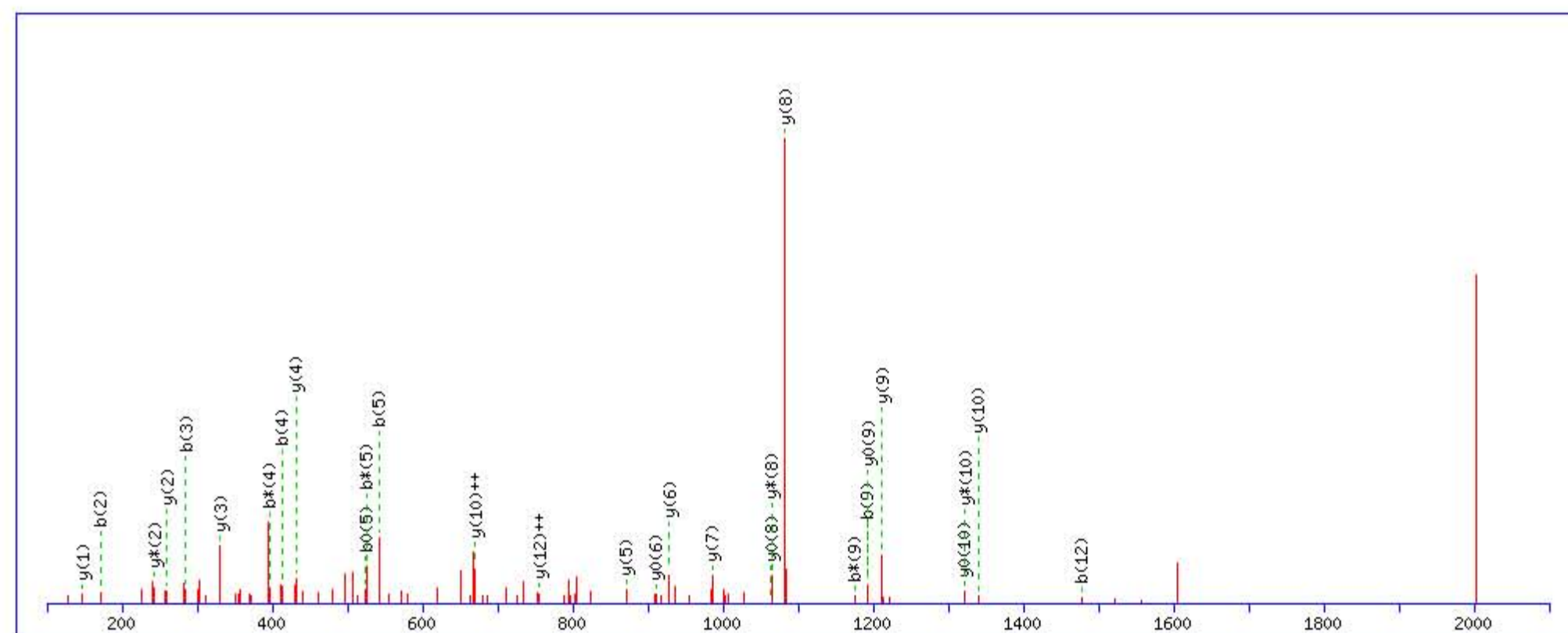
Title: Locus:1.1.1.1496.14 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1622.845016

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

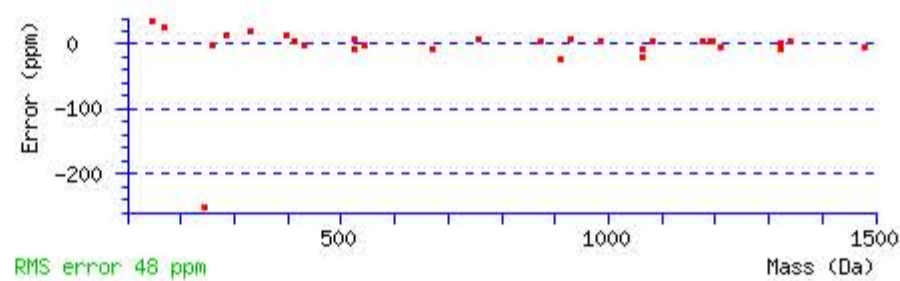
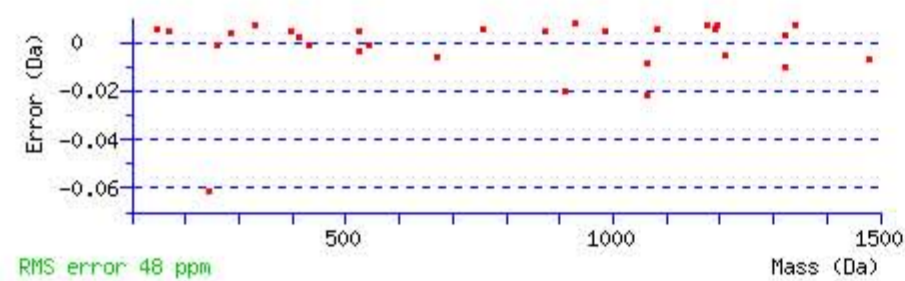
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.00038

Matches : 29/126 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					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
42.7	1622.845016	-0.013488	LGNQEPGGQTALK
6.8	1622.845016	-0.013488	LGNQEPGGQTALK
5.8	1622.831085	0.000443	GLNPNPSHQMTKRK
5.4	1622.813324	0.018204	NGLAQRMSHGK
5.1	1622.820511	0.011017	FPPEASGYLHIGHAK
2.3	1622.837601	-0.006073	SQSEKQTYLEVRR

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 45252: 1934.017128 from(968.015840,2+) rtinseconds(1971) index(5715)

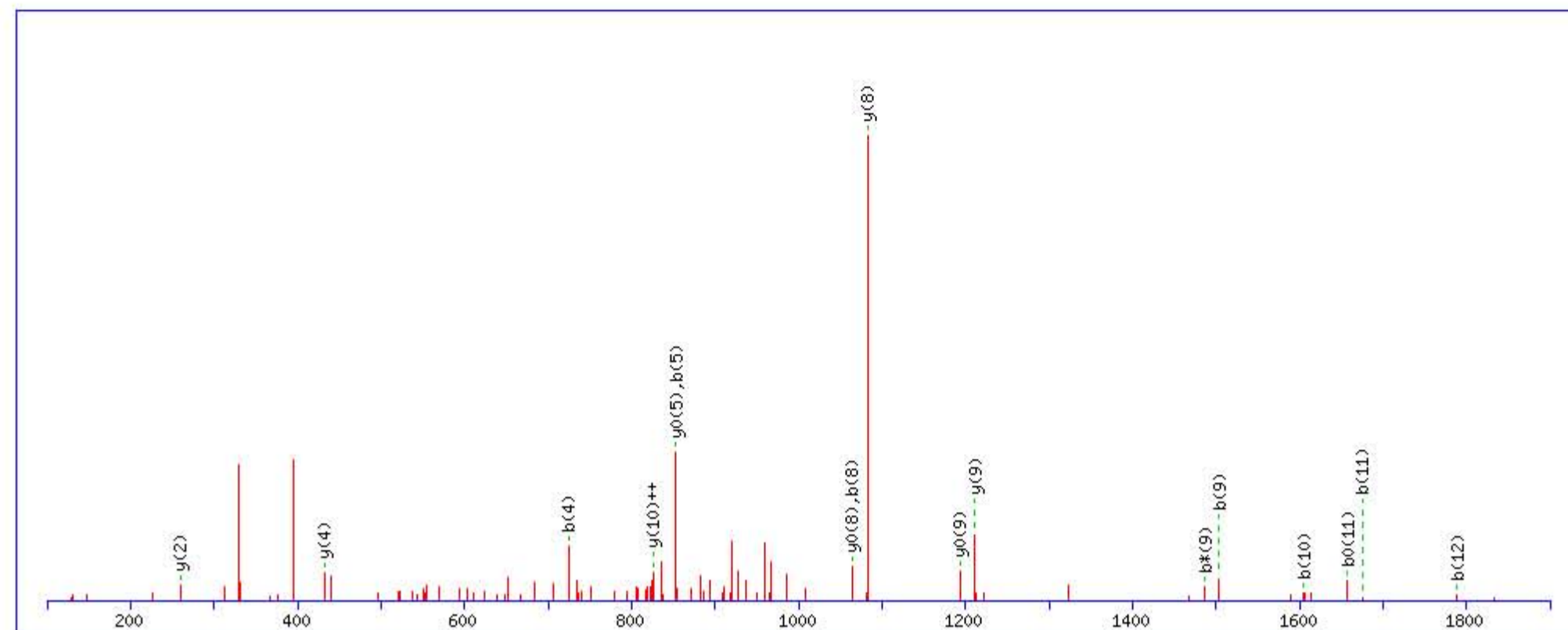
Title: Locus:1.1.1.1495.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1934.011765

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

Variable modifications:

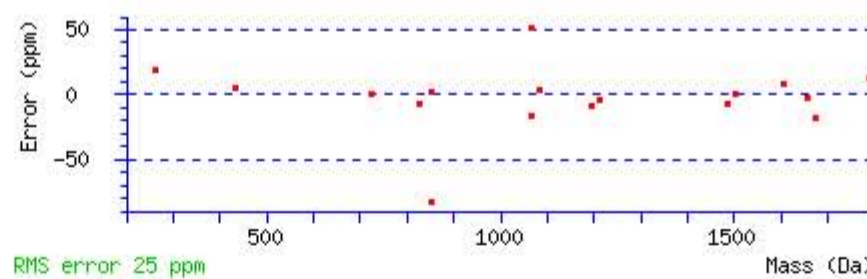
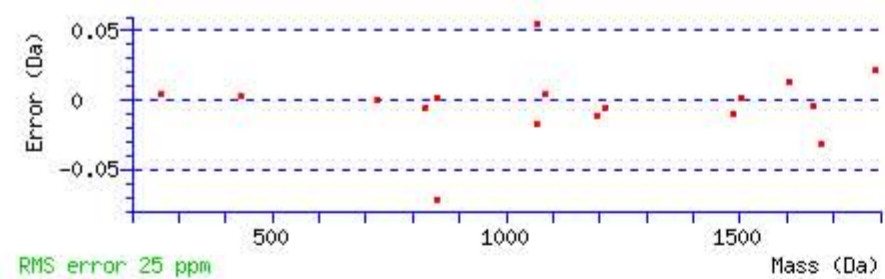
Q4 : Biotin:Thermo-21345 (Q)

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.019

Matches : 17/126 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							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
33.2	1934.011765	0.005363	LGNQEPGGQTALK
10.2	1934.032867	-0.015739	KSRPLTGLMDLAKEMTK
5.1	1934.032867	-0.015739	KSRPLTGLMDLAKEMTK
3.8	1934.037369	-0.020241	NYLEGIYNVPVAAVTR
1.7	1934.003647	0.013481	SSSLGYISKAEEYFLK
0.9	1934.026154	-0.009026	QPLRK YVTPSDFDQLK
0.8	1934.027008	-0.009880	VSFRLHITEPKMMFAK

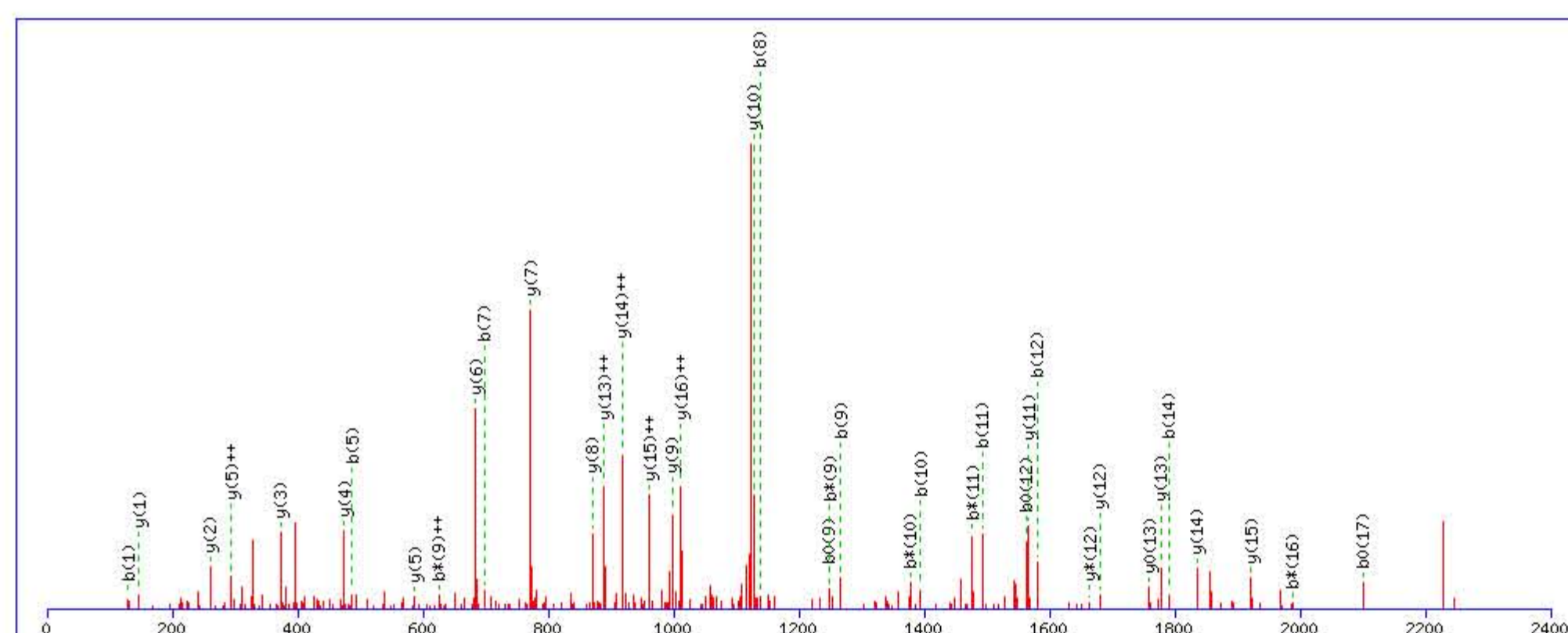
MASCOT Search Results

Peptide View

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

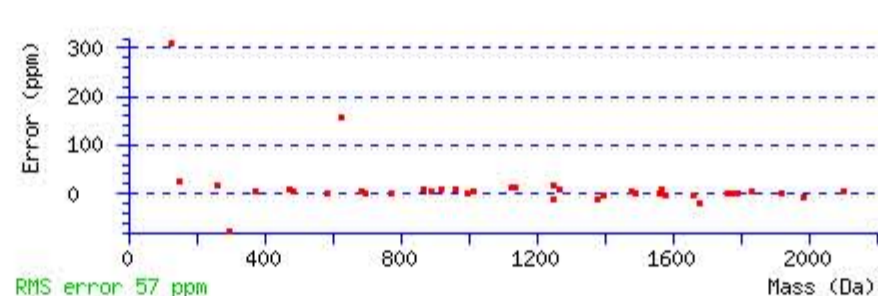
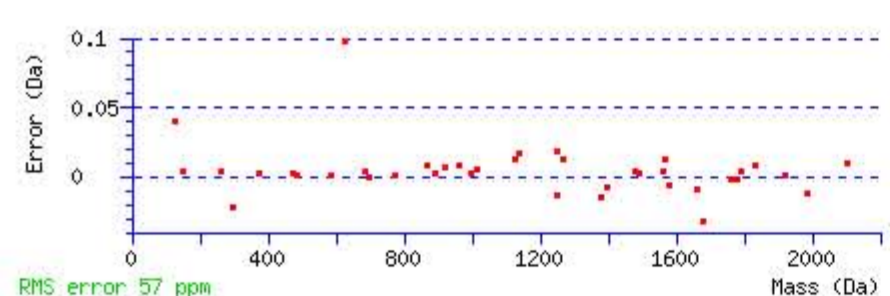
Match to Query 52312: 2263.243468 from(1132.629010,2+) rtinseconds(2502) index(8663)
 Title: Locus:1.1.1.1680.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2263.224594
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q8 : Biotin:Thermo-21345 (Q)
 Ions Score: 116 Expect: 6.6e-011
 Matches : 39/194 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	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 **QLTSGPNQEQVSPLTLK**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
115.6	2263.224594	0.018874	QLTSGPNQEQVSPLTLK
80.5	2263.224594	0.018874	QLTSGPNQEQVSPLTLK
45.3	2263.224594	0.018874	QLTSGPNQEQVSPLTLK
7.0	2263.231979	0.011489	LGKKIETIVMIFDCEGLGLK
6.4	2263.224594	0.018874	GLALSSNKVKSVMVVFENEK

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 54203: 2393.285896 from(599.328750,4+) rtinseconds(2111) index(6515)

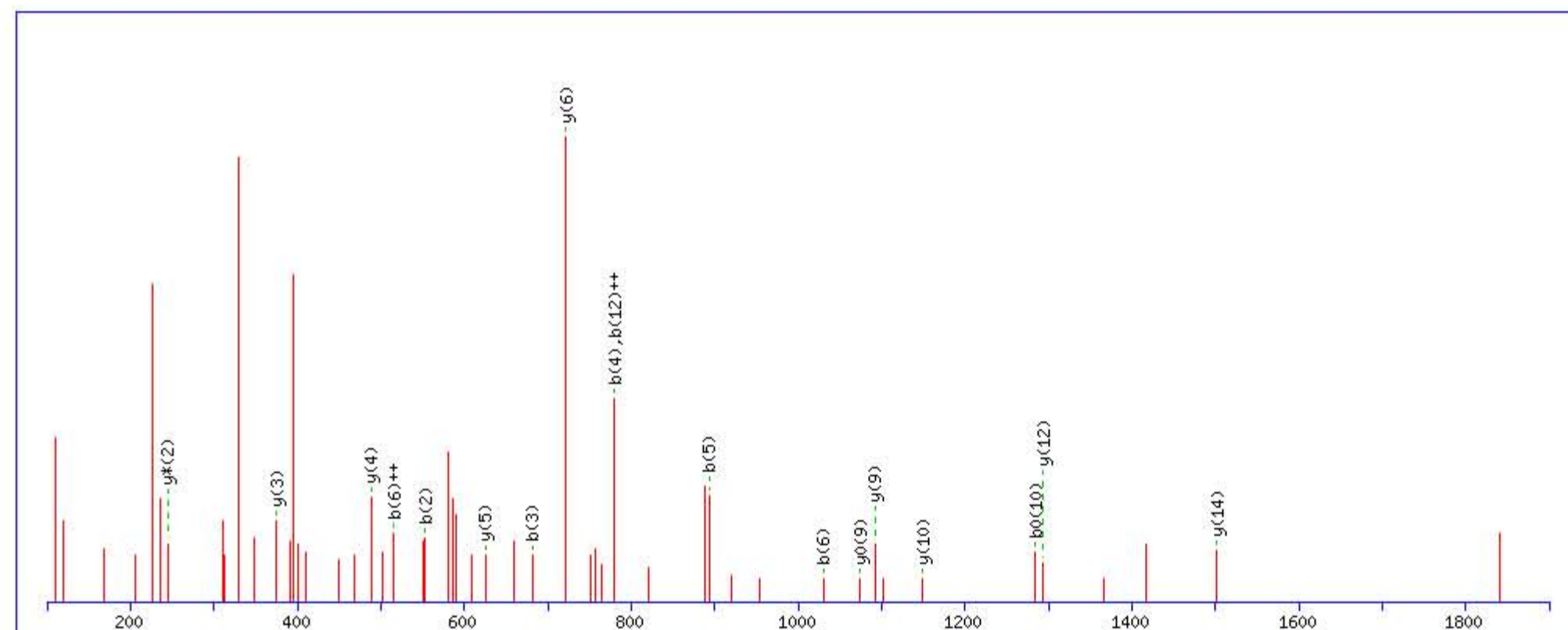
Title: Locus:1.1.1.1544.21 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2393.282410

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

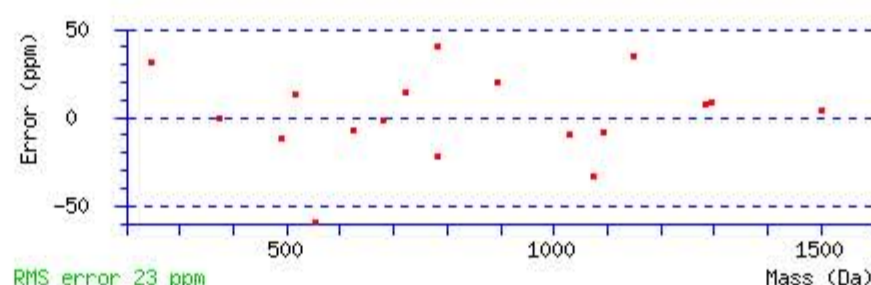
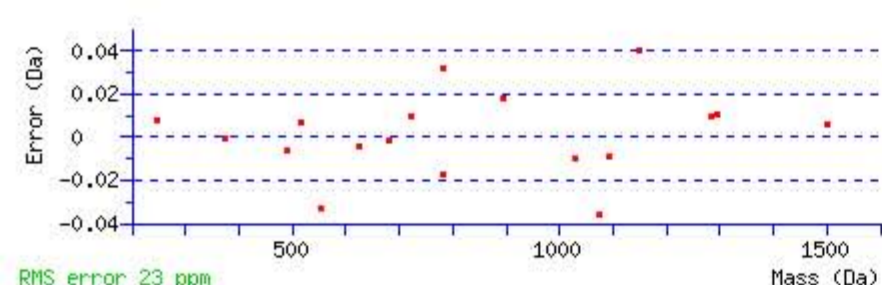
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.042

Matches : 18/196 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	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
27.1	2393.282410	0.003486	LQQVLHAGSGPCLPHLLSR
25.6	2393.282410	0.003486	LQQVLHAGSGPCLPHLLSR

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 56923: 2514.277136 from(629.576560,4+) rtinseconds(1896) index(5176)

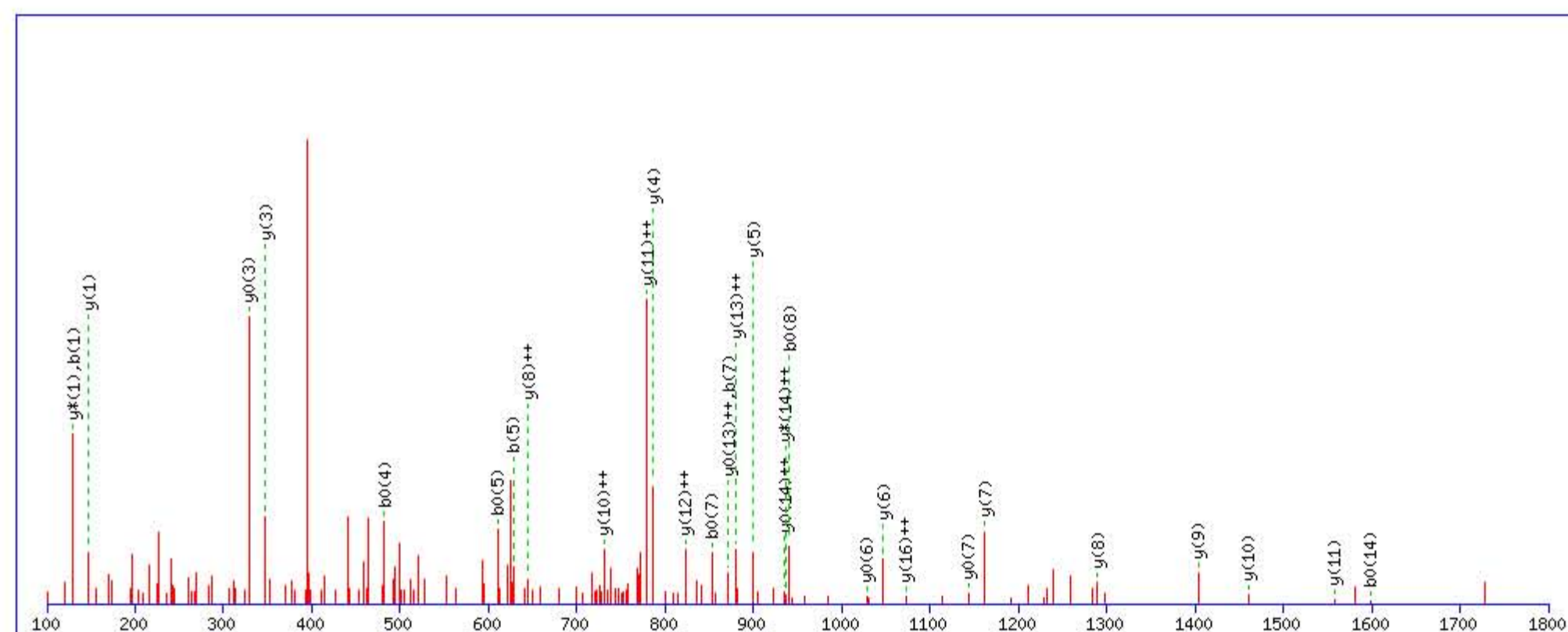
Title: Locus:1.1.1.1469.22 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2514.278793

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

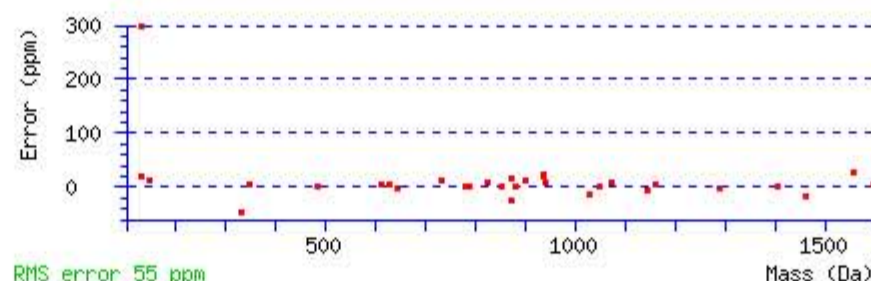
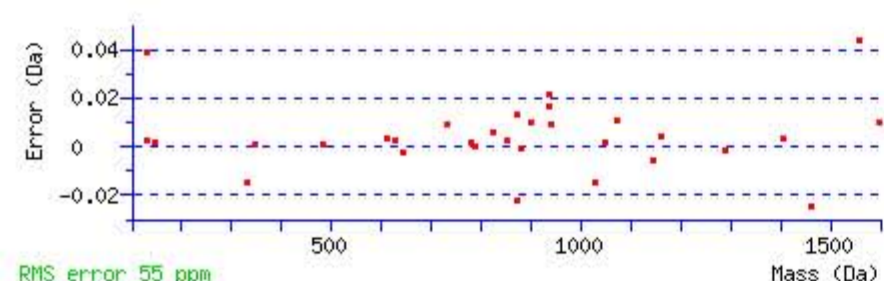
Variable modifications:

Q16 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.00085

Matches : 31/208 fragment ions using 65 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
39.7	2514.278793	-0.001657	ELKEQQDSPGNKDFLQSLK
7.0	2514.268951	0.008185	GNSGPPGIVGQKGDPGYPGAPGPK

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLTSGPNQEQVSPLTLK**

Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

Match to Query 57391: 2574.407772 from(859.143200,3+) rtinseconds(2698) index(9758)

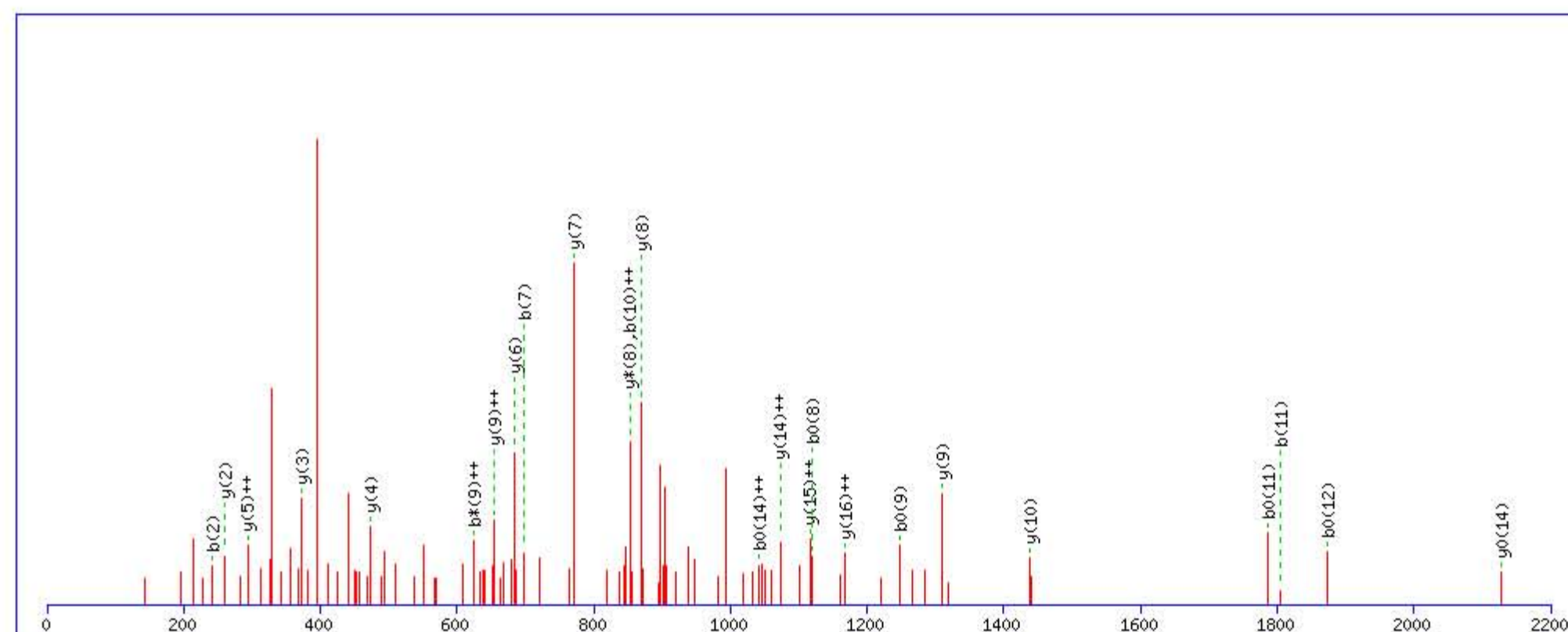
Title: Locus:1.1.1.1748.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2574.391342

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

Variable modifications:

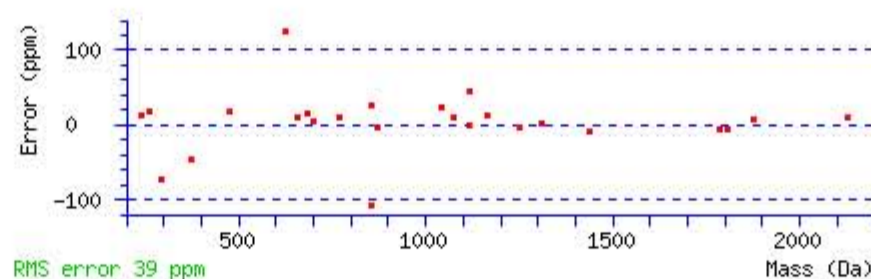
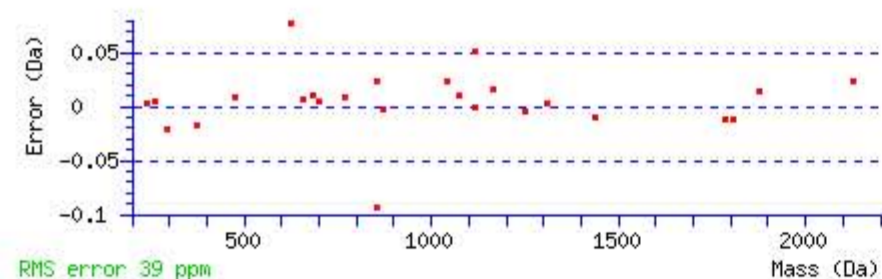
Q8 : Biotin:Thermo-21345 (Q)

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.001

Matches : 25/194 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	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 [QLTSGPNQEQVSPLTLK](#)

(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	2574.391342	0.016430	QLTSGPNQEQVSPLTLK
28.3	2574.391342	0.016430	QLTSGPNQEQVSPLTLK
9.6	2574.391342	0.016430	QLTSGPNQEQVSPLTLK

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 62986: 3175.678376 from(794.926870,4+) rtinseconds(2762) index(10173)

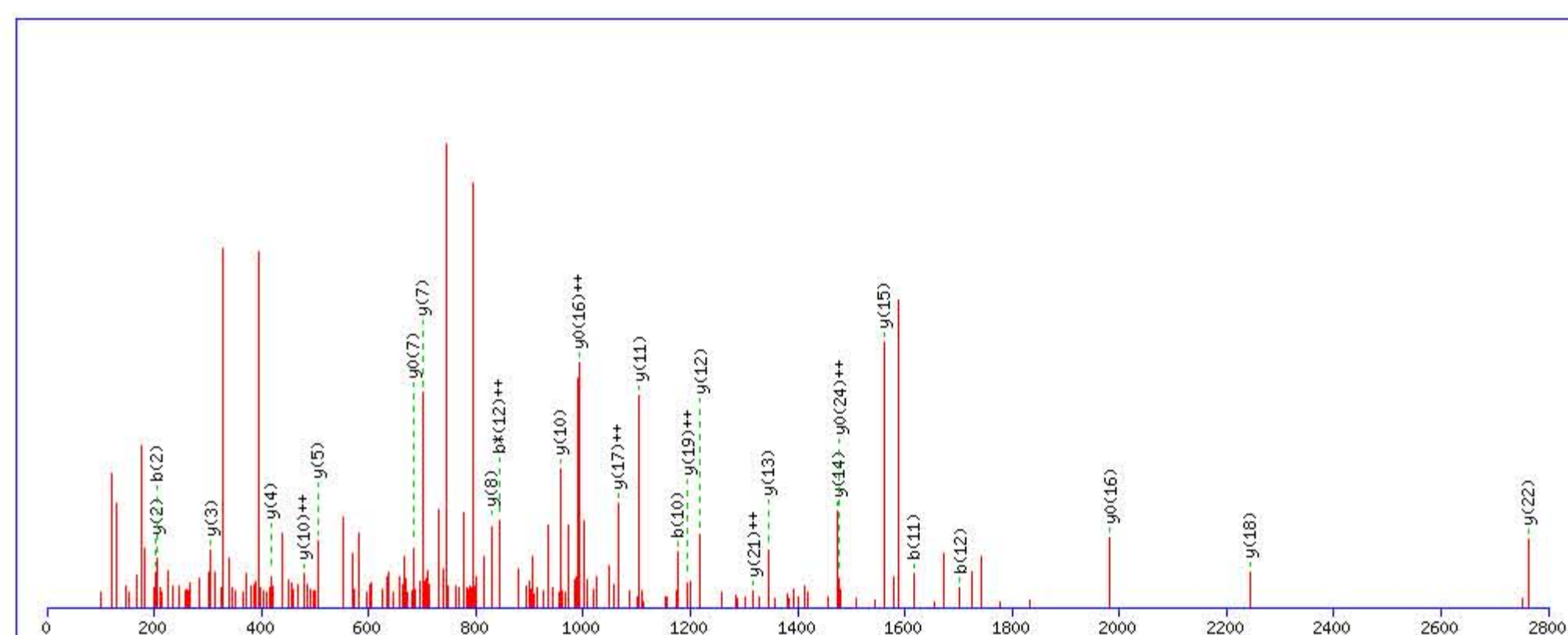
Title: Locus:1.1.1.1770.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3175.662750

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

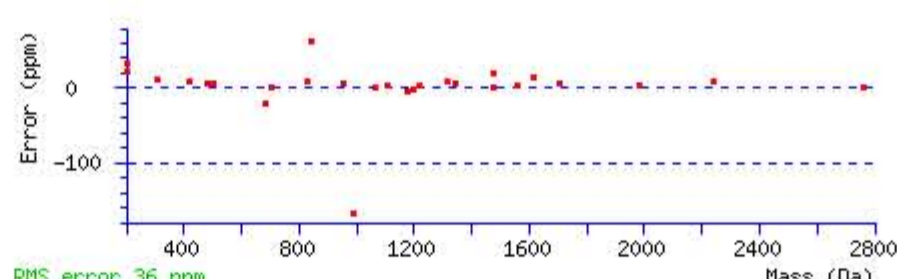
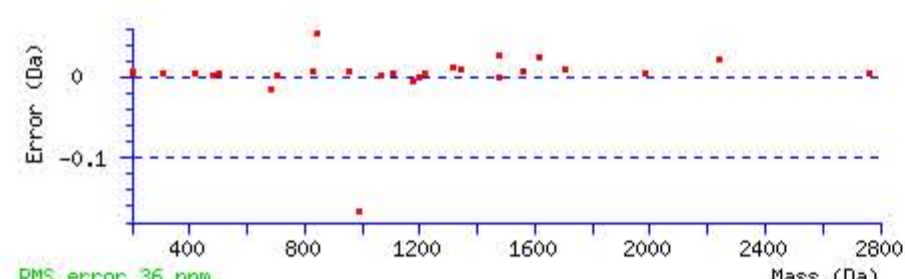
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 71 Expect: 1.6e-006

Matches : 27/278 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	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
71.2	3175.662750	0.015626	GFPIKEDFLEQSEQLFGAKPVSLTGK
37.4	3175.662750	0.015626	GFPIKEDFLEQSEQLFGAKPVSLTGK

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 34068: 1506.778888 from(754.396720,2+) rtinseconds(1576) index(18994)

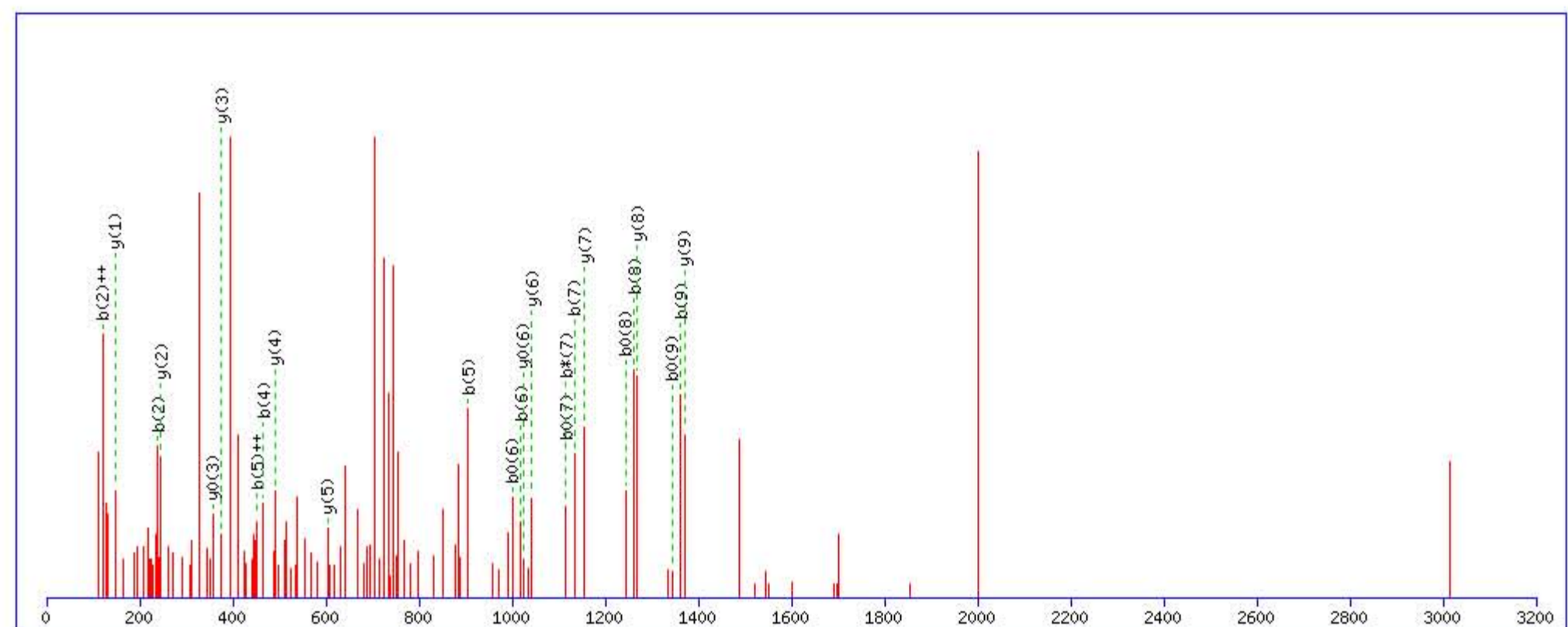
Title: Locus:1.1.1.551.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1506.786438

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

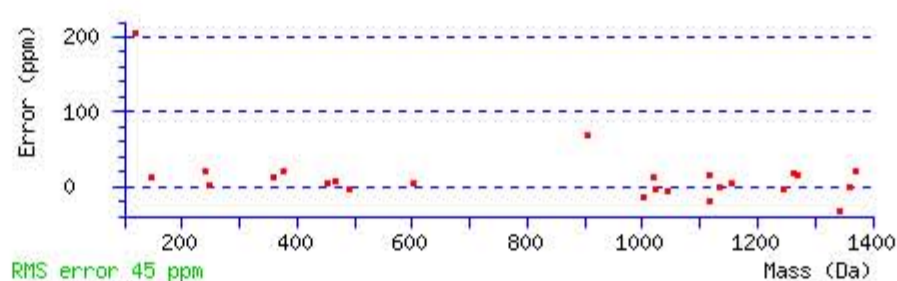
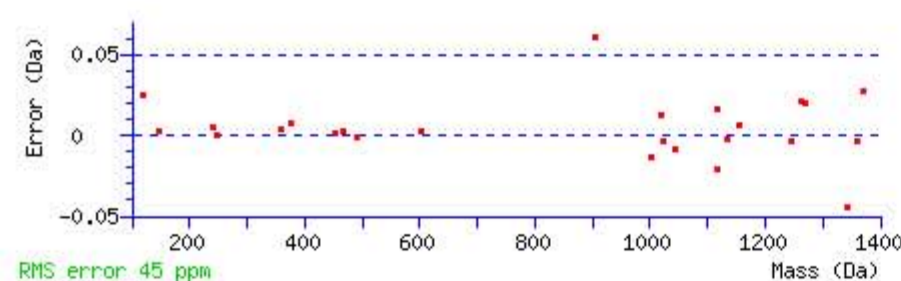
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 50 Expect: 6.6e-005

Matches : 25/96 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	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	$M_r(\text{calc})$:	Delta	Sequence
50.2	1506.786438	-0.007550	HTLNQIDEVK
5.3	1506.779037	-0.000149	EHQALQDLVDLAR
3.8	1506.790253	-0.011365	SSRFLKEGNNLSR
2.5	1506.771149	0.007739	GEKSSMERLLTEK
2.1	1506.767792	0.011096	SGTEYPENLRILK
1.8	1506.765320	0.013568	KPPWHLQVDVEK
1.3	1506.772507	0.006381	QHISRNAQDK
1.1	1506.759964	0.018924	QQVTMVSDEILK
0.5	1506.756577	0.022311	ITFDSEQLQEAVK

MASCOT 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 45981: 1970.925192 from(657.982340,3+) rtinseconds(2071) index(6273)

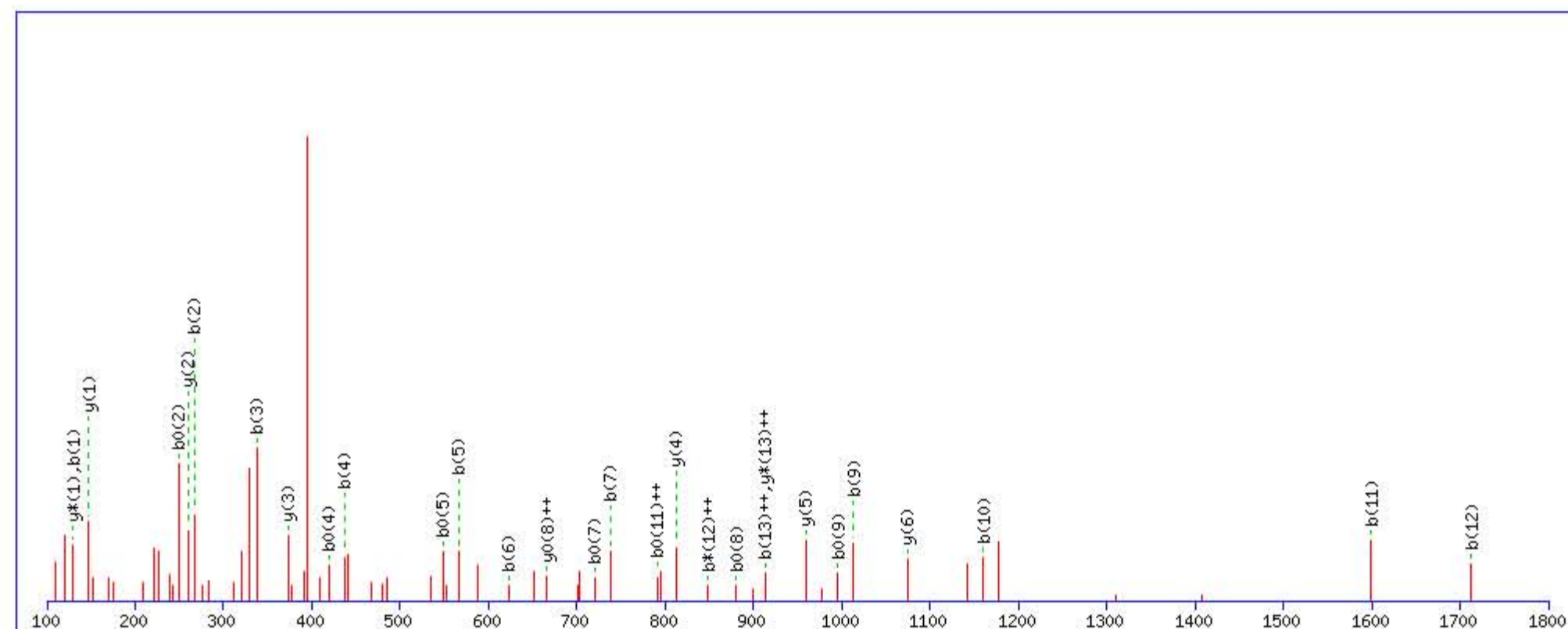
Title: Locus:1.1.1.1530.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1970.923019

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

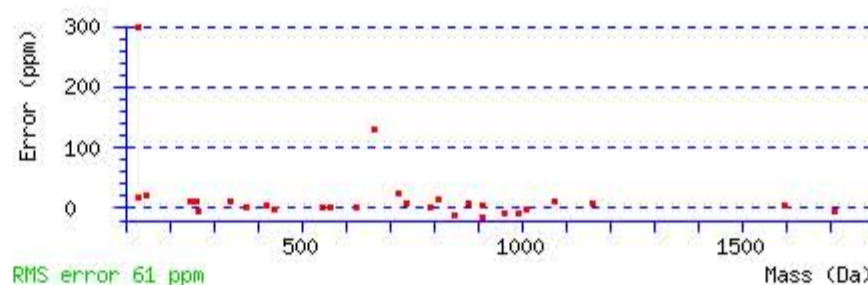
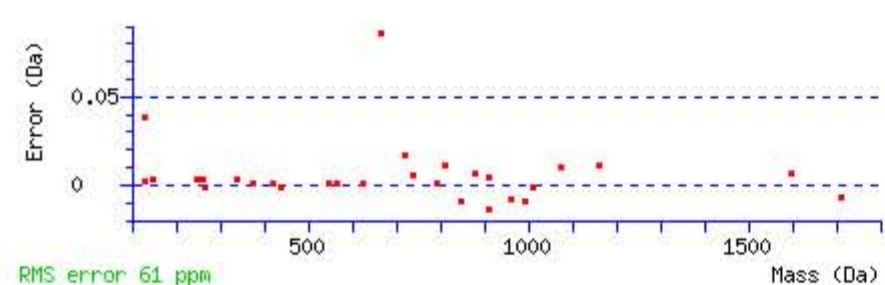
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 69 Expect: 4.3e-007

Matches : 29/126 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	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
69.2	1970.923019	0.002173	EHAVEGDCDFQLLK
1.3	1970.905258	0.019934	LDFNMTTNHSFMCLIK

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

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 36296: 1582.833728 from(792.424140,2+) rtinseconds(1806) index(20396)

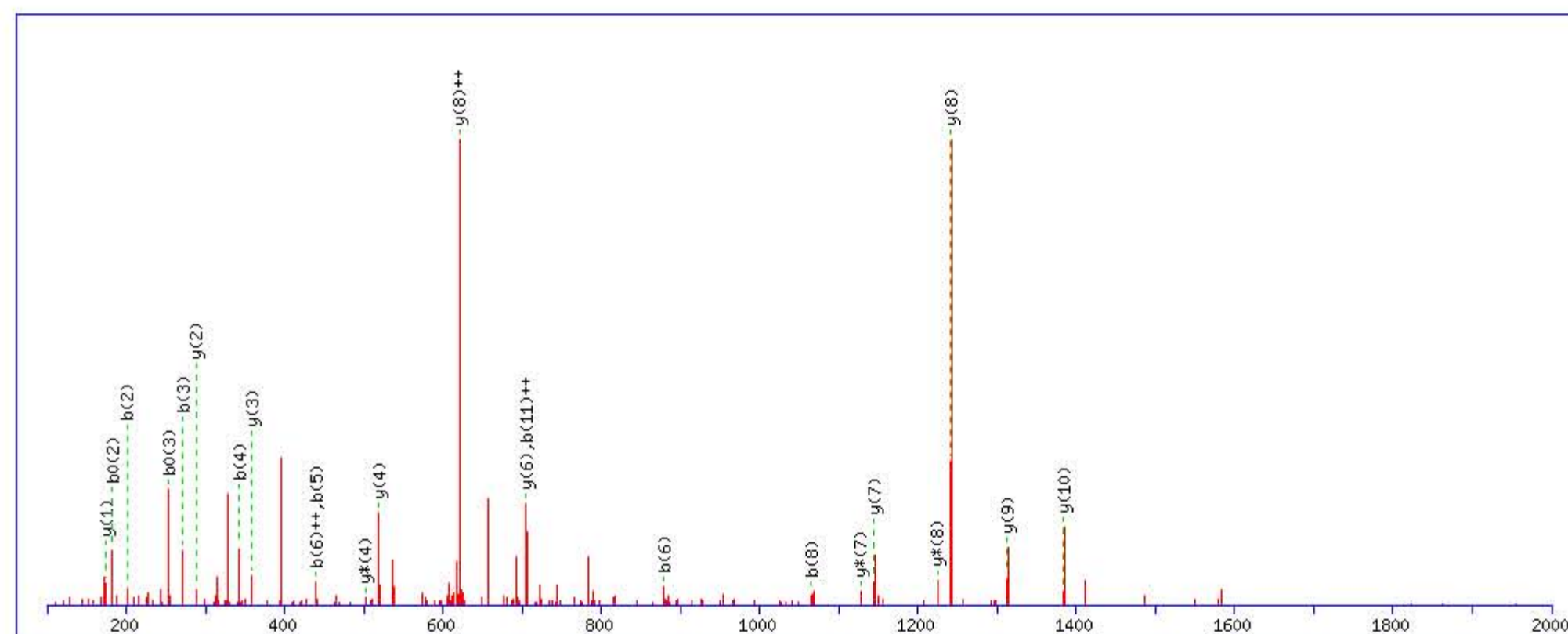
Title: Locus:1.1.1.631.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1582.832352

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

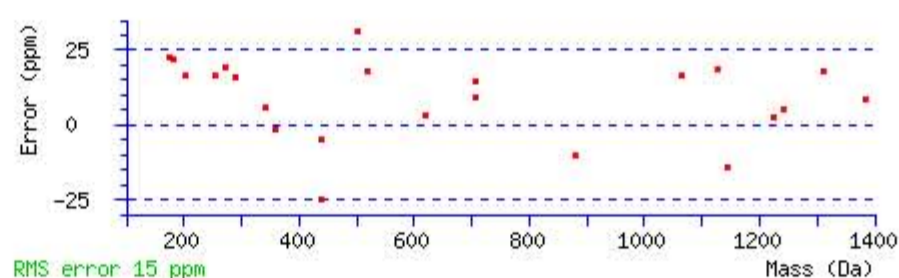
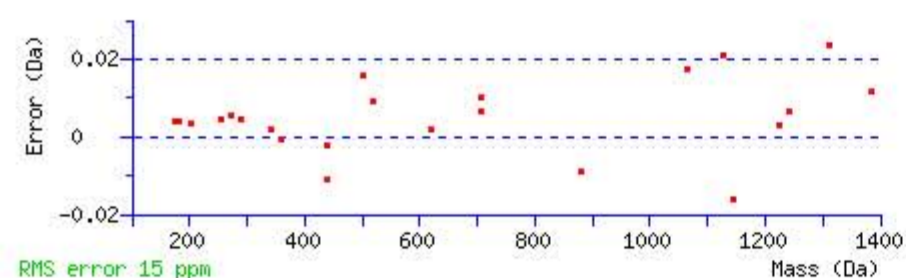
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.00044

Matches : 23/110 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							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
37.0	1582.832352	0.001376	VTAAPQSVCALR
1.2	1582.846710	-0.012982	LVEHLLDPSRYNK

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 47425: 3006.443742 from(1003.155190,3+) rtinseconds(2332) index(38404)

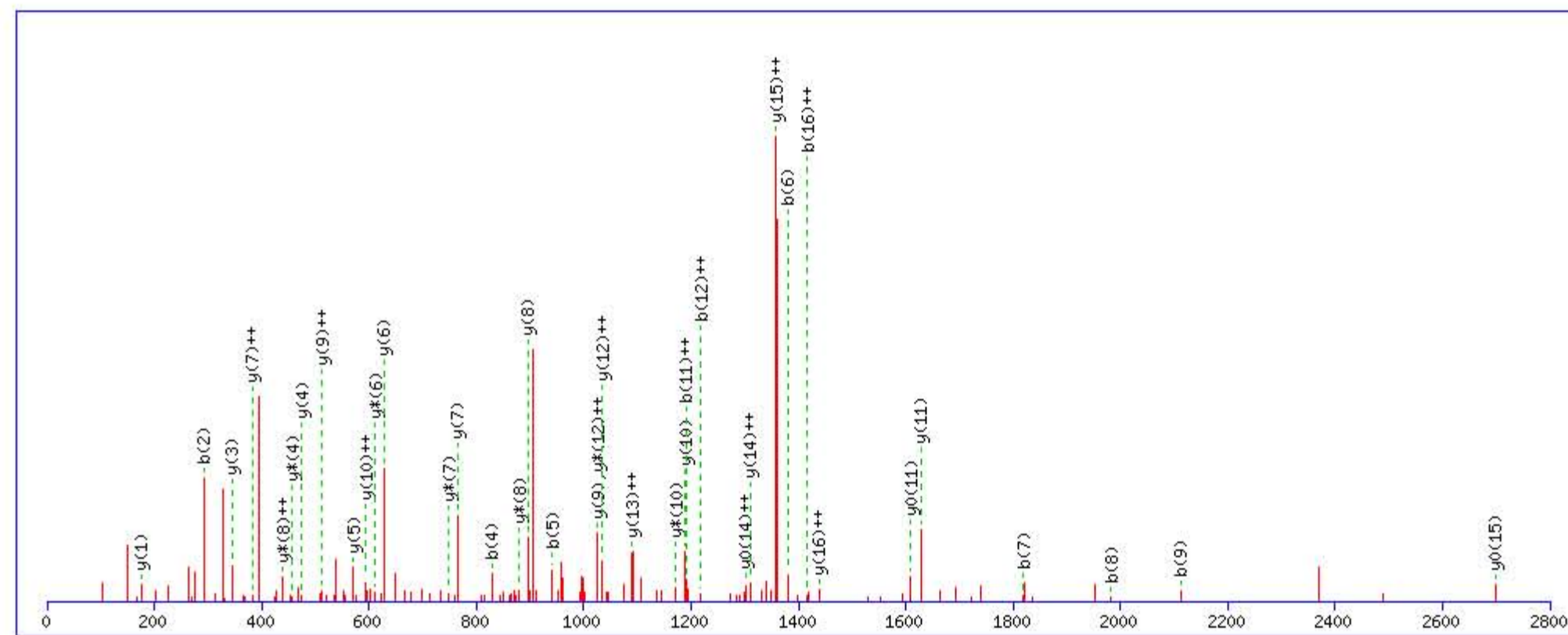
Title: Locus:1.1.1.3231.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3006.423264

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

Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

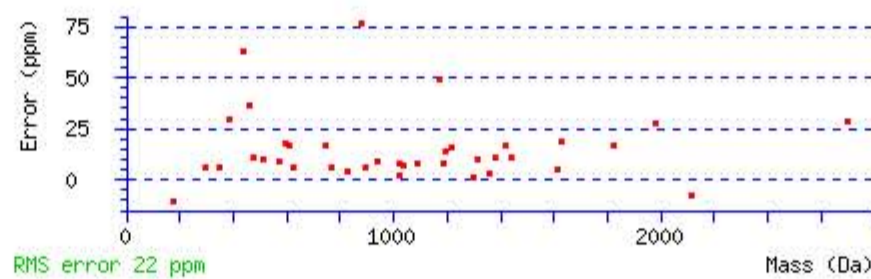
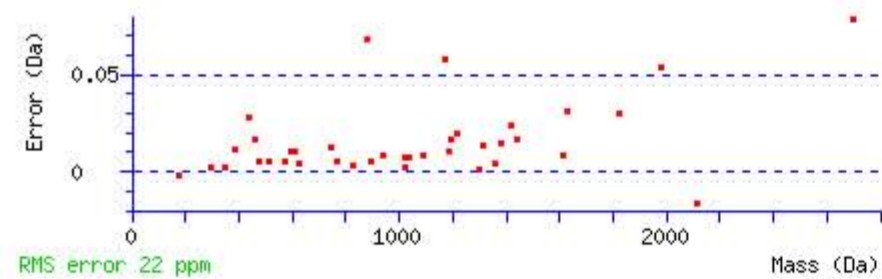
Q6 : Biotin:Thermo-21345 (Q)

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 31 Expect: 0.021

Matches : 38/164 fragment ions using 102 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
30.7	3006.423264	0.020478	MCPQLQQYEMHGPEGLR

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 51197: 2210.043942 from(737.688590,3+) rtinseconds(1863) index(35359)

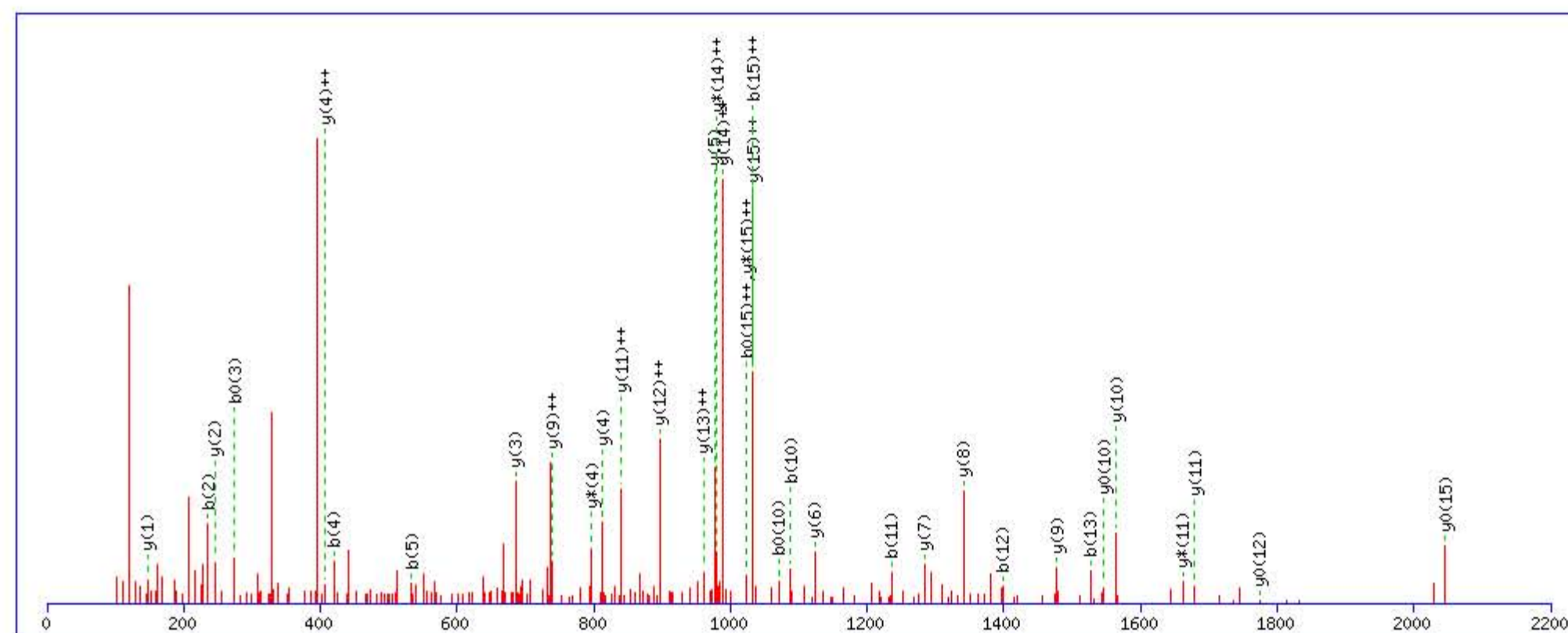
Title: Locus:1.1.1.3068.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2210.040131

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

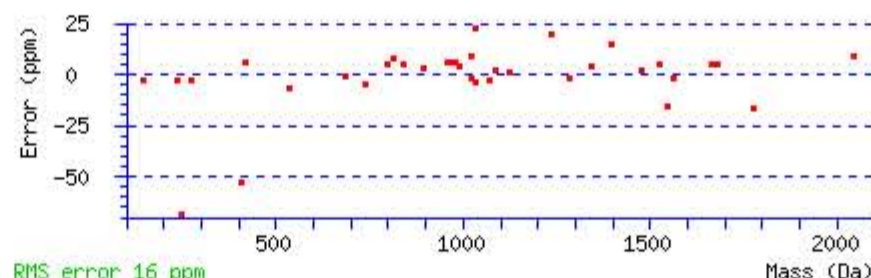
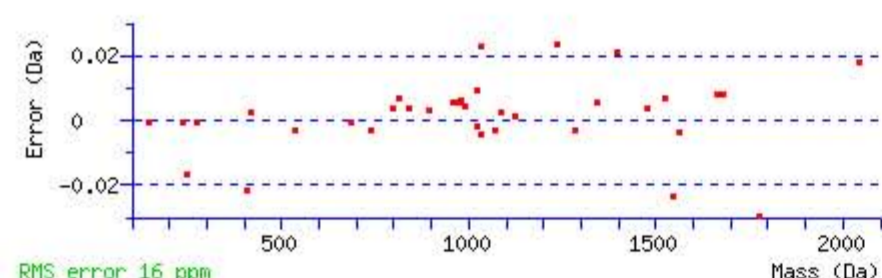
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 0.00045

Matches : 36/154 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	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
45.6	2210.040131	0.003811	FSGQLNSHGCFYQQVK
37.7	2210.040131	0.003811	FSGQLNSHGCFYQQVK

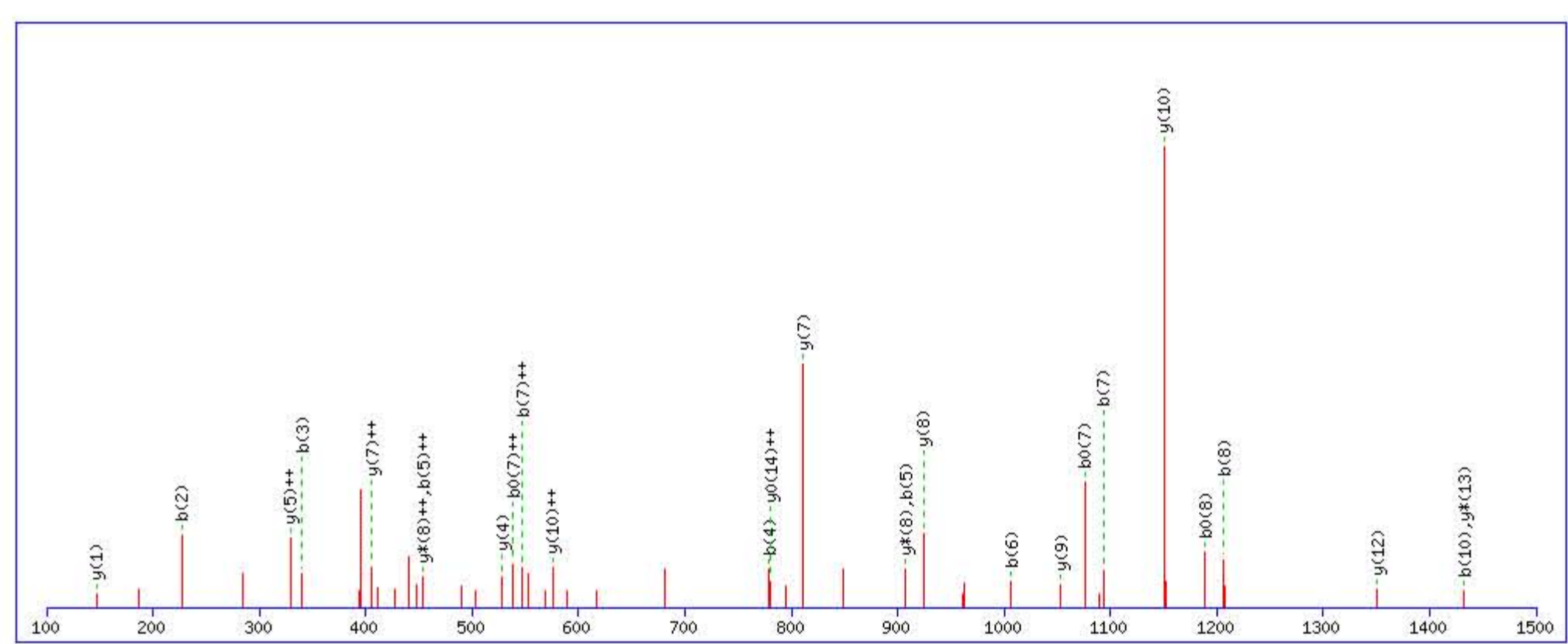
Mascot Search Results

Peptide View

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

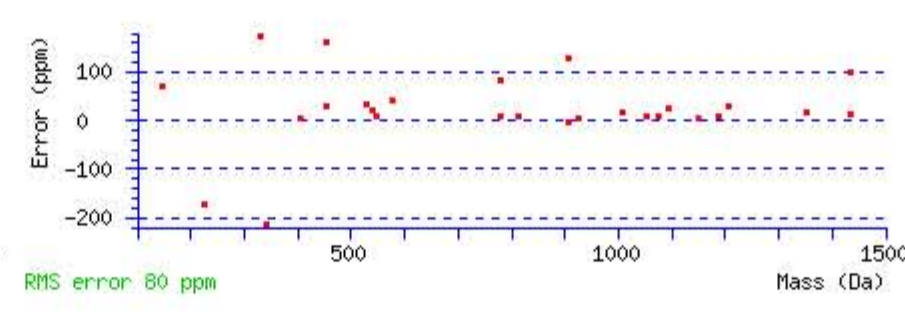
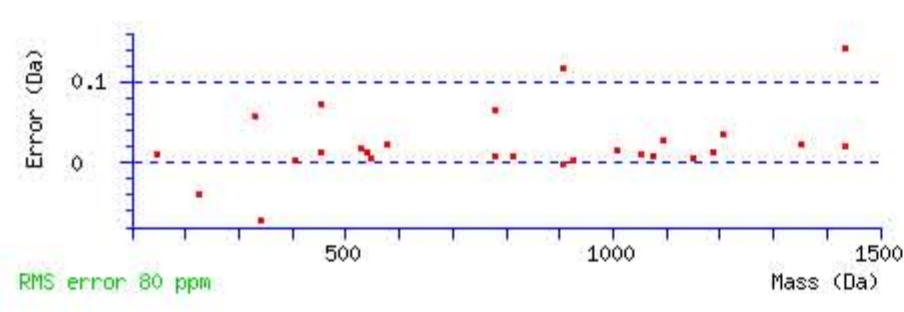
Match to Query 53813: 2355.271572 from(786.097800,3+) rtinseconds(2841) index(26709)
 Title: Locus:1.1.1.990.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2355.258179
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q4 : Biotin:Thermo-21345 (Q)
 Ions Score: 65 Expect: 1.3e-006
 Matches : 27/182 fragment ions using 33 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							18
2	227.175404	114.091340					L	2243.181426	1122.094351	2226.154877	1113.581076	2225.170861	1113.089068	17
3	340.259468	170.633372					L	2130.097362	1065.552319	2113.070813	1057.039044	2112.086797	1056.547036	16
4	779.484794	390.246035	762.458245	381.732760			Q	2017.013298	1009.010287	1999.986749	1000.497013	1999.002733	1000.005005	15
5	907.543372	454.275324	890.516823	445.762049			Q	1577.787972	789.397624	1560.761423	780.884350	1559.777407	780.392342	14
6	1006.611786	503.809531	989.585237	495.296256			V	1449.729394	725.368335	1432.702845	716.855061	1431.718829	716.363053	13
7	1093.643814	547.325545	1076.617265	538.812271	1075.633249	538.320263	S	1350.660980	675.834128	1333.634431	667.320854	1332.650415	666.828846	12
8	1206.727878	603.867577	1189.701329	595.354303	1188.717313	594.862294	L	1263.628952	632.318114	1246.602403	623.804840	1245.618387	623.312832	11
9	1303.780642	652.393959	1286.754093	643.880685	1285.770077	643.388676	P	1150.544888	575.776082	1133.518339	567.262808	1132.534323	566.770800	10
10	1432.823235	716.915256	1415.796686	708.401981	1414.812670	707.909973	E	1053.492124	527.249700	1036.465575	518.736426	1035.481559	518.244418	9
11	1545.907299	773.457288	1528.880750	764.944013	1527.896734	764.452005	L	924.449531	462.728404	907.422982	454.215129	906.438966	453.723121	8
12	1642.960063	821.983670	1625.933514	813.470395	1624.949498	812.978387	P	811.365467	406.186372	794.338918	397.673097	793.354902	397.181089	7
13	1699.981527	850.494401	1682.954978	841.981127	1681.970962	841.489119	G	714.312703	357.659990	697.286154	349.146715	696.302138	348.654707	6
14	1829.024120	915.015698	1811.997571	906.502423	1811.013555	906.010415	E	657.291239	329.149258	640.264690	320.635983	639.280674	320.143975	5
15	1992.087449	996.547362	1975.060900	988.034088	1974.076884	987.542080	Y	528.248646	264.627961	511.222097	256.114687	510.238081	255.622679	4
16	2079.119477	1040.063376	2062.092928	1031.550102	2061.108912	1031.058094	S	365.185317	183.096297	348.158768	174.583022	347.174752	174.091014	3
17	2210.159962	1105.583619	2193.133413	1097.070344	2192.149397	1096.578336	M	278.153289	139.580282	261.126740	131.067008			2
18							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
64.9	2355.258179	0.013393	LLLQQVSLPELPGEYSMK
53.6	2355.258179	0.013393	LLLQQVSLPELPGEYSMK
2.0	2355.259354	0.012218	SQPRASGPPRSIQPVSPR
1.8	2355.273926	-0.002354	LGLYTFVNLANFVKSWTNLR
0.6	2355.288498	-0.016926	LIQKERALLNFTWKR
0.6	2355.288498	-0.016926	LIQKERALLNFTWKR
0.5	2355.240891	0.030681	IQQIRSLSEDVRFYYK

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 54075: 2384.095212 from(795.705680,3+) rtinseconds(1985) index(21610)

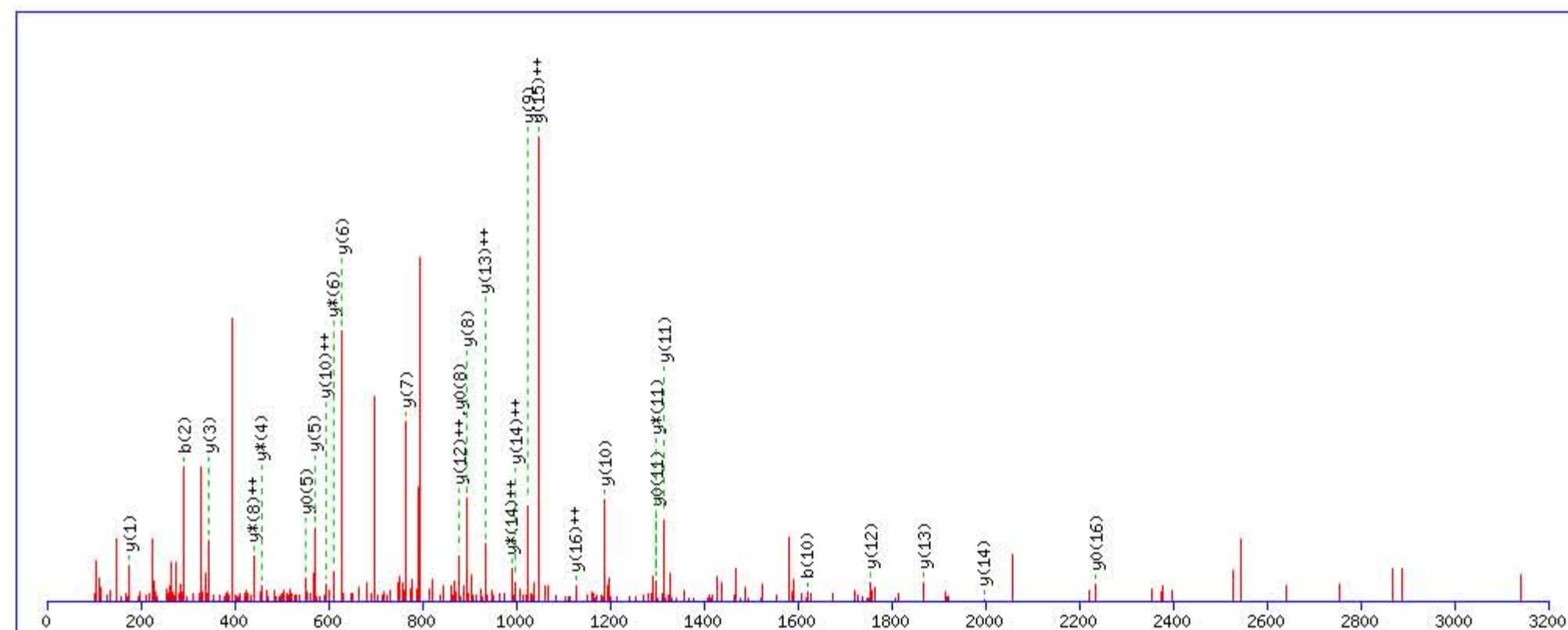
Title: Locus:1.1.1.693.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2384.089767

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

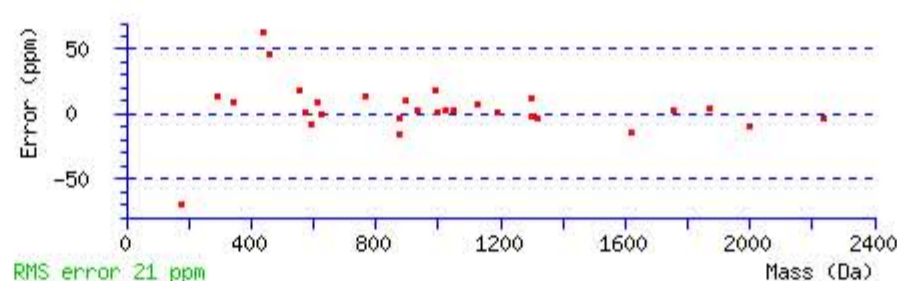
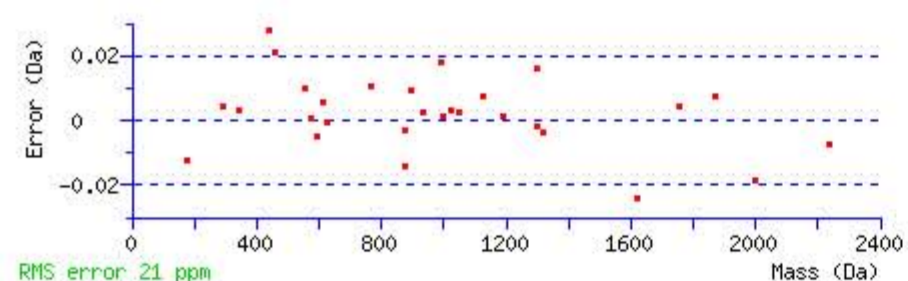
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.001

Matches : 29/164 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	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
40.7	2384.089767	0.005445	MCPQLQQYEMHGPEGLR
39.4	2384.089767	0.005445	MCPQLQQYEMHGPEGLR
25.7	2384.089767	0.005445	MCPQLQQYEMHGPEGLR

MASCOT 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 54085: 2384.108908 from(1193.061730,2+) rtinseconds(2028) index(36558)

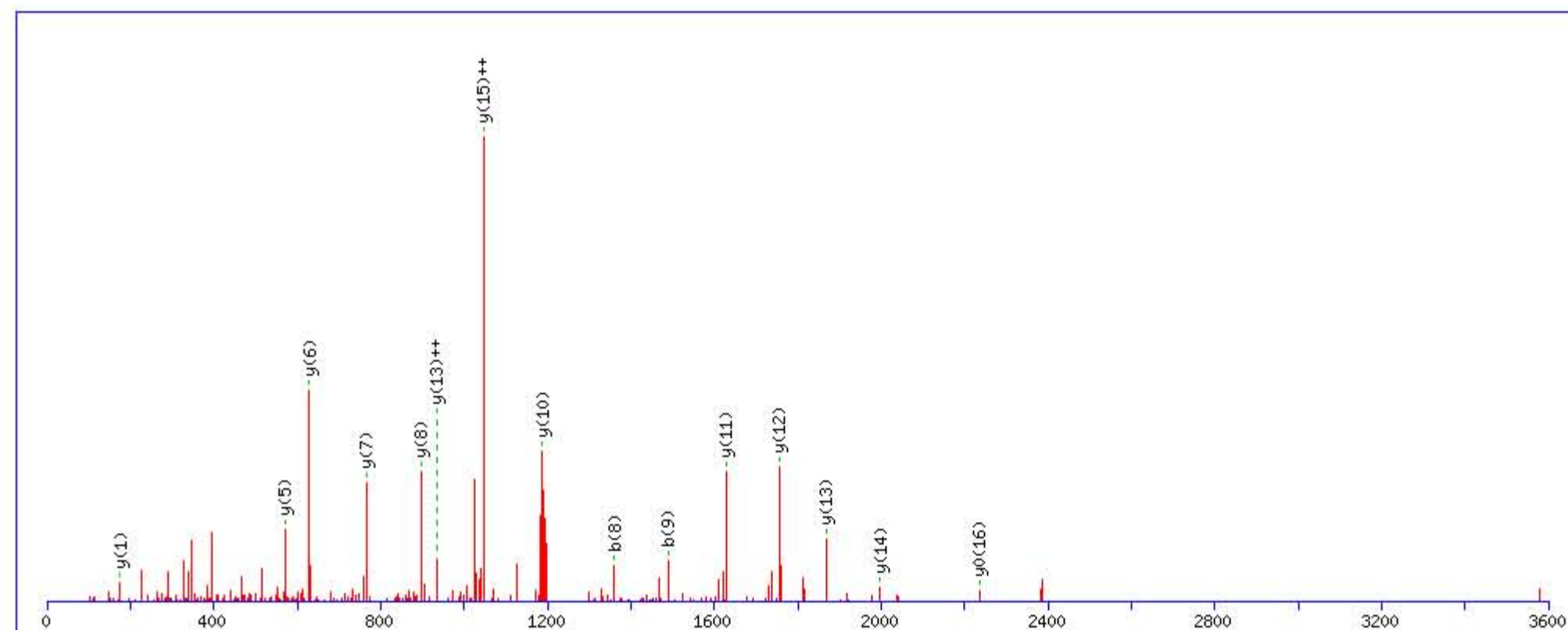
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2384.089767

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

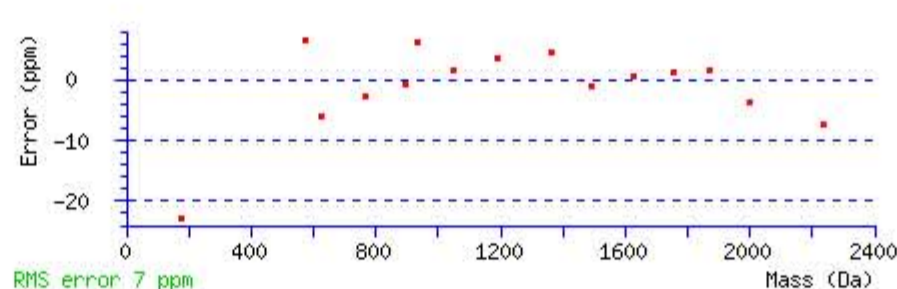
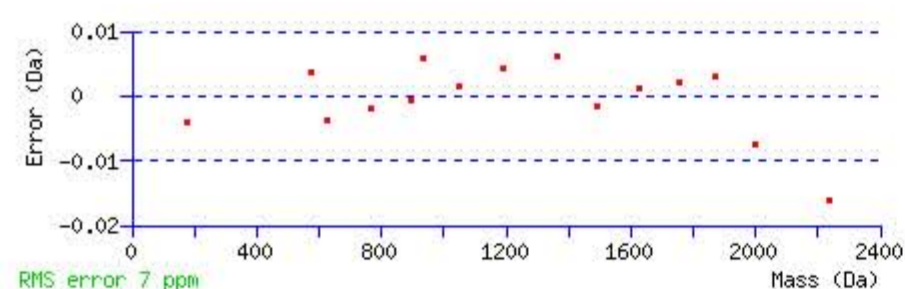
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 70 Expect: 1.5e-006

Matches : 15/164 fragment ions using 22 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	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
70.0	2384.089767	0.019141	MCPQLQQYEMHGPEGLR
59.4	2384.089767	0.019141	MCPQLQQYEMHGPEGLR
31.4	2384.089767	0.019141	MCPQLQQYEMHGPEGLR

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 54704: 2415.935772 from(806.319200,3+) rtinseconds(1528) index(18656)

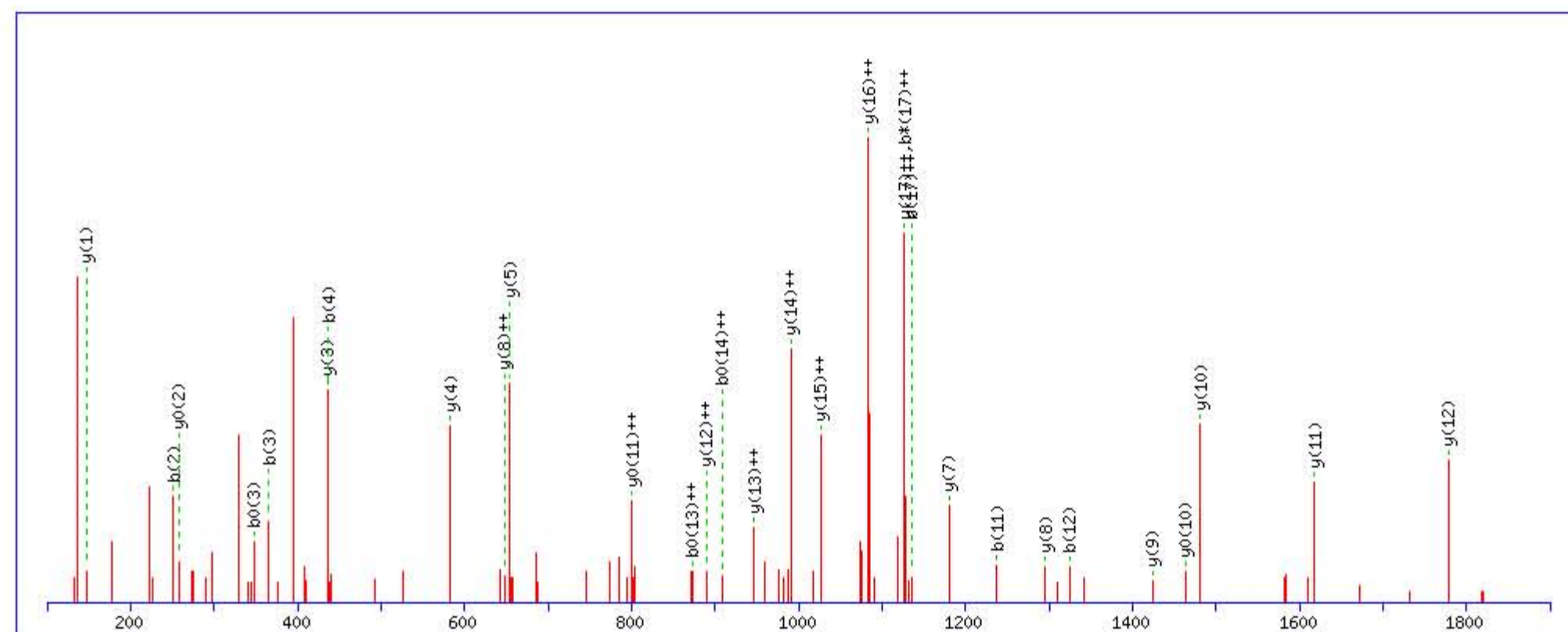
Title: Locus:1.1.1.534.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2415.940598

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

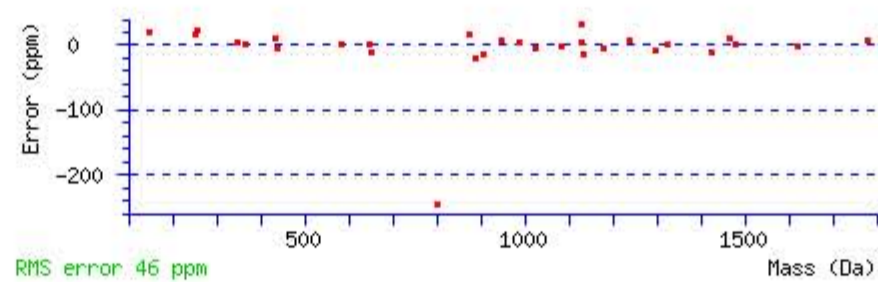
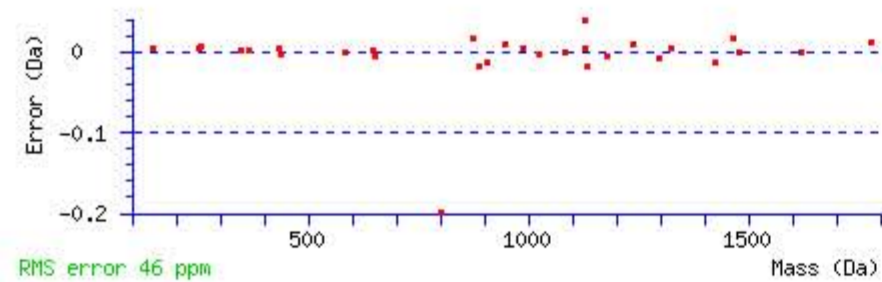
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 2e-006

Matches : 30/176 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	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
57.0	2415.940598	-0.004826	YSDASDCHGEDSQAFCEK

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 58296: 2695.265892 from(899.429240,3+) rtinseconds(2212) index(22970)

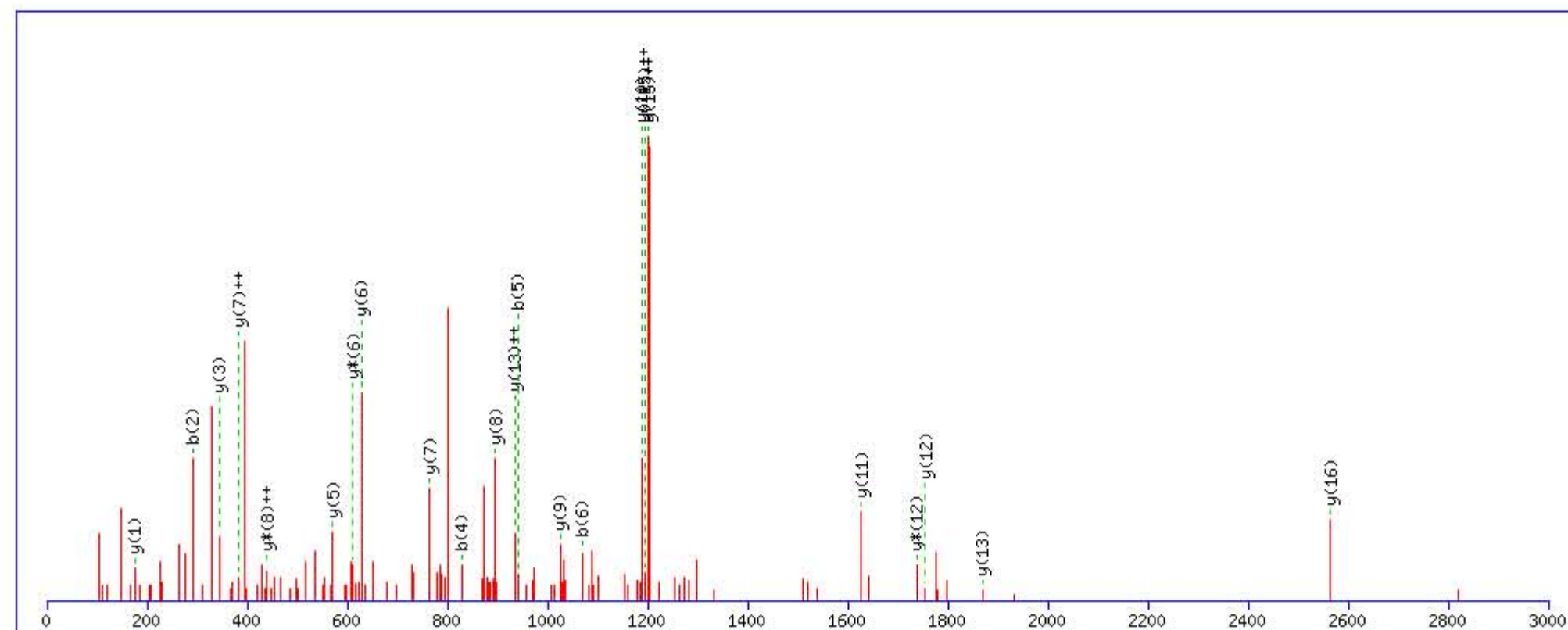
Title: Locus:1.1.1.772.23 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2695.256516

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

Variable modifications:

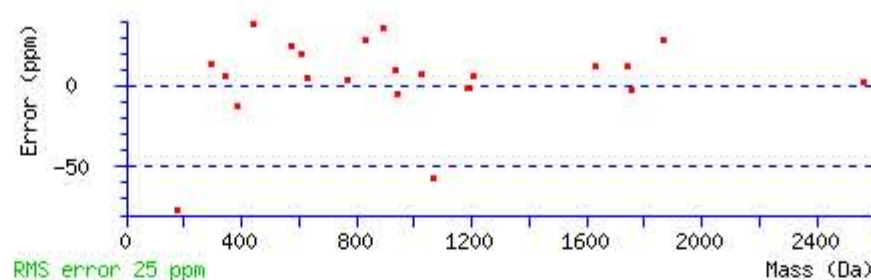
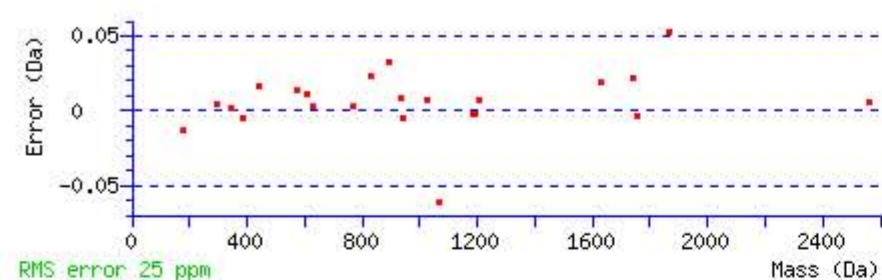
Q4 : Biotin:Thermo-21345 (Q)

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 44 Expect: 0.00064

Matches : 23/164 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	292.078410	146.542843					C	2565.223327	1283.115301	2548.196778	1274.602027	2547.212762	1274.110019	16
3	389.131174	195.069225					P	2405.192678	1203.099977	2388.166129	1194.586702	2387.182113	1194.094694	15
4	828.356500	414.681888	811.329951	406.168614			Q	2308.139914	1154.573595	2291.113365	1146.060320	2290.129349	1145.568312	14
5	941.440564	471.223920	924.414015	462.710646			L	1868.914588	934.960932	1851.888039	926.447658	1850.904023	925.955650	13
6	1069.499142	535.253209	1052.472593	526.739935			Q	1755.830524	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	1508.724468	754.865872	1491.697919	746.352598			Q	1627.771946	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
8	1671.787797	836.397537	1654.761248	827.884262			Y	1188.546620	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1800.830390	900.918833	1783.803841	892.405559	1782.819825	891.913551	E	1025.483291	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1931.870875	966.439076	1914.844326	957.925801	1913.860310	957.433793	M	896.440698	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	2068.929787	1034.968531	2051.903238	1026.455257	2050.919222	1025.963249	H	765.400213	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	2125.951251	1063.479263	2108.924702	1054.965989	2107.940686	1054.473981	G	628.341301	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	2223.004015	1112.005645	2205.977466	1103.492371	2204.993450	1103.000363	P	571.319837	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2352.046608	1176.526942	2335.020059	1168.013667	2334.036043	1167.521659	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2409.068072	1205.037674	2392.041523	1196.524399	2391.057507	1196.032391	G	345.224480	173.115878	328.197931	164.602603			3
16	2522.152136	1261.579706	2505.125587	1253.066431	2504.141571	1252.574424	L	288.203016	144.605146	271.176467	136.091872			2
17							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [MCPQLQQYEMHGPEGLR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.4	2695.256516	0.009376	MCPQLQQYEMHGPEGLR
37.2	2695.256516	0.009376	MCPQLQQYEMHGPEGLR
30.7	2695.256516	0.009376	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 58427: 2711.253016 from(678.820530,4+) rtinseconds(2053) index(6150)

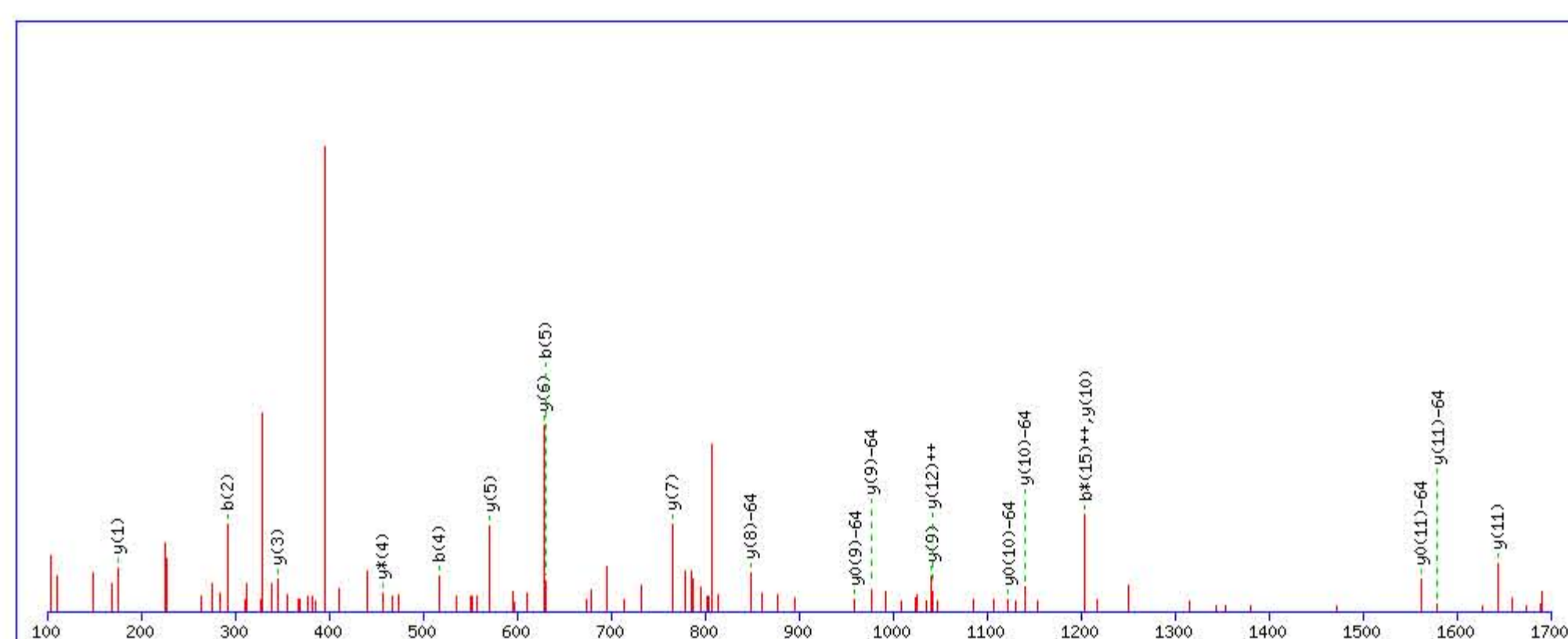
Title: Locus:1.1.1.1524.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2711.251434

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

Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

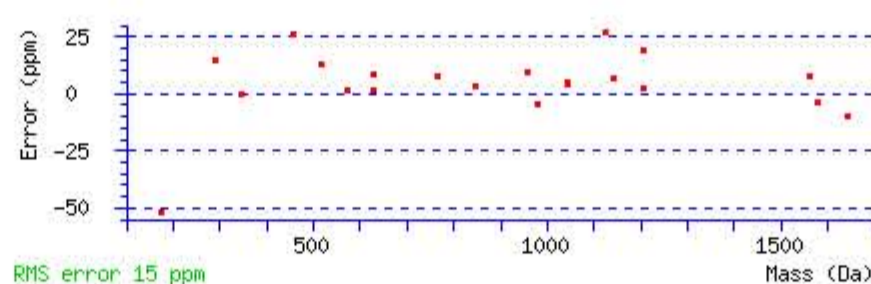
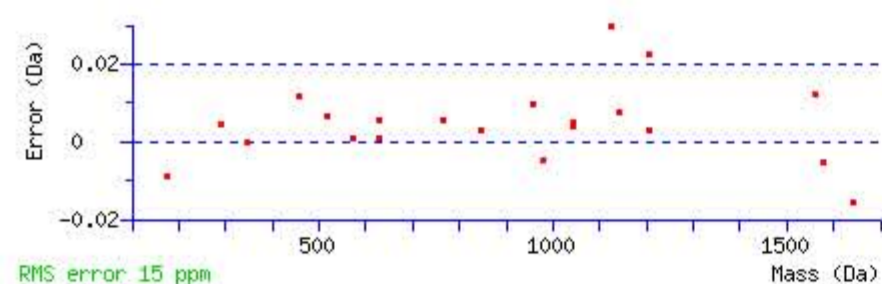
Q7 : Biotin:Thermo-21345 (Q)

M10 : Oxidation (M), with neutral losses 63.998285 (shown in table), 0.000000

Ions Score: 28 Expect: 0.0027

Matches : 21/260 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	132.047761	66.527518					M							17
2	292.078410	146.542843					C	2517.219957	1259.113616	2500.193408	1250.600342	2499.209392	1250.108334	16
3	389.131174	195.069225					P	2357.189308	1179.098292	2340.162759	1170.585017	2339.178743	1170.093009	15
4	517.189752	259.098514	500.163203	250.585240			Q	2260.136544	1130.571910	2243.109995	1122.058635	2242.125979	1121.566627	14
5	630.273816	315.640546	613.247267	307.127272			L	2132.077966	1066.542621	2115.051417	1058.029346	2114.067401	1057.537338	13
6	1069.499142	535.253209	1052.472593	526.739935			Q	2018.993902	1010.000589	2001.967353	1001.487315	2000.983337	1000.995307	12
7	1508.724468	754.865872	1491.697919	746.352598			Q	1579.768576	790.387926	1562.742027	781.874652	1561.758011	781.382644	11
8	1671.787797	836.397537	1654.761248	827.884262			Y	1140.543250	570.775263	1123.516701	562.261989	1122.532685	561.769981	10
9	1800.830390	900.918833	1783.803841	892.405559	1782.819825	891.913551	E	977.479921	489.243599	960.453372	480.730324	959.469356	480.238316	9
10	1883.867505	942.437391	1866.840956	933.924116	1865.856940	933.432108	M	848.437328	424.722302	831.410779	416.209028	830.426763	415.717020	8
11	2020.926417	1010.966847	2003.899868	1002.453572	2002.915852	1001.961564	H	765.400213	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	2077.947881	1039.477578	2060.921332	1030.964304	2059.937316	1030.472296	G	628.341301	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	2175.000645	1088.003960	2157.974096	1079.490686	2156.990080	1078.998678	P	571.319837	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2304.043238	1152.525257	2287.016689	1144.011982	2286.032673	1143.519975	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2361.064702	1181.035989	2344.038153	1172.522714	2343.054137	1172.030707	G	345.224480	173.115878	328.197931	164.602603			3
16	2474.148766	1237.578021	2457.122217	1229.064747	2456.138201	1228.572739	L	288.203016	144.605146	271.176467	136.091872			2
17							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **MCPQLQQYEMHGPEGLR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.8	2711.251434	0.001582	MCPQLQQYEMHGPEGLR
24.8	2711.251434	0.001582	MCPQLQQYEMHGPEGLR
18.3	2711.251434	0.001582	MCPQLQQYEMHGPEGLR
9.0	2711.251434	0.001582	MCPQLQQYEMHGPEGLR
9.0	2711.251434	0.001582	MCPQLQQYEMHGPEGLR
5.1	2711.251434	0.001582	MCPQLQQYEMHGPEGLR
0.4	2711.226059	0.026957	FHYGEKPYECKECKGKAFSVYGR

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 58448: 2711.264862 from(904.762230,3+) rtinseconds(2087) index(36932)

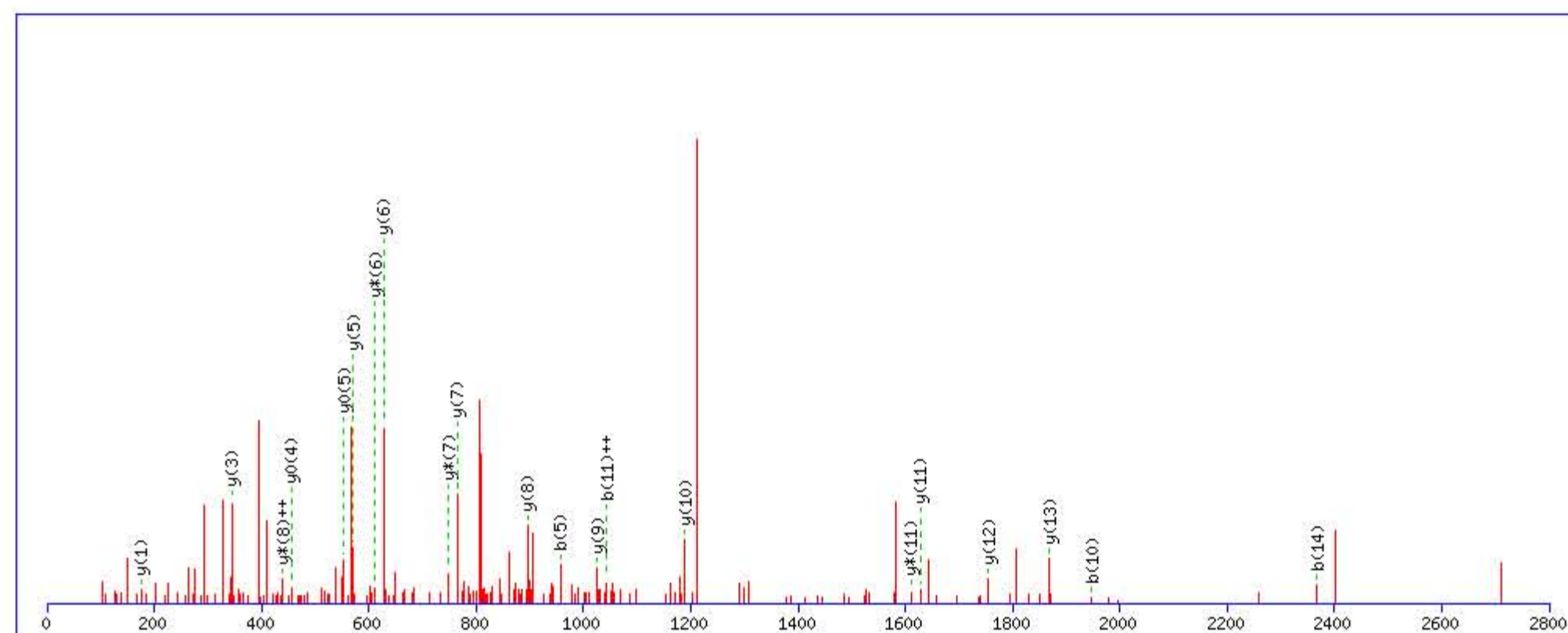
Title: Locus:1.1.1.3146.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2711.251434

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

Variable modifications:

M1 : Oxidation (M), with neutral losses 0.000000 (shown in table), 63.998285

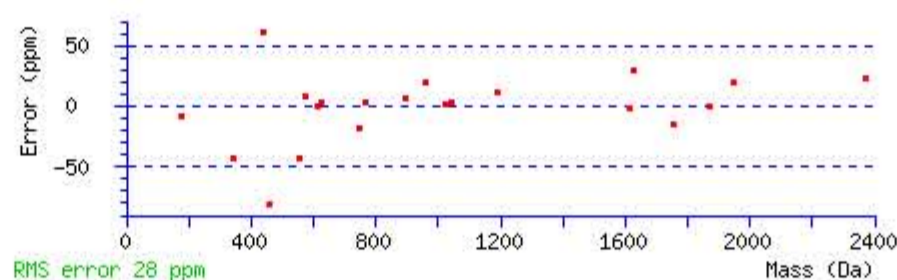
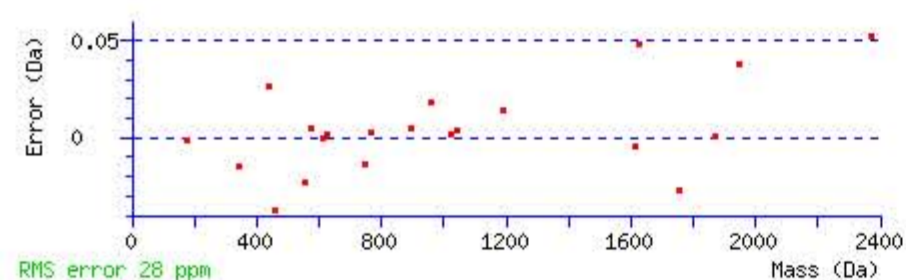
Q4 : Biotin:Thermo-21345 (Q)

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 32 Expect: 0.0094

Matches : 21/238 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	148.042676	74.524976					M							17
2	308.073325	154.540301					C	2565.223327	1283.115302	2548.196778	1274.602027	2547.212762	1274.110019	16
3	405.126089	203.066683					P	2405.192678	1203.099977	2388.166129	1194.586702	2387.182113	1194.094694	15
4	844.351415	422.679346	827.324866	414.166071			Q	2308.139914	1154.573595	2291.113365	1146.060320	2290.129349	1145.568312	14
5	957.435479	479.221378	940.408930	470.708103			L	1868.914588	934.960932	1851.888039	926.447658	1850.904023	925.955650	13
6	1085.494057	543.250667	1068.467508	534.737392			Q	1755.830524	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	1524.719383	762.863330	1507.692834	754.350055			Q	1627.771946	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
8	1687.782712	844.394994	1670.756163	835.881720			Y	1188.546620	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1816.825305	908.916291	1799.798756	900.403016	1798.814740	899.911008	E	1025.483291	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1947.865790	974.436533	1930.839241	965.923259	1929.855225	965.431251	M	896.440698	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	2084.924702	1042.965989	2067.898153	1034.452715	2066.914137	1033.960707	H	765.400213	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	2141.946166	1071.476721	2124.919617	1062.963446	2123.935601	1062.471439	G	628.341301	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	2238.998930	1120.003103	2221.972381	1111.489828	2220.988365	1110.997821	P	571.319837	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2368.041523	1184.524400	2351.014974	1176.011125	2350.030958	1175.519117	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2425.062987	1213.035132	2408.036438	1204.521857	2407.052422	1204.029849	G	345.224480	173.115878	328.197931	164.602603			3
16	2538.147051	1269.577164	2521.120502	1261.063889	2520.136486	1260.571881	L	288.203016	144.605146	271.176467	136.091872			2
17							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [MCPQLQQYEMHGPEGLR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.4	2711.251434	0.013428	MCPQLQQYEMHGPEGLR
25.0	2711.251434	0.013428	MCPQLQQYEMHGPEGLR
16.9	2711.251434	0.013428	MCPQLQQYEMHGPEGLR
9.4	2711.251434	0.013428	MCPQLQQYEMHGPEGLR
7.4	2711.251434	0.013428	MCPQLQQYEMHGPEGLR
6.2	2711.251434	0.013428	MCPQLQQYEMHGPEGLR

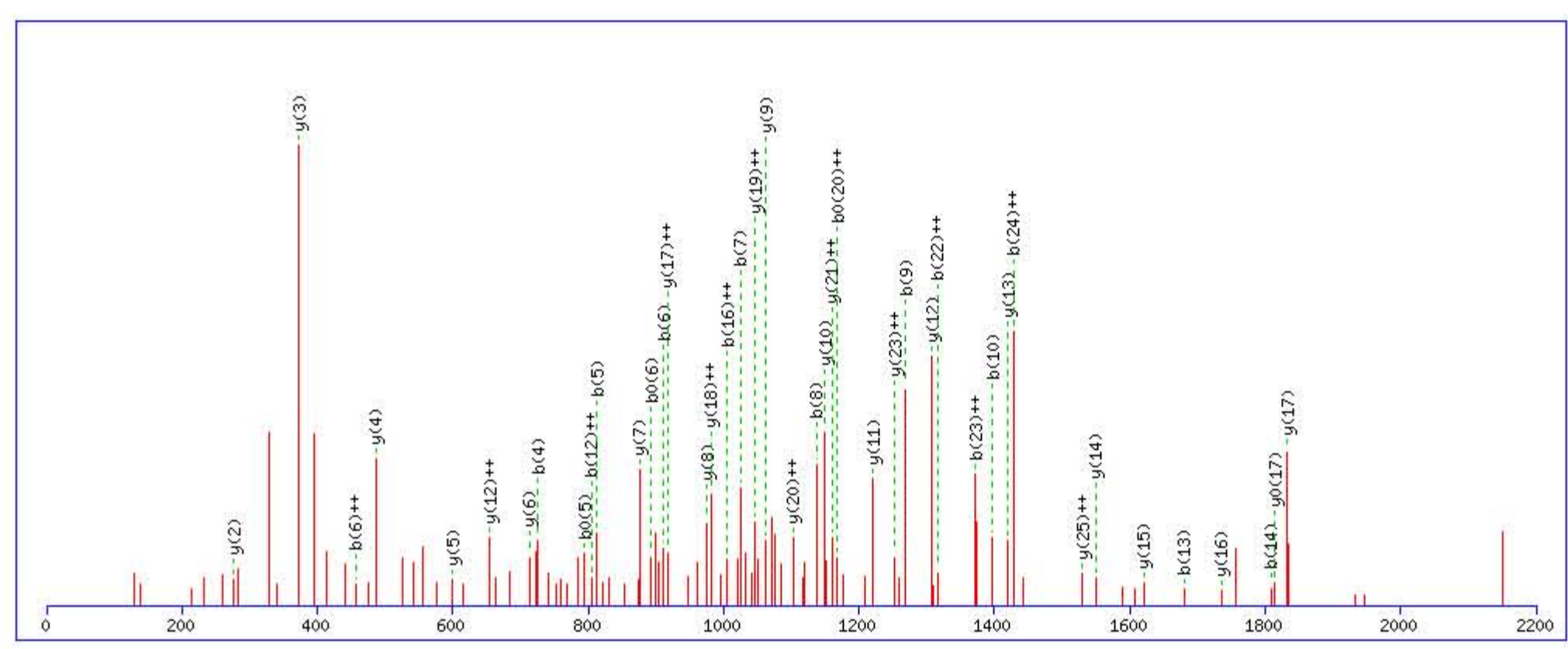
MASCOT Search Results

Peptide View

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

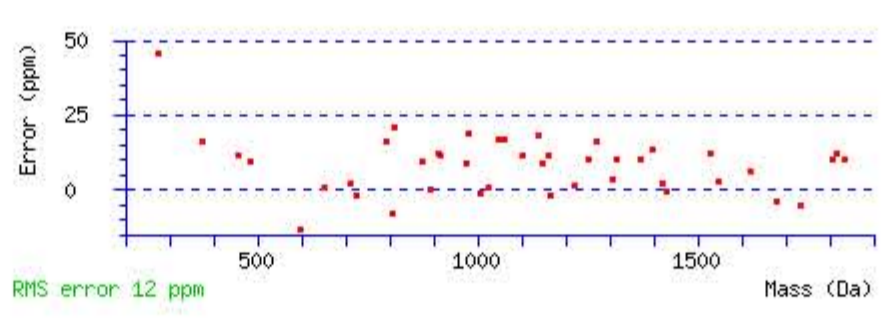
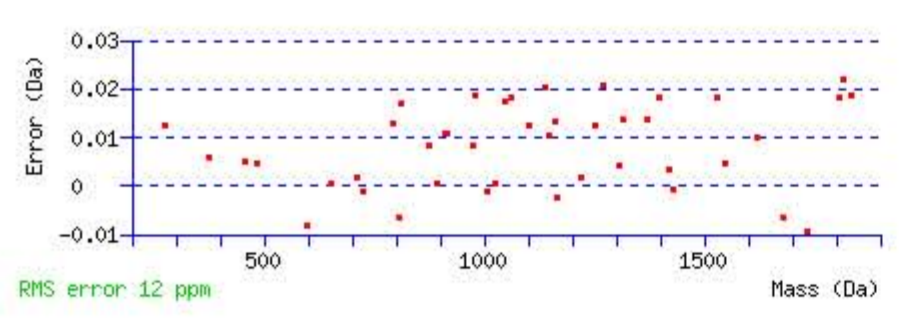
Match to Query 64174: 3227.705652 from(1076.909160,3+) rtinseconds(2761) index(26239)
 Title: Locus:1.1.1.962.25 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 3227.682129
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q4 : Biotin:Thermo-21345 (Q)
 Ions Score: 91 Expect: 1.4e-008
 Matches : 43/300 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	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
91.4	3227.682129	0.023523	AVDQSVLLMKPDAELSASSVYNLLPEK

MASCOT SCIENCE } Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENAEQSR**

Found in **ANT3_HUMAN**, Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

Match to Query 21427: 1143.530328 from(572.772440,2+) rtinseconds(1132) index(31086)

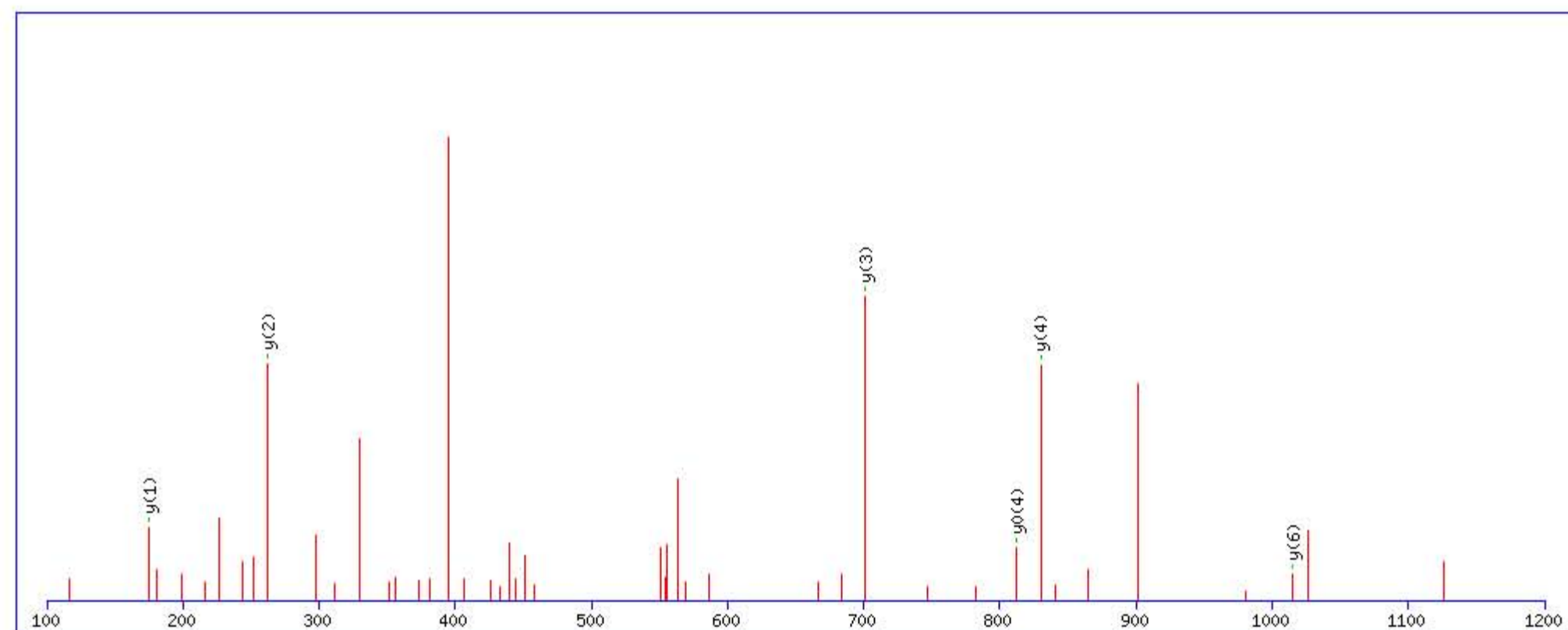
Title: Locus:1.1.1.2813.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1143.534225

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

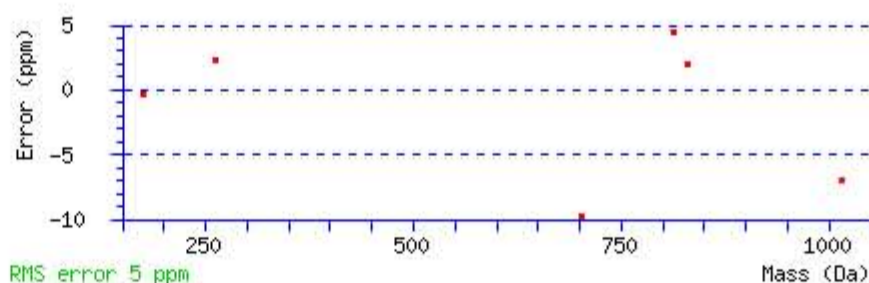
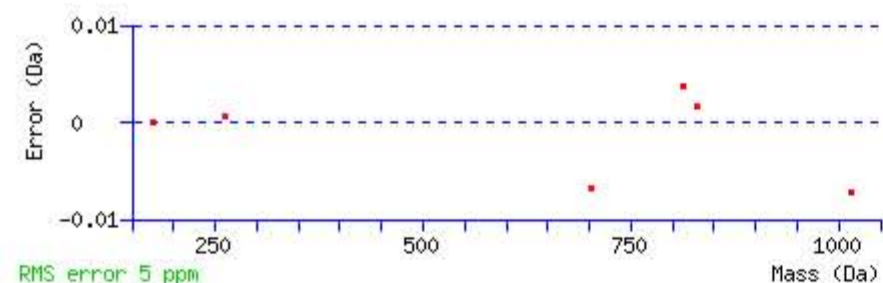
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.0021

Matches : 6/68 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	130.049869	65.528572			112.039304	56.523290	E							7
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	N	1015.498940	508.253108	998.472391	499.739834	997.488375	499.247826	6
3	315.129910	158.068593	298.103361	149.555319	297.119345	149.063311	A	901.456013	451.231645	884.429464	442.718370	883.445448	442.226362	5
4	444.172503	222.589890	427.145954	214.076615	426.161938	213.584607	E	830.418899	415.713088	813.392350	407.199813	812.408334	406.707805	4
5	883.397829	442.202553	866.371280	433.689278	865.387264	433.197270	Q	701.376306	351.191791	684.349757	342.678517	683.365741	342.186509	3
6	970.429857	485.718567	953.403308	477.205292	952.419292	476.713284	S	262.150980	131.579128	245.124431	123.065853	244.140415	122.573845	2
7							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [ENAEQSR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.4	1143.534225	-0.003897	ENAEQSR
10.6	1143.526840	0.003488	EGEGASAPRDR
1.4	1143.515625	0.014703	SYSVGASGSSSR

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 34703: 1531.713552 from(511.578460,3+) rtinseconds(1023) index(16161)

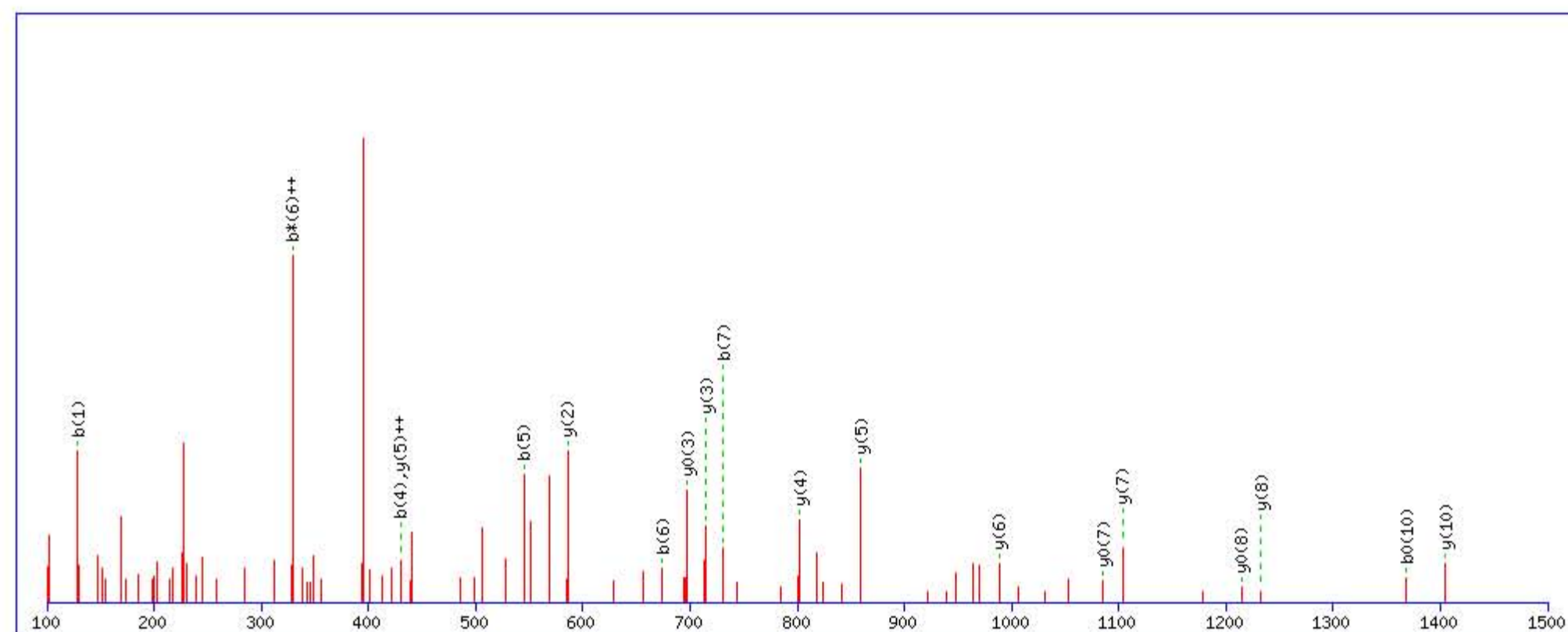
Title: Locus:1.1.1.358.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1531.718796

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

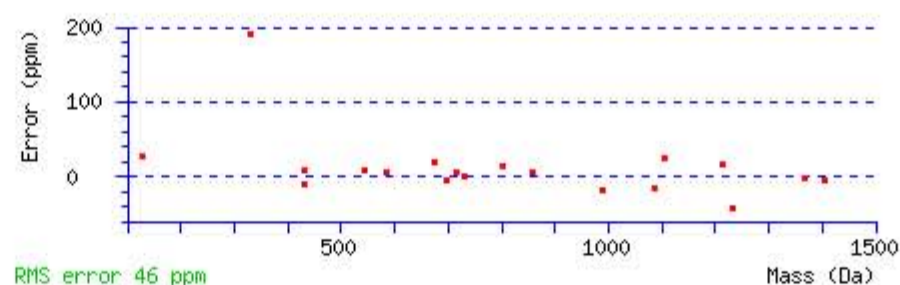
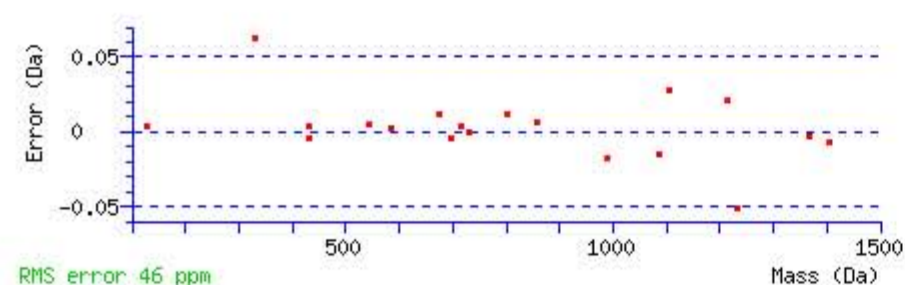
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 2.8e-005

Matches : 19/112 fragment ions using 26 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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
57.2	1531.718796	-0.005244	KATEDEGSEQK
13.1	1531.716309	-0.002757	QVDSMWAEQK
7.2	1531.734055	-0.020503	VNPQEESYQK
7.0	1531.715454	-0.001902	EWNGVVSESDSPVK
2.9	1531.701523	0.012029	EGFDPQGASQLNNR
2.3	1531.730072	-0.016520	DGQQSGTVSSQK
1.9	1531.722626	-0.009074	EAQQATETQRNEK

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **VAEGTQVLELPPFK**

Found in **ANT3_HUMAN**, Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

Match to Query 41310: 1740.957428 from(871.485990,2+) rtinseconds(2545) index(24773)

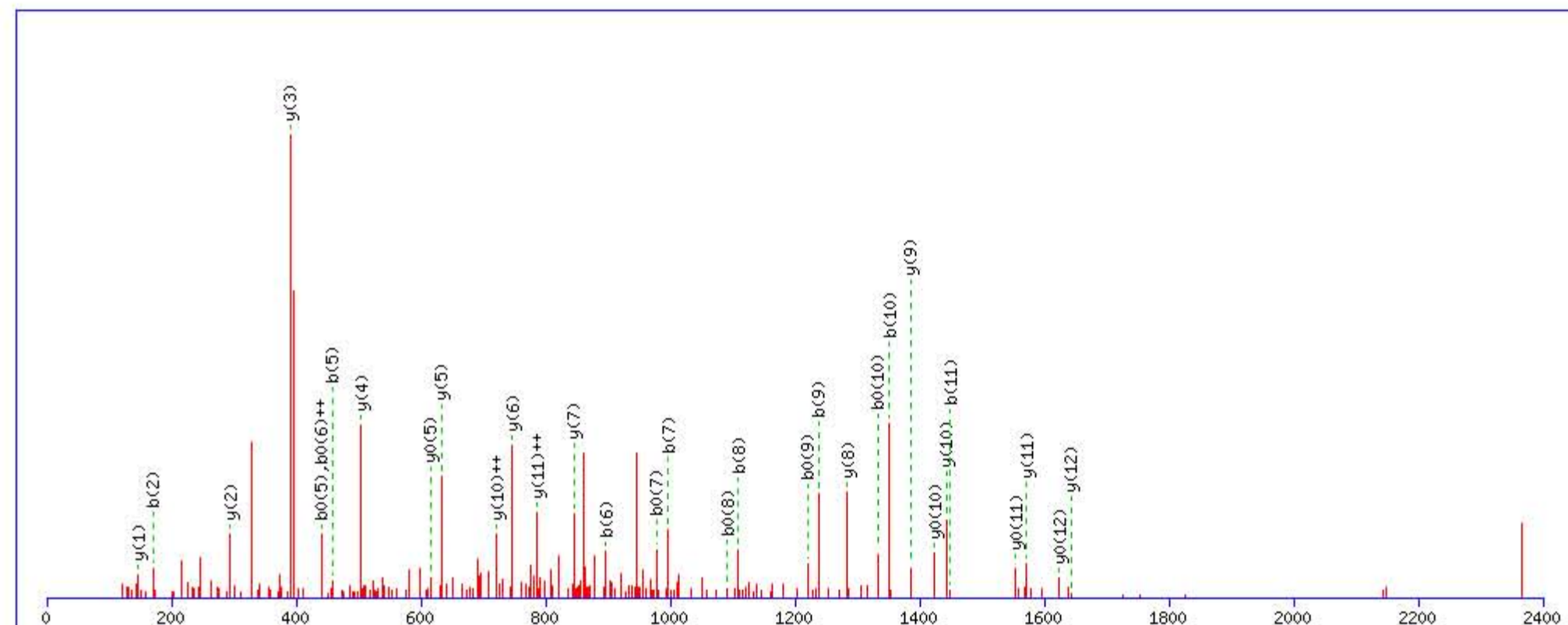
Title: Locus:1.1.1.888.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1740.948425

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

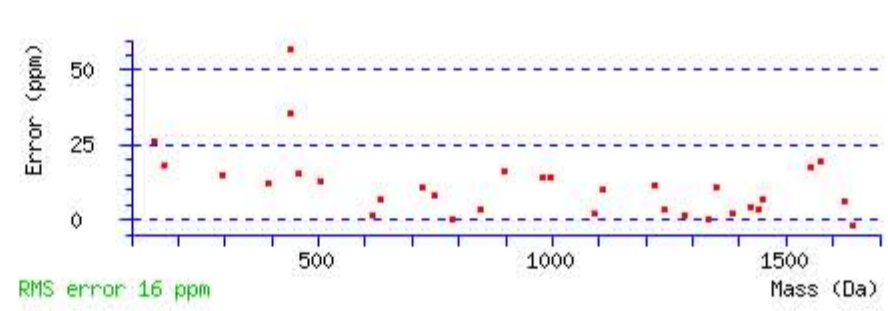
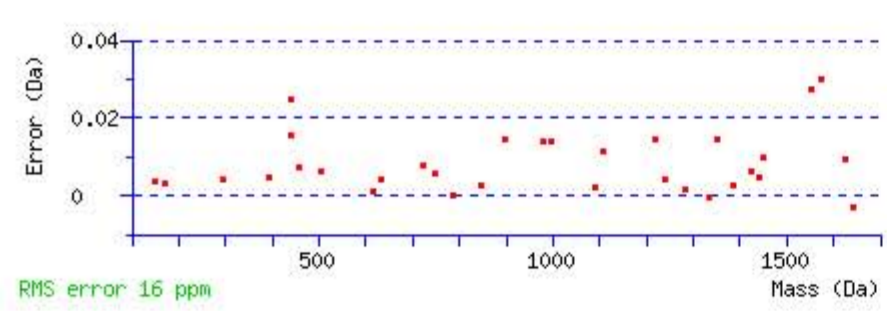
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 90 Expect: 1.7e-008

Matches : 32/122 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	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 **VAEGTQVLELPPFK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
89.9	1740.948425	0.009003	VAEGTQVLELPPFK
6.9	1740.962982	-0.005554	ISRQLAEEILMK

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 22870: 1183.598148 from(592.806350,2+) rtinseconds(1454) index(32954)

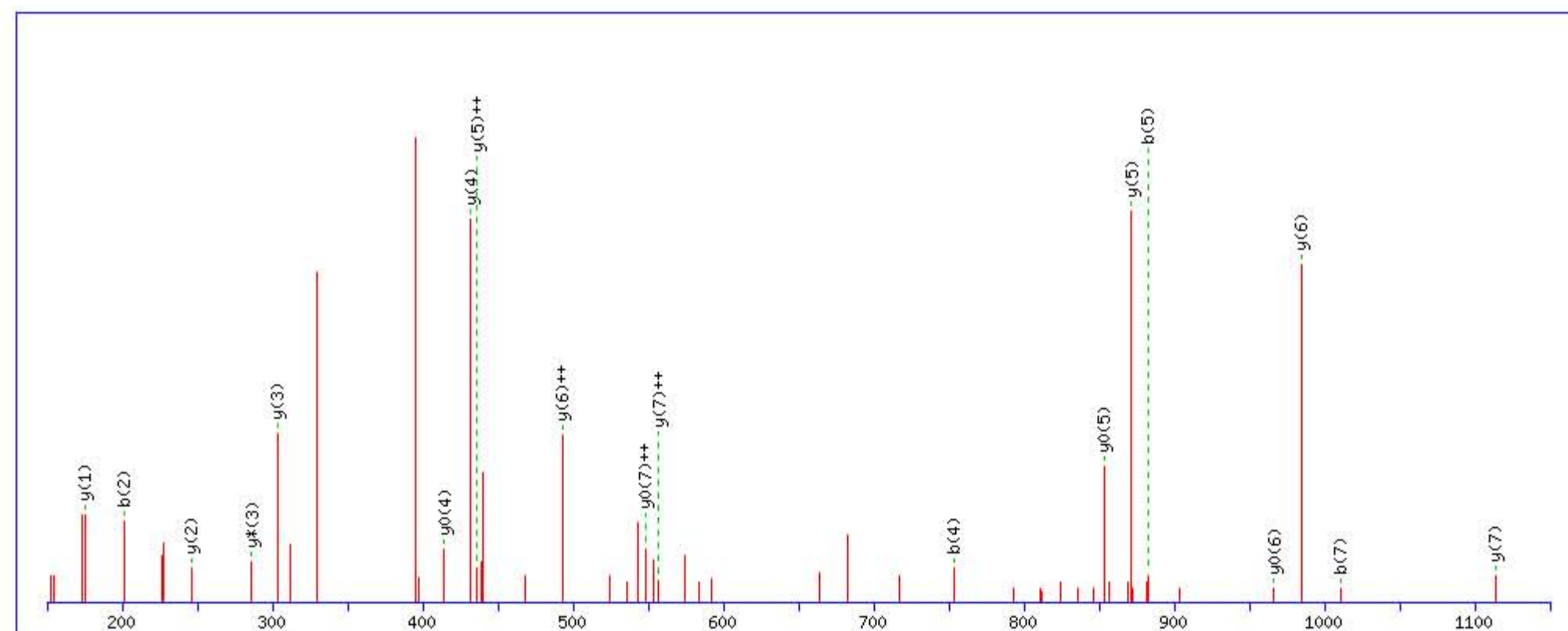
Title: Locus:1.1.1.2925.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1183.601913

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

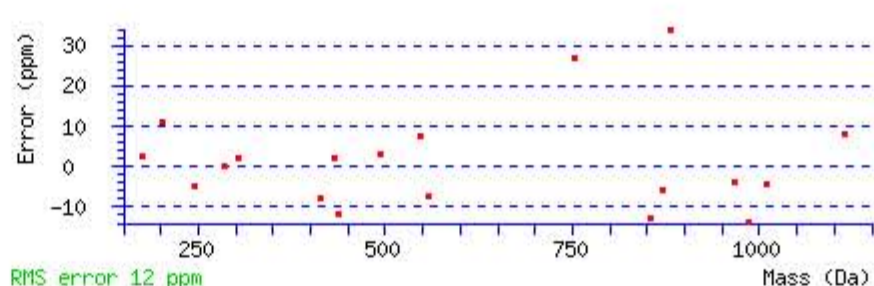
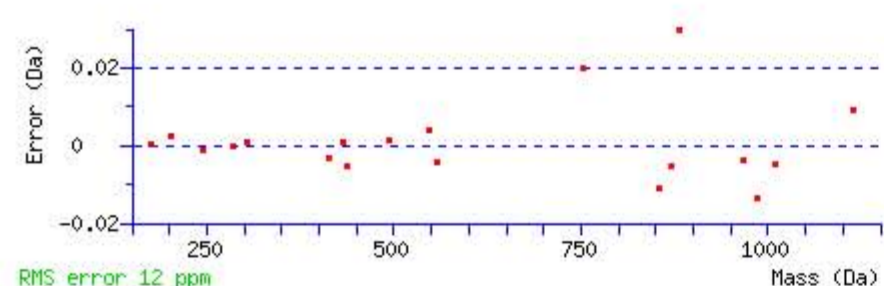
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 35 Expect: 0.0054

Matches : 19/70 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	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
35.0	1183.601913	-0.003765	AELQEGAR
11.9	1183.601913	-0.003765	EALEQQR
10.6	1183.601913	-0.003765	QLAEQER
10.0	1183.601913	-0.003765	LQEAQER
9.5	1183.601913	-0.003765	EALEQQR
9.4	1183.613815	-0.015667	FHFEALPPAR
7.8	1183.601913	-0.003765	ELQAEAGR
7.1	1183.587997	0.010151	EAKLDHCRR
5.6	1183.609802	-0.011654	ATPHFSGLAAGR
3.7	1183.601913	-0.003765	LEQEAGAR

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 34898: 1540.870848 from(771.442700,2+) rtinseconds(2823) index(73793)

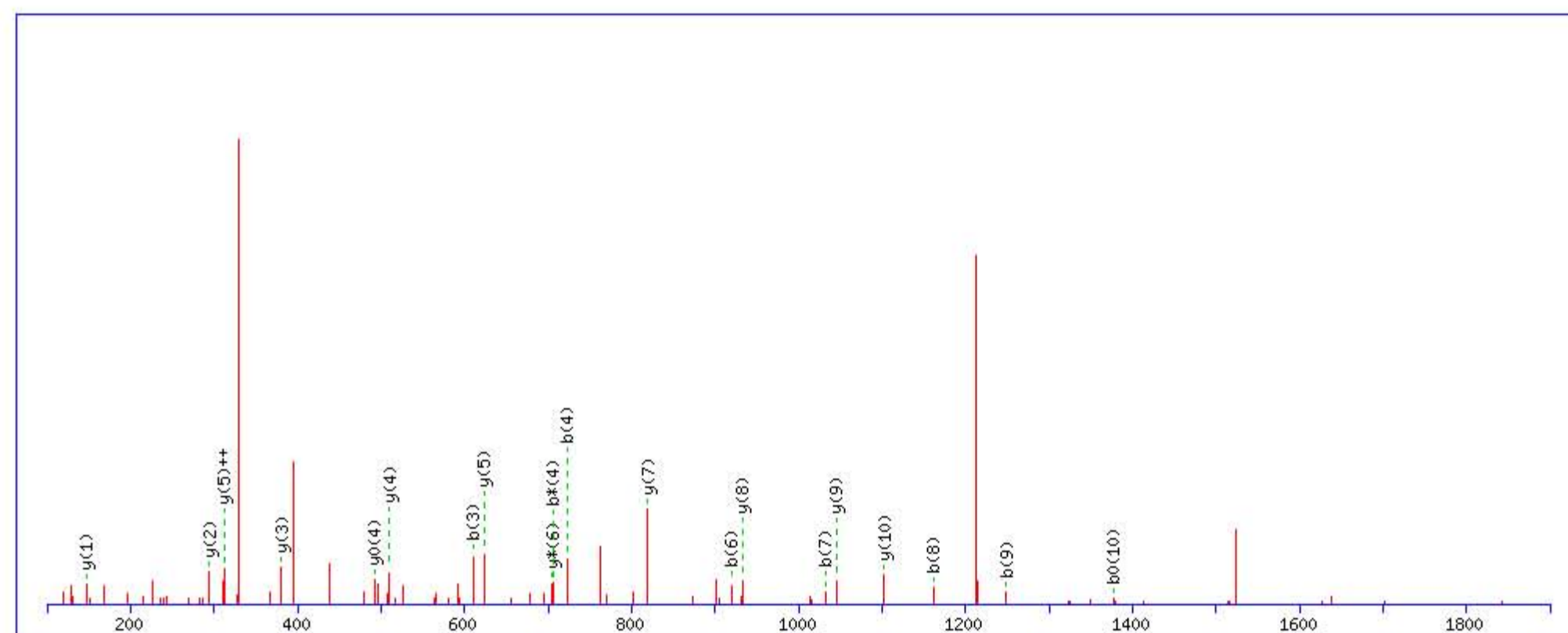
Title: Locus:1.1.1.1919.8 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1540.868713

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

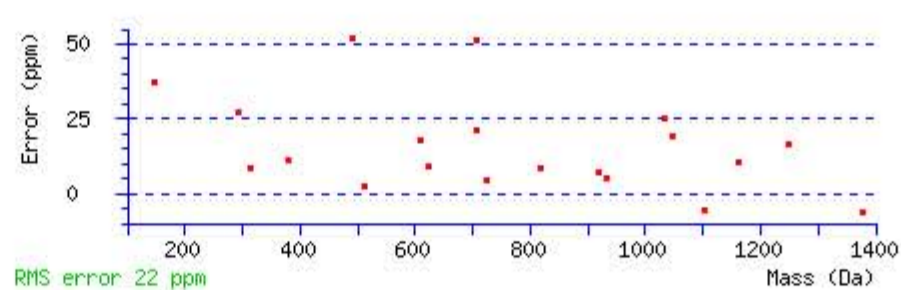
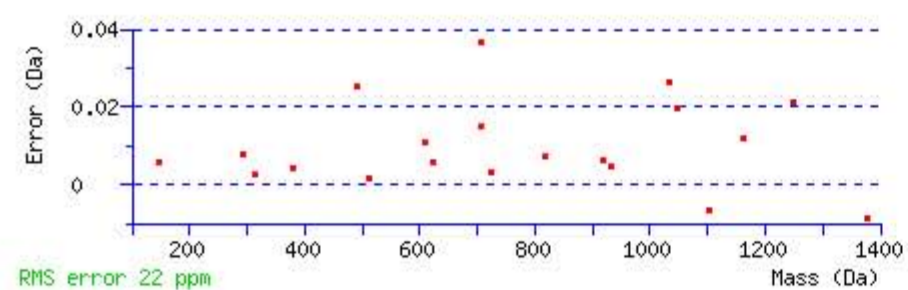
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 51 Expect: 3.1e-005

Matches : 20/102 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	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
50.8	1540.868713	0.002135	QGLLPVLESFK
2.6	1540.872559	-0.001711	GALHKTVQNLVFSK
1.2	1540.887146	-0.016298	KTVRVGLNAPSMLR
0.8	1540.864700	0.006148	KVTVGKDDIQK
0.6	1540.893677	-0.022829	LKSVDVGLQGLREK
0.6	1540.858139	0.012709	LTNLRQLQNMK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VQPYLDDDFQK**

Found in **APOA1_HUMAN**, Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1

Match to Query 35478: 1562.791308 from(782.402930,2+) rtinseconds(2184) index(37540)

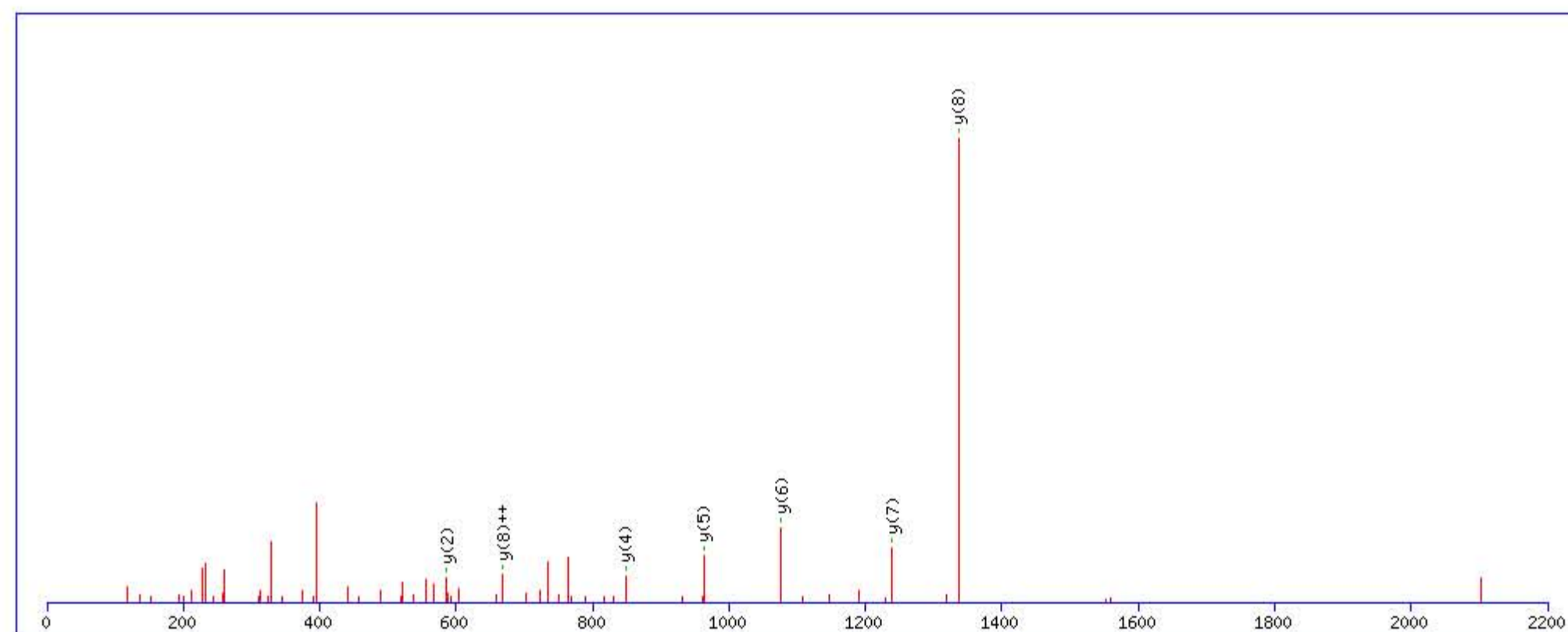
Title: Locus:1.1.1.3180.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1562.780304

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

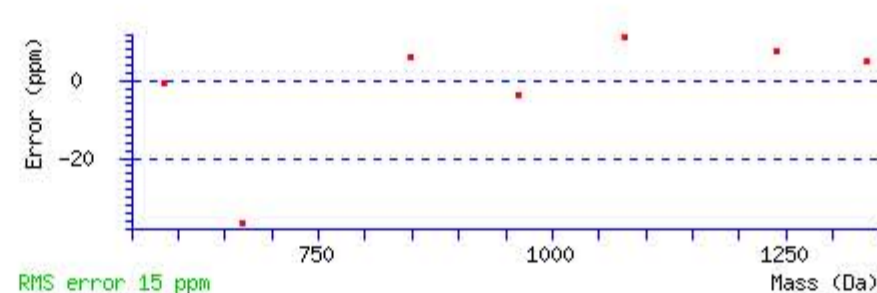
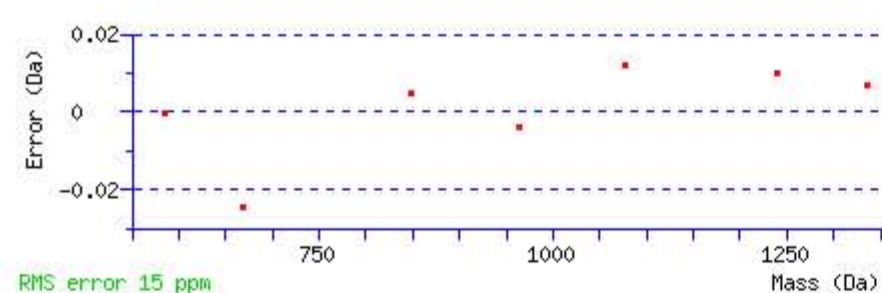
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 34 Expect: 0.0031

Matches : 7/90 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	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 **VQPYLDDDFQK**

(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	1562.780304	0.011004	VQPYLDDDFQK
7.1	1562.808624	-0.017316	LNSPTTTSQIMARK
5.6	1562.804764	-0.013456	QVEELLMAMEKVK
1.6	1562.768875	0.022433	VQQGERDFEQISK
1.4	1562.780960	0.010348	MERHMVRGQLYK
1.2	1562.787521	0.003787	VQLVDNVYCIGQR
1.1	1562.804764	-0.013456	QVEELLMAMEKVK
0.7	1562.769714	0.021594	YAVMRAAEMHQLK

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 40698: 1710.849728 from(856.432140,2+) rtinseconds(2432) index(55595)

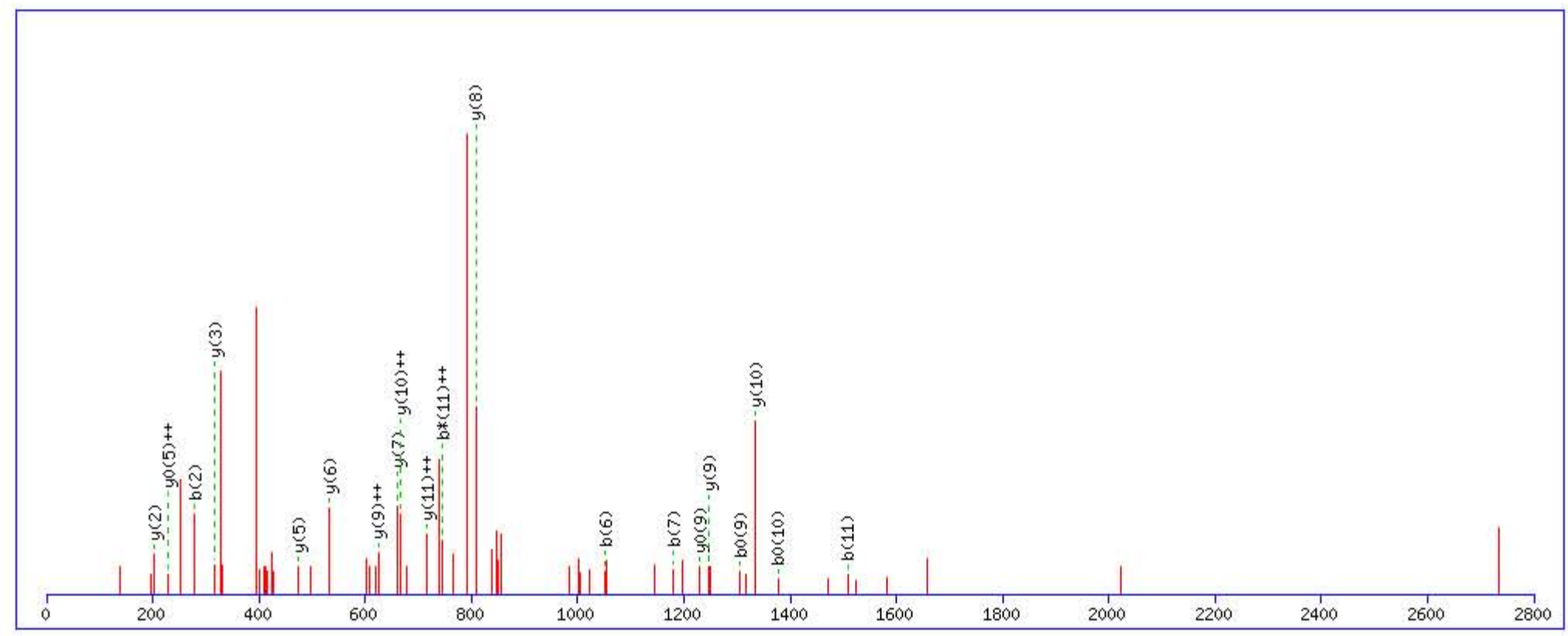
Title: Locus:1.1.1.1461.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1710.828705

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

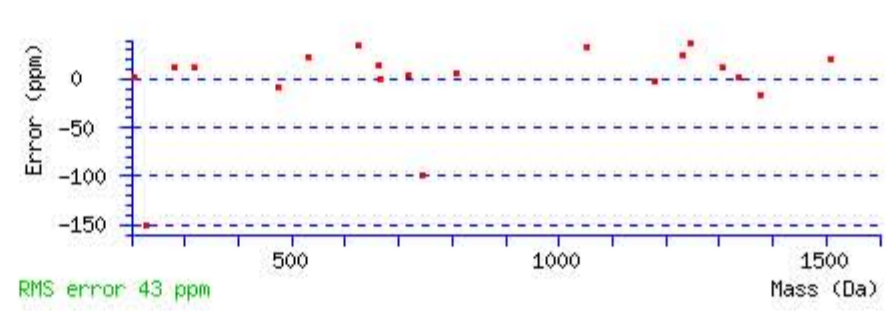
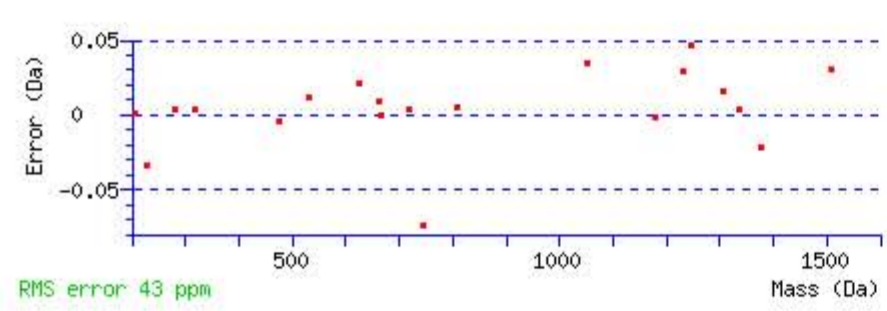
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 32 Expect: 0.0015

Matches : 20/128 fragment ions using 51 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.034219	58.520748			98.023654	49.515465	D							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
32.0	1710.828705	0.021023	DYVSQFEGSALGK
1.7	1710.833420	0.016308	YDPVWMTVTRKCR

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 25787: 1282.654828 from(642.334690,2+) rtinseconds(1531) index(33483)

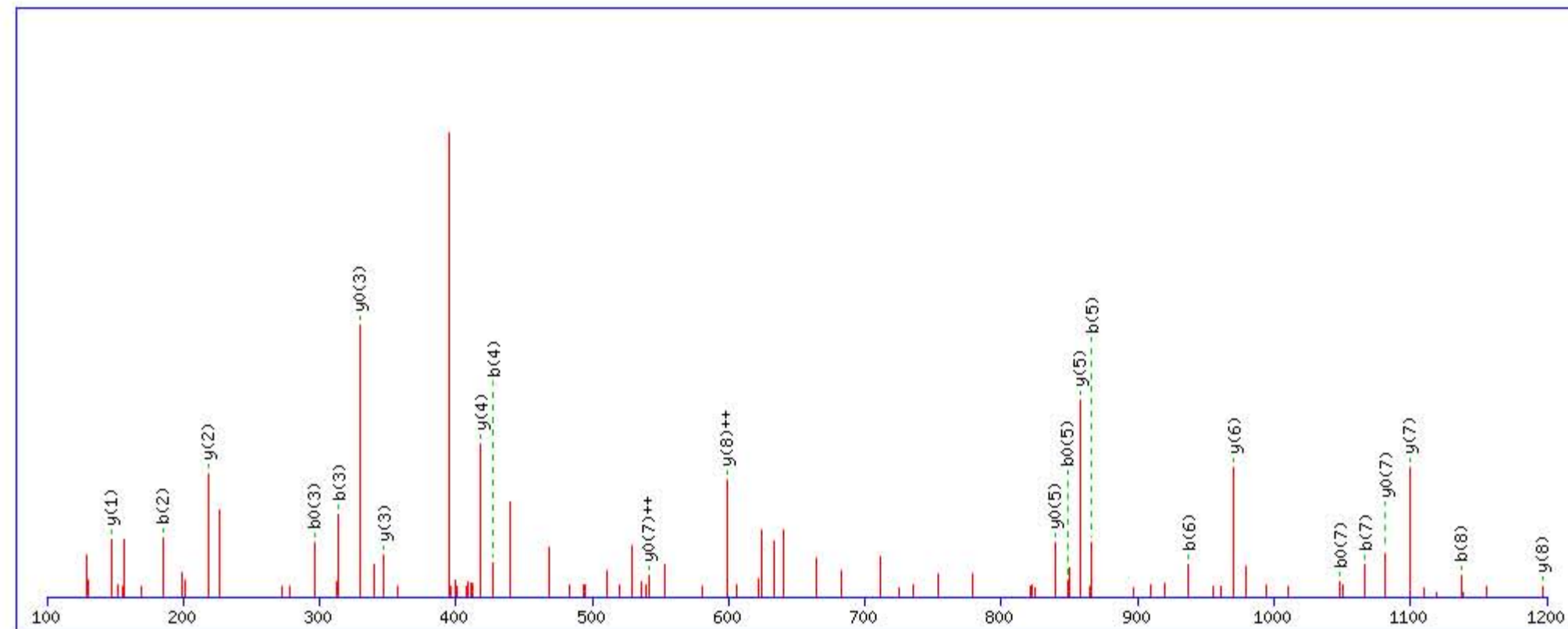
Title: Locus:1.1.1.2952.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1282.659088

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

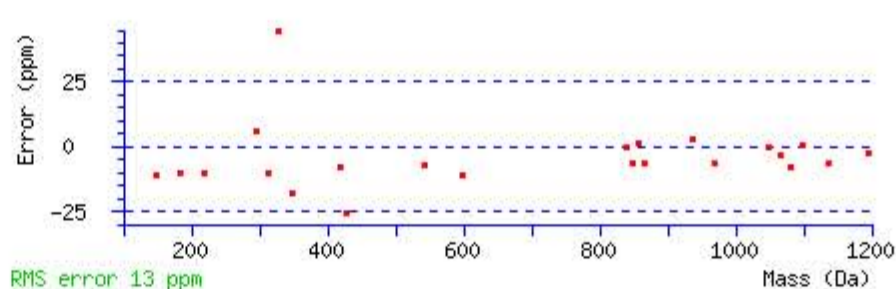
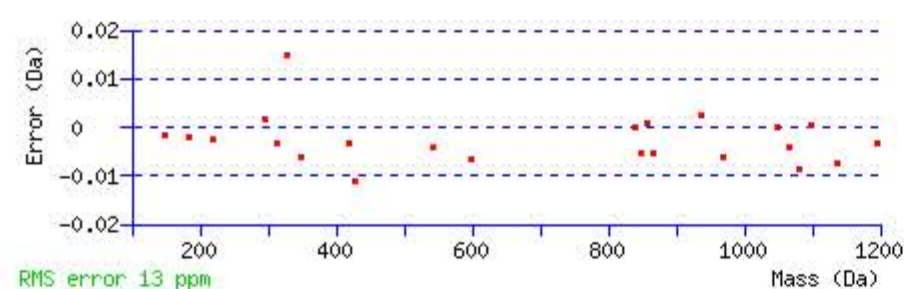
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.0022

Matches : 23/84 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	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
39.6	1282.659088	-0.004260	SPELQAEAK
12.5	1282.637802	0.017026	KGHETLRDGD
3.1	1282.670334	-0.015506	EPIQASTAR
1.3	1282.655716	-0.000888	ALEAEKYGFQK
1.1	1282.662949	-0.008121	DLSDTQRHLAK
0.8	1282.645203	0.009625	AAGPGLGNVAMGPR
0.7	1282.645187	0.009641	KCGHENLQLGK
0.6	1282.641830	0.012998	SYPGHVQPATAR

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 58048: 2660.263062 from(887.761630,3+) rtinseconds(3114) index(28264)

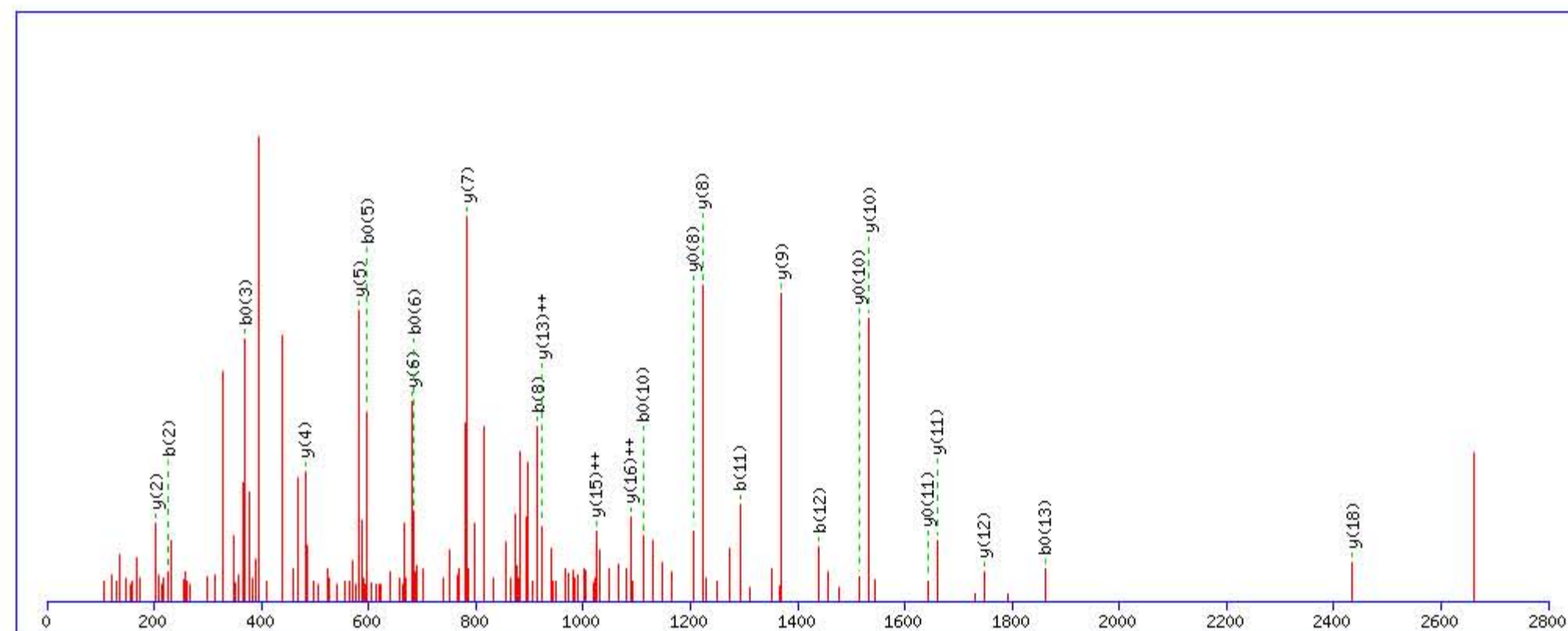
Title: Locus:1.1.1.1083.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2660.250244

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

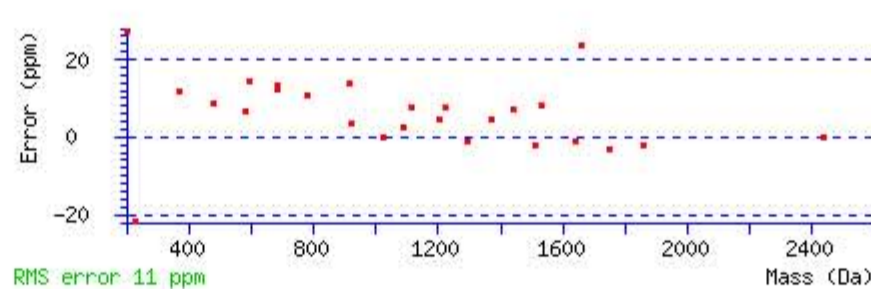
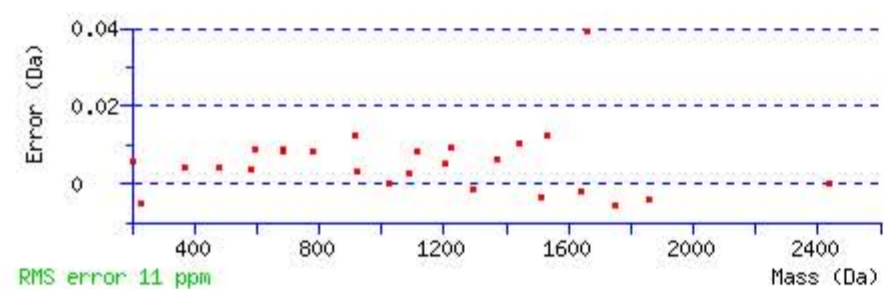
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 75 Expect: 7.3e-007

Matches : 26/204 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	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
74.8	2660.250244	0.012818	EPCVESLVSQYFQTVTDYGK
33.1	2660.250244	0.012818	EPCVESLVSQYFQTVTDYGK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **EPCVESLVSQYFQTVTDYGK**

Found in **APOA2_HUMAN**, Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1

Match to Query 58051: 2660.265912 from(887.762580,3+) rtinseconds(3178) index(28557)

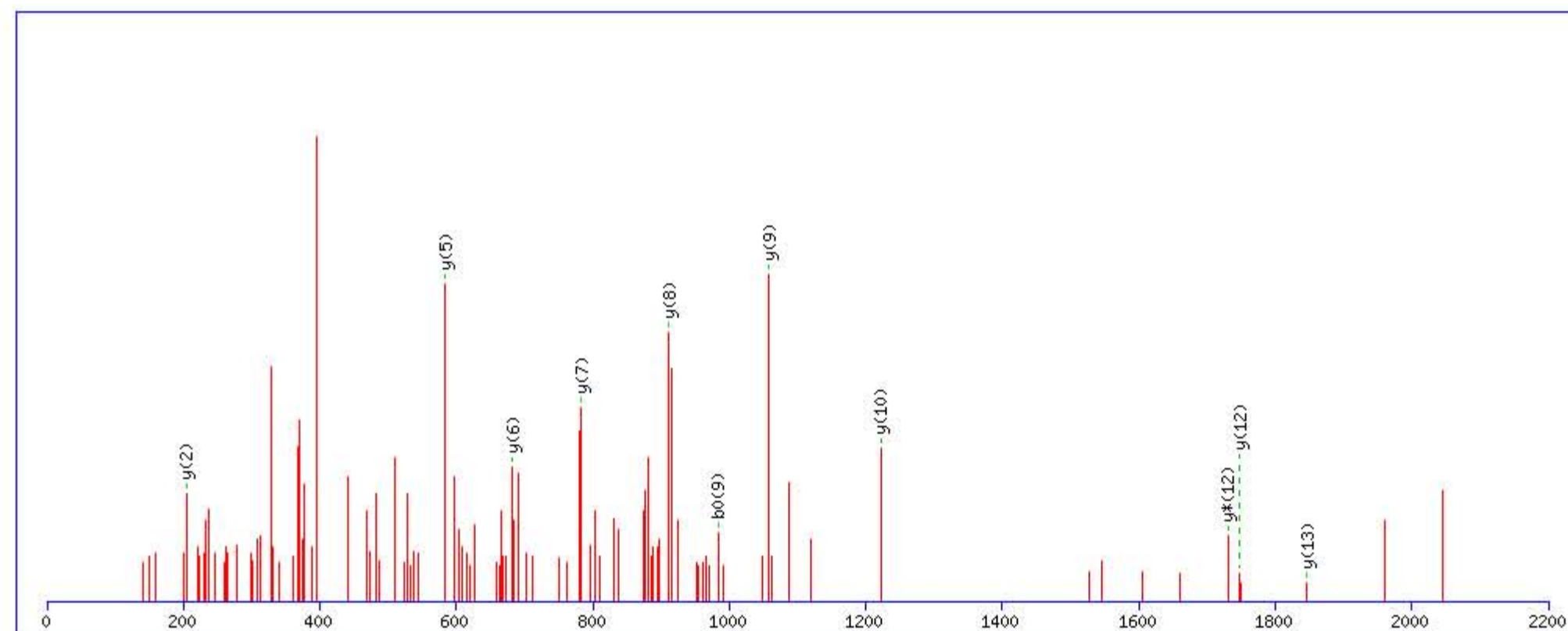
Title: Locus:1.1.1.1105.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2660.250244

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

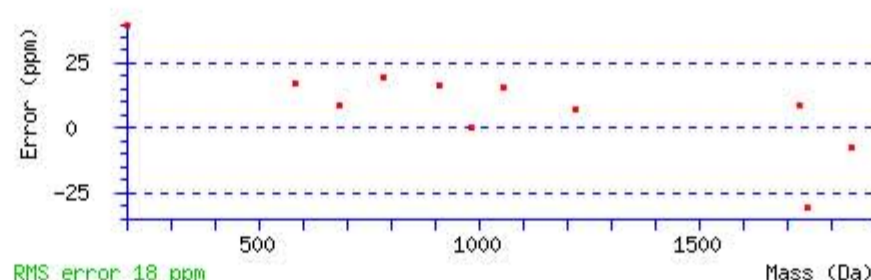
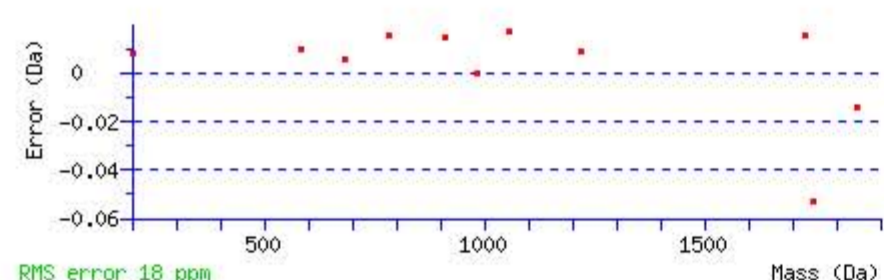
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 50 Expect: 0.00023

Matches : 11/204 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							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
50.0	2660.250244	0.015668	EPCVESLVSQYFQTVTDYGK
28.6	2660.250244	0.015668	EPCVESLVSQYFQTVTDYGK

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

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 21820: 1156.585268 from(579.299910,2+) rtinseconds(1399) index(32517)

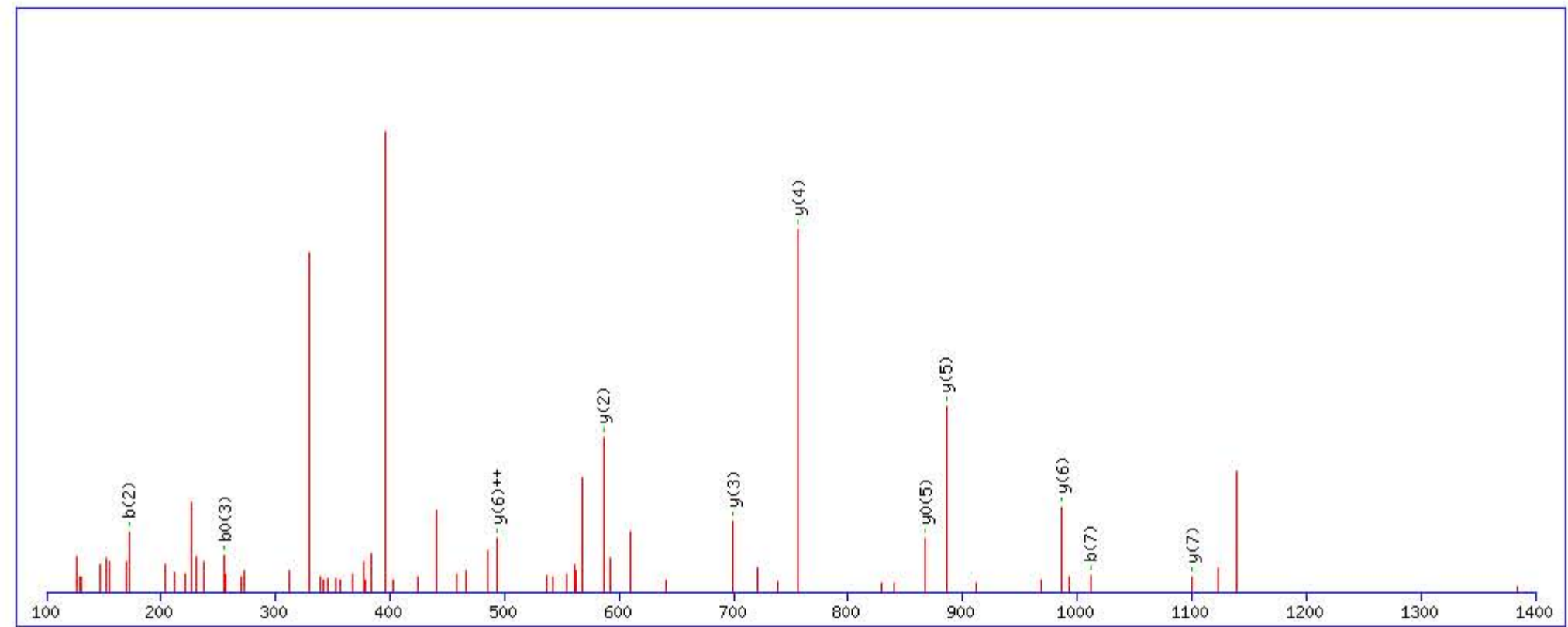
Title: Locus:1.1.1.2906.15 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1156.591034

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

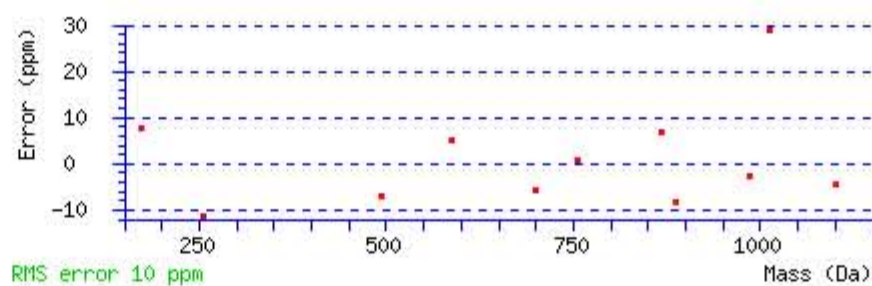
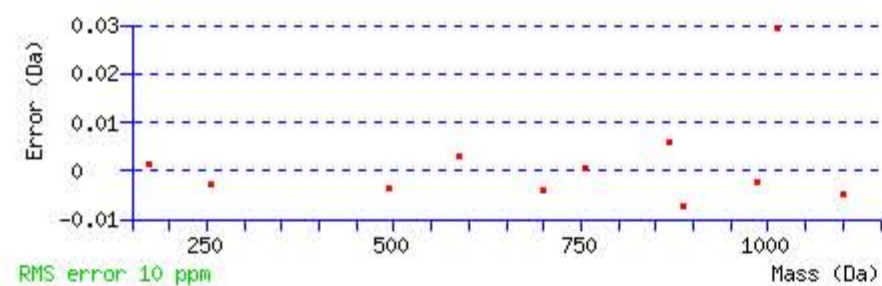
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.004

Matches : 11/70 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	58.028740	29.518008					G							8
2	172.071667	86.539471	155.045118	78.026197			N	1100.576857	550.792067	1083.550308	542.278792	1082.566292	541.786784	7
3	273.119346	137.063311	256.092797	128.550037	255.108781	128.058029	T	986.533930	493.770603	969.507381	485.257329	968.523365	484.765321	6
4	402.161939	201.584608	385.135390	193.071333	384.151374	192.579325	E	885.486251	443.246764	868.459702	434.733489	867.475686	434.241481	5
5	459.183403	230.095339	442.156854	221.582065	441.172838	221.090057	G	756.443658	378.725467	739.417109	370.212193			4
6	572.267467	286.637372	555.240918	278.124097	554.256902	277.632089	L	699.422194	350.214735	682.395645	341.701461			3
7	1011.492793	506.250035	994.466244	497.736760	993.482228	497.244752	Q	586.338130	293.672703	569.311581	285.159429			2
8							K	147.112804	74.060040	130.086255	65.546766			1



NCBI BLAST search of **GNTEGLQK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.7	1156.591034	-0.005766	GNTEGLQK
12.7	1156.572418	0.012850	GPQTSTSPASPK
7.2	1156.598923	-0.013655	GDRGGPGIPGFK
6.0	1156.577118	0.008150	QLSTRCHQK
3.1	1156.591019	-0.005751	SQLENQK
2.3	1156.576416	0.008852	IKSQDFYEK
2.1	1156.595047	-0.009779	CDYFLAKIK
1.3	1156.602249	-0.016981	MVHKEKGANK
1.0	1156.591034	-0.005766	IQVEQNK

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 30079: 1397.714368 from(699.864460,2+) rtinseconds(1817) index(35136)

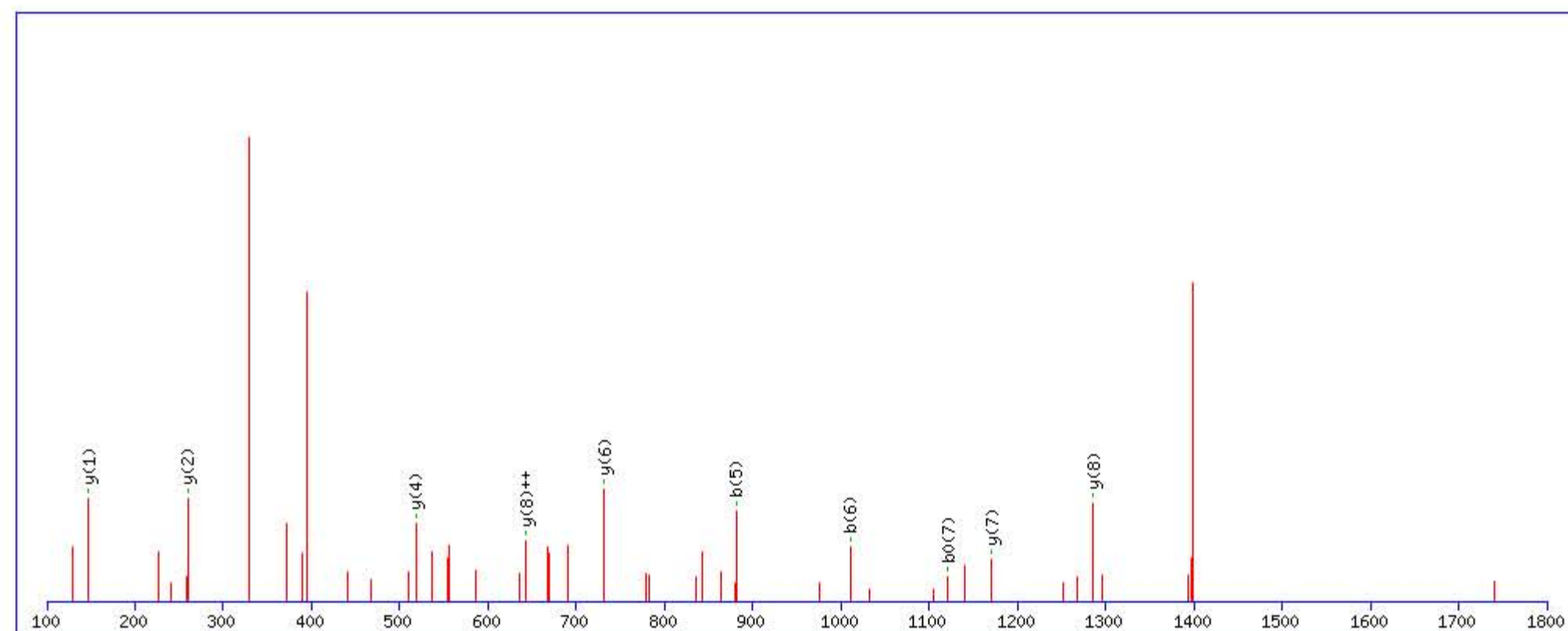
Title: Locus:1.1.1.3052.14 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1397.722427

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

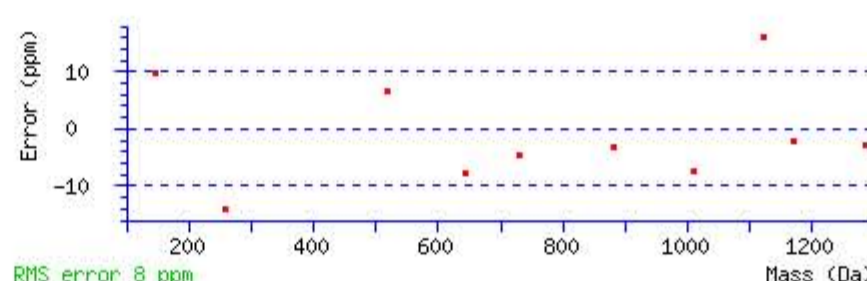
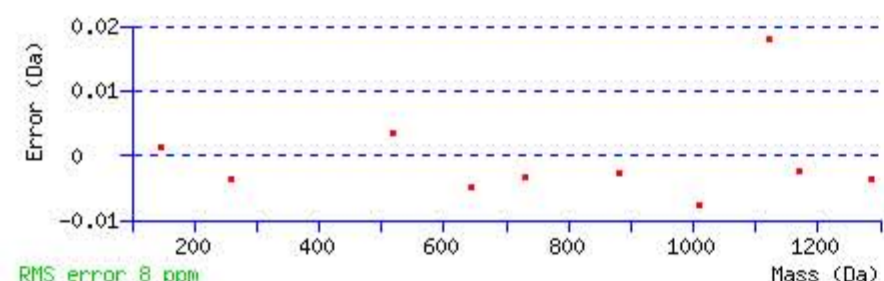
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 45 Expect: 0.00086

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	$M_r(\text{calc})$:	Delta	Sequence
44.5	1397.722427	-0.008059	IDQNVEELK
13.5	1397.704681	0.009687	EQVDPLQMK
8.9	1397.733658	-0.019290	QNITNQLEK
8.8	1397.722427	-0.008059	EQKDTYVMKIK
8.4	1397.722412	-0.008044	EELEQAQIK
7.4	1397.697296	0.017072	LPNTESHQVVMK
4.8	1397.722412	-0.008044	QLEAQLQEK
4.7	1397.712540	0.001828	LMFDAFNQRLK
4.3	1397.719070	-0.004702	EFATSQLSFLQK
3.7	1397.723785	-0.009417	LFVSHMIDKHR

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 31041: 1412.731008 from(707.372780,2+) rtinseconds(1889) index(35570)

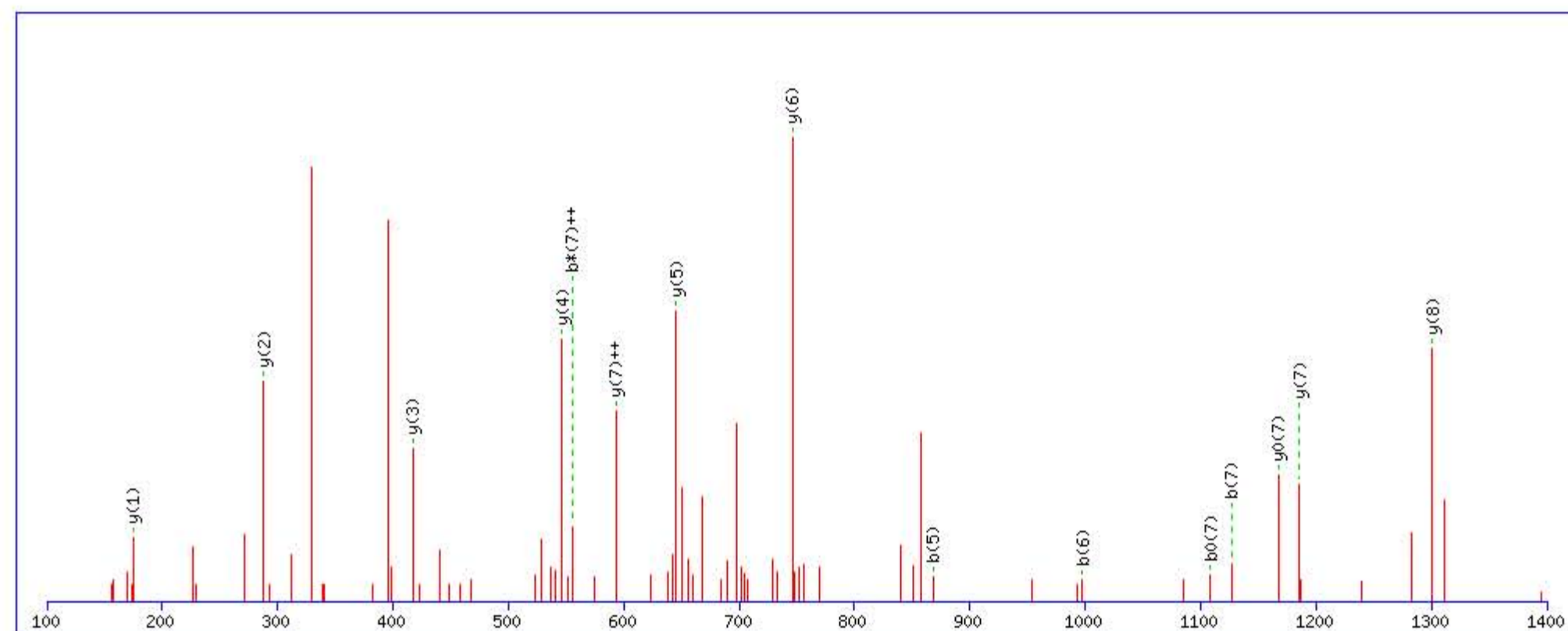
Title: Locus:1.1.1.3077.22 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1412.733337

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

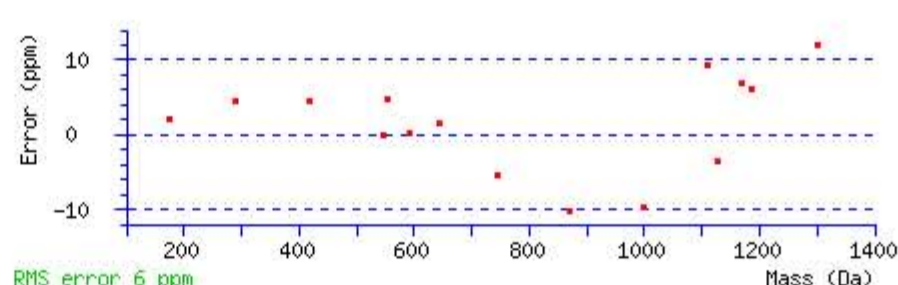
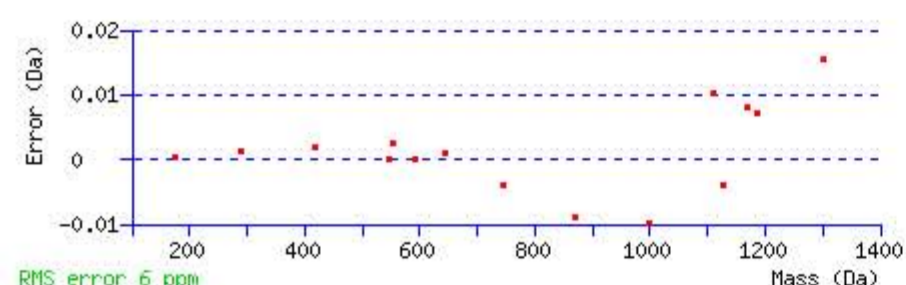
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 4e-005

Matches : 15/86 fragment ions using 25 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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	$M_r(\text{calc})$:	Delta	Sequence
57.4	1412.733337	-0.002329	IDQTVEELR
9.9	1412.744537	-0.013529	IPPEKMLELER
7.2	1412.734665	-0.003657	MPADWRQQLR
6.3	1412.741211	-0.010203	KVTIYSFTGNQR
5.8	1412.737167	-0.006159	ARPEDVISEGRGK
4.9	1412.741196	-0.010188	SSLHYKTPDLR
2.5	1412.730621	0.000387	ARMEHSRELLR
1.9	1412.719421	0.011587	VSTLHCKADNIR
1.9	1412.716034	0.014974	SWRESHLTEIR
1.9	1412.741180	-0.010172	WQQQELIAELR

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 31067: 1414.726348 from(708.370450,2+) rtinseconds(1990) index(68722)

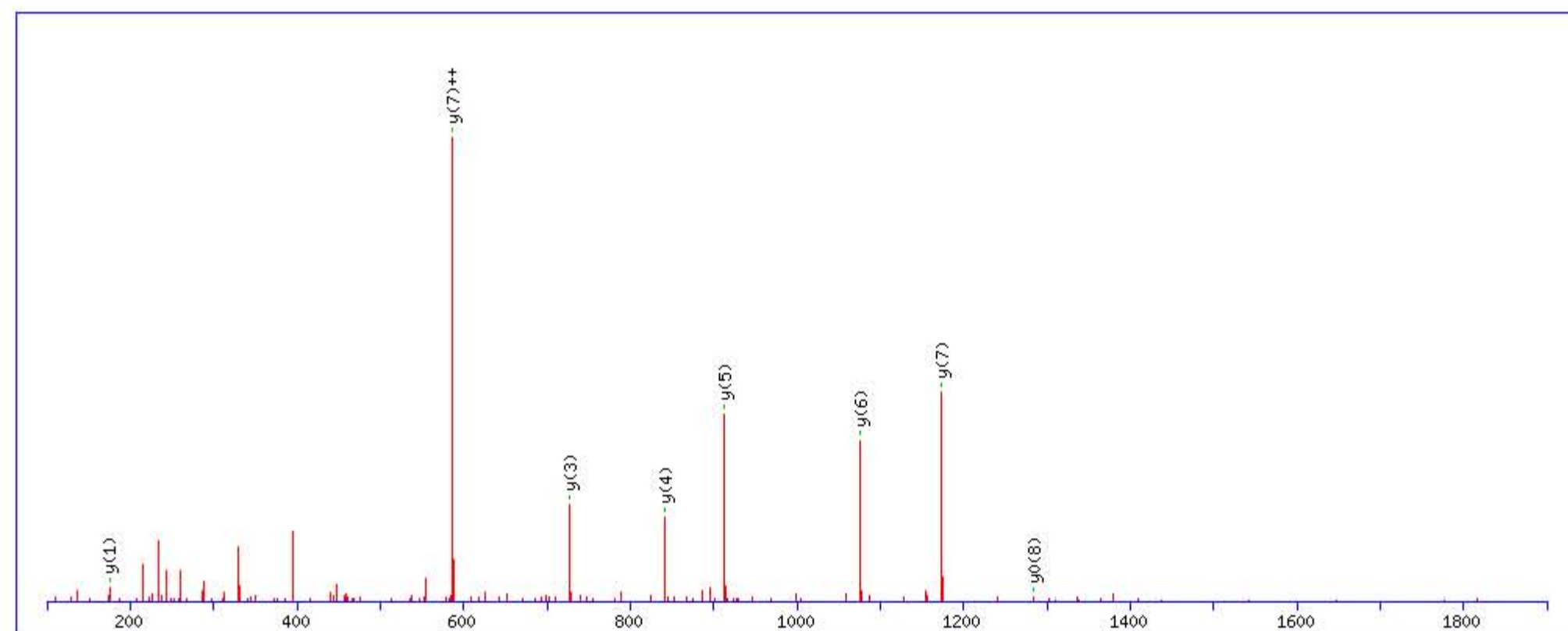
Title: Locus:1.1.1.1630.12 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1414.727844

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

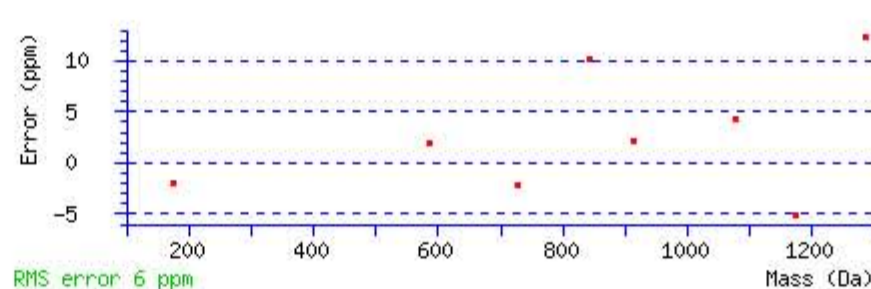
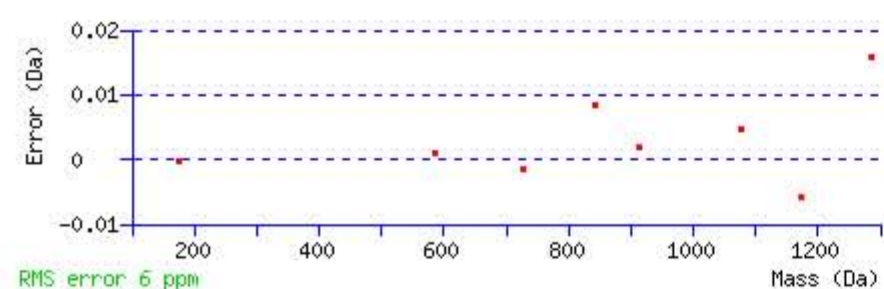
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.001

Matches : 8/76 fragment ions using 14 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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
39.5	1414.727844	-0.001496	LEPYADQLR
7.3	1414.712585	0.013763	EISTEEQLR
6.5	1414.713943	0.012405	KLQCIADQFHR
5.0	1414.735931	-0.009583	LMRGLLHCMIR
1.8	1414.731216	-0.004868	LMELQEAVR
1.5	1414.731689	-0.005341	NKAEFHQSVISR
0.8	1414.735077	-0.008729	SSMSGLHLVKQGR
0.4	1414.741577	-0.015229	ELDVEVSRLEAR
0.3	1414.716400	0.009948	LEEDARLEERR
0.1	1414.717789	0.008559	GKGAAGGSWQQRGR

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 34589: 1525.813928 from(763.914240,2+) rtinseconds(2097) index(6396)

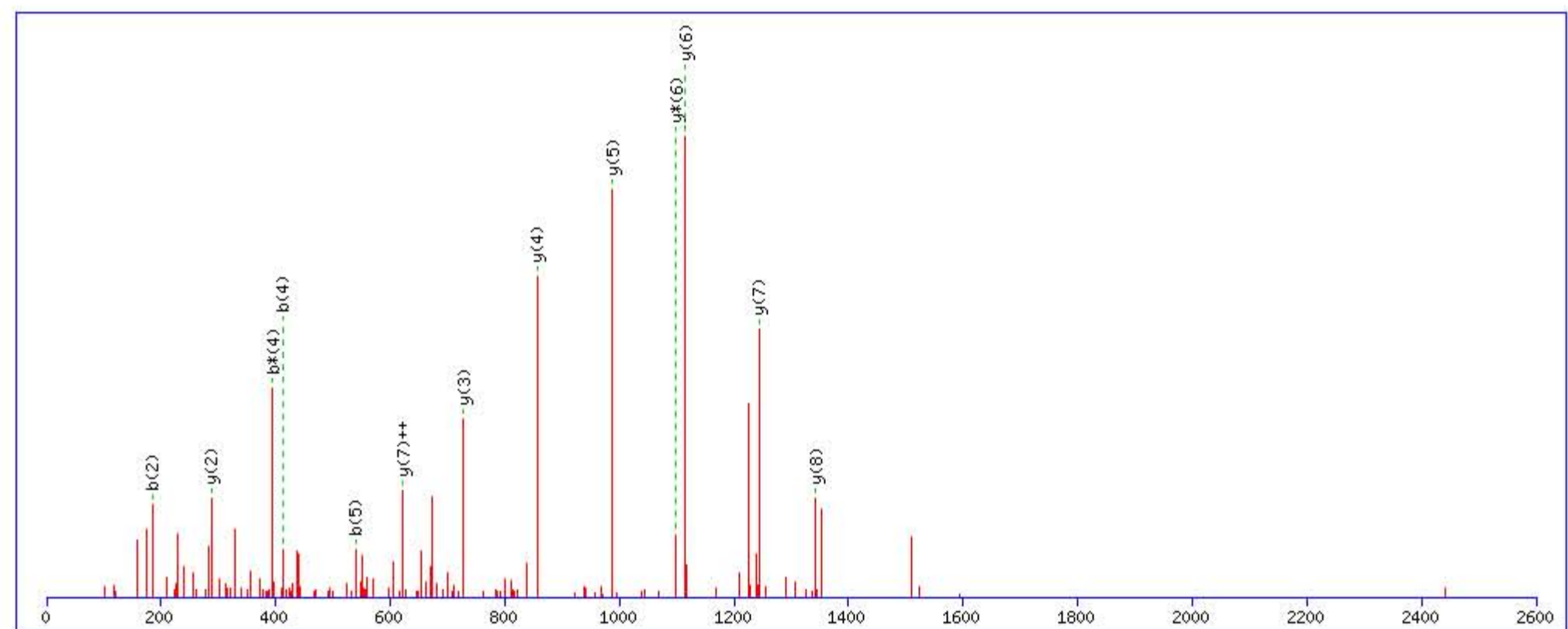
Title: Locus:1.1.1.1539.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1525.810867

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

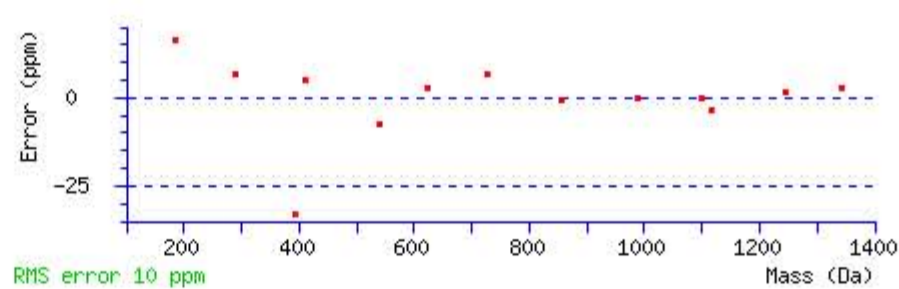
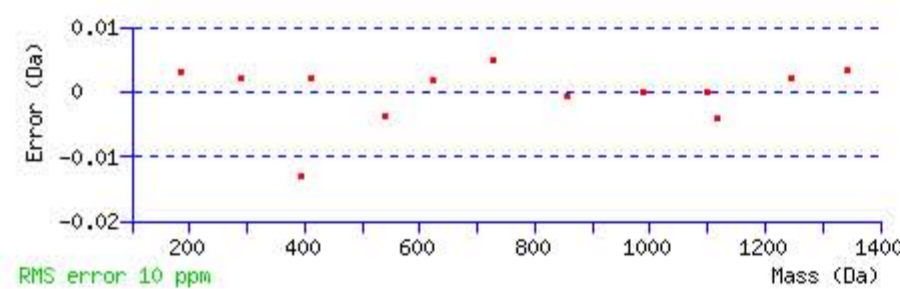
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 71 Expect: 2.1e-006

Matches : 13/84 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							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
71.4	1525.810867	0.003061	ALVQQMEQLR
23.1	1525.810867	0.003061	ALVQQMEQLR
16.7	1525.798752	0.015176	SPVKEEEEKPOEVK
14.9	1525.792236	0.021692	ALTEQQEQLR
10.3	1525.800064	0.013864	ARALQSYEAKAR
9.9	1525.810867	0.003061	ALVQQMEQLR
7.7	1525.803467	0.010461	SPPSPRSSMAAVALR
5.5	1525.803482	0.010446	VNTFAGSSQKAR
5.2	1525.807495	0.006433	WPPQQLMLSAALR
4.9	1525.814682	-0.000754	LARASEQERR

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 35002: 1545.829928 from(773.922240,2+) rtinseconds(1531) index(66052)

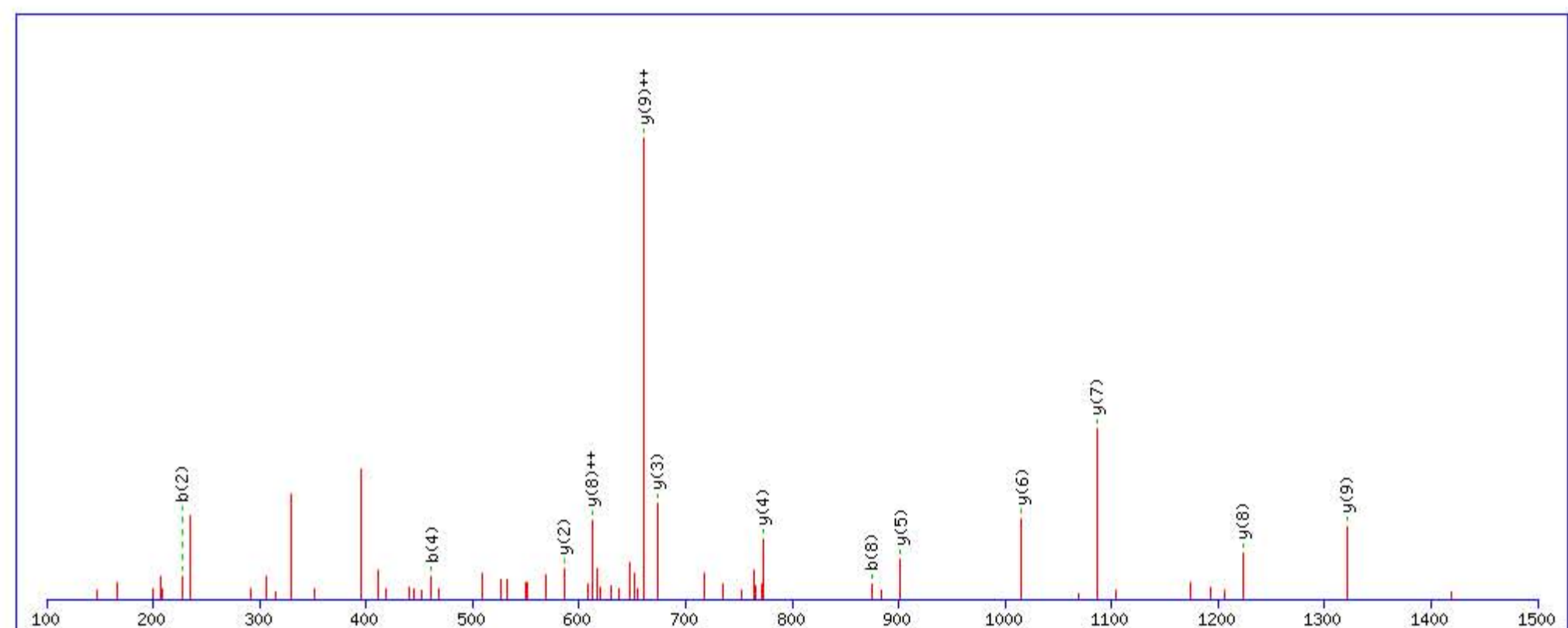
Title: Locus:1.1.1.1470.18 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1545.833710

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

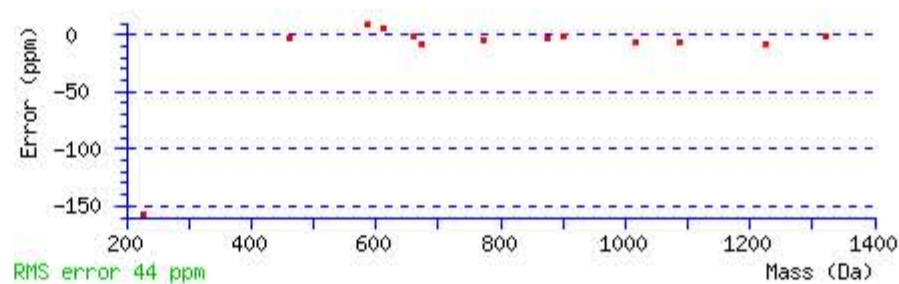
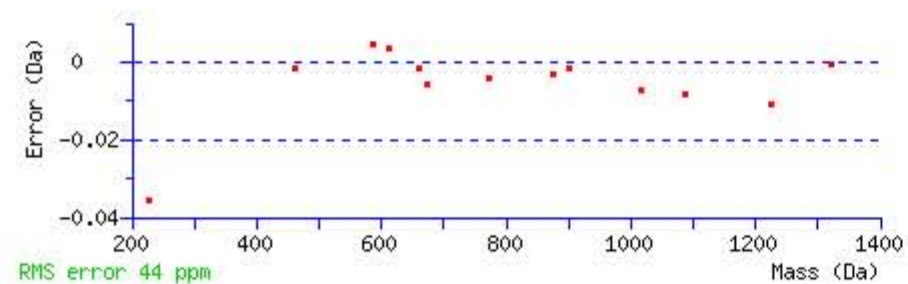
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 56 Expect: 9.2e-006

Matches : 13/94 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							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
55.6	1545.833710	-0.003782	LLPHANEVSQK
1.8	1545.837738	-0.007810	LIPGQEYIFR
0.9	1545.832352	-0.002424	LLSEVMEELEKVK

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 37125: 1597.818132 from(533.613320,3+) rtinseconds(1582) index(66370)

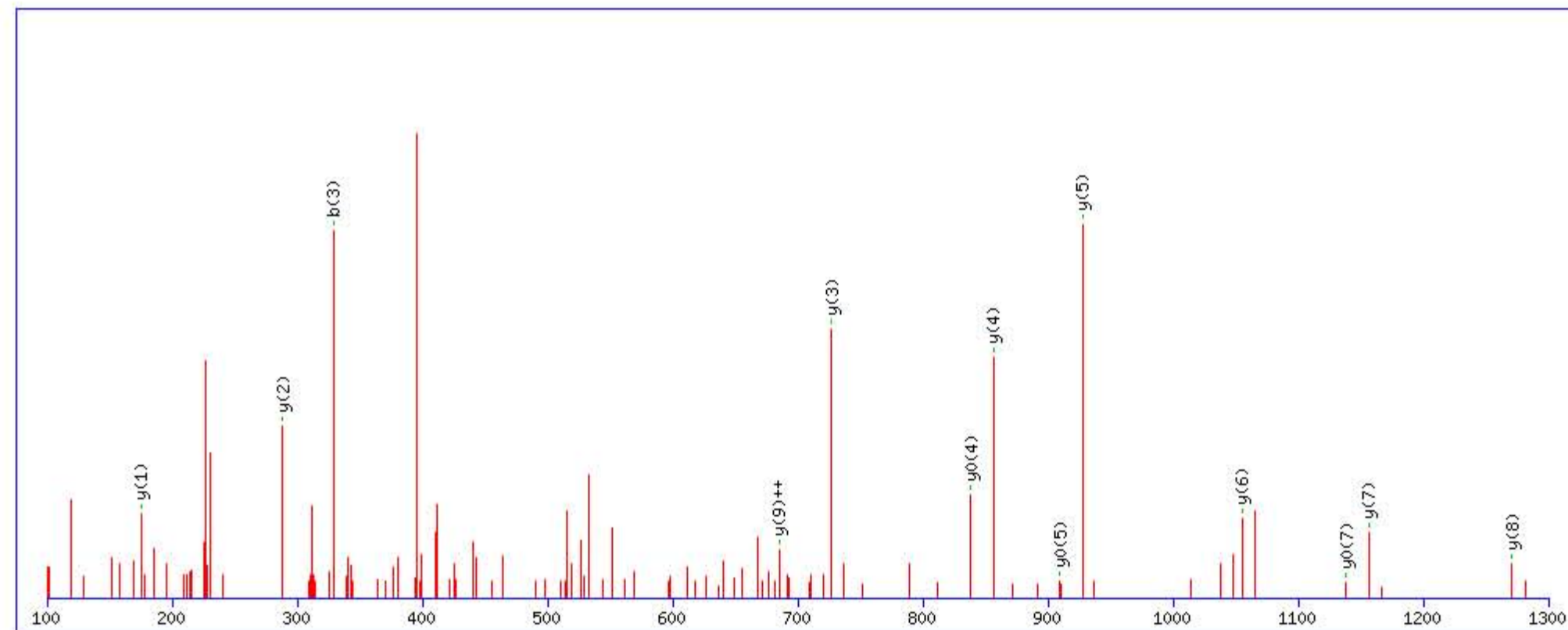
Title: Locus:1.1.1.1488.10 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1597.824615

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

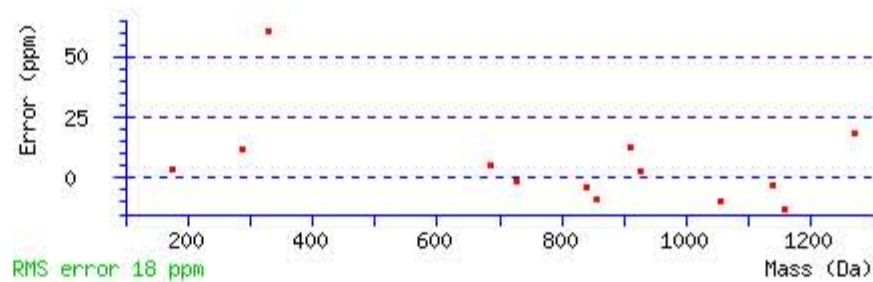
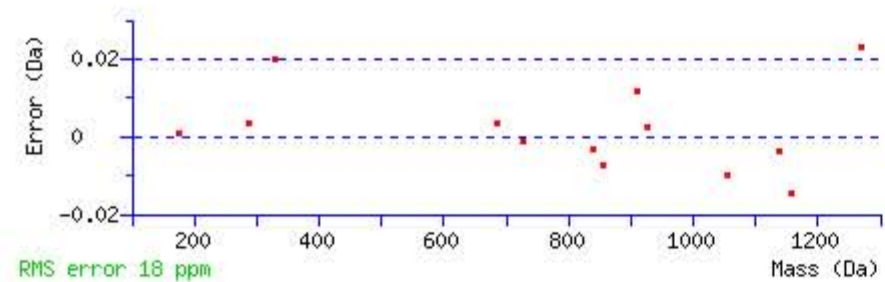
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 44 Expect: 0.00015

Matches : 13/112 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							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
43.6	1597.824615	-0.006483	TQVNTQAEQLR
9.0	1597.824615	-0.006483	TQVNTQAEQLR
2.8	1597.828400	-0.010268	RALQEEERAAAQAR
2.5	1597.835846	-0.017714	TKAAATAGGQGAAR
0.6	1597.828629	-0.010497	AWDILSGEQLR

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

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 39610: 1660.812208 from(831.413380,2+) rtinseconds(1720) index(4209)

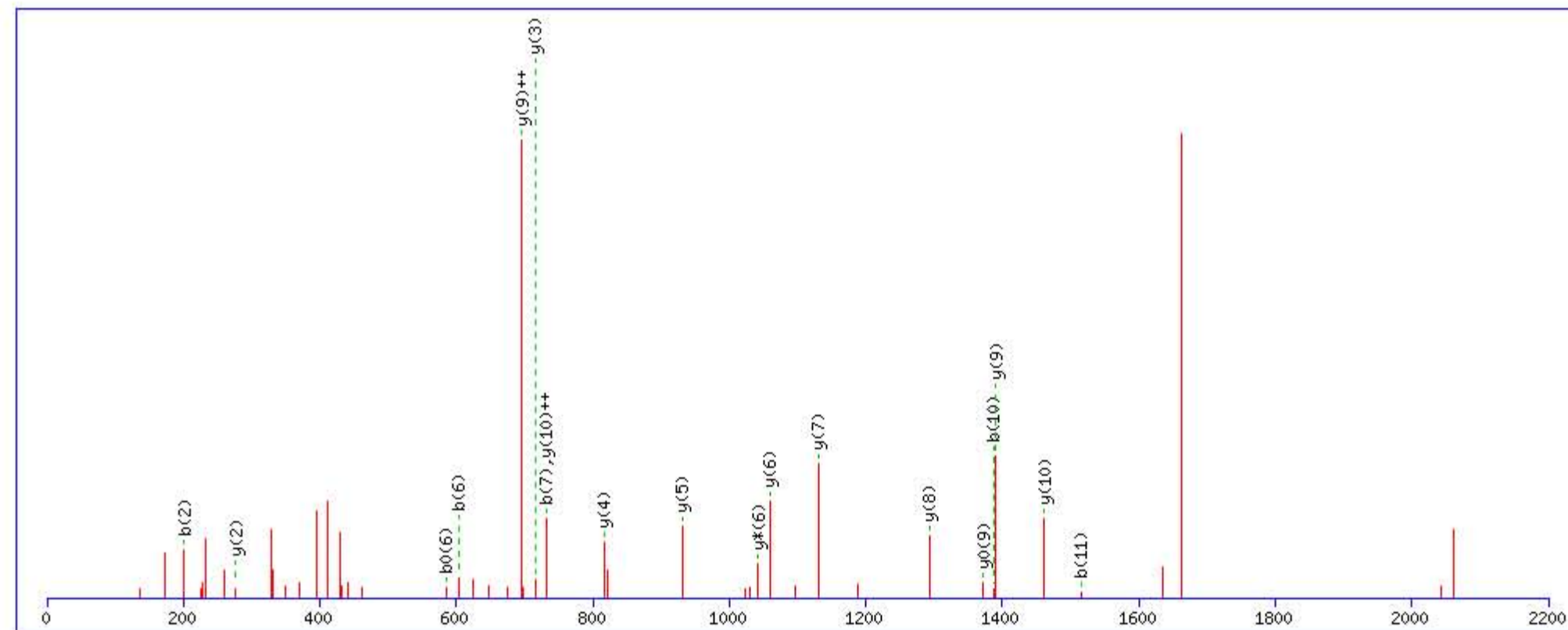
Title: Locus:1.1.1.1408.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1660.813034

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

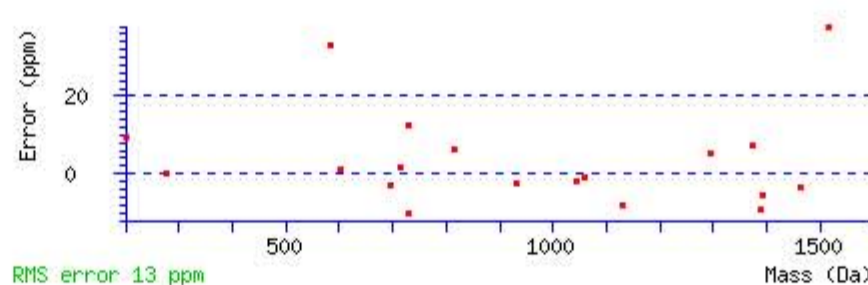
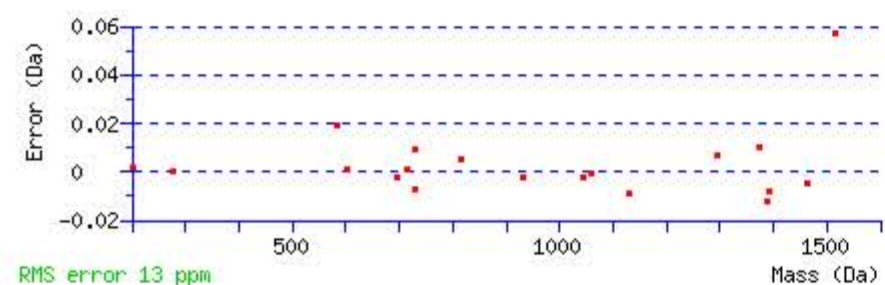
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 52 Expect: 6.7e-005

Matches : 19/118 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	88.039304	44.523290			70.028739	35.518008	S							12
2	201.123368	101.065322			183.112803	92.060039	L	1574.788308	787.897792	1557.761759	779.384518	1556.777743	778.892510	11
3	272.160482	136.583879			254.149917	127.578596	A	1461.704244	731.355760	1444.677695	722.842486	1443.693679	722.350478	10
4	369.213246	185.110261			351.202681	176.104978	P	1390.667130	695.837203	1373.640581	687.323929	1372.656565	686.831921	9
5	532.276575	266.641926			514.266010	257.636643	Y	1293.614366	647.310821	1276.587817	638.797547	1275.603801	638.305539	8
6	603.313689	302.160483			585.303124	293.155200	A	1130.551037	565.779157	1113.524488	557.265882	1112.540472	556.773874	7
7	731.372267	366.189772	714.345718	357.676497	713.361702	357.184489	Q	1059.513923	530.260600	1042.487374	521.747325	1041.503358	521.255317	6
8	846.399210	423.703243	829.372661	415.189969	828.388645	414.697961	D	931.455345	466.231311	914.428796	457.718036	913.444780	457.226028	5
9	947.446889	474.227083	930.420340	465.713808	929.436324	465.221800	T	816.428402	408.717839	799.401853	400.204565	798.417837	399.712557	4
10	1386.672215	693.839746	1369.645666	685.326471	1368.661650	684.834463	Q	715.380723	358.194000	698.354174	349.680725	697.370158	349.188717	3
11	1515.714808	758.361042	1498.688259	749.847768	1497.704243	749.355760	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
12							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **SLAPYAQDTQEK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.3	1660.813034	-0.000826	SLAPYAQDTQEK
28.1	1660.813034	-0.000826	SLAPYAQDTQEK
7.4	1660.820908	-0.008700	SLARAGFYITGVNDK
2.1	1660.826782	-0.014574	EAATQAQQTLGSTIDK

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

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGEVNTYAGDLQK**

Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

Match to Query 40840: 1717.866492 from(573.629440,3+) rtinseconds(1999) index(68793)

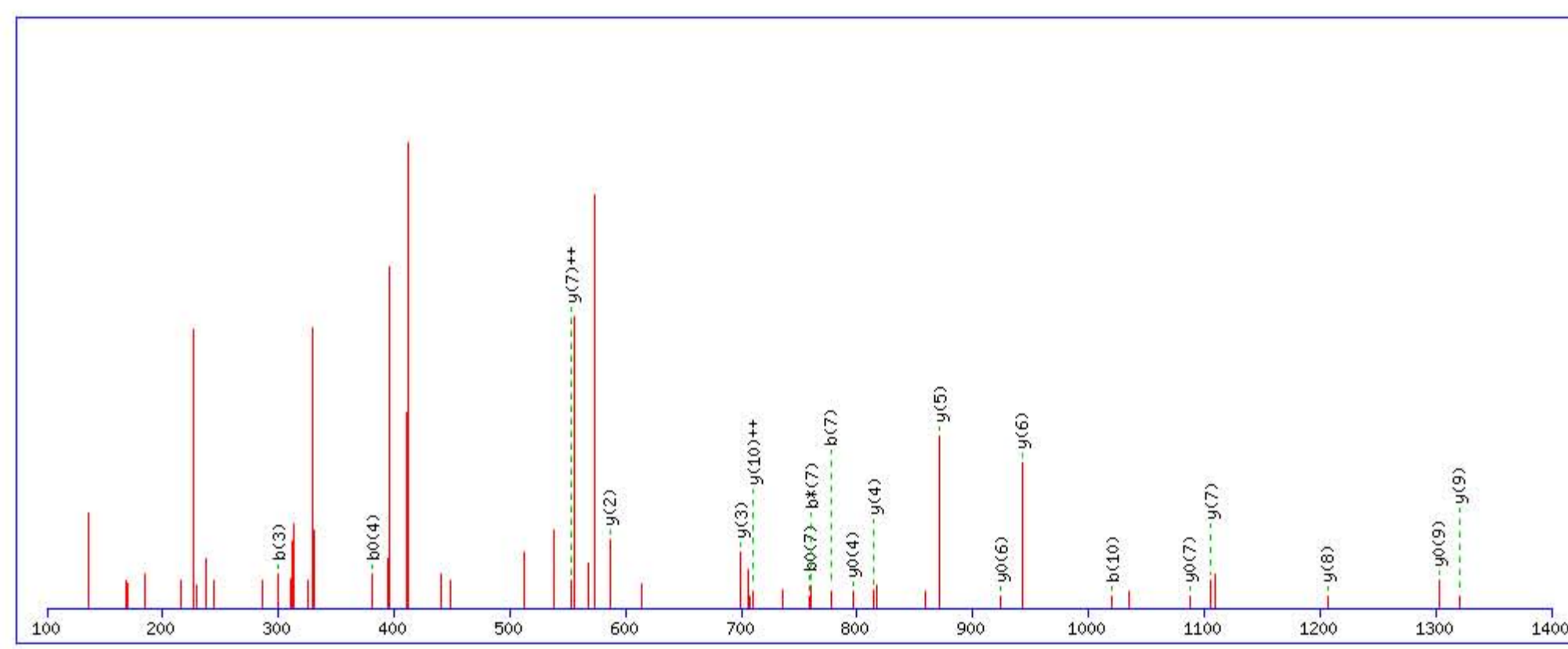
Title: Locus:1.1.1.1633.20 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1717.870895

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

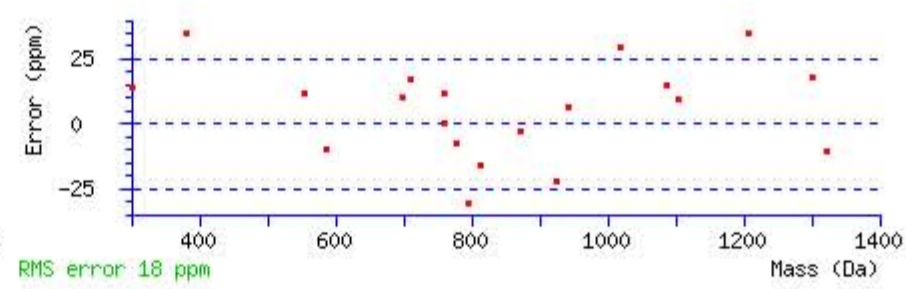
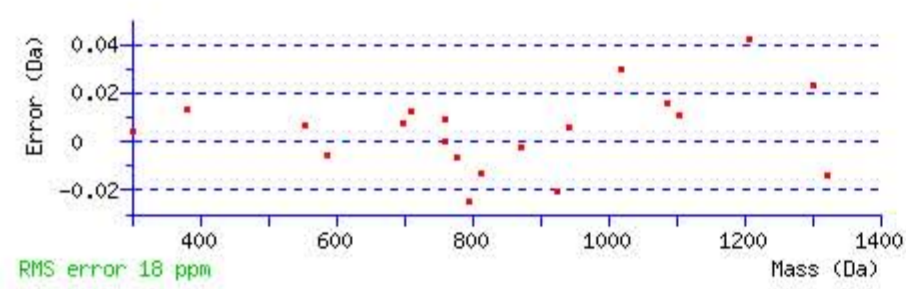
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.041

Matches : 20/126 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							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
28.0	1717.870895	-0.004403	LGEVNTYAGDLQK

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALVQQMEQLR**

Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

Match to Query 43403: 1836.982512 from(613.334780,3+) rtinseconds(2342) index(70733)

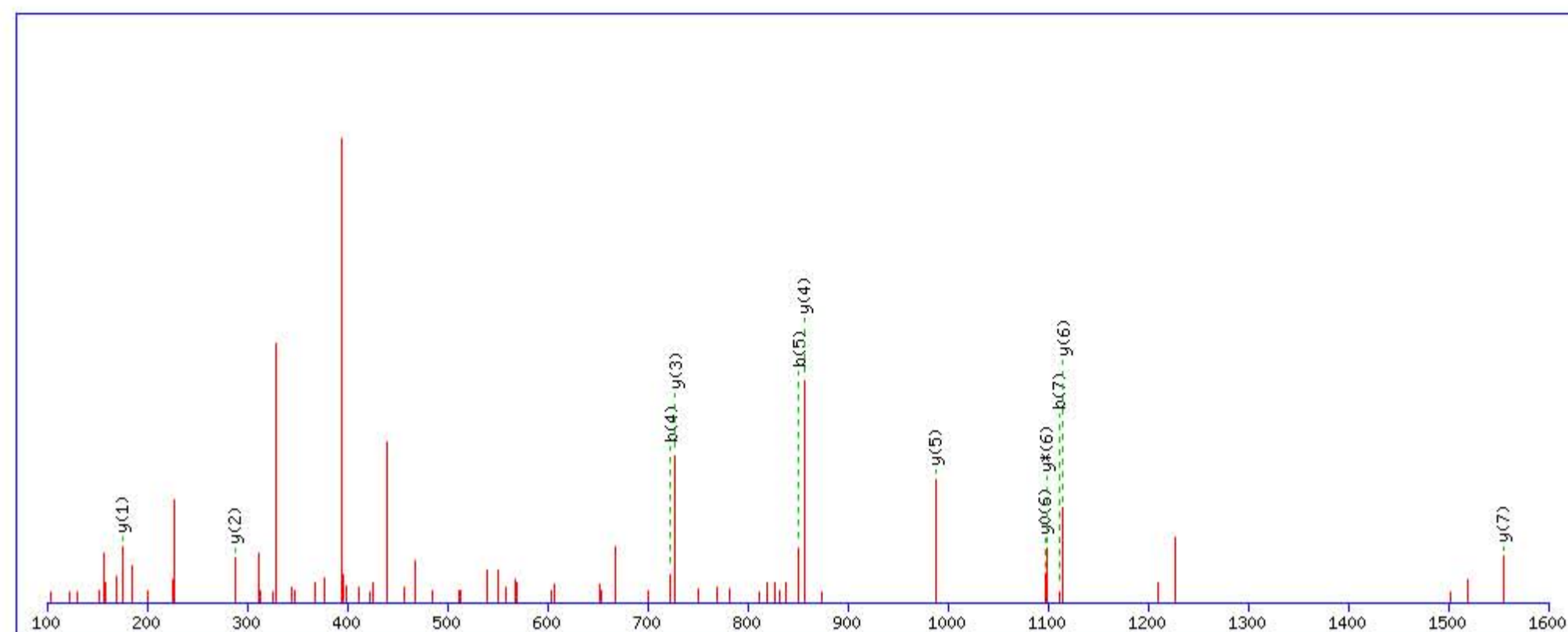
Title: Locus:1.1.1.1753.6 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1836.977615

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

Variable modifications:

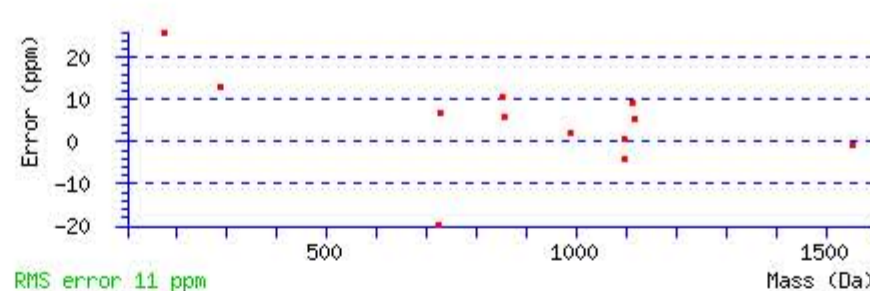
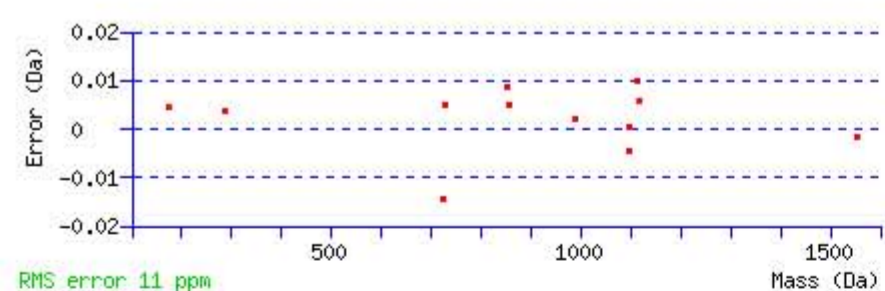
Q4 : Biotin:Thermo-21345 (Q)

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 31 Expect: 0.0042

Matches : 12/84 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							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
31.3	1836.977615	0.004897	ALVQQMEQLR
20.2	1836.977615	0.004897	ALVQQMEQLR
5.8	1836.999207	-0.016695	QQLRQLEQLR
5.5	1837.004578	-0.022066	RHSWRQQIFLR
2.3	1836.969360	0.013152	EPSAAGGLETTLVSPR

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

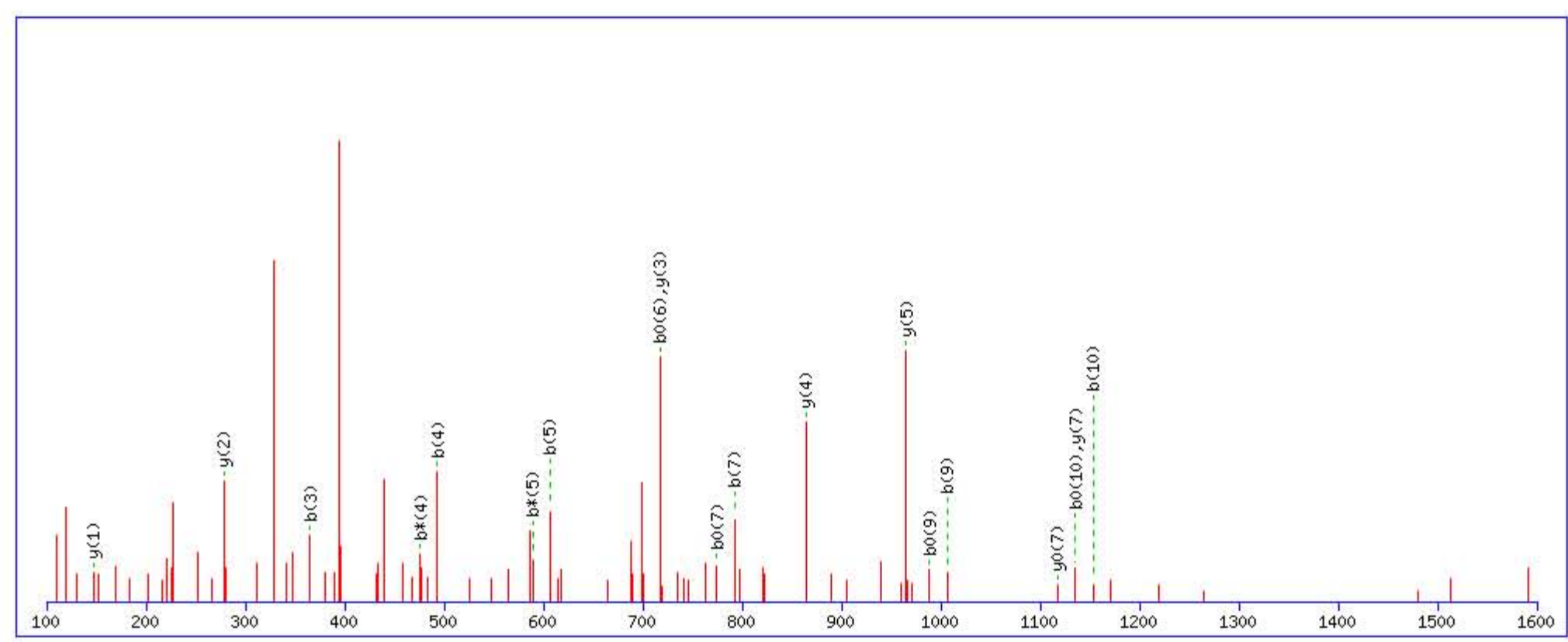
MASCOT SEARCH RESULTS

Peptide View

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

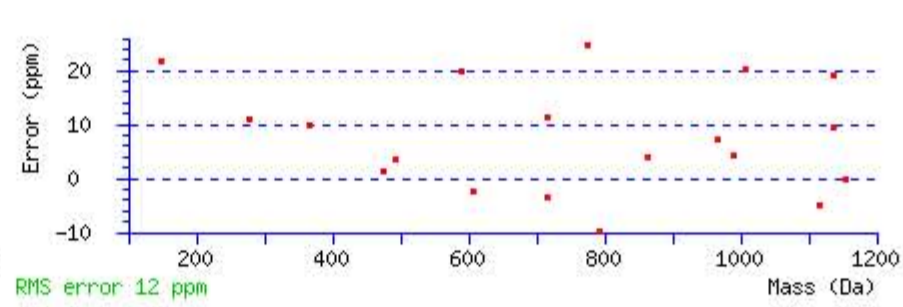
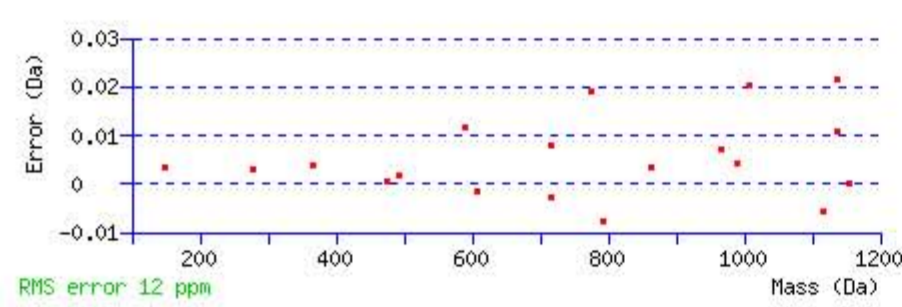
Match to Query 44101: 1868.962812 from(623.994880,3+) rtinseconds(2153) index(69686)
 Title: Locus:1.1.1.1687.14 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 1868.964081
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q11 : Biotin:Thermo-21345 (Q)
 Ions Score: 27 Expect: 0.057
 Matches : 19/124 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	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
26.8	1868.964081	-0.001269	LNHQLEGLTFQMK

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQVNTQAEQLR**

Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

Match to Query 44739: 1908.989982 from(637.337270,3+) rtinseconds(1935) index(68265)

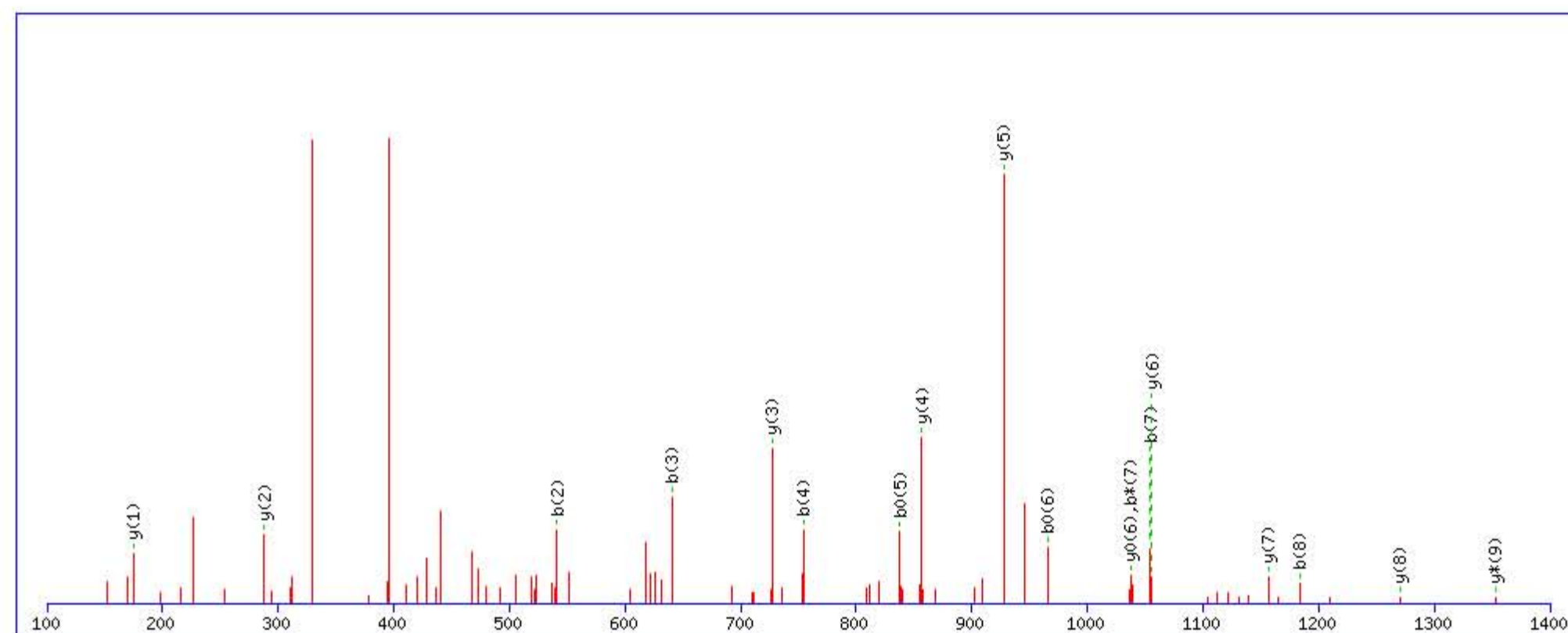
Title: Locus:1.1.1.1611.21 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1908.991364

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

Variable modifications:

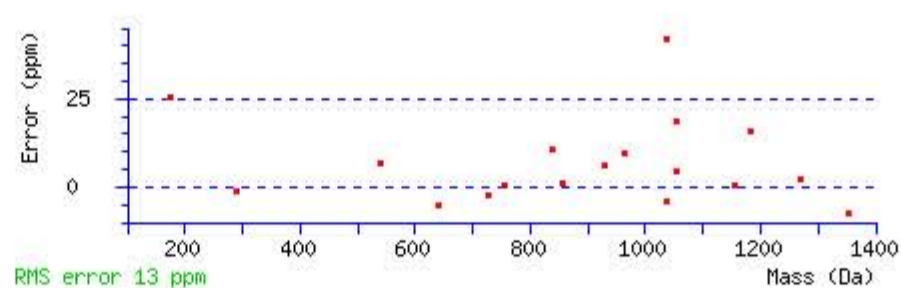
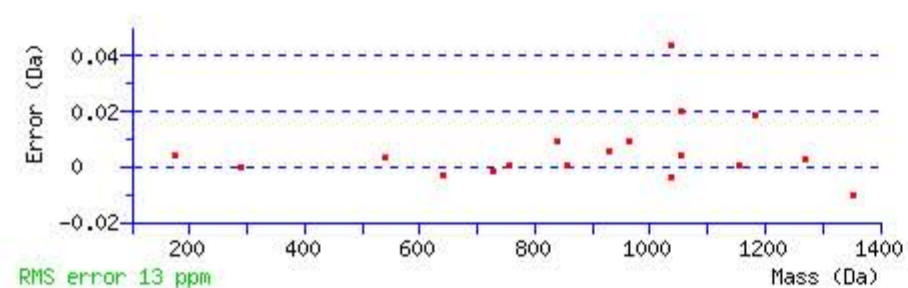
Q2 : Biotin:Thermo-21345 (Q)

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 54 Expect: 1.4e-005

Matches : 18/112 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							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
53.9	1908.991364	-0.001382	TQVNTQAEQLR
16.6	1908.991364	-0.001382	TQVNTQAEQLR
13.4	1908.991364	-0.001382	TQVNTQAEQLR
2.0	1909.015610	-0.025628	SSIALTAPDAAADPKEKPK
0.9	1908.974045	0.015937	SAQWAINRVAMEIQHR

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

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 45445: 1944.999408 from(973.506980,2+) rtinseconds(2880) index(74176)

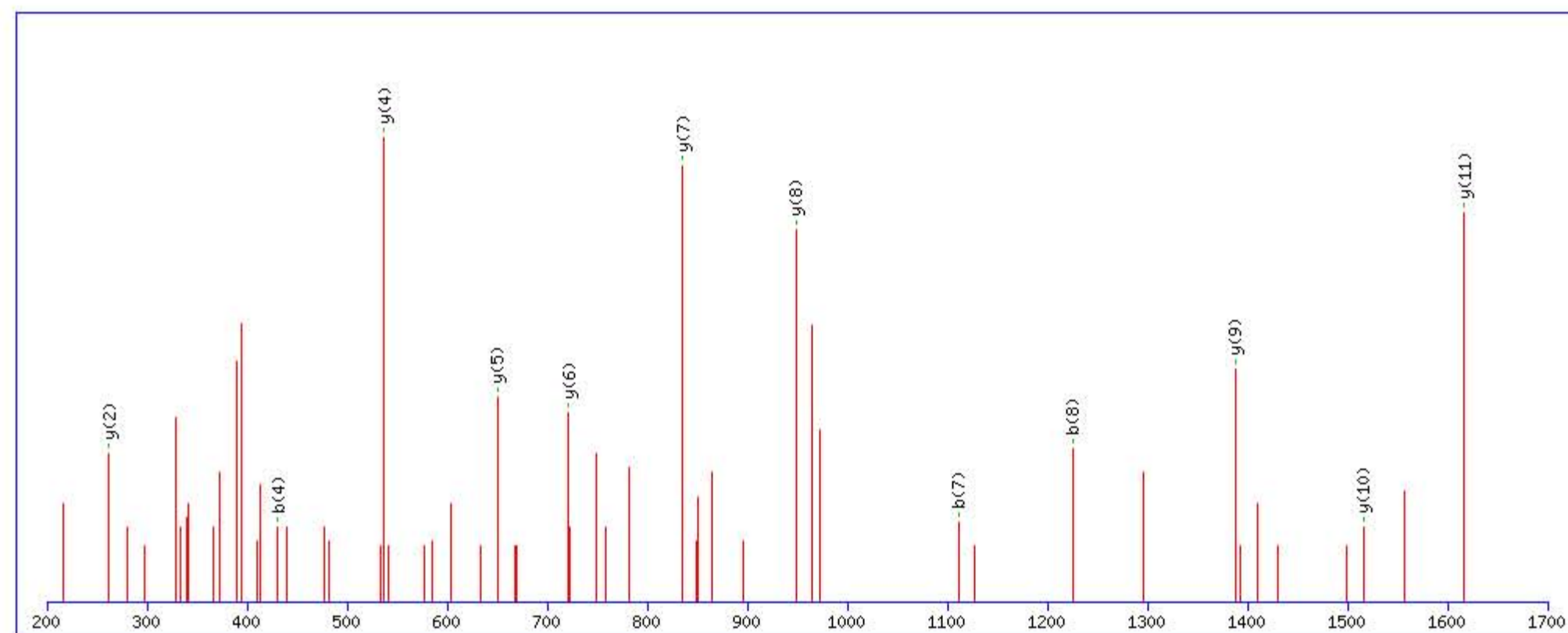
Title: Locus:1.1.1.1938.19 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1944.997879

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

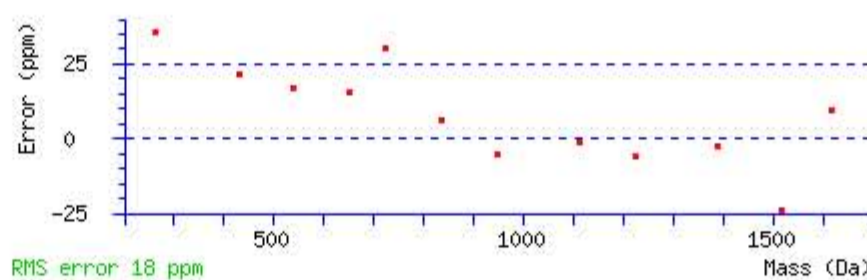
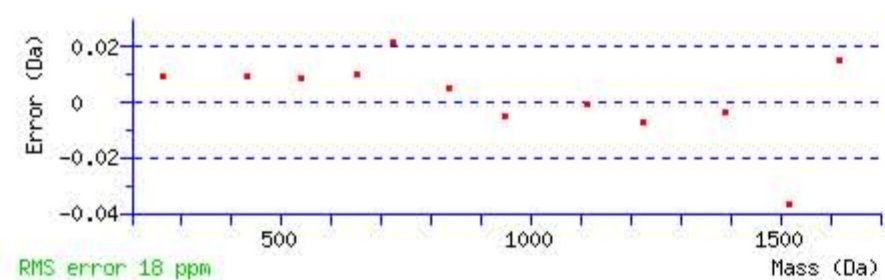
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 79 Expect: 1.3e-007

Matches : 12/146 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							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
79.3	1944.997879	0.001529	SELTQQLNALFQDK
64.2	1944.997879	0.001529	SELTQQLNALFQDK
8.2	1944.997879	0.001529	SELTQQLNALFQDK
5.4	1945.005280	-0.005872	QPPSDAALTMLSFIK
2.1	1945.024384	-0.024976	QASLWVQGDIKFRSK
1.5	1945.024384	-0.024976	QASLWVQGDIKFRSK
0.3	1945.027740	-0.028332	GGFGSMLRALGAQIEK

MASCOT Search Results

Peptide View

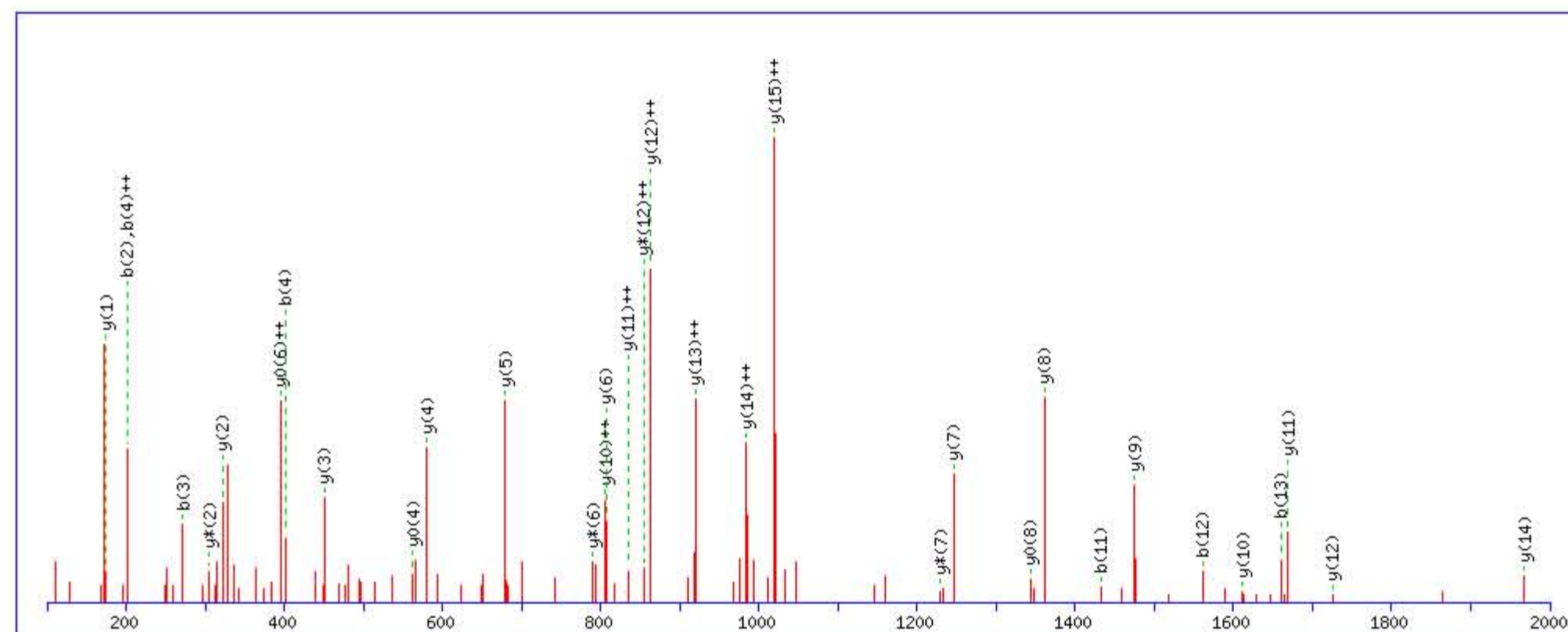
MS/MS Fragmentation of **SLAELGGHLDQQVEEFR**
 Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

Match to Query 51791: 2238.110412 from(747.044080,3+) rtinseconds(2262) index(70361)
 Title: Locus:1.1.1.1725.9 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

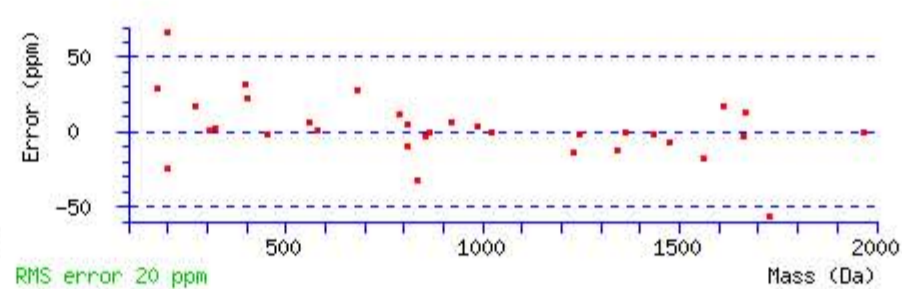
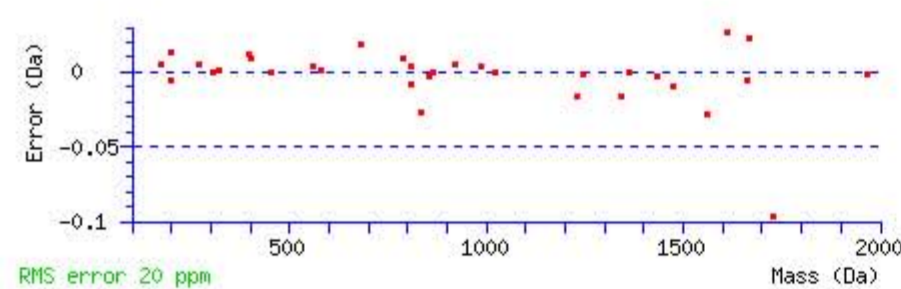
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2238.110291
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q11 : Biotin:Thermo-21345 (Q)
 Ions Score: 74 Expect: 1.1e-006
 Matches : 33/168 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	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
73.8	2238.110291	0.000121	SLAELGGHLDQQVEEFR
69.0	2238.110291	0.000121	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 53077: 2304.154176 from(577.045820,4+) rtinseconds(1900) index(67967)

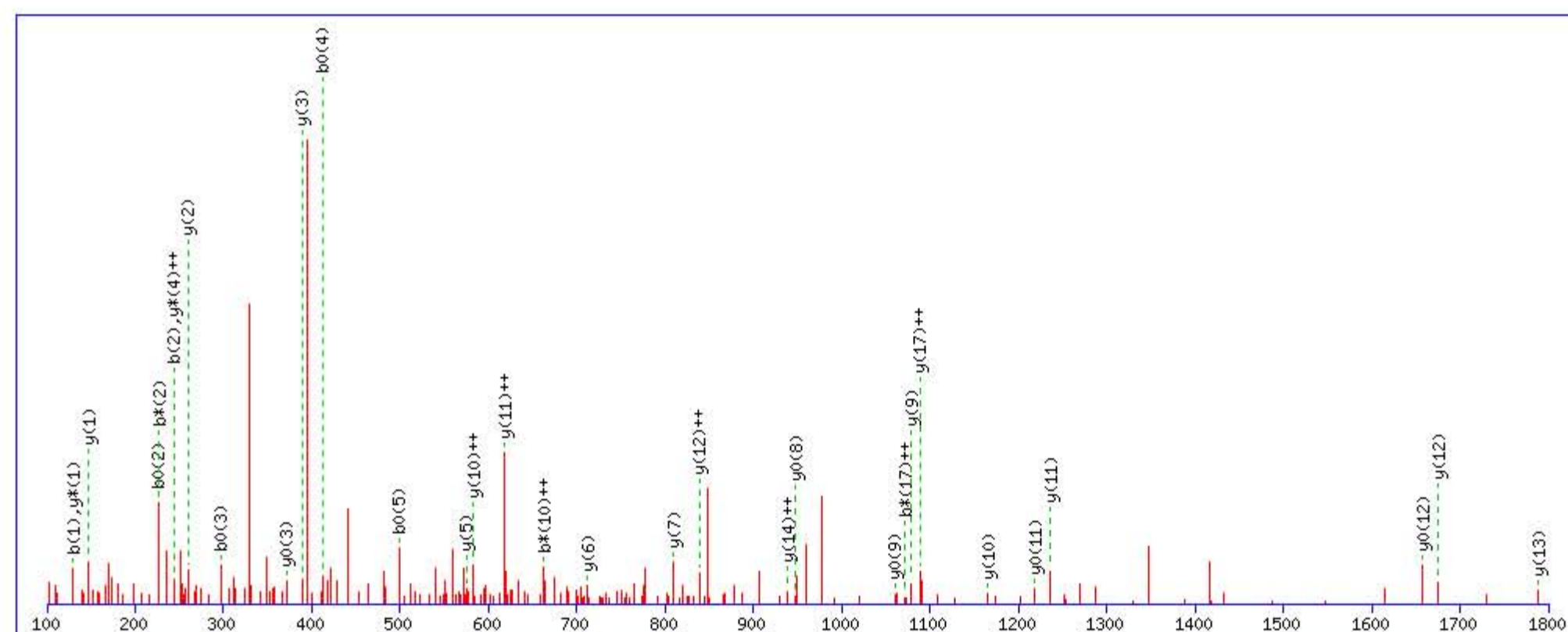
Title: Locus:1.1.1.1599.13 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2304.153183

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

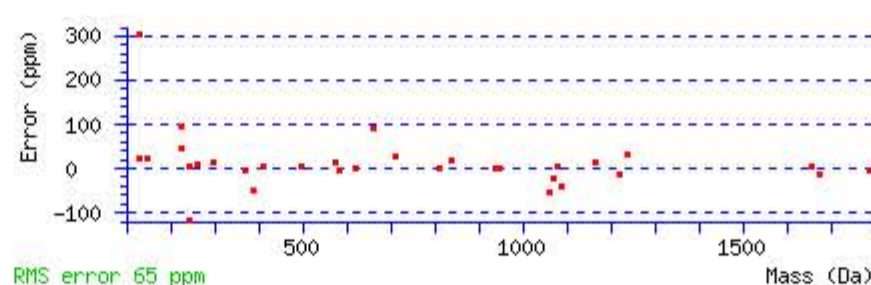
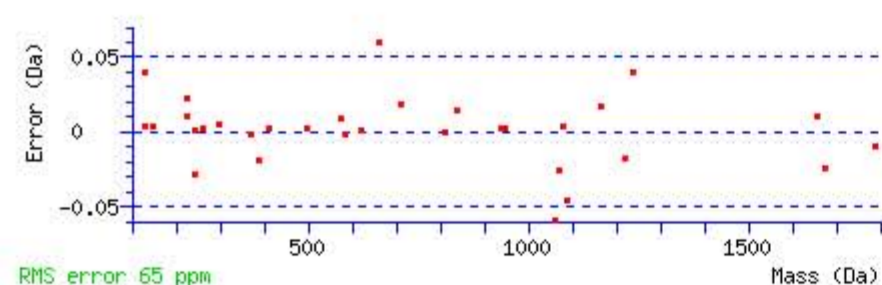
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.0065

Matches : 32/198 fragment ions using 104 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							18
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	N	2176.117913	1088.562594	2159.091364	1080.049320	2158.107348	1079.557312	17
3	315.129910	158.068593	298.103361	149.555319	297.119345	149.063311	A	2062.074986	1031.541131	2045.048437	1023.027856	2044.064421	1022.535848	16
4	430.156853	215.582065	413.130304	207.068790	412.146288	206.576782	D	1991.037872	996.022574	1974.011323	987.509300	1973.027307	987.017292	15
5	517.188881	259.098079	500.162332	250.584804	499.178316	250.092796	S	1876.010929	938.509103	1858.984380	929.995828	1858.000364	929.503820	14
6	630.272945	315.640111	613.246396	307.126836	612.262380	306.634828	L	1788.978901	894.993089	1771.952352	886.479814	1770.968336	885.987806	13
7	1069.498271	535.252774	1052.471722	526.739499	1051.487706	526.247491	Q	1675.894837	838.451057	1658.868288	829.937782	1657.884272	829.445774	12
8	1140.535385	570.771331	1123.508836	562.258056	1122.524820	561.766048	A	1236.669511	618.838394	1219.642962	610.325119	1218.658946	609.833111	11
9	1227.567413	614.287345	1210.540864	605.774070	1209.556848	605.282062	S	1165.632397	583.319837	1148.605848	574.806562	1147.621832	574.314554	10
10	1340.651477	670.829377	1323.624928	662.316102	1322.640912	661.824094	L	1078.600369	539.803823	1061.573820	531.290548	1060.589804	530.798540	9
11	1496.752588	748.879932	1479.726039	740.366658	1478.742023	739.874650	R	965.516305	483.261791	948.489756	474.748516	947.505740	474.256508	8
12	1593.805352	797.406314	1576.778803	788.893040	1575.794787	788.401032	P	809.415194	405.211235	792.388645	396.697961	791.404629	396.205953	7
13	1730.864264	865.935770	1713.837715	857.422496	1712.853699	856.930488	H	712.362430	356.684853	695.335881	348.171579	694.351865	347.679571	6
14	1801.901378	901.454327	1784.874829	892.941053	1783.890813	892.449045	A	575.303518	288.155397	558.276969	279.642123	557.292953	279.150115	5
15	1916.928321	958.967799	1899.901772	950.454524	1898.917756	949.962516	D	504.266404	252.636840	487.239855	244.123566	486.255839	243.631558	4
16	2045.970914	1023.489095	2028.944365	1014.975821	2027.960349	1014.483813	E	389.239461	195.123369	372.212912	186.610094	371.228896	186.118086	3
17	2159.054978	1080.031127	2142.028429	1071.517852	2141.044413	1071.025844	L	260.196868	130.602072	243.170319	122.088798			2
18							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **ENADSLQASLRPHADELK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.7	2304.153183	0.000993	ENADSLQASLRPHADELK
2.3	2304.149384	0.004792	LNCMETFEVKVDSPVKPAPK
0.8	2304.124191	0.029985	TAAMLSSAESFSKHAHEIMLK

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **STAAMSTYTGIFTDQVLSVLK**

Found in **APOC2_HUMAN**, Apolipoprotein C-II OS=Homo sapiens GN=APOC2 PE=1 SV=1

Match to Query 57186: 2543.312562 from(848.778130,3+) rtinseconds(3224) index(44528)

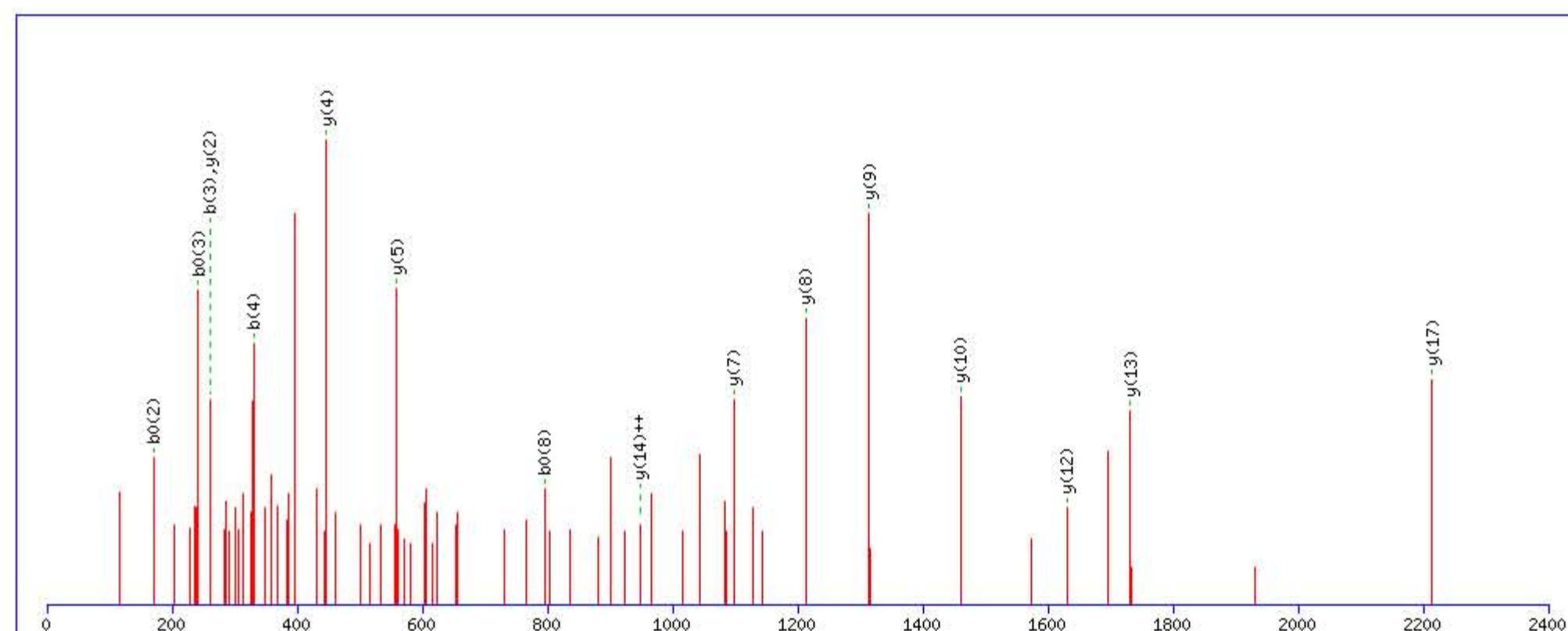
Title: Locus:1.1.1.3537.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2543.301544

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

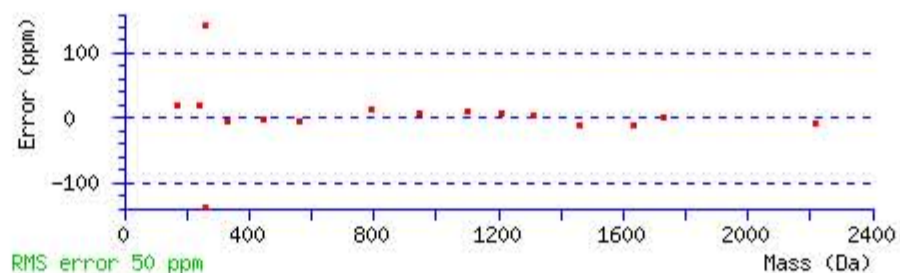
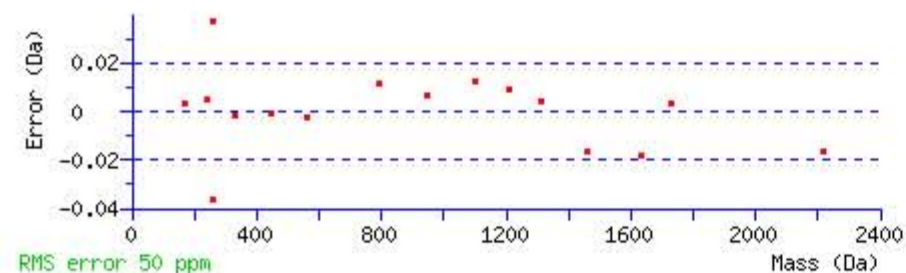
Variable modifications:

Q15 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 0.00069

Matches : 16/206 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							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
46.1	2543.301544	0.011018	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 47816: 2027.010522 from(676.677450,3+) rtinseconds(1944) index(36032)

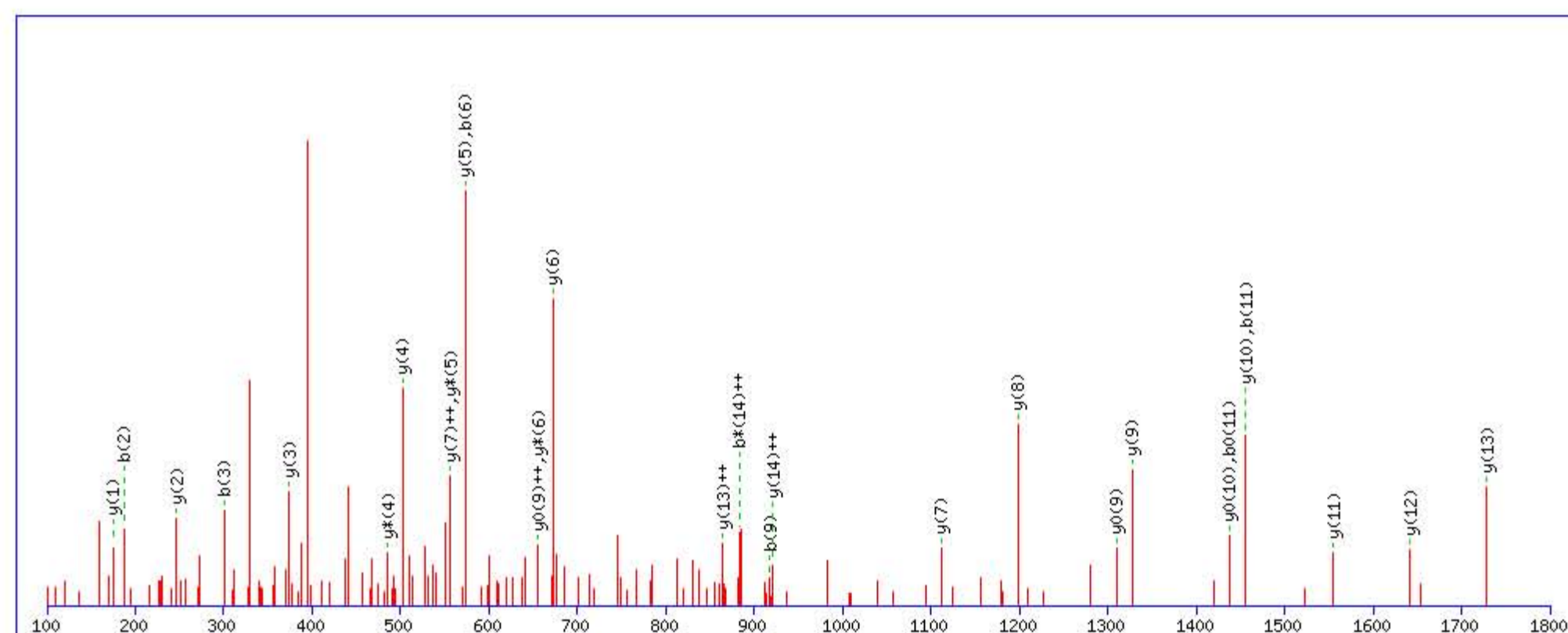
Title: Locus:1.1.1.3096.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2027.010574

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

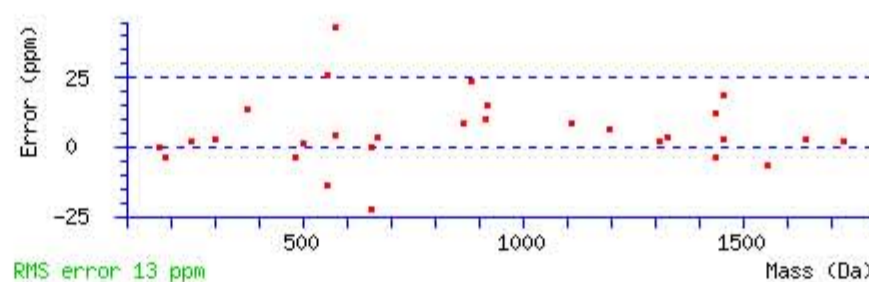
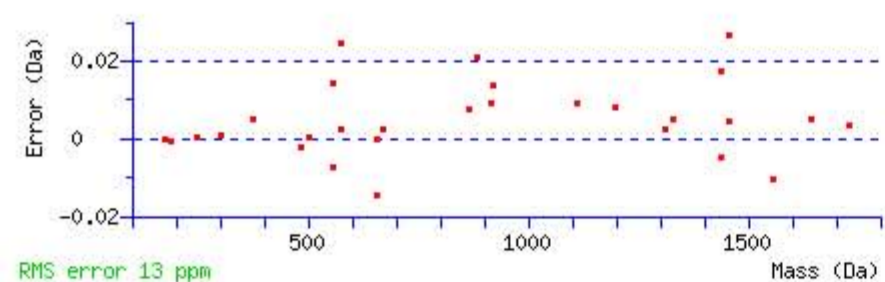
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 81 Expect: 2.7e-008

Matches : 29/154 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	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
81.4	2027.010574	-0.000052	DALSSVQESQVAQQAR
74.7	2027.010574	-0.000052	DALSSVQESQVAQQAR
68.6	2027.010574	-0.000052	DALSSVQESQVAQQAR
43.5	2027.010574	-0.000052	DALSSVQESQVAQQAR
0.6	2027.027161	-0.016639	IHSGKKPYQCGKAFNHR

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 47817: 2027.010522 from(676.677450,3+) rtinseconds(1927) index(35894)

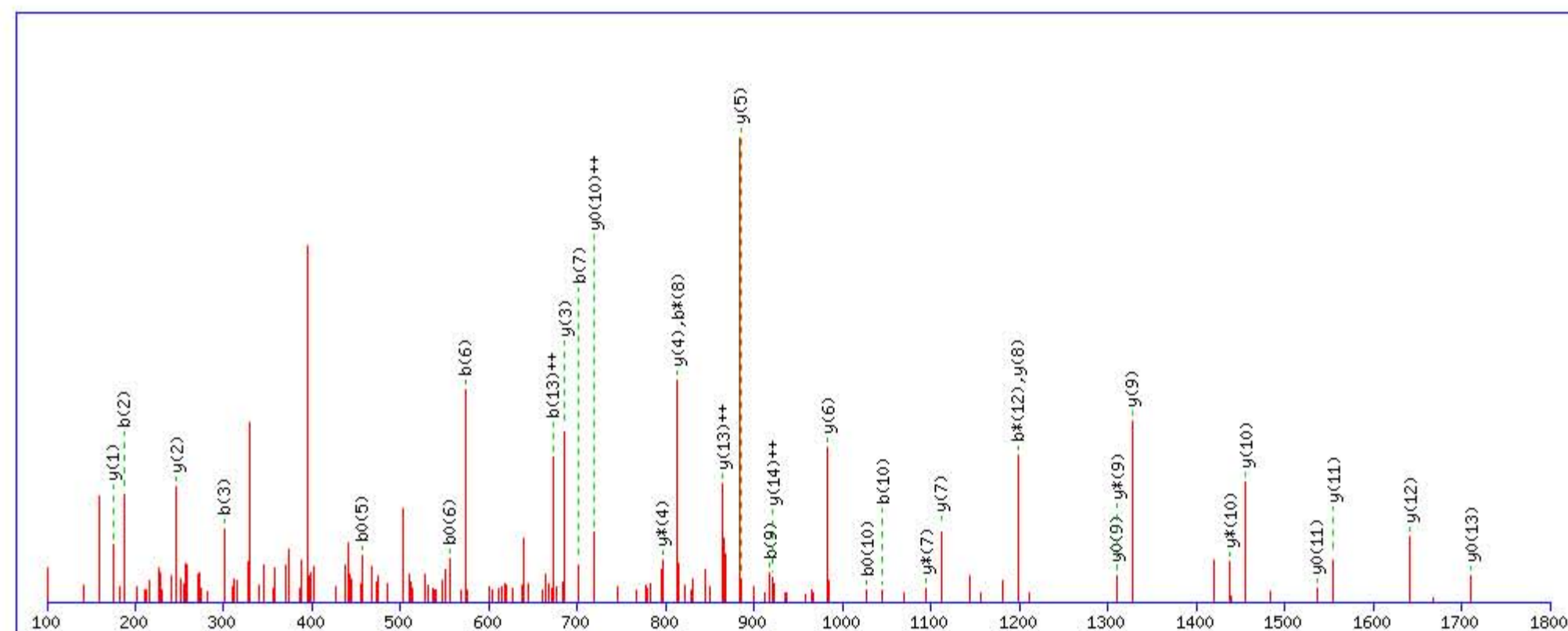
Title: Locus:1.1.1.3090.21 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2027.010574

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

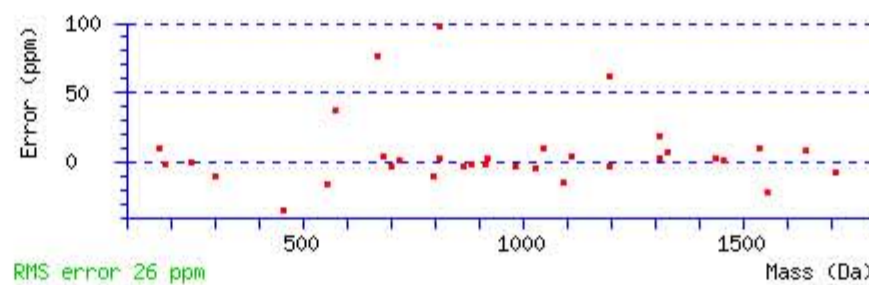
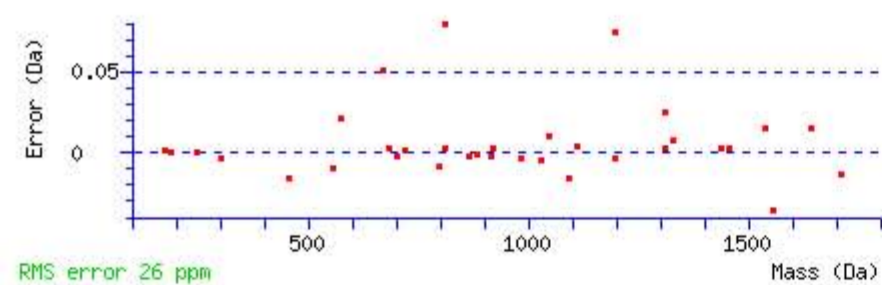
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 88 Expect: 4.3e-008

Matches : 34/154 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							16
2	187.071333	94.039304			169.060768	85.034022	A	1912.990923	956.999100	1895.964374	948.485825	1894.980358	947.993817	15
3	300.155397	150.581336			282.144832	141.576054	L	1841.953809	921.480543	1824.927260	912.967268	1823.943244	912.475260	14
4	387.187425	194.097351			369.176860	185.092068	S	1728.869745	864.938511	1711.843196	856.425236	1710.859180	855.933228	13
5	474.219453	237.613364			456.208888	228.608082	S	1641.837717	821.422497	1624.811168	812.909222	1623.827152	812.417214	12
6	573.287867	287.147572			555.277302	278.142289	V	1554.805689	777.906483	1537.779140	769.393208	1536.795124	768.901200	11
7	701.346445	351.176861	684.319896	342.663586	683.335880	342.171578	Q	1455.737275	728.372276	1438.710726	719.859001	1437.726710	719.366993	10
8	830.389038	415.698157	813.362489	407.184883	812.378473	406.692875	E	1327.678697	664.342987	1310.652148	655.829712	1309.668132	655.337704	9
9	917.421066	459.214171	900.394517	450.700897	899.410501	450.208889	S	1198.636104	599.821690	1181.609555	591.308416	1180.625539	590.816408	8
10	1045.479644	523.243460	1028.453095	514.730186	1027.469079	514.238178	Q	1111.604076	556.305676	1094.577527	547.792402			7
11	1144.548058	572.777667	1127.521509	564.264393	1126.537493	563.772385	V	983.545498	492.276387	966.518949	483.763113			6
12	1215.585172	608.296224	1198.558623	599.782950	1197.574607	599.290942	A	884.477084	442.742180	867.450535	434.228906			5
13	1343.643750	672.325513	1326.617201	663.812239	1325.633185	663.320230	Q	813.439970	407.223623	796.413421	398.710349			4
14	1782.869076	891.938176	1765.842527	883.424902	1764.858511	882.932894	Q	685.381392	343.194334	668.354843	334.681060			3
15	1853.906190	927.456733	1836.879641	918.943459	1835.895625	918.451451	A	246.156066	123.581671	229.129517	115.068396			2
16							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **DALSSVQESQVAQQAR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.7	2027.010574	-0.000052	DALSSVQESQVAQQAR
87.3	2027.010574	-0.000052	DALSSVQESQVAQQAR
80.7	2027.010574	-0.000052	DALSSVQESQVAQQAR
37.3	2027.010574	-0.000052	DALSSVQESQVAQQAR

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 47819: 2027.012172 from(676.678000,3+) rtinseconds(1962) index(36184)

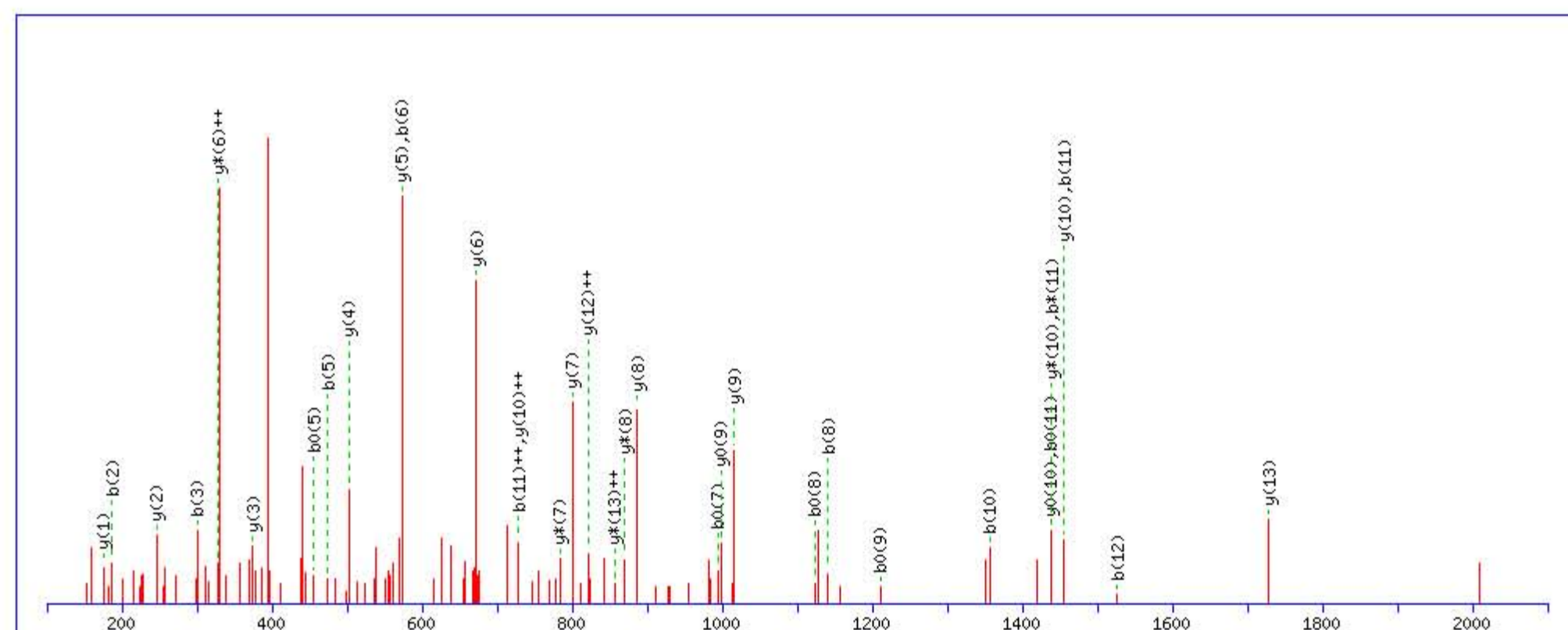
Title: Locus:1.1.1.3102.22 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\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): 2027.010574

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

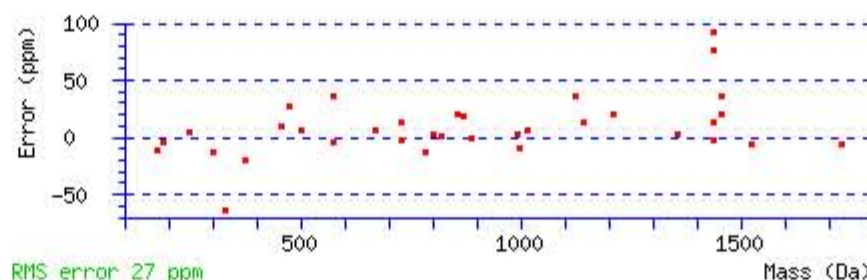
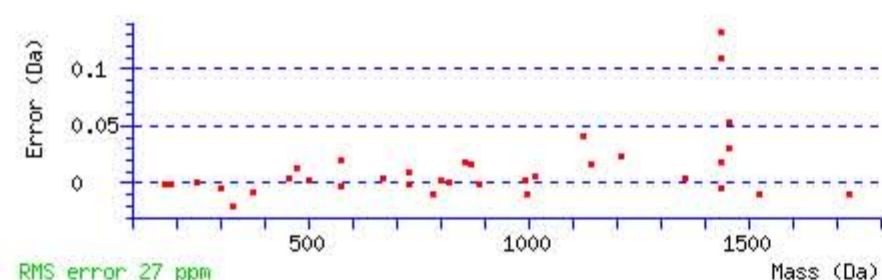
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 69 Expect: 5.8e-007

Matches : 35/154 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	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
68.6	2027.010574	0.001598	DALSSVQESQVAQQAR
31.7	2027.010574	0.001598	DALSSVQESQVAQQAR
12.1	2027.010574	0.001598	DALSSVQESQVAQQAR
10.1	2027.010574	0.001598	DALSSVQESQVAQQAR
2.0	2027.010559	0.001613	LTGRGAEDSLADQAANK
0.5	2027.000870	0.011302	QMSEPNIPFPQGFK

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 47821: 2027.012772 from(676.678200,3+) rtinseconds(1883) index(35519)

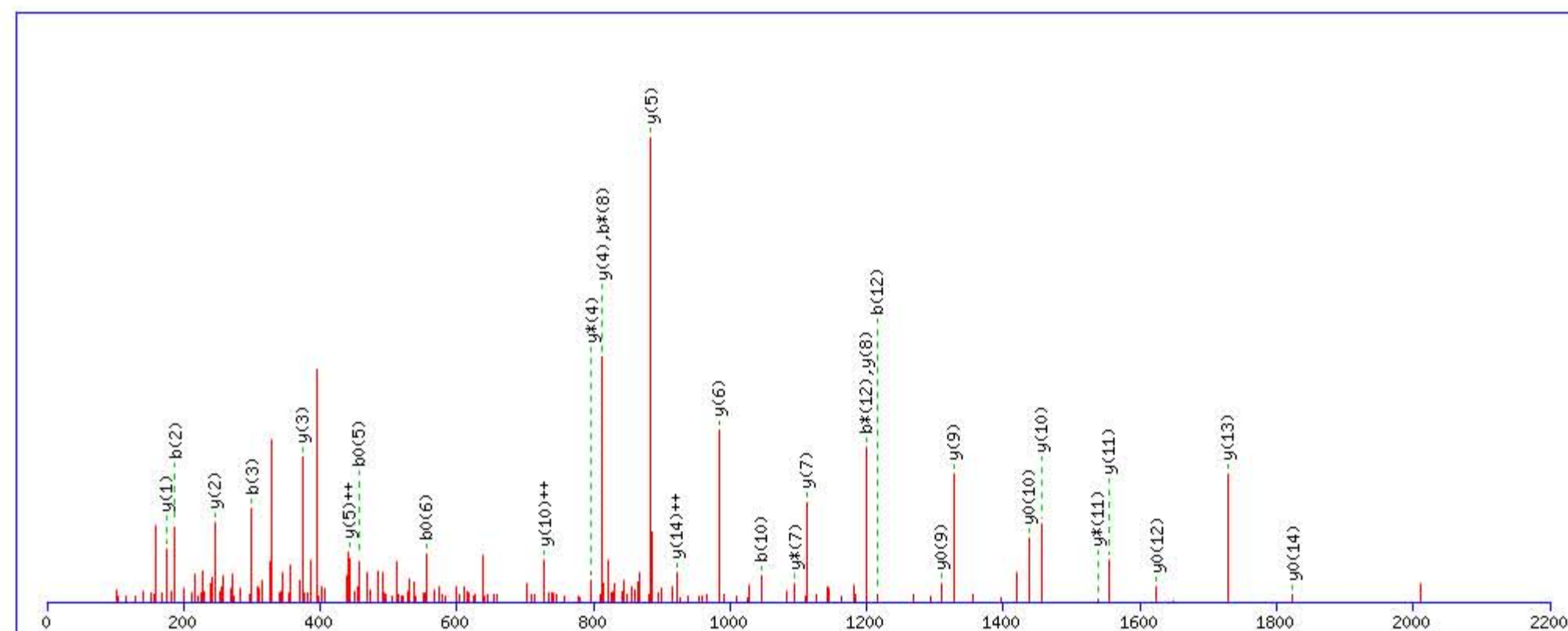
Title: Locus:1.1.1.3075.21 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2027.010574

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

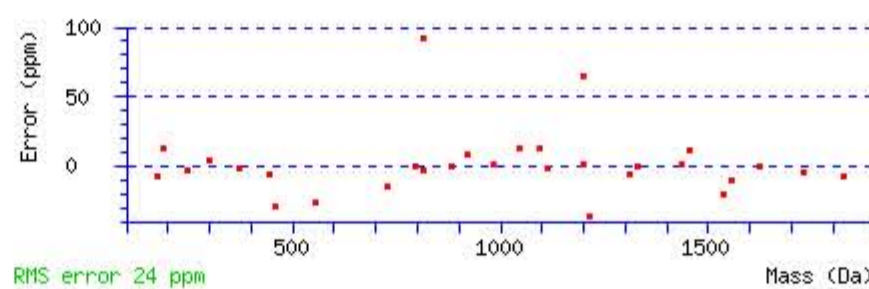
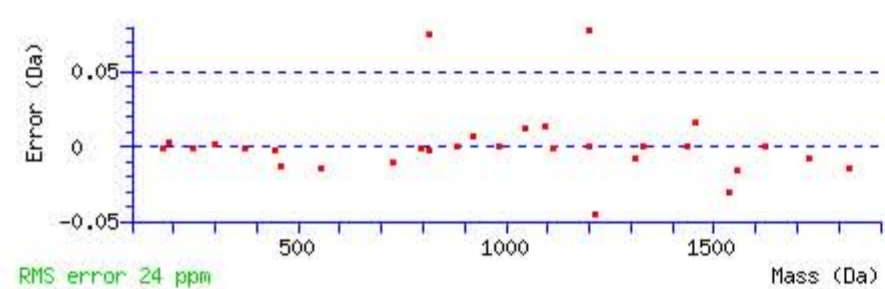
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 76 Expect: 5.5e-007

Matches : 30/154 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	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
76.5	2027.010574	0.002198	DALSSVQESQVAQQAR
66.5	2027.010574	0.002198	DALSSVQESQVAQQAR
38.2	2027.010574	0.002198	DALSSVQESQVAQQAR
11.5	2027.010574	0.002198	DALSSVQESQVAQQAR

MASCOT 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 23251: 1196.634708 from(599.324630,2+) rtinseconds(1508) index(49626)

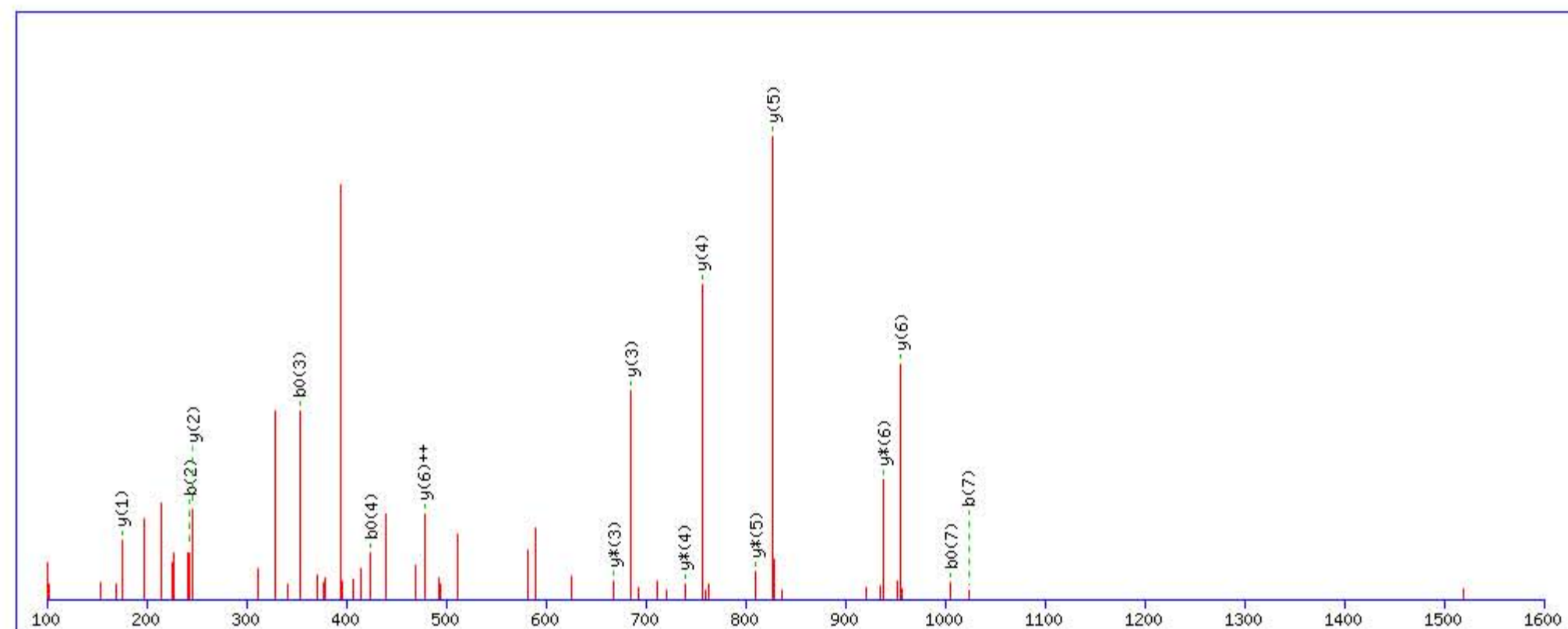
Title: Locus:1.1.1.1140.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide **Mr(calc)**: 1196.633545

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

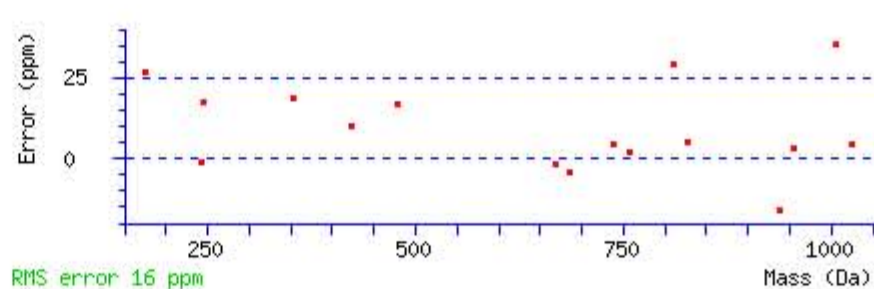
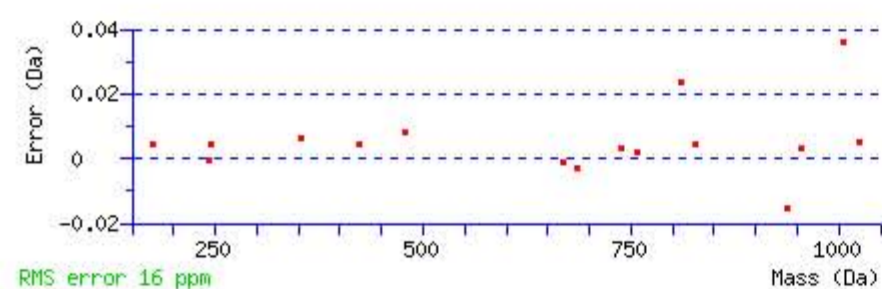
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 34 Expect: 0.0034

Matches : 16/66 fragment ions using 29 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
34.4	1196.633545	0.001163	ELQAAQAR
7.6	1196.633575	0.001133	QASTQVPR
4.6	1196.637390	-0.002682	TLRQAGAPNNR
2.0	1196.641434	-0.006726	STRPQAWVPR
1.3	1196.633545	0.001163	ELQAAQAR
1.2	1196.627029	0.007679	AGMPRQAR

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

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 25534: 1278.711268 from(640.362910,2+) rtinseconds(1962) index(36182)

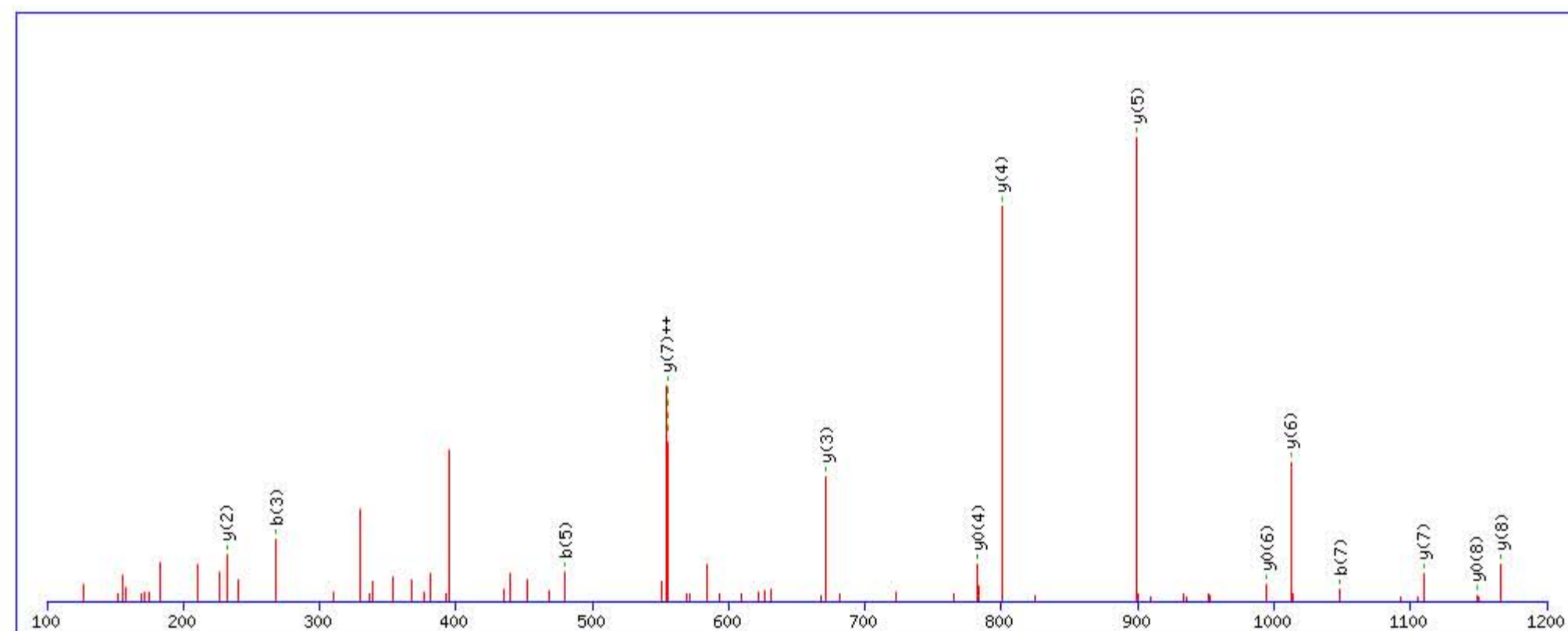
Title: Locus:1.1.1.3102.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1278.711823

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

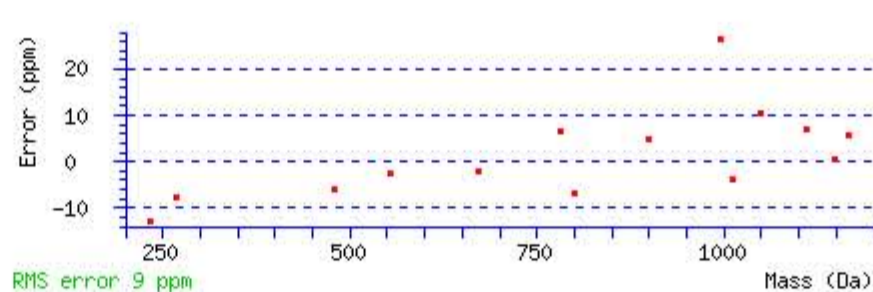
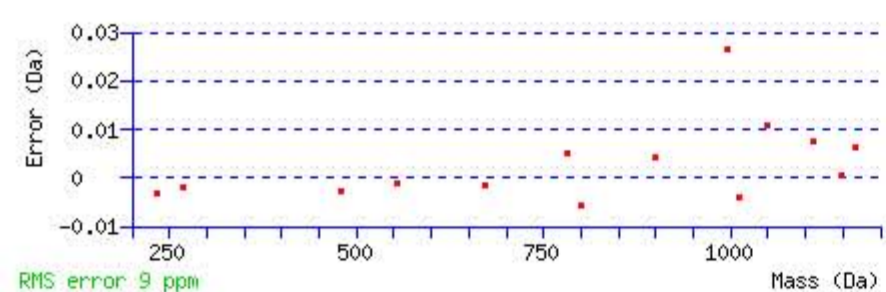
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 50 Expect: 6.3e-005

Matches : 14/68 fragment ions using 22 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							9
2	171.112804	86.060040					G	1166.635041	583.821159	1149.608492	575.307884	1148.624476	574.815876	8
3	268.165568	134.586422					P	1109.613577	555.310426	1092.587028	546.797152	1091.603012	546.305144	7
4	381.249632	191.128454					L	1012.560813	506.784044	995.534264	498.270770	994.550248	497.778762	6
5	480.318046	240.662661					V	899.476749	450.242012	882.450200	441.728738	881.466184	441.236730	5
6	609.360639	305.183958			591.350074	296.178675	E	800.408335	400.707805	783.381786	392.194531	782.397770	391.702523	4
7	1048.585965	524.796621	1031.559416	516.283346	1030.575400	515.791338	Q	671.365742	336.186509	654.339193	327.673234			3
8	1105.607429	553.307352	1088.580880	544.794078	1087.596864	544.302070	G	232.140416	116.573846	215.113867	108.060571			2
9							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **LGPLVEQGR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.1	1278.711823	-0.000555	LGPLVEQGR
5.0	1278.729584	-0.018316	IVIVPSLNPDGR
0.3	1278.704422	0.006846	ERGGLPVIEGPR
0.3	1278.693192	0.018076	LGDL DVALHQAK

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

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 31712: 1424.740448 from(713.377500,2+) rtinseconds(1547) index(18797)

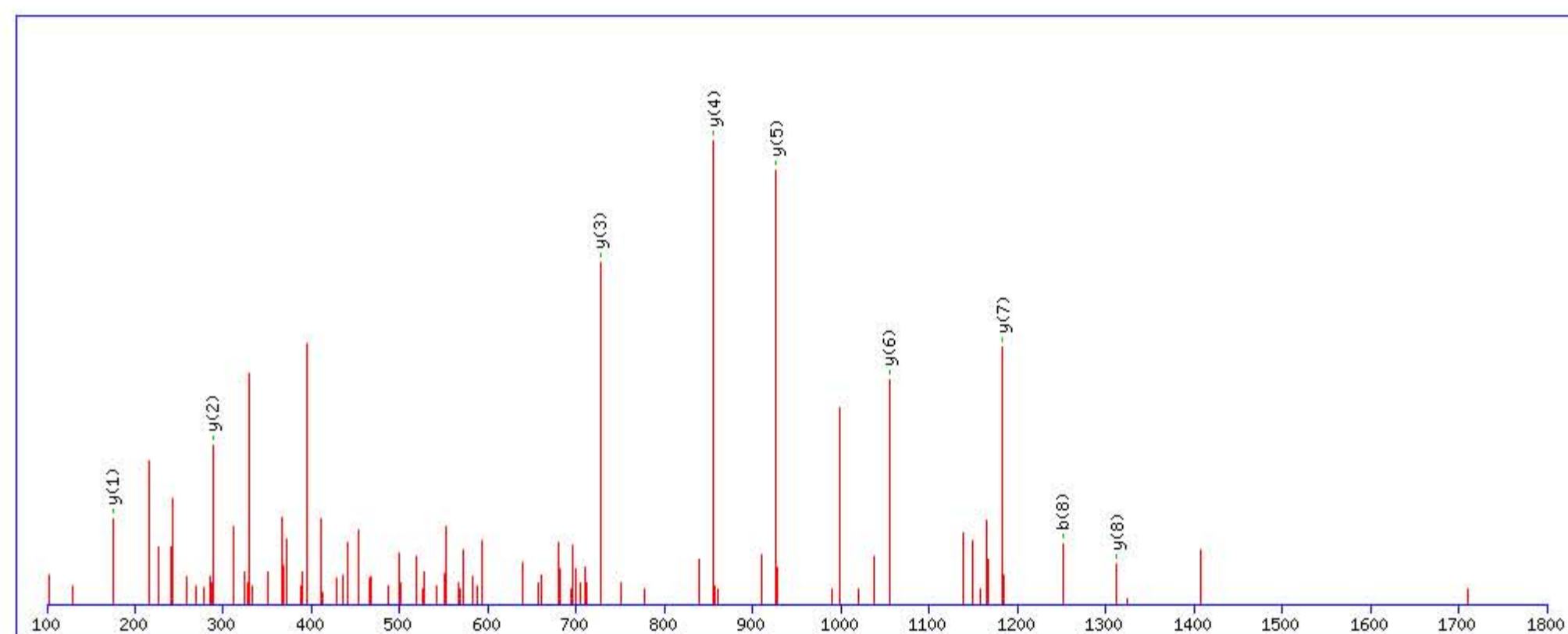
Title: Locus:1.1.1.541.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1424.744553

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

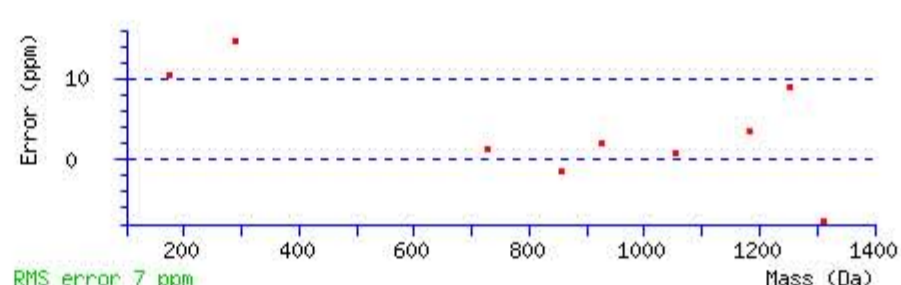
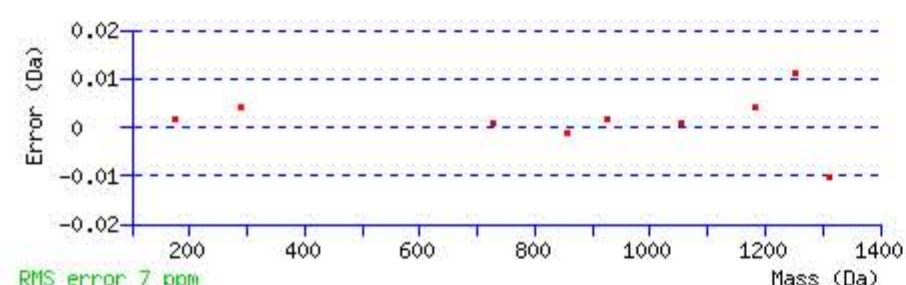
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 1.7e-005

Matches : 9/76 fragment ions using 14 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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
66.1	1424.744553	-0.004105	LEEQAQQIR
50.2	1424.744553	-0.004105	LEEQAQQIR
22.0	1424.744553	-0.004105	LEEQAQQIR
14.4	1424.733322	0.007126	LEQETEPLR
13.4	1424.745438	-0.004990	QMQQIR
10.3	1424.730667	0.009781	QPGCAVPQSGRLR
8.9	1424.723465	0.016983	TWTVLPPMSTHR
5.5	1424.734680	0.005768	WVLTAHCLAQR
5.4	1424.744583	-0.004135	QLSGDQPTIR
4.3	1424.744583	-0.004135	QLSGDQPTIR

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 35208: 1557.731388 from(779.872970,2+) rtinseconds(1534) index(33507)

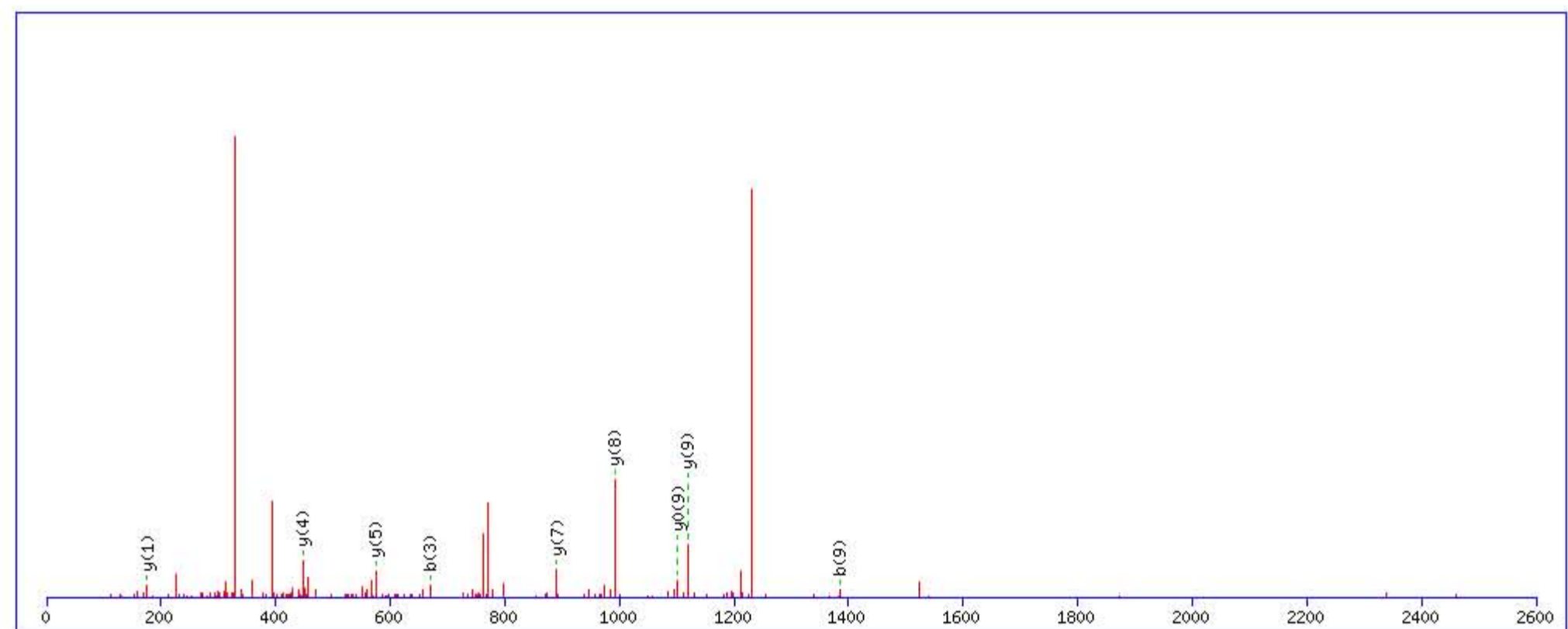
Title: Locus:1.1.1.2953.22 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1557.735809

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

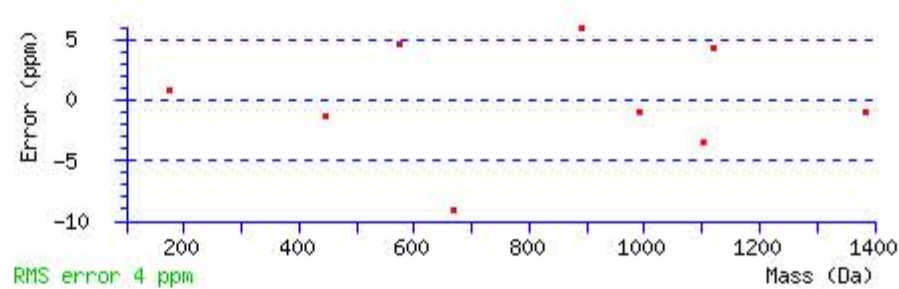
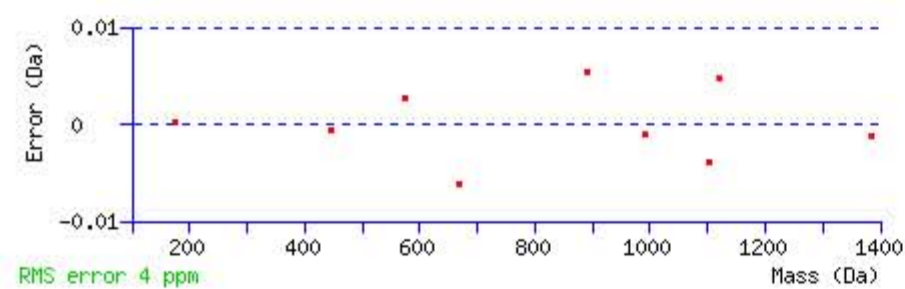
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.00098

Matches : 9/98 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	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
41.5	1557.735809	-0.004421	QQTEWQSGQR
28.7	1557.735809	-0.004421	QQTEWQSGQR
16.9	1557.747040	-0.015652	AFSHCSSLTKHQR
6.8	1557.745697	-0.014309	GSSLFMDTEKSGKR
5.8	1557.742340	-0.010952	TQSFEIPQPDSPGR
5.1	1557.739182	-0.007794	GPMIDQRGLPMDGR
5.0	1557.720566	0.010822	QEAAATGVDTICTHR
4.4	1557.720551	0.010837	LSQVSPEDDRPCR
4.4	1557.749496	-0.018108	QAEATRQAAAQEER
4.4	1557.709305	0.022083	QLSDQQDEER

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AATVGS LAGQPLQER**

Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

Match to Query 42837: 1807.960542 from(603.660790,3+) rtinseconds(1953) index(36106)

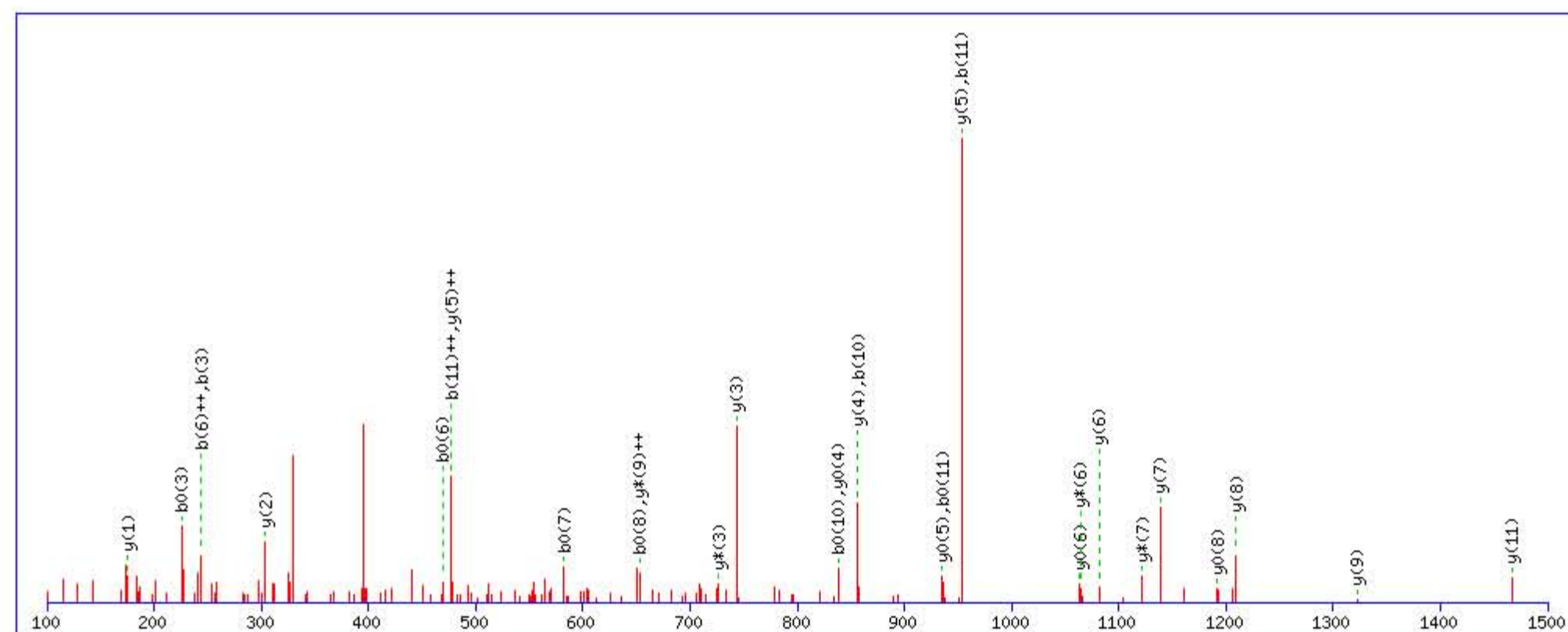
Title: Locus:1.1.1.3099.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1807.961441

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

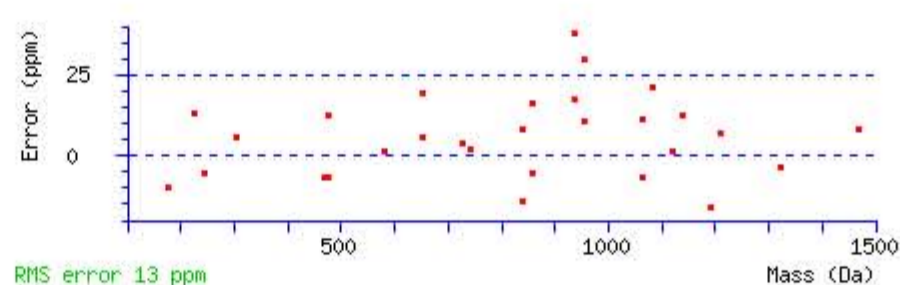
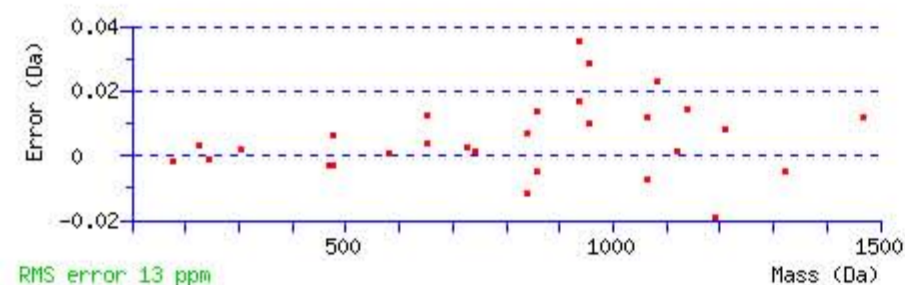
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 65 Expect: 3.9e-006

Matches : 30/144 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	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 **AATVGS LAGQPLQER**

(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	1807.961441	-0.000899	AATVGS LAGQPLQER
18.2	1807.961441	-0.000899	AATVGS LAGQPLQER
7.1	1807.947510	0.013032	VGLAQIAAMDISRGNHR
2.6	1807.942795	0.017747	ENKDQLESVLEVLHR

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 43580: 1846.875492 from(616.632440,3+) rtinseconds(2818) index(41692)

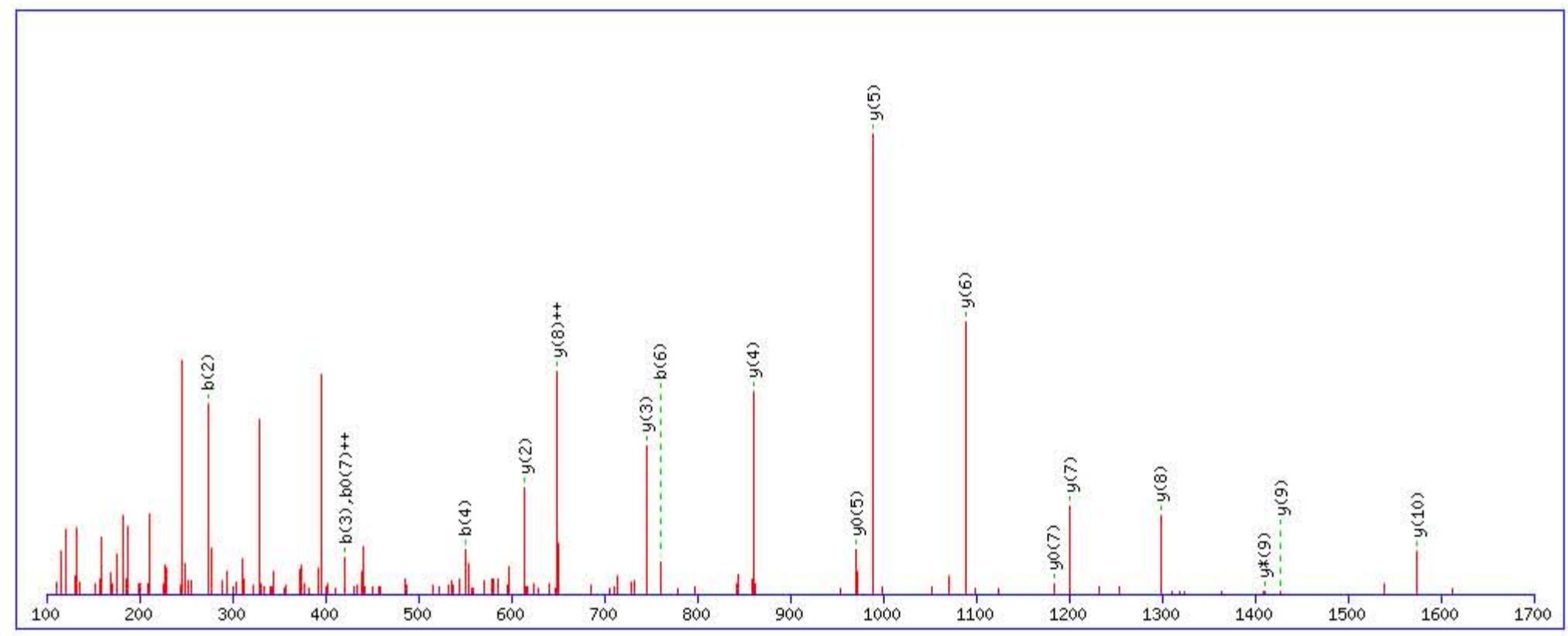
Title: Locus:1.1.1.3399.3 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1846.874603

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

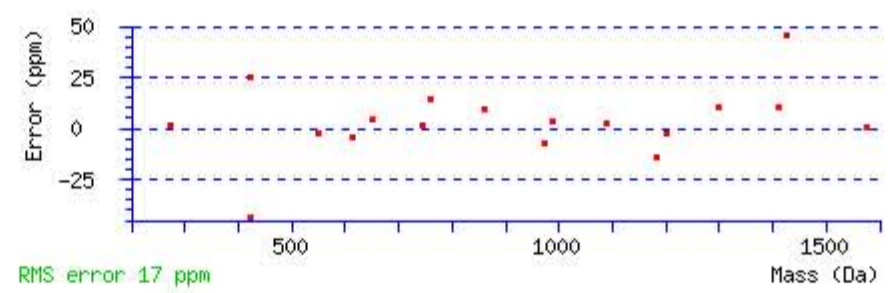
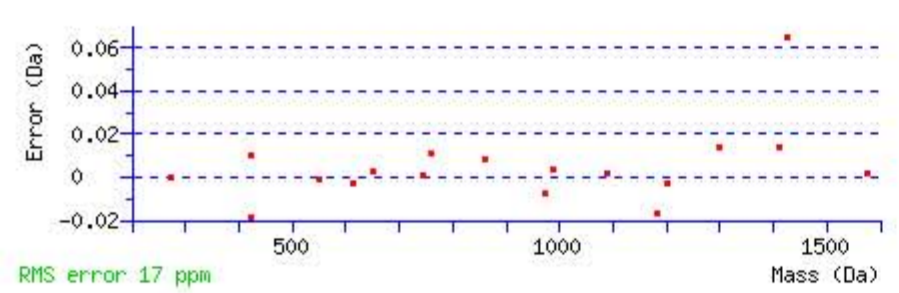
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 52 Expect: 2.8e-005

Matches : 18/106 fragment ions using 31 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							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
51.7	1846.874603	0.000889	SWFEPLVEDMQR
3.0	1846.849426	0.026066	SFWENNCKMIYLAR
0.4	1846.895721	-0.020229	LQLEETMPSPYGR

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 47485: 2008.016472 from(670.346100,3+) rtinseconds(2469) index(39224)

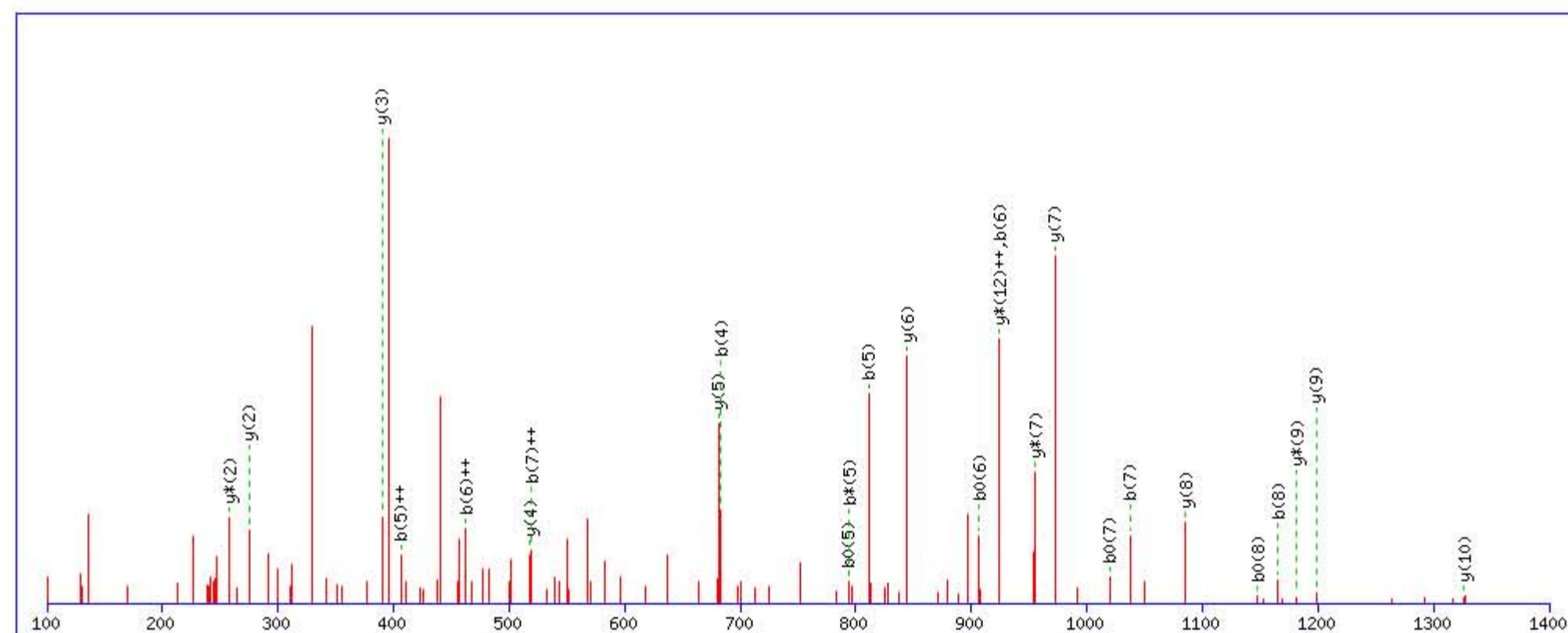
Title: Locus:1.1.1.3279.14 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2008.008789

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

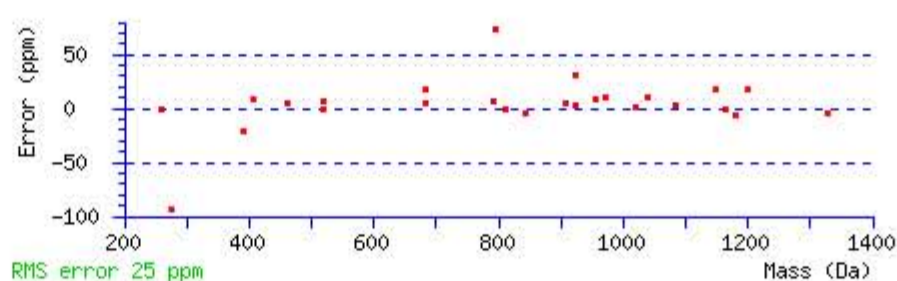
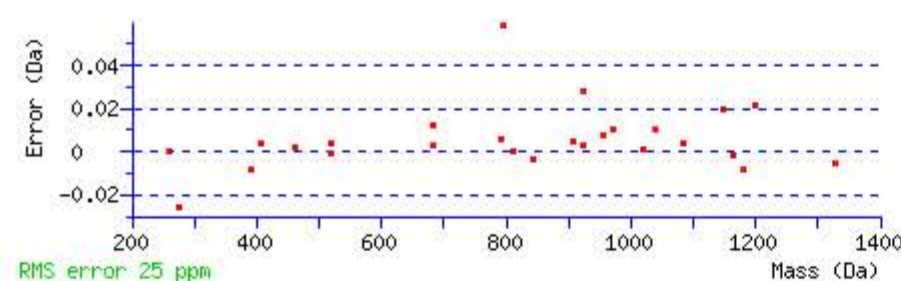
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.00088

Matches : 26/146 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	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
42.6	2008.008789	0.007683	SGVQQLIQYYQDQK
32.2	2008.008789	0.007683	SGVQQLIQYYQDQK
9.4	2007.998215	0.018257	QQLNLRTHMADENK
7.6	2008.037308	-0.020836	VVPVLSLSLYLLQCNMK
0.6	2008.026535	-0.010063	HYSNTLKALGISDEFVSK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VTEPISAESGEQVER**

Found in **APOLI_HUMAN**, Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5

Match to Query 45380: 1940.949702 from(647.990510,3+) rtinseconds(1702) index(19696)

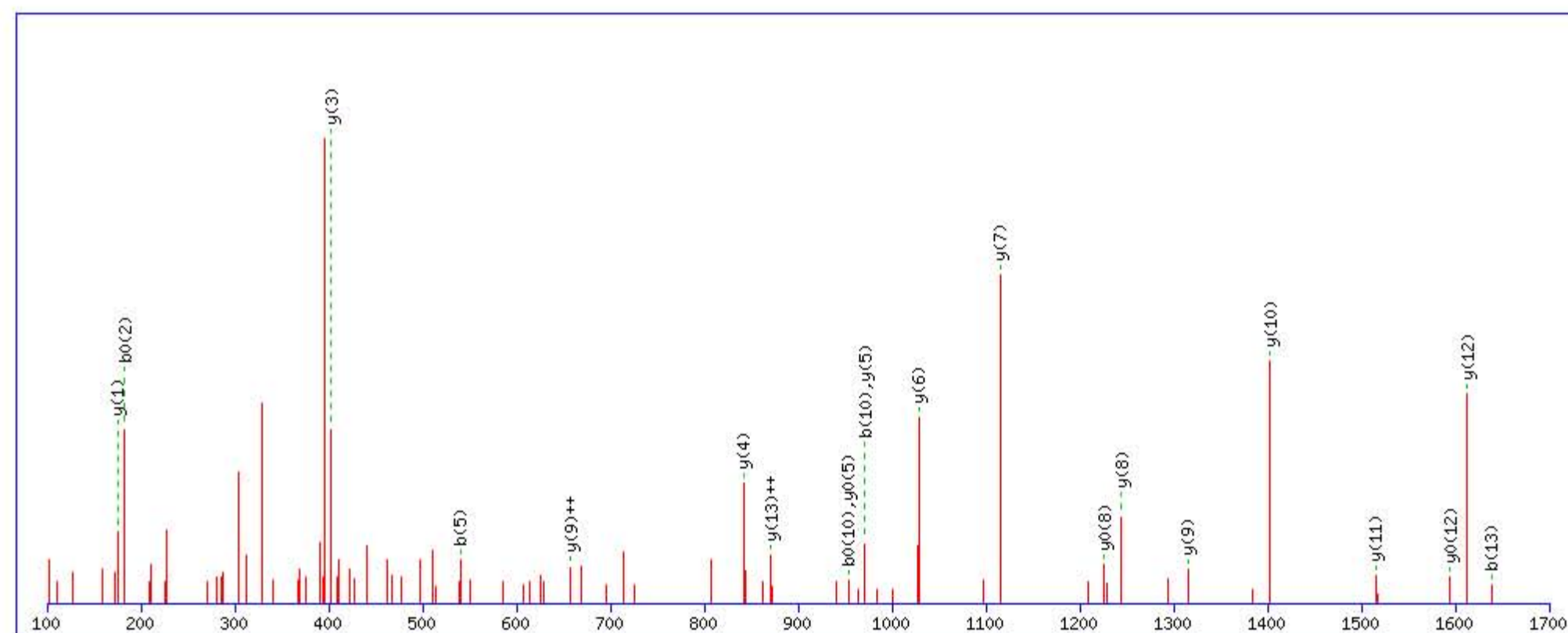
Title: Locus:1.1.1.595.8 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1940.951324

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

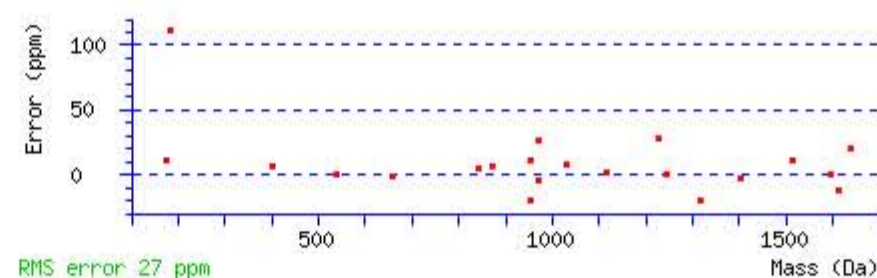
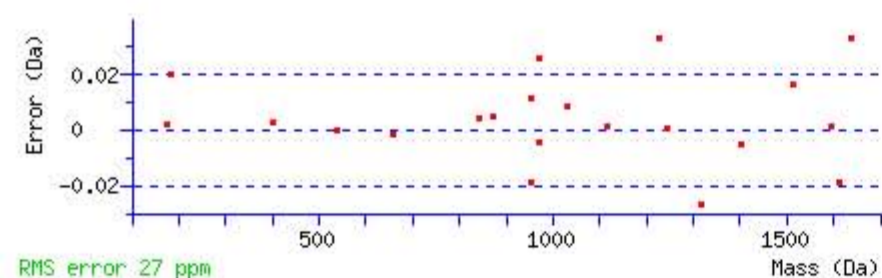
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 79 Expect: 2.8e-007

Matches : 21/142 fragment ions using 30 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483					V							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
79.2	1940.951324	-0.001622	VTEPISAESGEQVER
11.1	1940.962540	-0.012838	LLNDQEEEGTQRAK
2.5	1940.937378	0.012324	SNNLEREQEQLDR

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

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 33528: 1488.631988 from(745.323270,2+) rtinseconds(1637) index(34042)

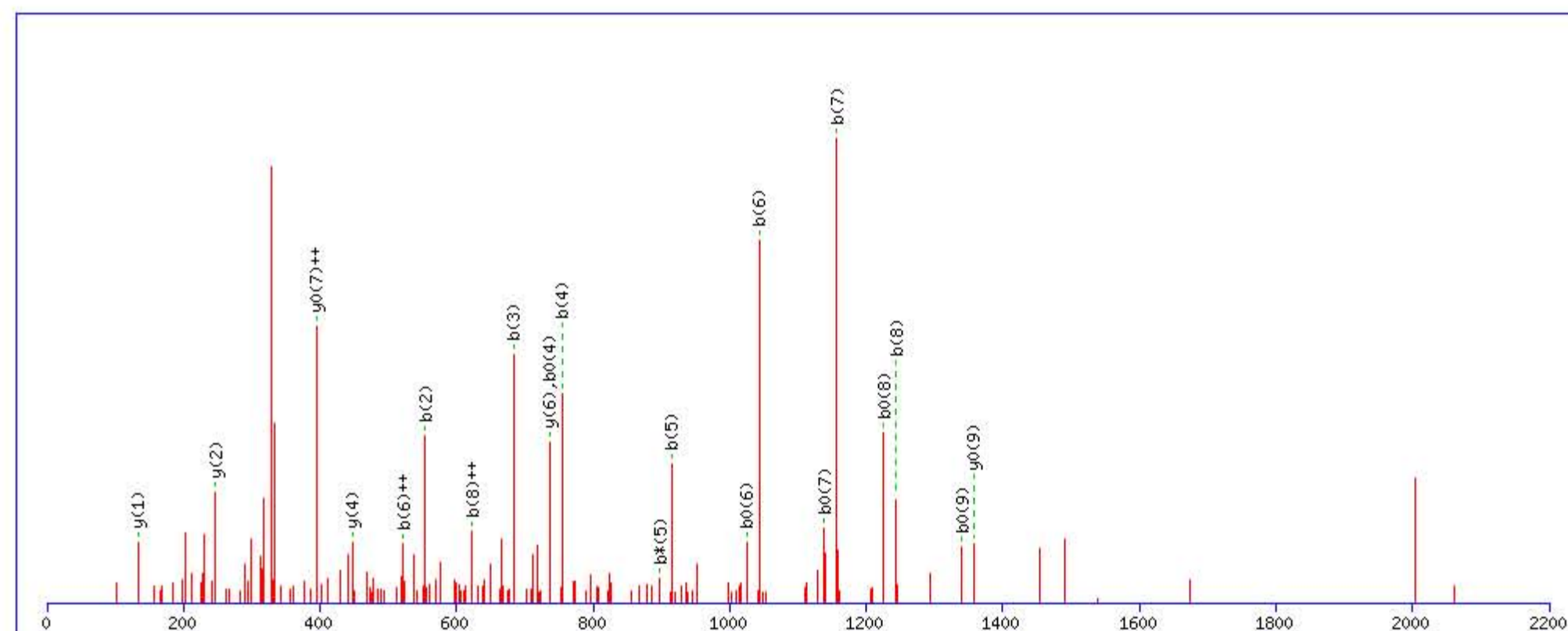
Title: Locus:1.1.1.2989.17 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1488.633682

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

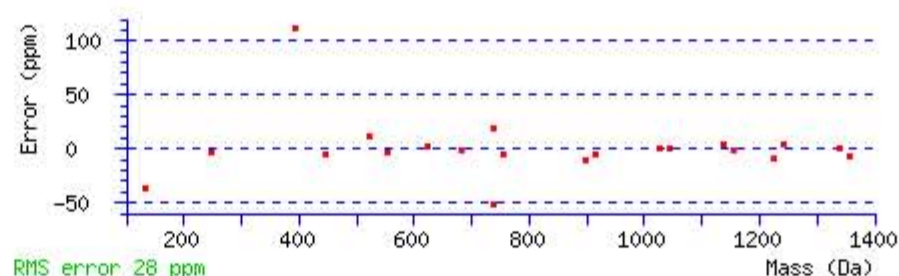
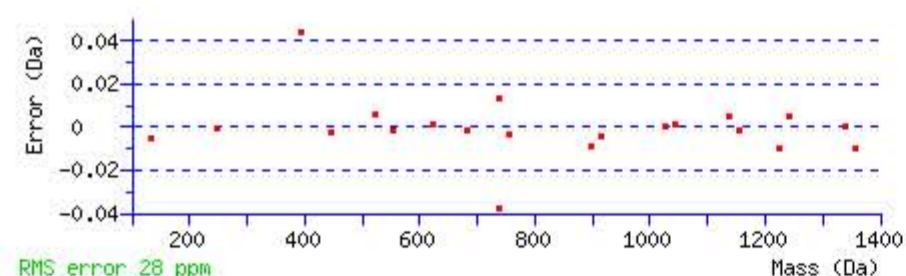
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 63 Expect: 1.5e-006

Matches : 22/100 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	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
63.5	1488.633682	-0.001694	NQEACELSNN

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

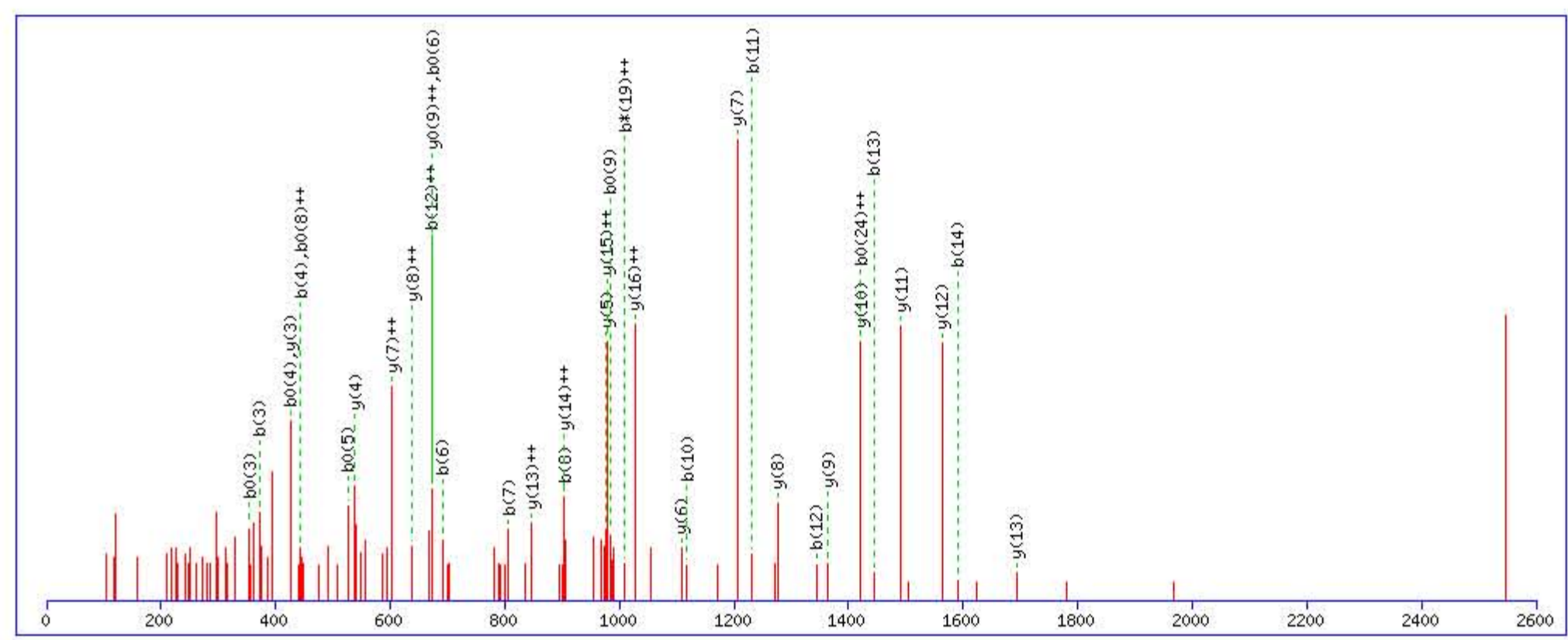
MASCOT Mascot Search Results

Peptide View

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

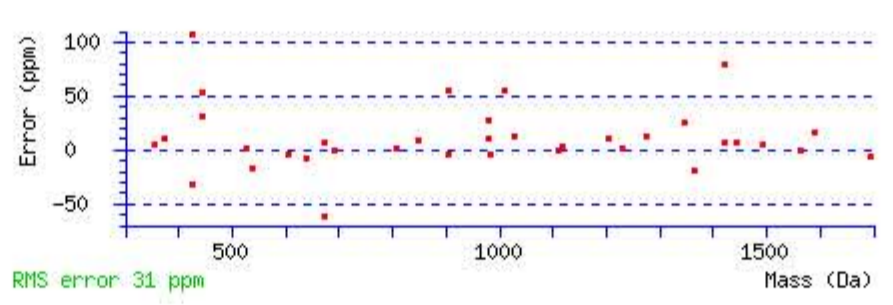
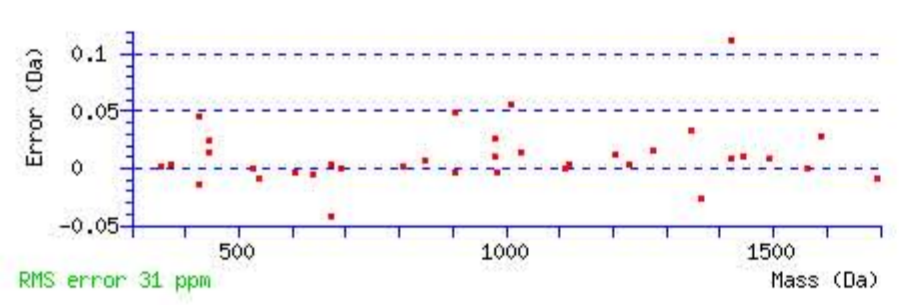
Match to Query 66282: 3396.690376 from(850.179870,4+) rtinseconds(3152) index(44024)
 Title: Locus:1.1.1.3513.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 3396.666855
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q24 : Biotin:Thermo-21345 (Q)
 Ions Score: 72 Expect: 1.7e-006
 Matches : 37/288 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	130.049869	65.528572			112.039304	56.523290	E							28
2	259.092462	130.049869			241.081897	121.044587	E	3268.631560	1634.819418	3251.605011	1626.306143	3250.620995	1625.814135	27
3	372.176526	186.591901			354.165961	177.586619	L	3139.588967	1570.298122	3122.562418	1561.784847	3121.578402	1561.292839	26
4	443.213640	222.110458			425.203075	213.105176	A	3026.504903	1513.756089	3009.478354	1505.242815	3008.494338	1504.750807	25
5	544.261319	272.634298			526.250754	263.629015	T	2955.467789	1478.237532	2938.441240	1469.724258	2937.457224	1469.232250	24
6	691.329733	346.168505			673.319168	337.163222	F	2854.420110	1427.713693	2837.393561	1419.200418	2836.409545	1418.708410	23
7	806.356676	403.681976			788.346111	394.676694	D	2707.351696	1354.179486	2690.325147	1345.666211	2689.341131	1345.174204	22
8	903.409440	452.208358			885.398875	443.203076	P	2592.324753	1296.666014	2575.298204	1288.152740	2574.314188	1287.660732	21
9	1002.477854	501.742565			984.467289	492.737282	V	2495.271989	1248.139632	2478.245440	1239.626358	2477.261424	1239.134350	20
10	1117.504797	559.256037			1099.494232	550.250754	D	2396.203575	1198.605425	2379.177026	1190.092151	2378.193010	1189.600143	19
11	1231.547724	616.277500	1214.521175	607.764226	1213.537159	607.272218	N	2281.176632	1141.091954	2264.150083	1132.578679	2263.166067	1132.086672	18
12	1344.631788	672.819532	1327.605239	664.306258	1326.621223	663.814249	I	2167.133705	1084.070490	2150.107156	1075.557216	2149.123140	1075.065208	17
13	1443.700202	722.353739	1426.673653	713.840465	1425.689637	713.348457	V	2054.049641	1027.528458	2037.023092	1019.015184	2036.039076	1018.523176	16
14	1590.768616	795.887946	1573.742067	787.374672	1572.758051	786.882664	F	1954.981227	977.994252	1937.954678	969.480977	1936.970662	968.988969	15
15	1704.811543	852.909410	1687.784994	844.396135	1686.800978	843.904127	N	1807.912813	904.460045	1790.886264	895.946770	1789.902248	895.454762	14
16	1835.852028	918.429652	1818.825479	909.916378	1817.841463	909.424370	M	1693.869886	847.438581	1676.843337	838.925307	1675.859321	838.433299	13
17	1906.889142	953.948209	1889.862593	945.434935	1888.878577	944.942927	A	1562.829401	781.918339	1545.802852	773.405064	1544.818836	772.913056	12
18	1977.926256	989.466766	1960.899707	980.953492	1959.915691	980.461483	A	1491.792287	746.399782	1474.765738	737.886507	1473.781722	737.394499	11
19	2034.947720	1017.977498	2017.921171	1009.464224	2016.937155	1008.972215	G	1420.755173	710.881225	1403.728624	702.367950	1402.744608	701.875942	10
20	2121.979748	1061.493512	2104.953199	1052.980237	2103.969183	1052.488229	S	1363.733709	682.370493	1346.707160	673.857218	1345.723144	673.365210	9
21	2193.016862	1097.012069	2175.990313	1088.498794	2175.006297	1088.006786	A	1276.701681	638.854479	1259.675132	630.341204			8
22	2290.069626	1145.538451	2273.043077	1137.025176	2272.059061	1136.533168	P	1205.664567	603.335922	1188.638018	594.822647			7
23	2421.110111	1211.058693	2404.083562	1202.545419	2403.099546	1202.053411	M	1108.611803	554.809540	1091.585254	546.296265			6
24	2860.335437	1430.671357	2843.308888	1422.158082	2842.324872	1421.666074	Q	977.571318	489.289297	960.544769	480.776023			5
25	2973.419501	1487.213389	2956.392952	1478.700114	2955.408936	1478.208106	L	538.345992	269.676634	521.319443	261.163360			4
26	3110.478413	1555.742845	3093.451864	1547.229570	3092.467848	1546.737562	H	425.261928	213.134602	408.235379	204.621328			3
27	3223.562477	1612.284877	3206.535928	1603.771602	3205.551912	1603.279594	L	288.203016	144.605146	271.176467	136.091872			2
28							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.0	3396.666855	0.023521	EELATFDPVDNIVFNMAAGSAPMQLHLR

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 46012: 1973.853792 from(658.958540,3+) rtinseconds(1990) index(5796)

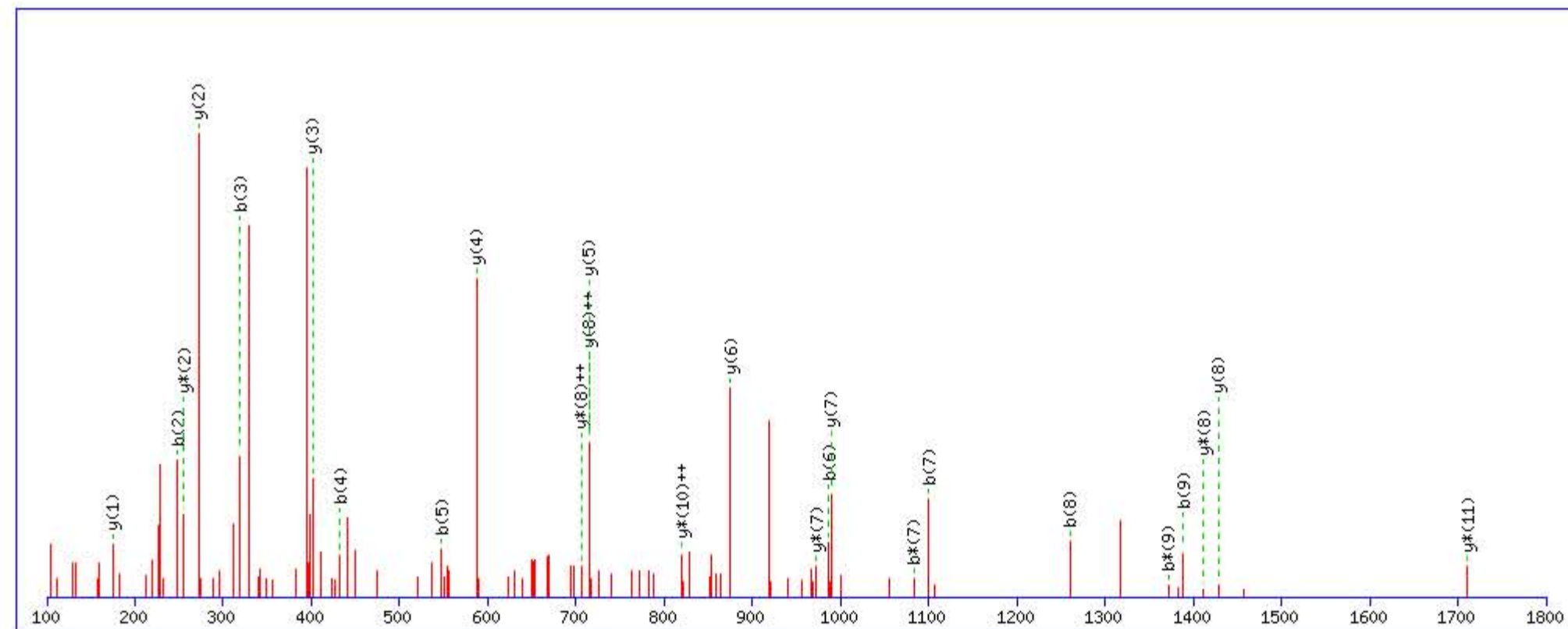
Title: Locus:1.1.1.1502.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1973.854614

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

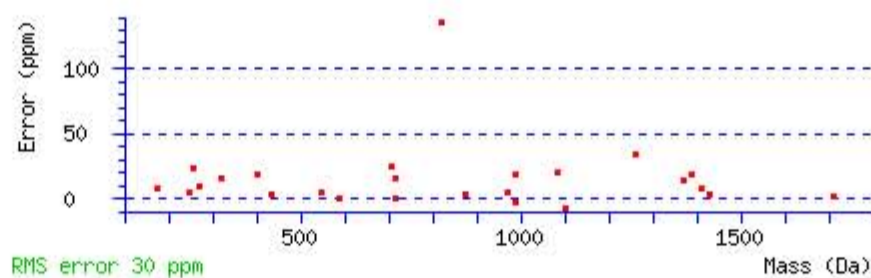
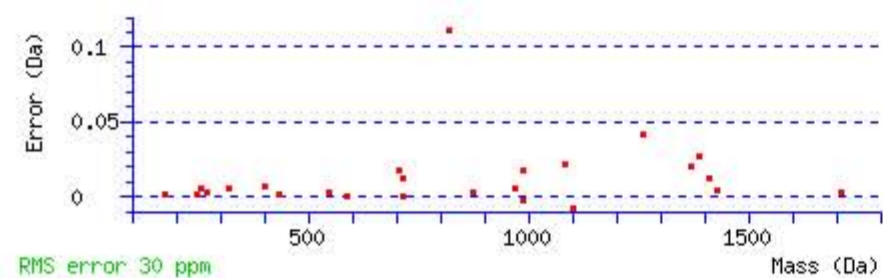
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 44 Expect: 0.00016

Matches : 25/130 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							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
44.2	1973.854614	-0.000822	SCALDQNCQWEPR
16.2	1973.854614	-0.000822	SCALDQNCQWEPR
1.7	1973.853729	0.000063	DSPETGEEMGRAEGAWPR

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

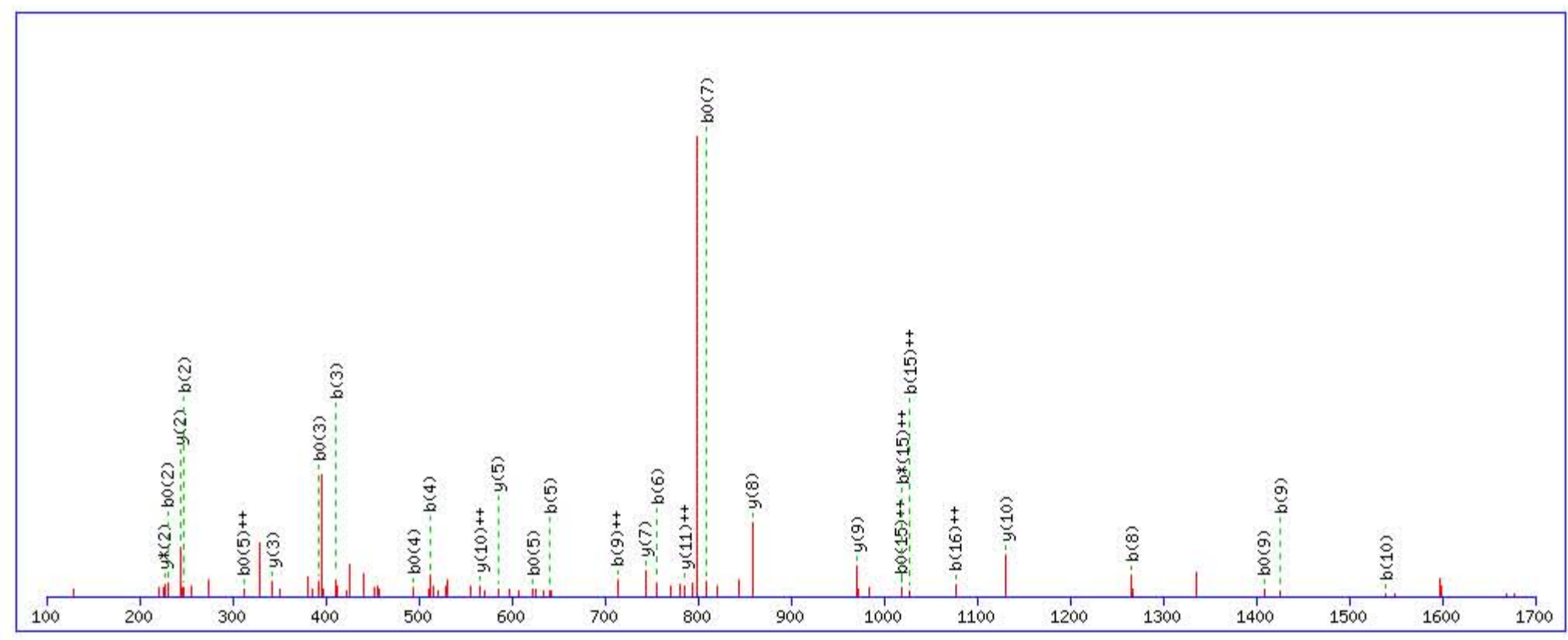
MASCOT Search Results

Peptide View

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

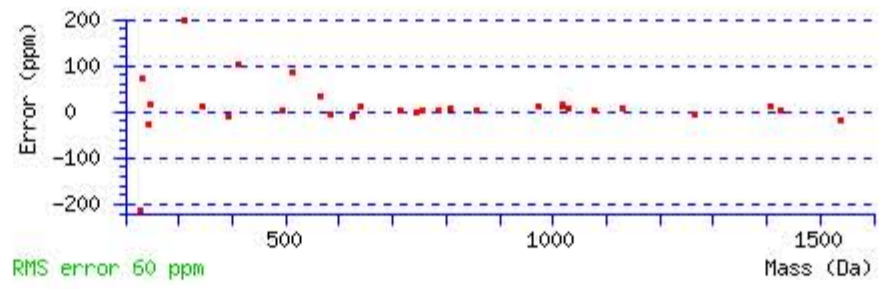
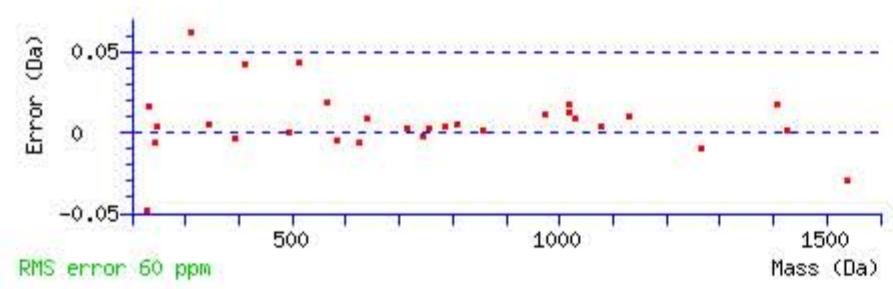
Match to Query 54239: 2396.073612 from(799.698480,3+) rtinseconds(2156) index(69708)
 Title: Locus:1.1.1.1688.17 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2396.069824
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q8 : Biotin:Thermo-21345 (Q)
 Ions Score: 33 Expect: 0.0042
 Matches : 30/182 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	161.037925	81.022600					C							18
2	248.069953	124.538614			230.059388	115.533332	S	2237.046450	1119.026863	2220.019901	1110.513588	2219.035885	1110.021580	17
3	411.133282	206.070279			393.122717	197.064997	Y	2150.014422	1075.510849	2132.987873	1066.997574	2132.003857	1066.505566	16
4	512.180961	256.594119			494.170396	247.588836	T	1986.951093	993.979184	1969.924544	985.465910	1968.940528	984.973902	15
5	641.223554	321.115415			623.212989	312.110133	E	1885.903414	943.455345	1868.876865	934.942071	1867.892849	934.450062	14
6	756.250497	378.628887			738.239932	369.623604	D	1756.860821	878.934048	1739.834272	870.420774	1738.850256	869.928766	13
7	827.287611	414.147444			809.277046	405.142161	A	1641.833878	821.420577	1624.807329	812.907302	1623.823313	812.415294	12
8	1266.512937	633.760107	1249.486388	625.246832	1248.502372	624.754824	Q	1570.796764	785.902020	1553.770215	777.388746	1552.786199	776.896737	11
9	1426.543586	713.775431	1409.517037	705.262157	1408.533021	704.770149	C	1131.571438	566.289357	1114.544889	557.776082	1113.560873	557.284074	10
10	1539.627650	770.317463	1522.601101	761.804189	1521.617085	761.312181	I	971.540789	486.274032	954.514240	477.760758	953.530224	477.268750	9
11	1654.654593	827.830935	1637.628044	819.317660	1636.644028	818.825652	D	858.456725	429.732000	841.430176	421.218726	840.446160	420.726718	8
12	1711.676057	856.341667	1694.649508	847.828392	1693.665492	847.336384	G	743.429782	372.218529	726.403233	363.705254	725.419217	363.213246	7
13	1812.723736	906.865506	1795.697187	898.352232	1794.713171	897.860224	T	686.408318	343.707797	669.381769	335.194522	668.397753	334.702514	6
14	1925.807800	963.407538	1908.781251	954.894264	1907.797235	954.402256	I	585.360639	293.183957	568.334090	284.670683	567.350074	284.178675	5
15	2054.850393	1027.928834	2037.823844	1019.415560	2036.839828	1018.923552	E	472.276575	236.641925	455.250026	228.128651	454.266010	227.636643	4
16	2153.918807	1077.463041	2136.892258	1068.949767	2135.908242	1068.457759	V	343.233982	172.120629	326.207433	163.607354			3
17	2250.971571	1125.989423	2233.945022	1117.476149	2232.961006	1116.984141	P	244.165568	122.586422	227.139019	114.073148			2
18							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **CSYTEDAQCIDGTIEVPK**
 (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	2396.069824	0.003788	CSYTEDAQCIDGTIEVPK

MASCOT 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 24918: 1258.713068 from(630.363810,2+) rtinseconds(2050) index(36718)

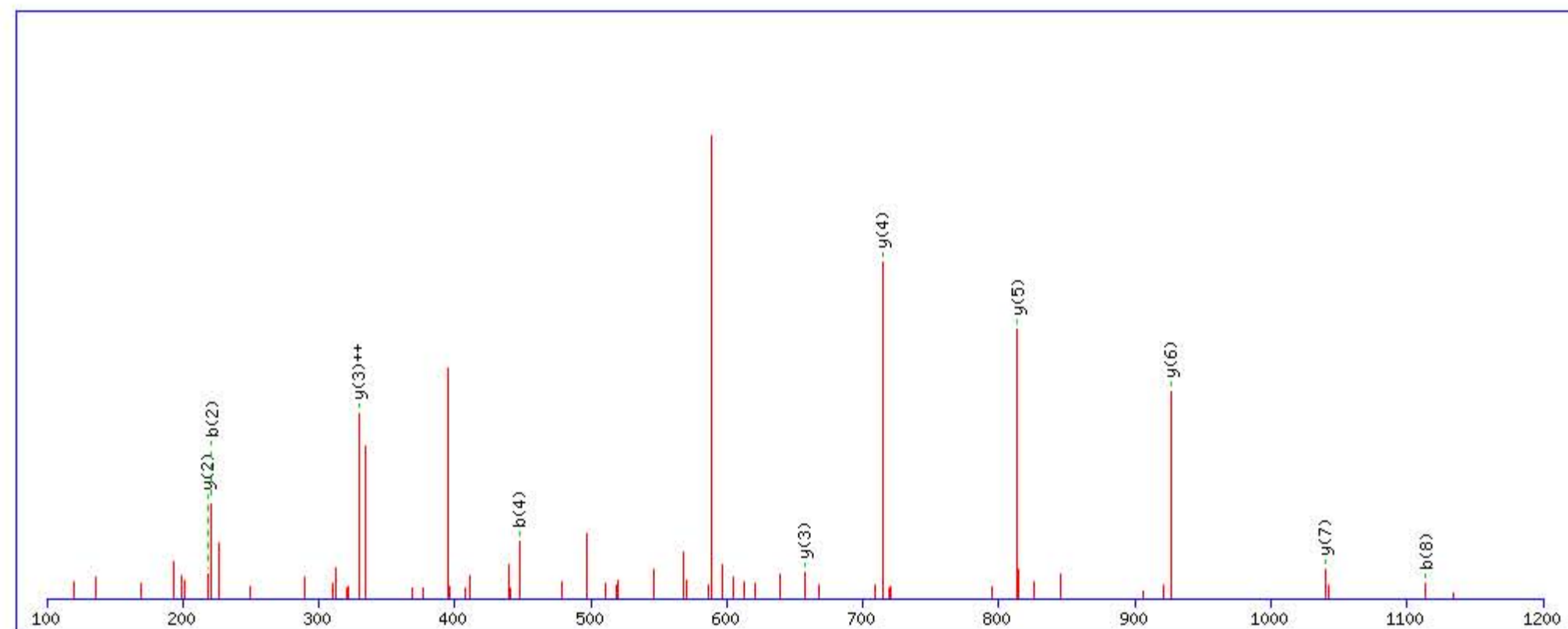
Title: Locus:1.1.1.3133.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1258.710754

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

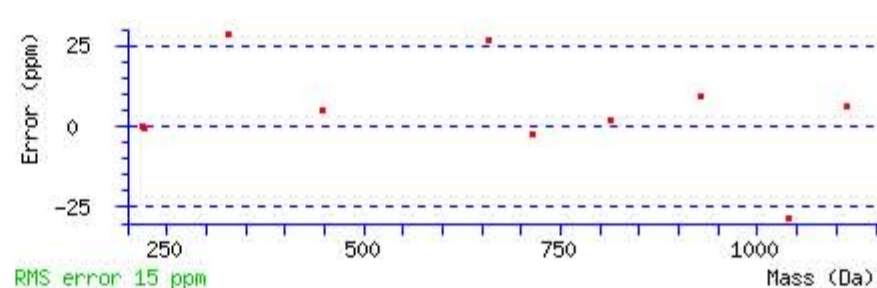
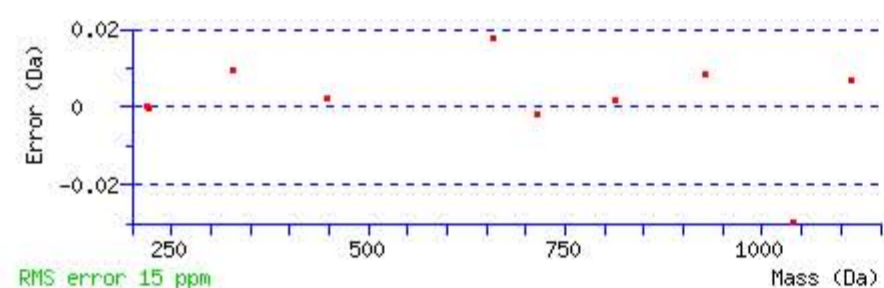
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.0071

Matches : 10/52 fragment ions using 21 most intense peaks [\(help\)](#)

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



NCBI BLAST search of [GYILVGQAK](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.9	1258.710754	0.002314	GYILVGQAK
6.9	1258.721970	-0.008902	GYILQAKR
6.7	1258.717941	-0.004873	RILAKVQEMR

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

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **QSSSYSFFK**

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

Match to Query 29789: 1390.665948 from(696.340250,2+) rtinseconds(2139) index(37248)

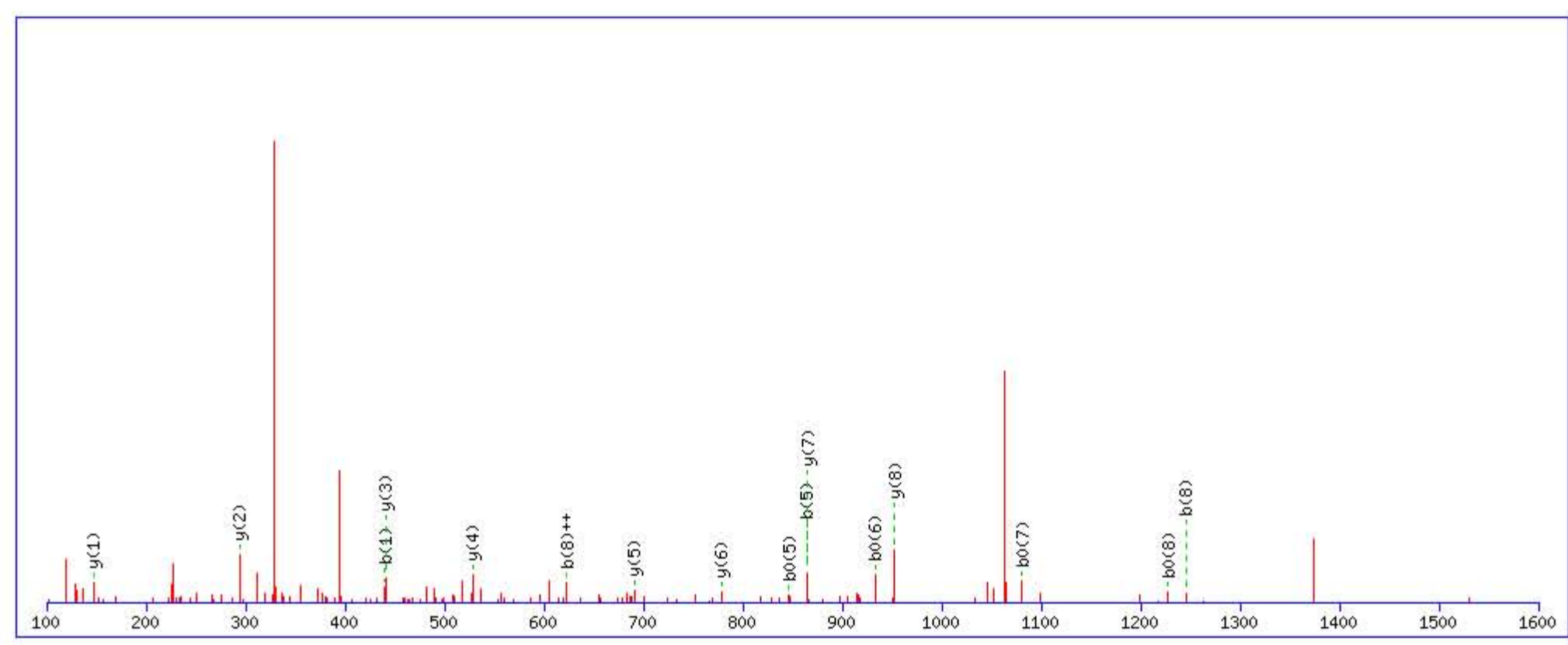
Title: Locus:1.1.1.3164.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1390.659119

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

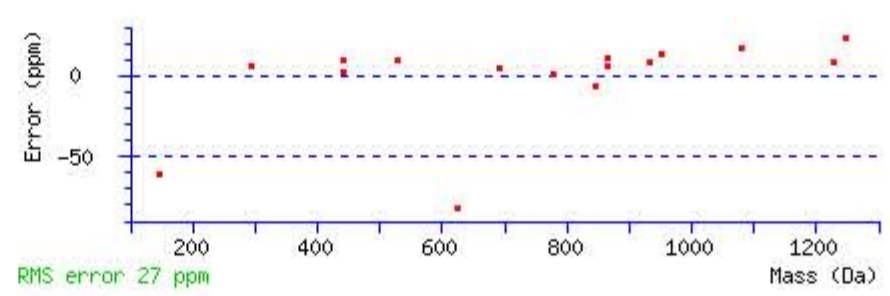
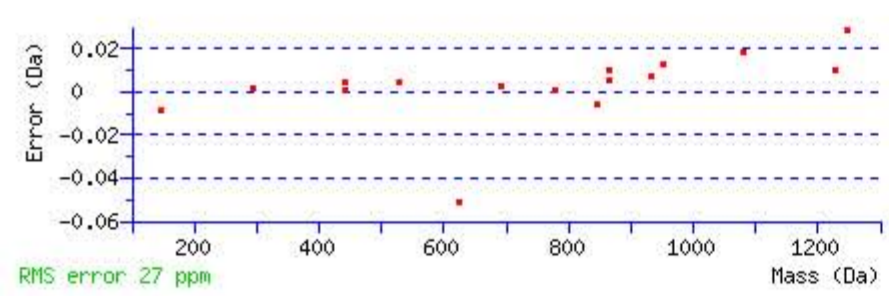
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.00036

Matches : 16/88 fragment ions using 36 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	440.232602	220.619939	423.206053	212.106664			Q							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
40.4	1390.659119	0.006829	QSSSYSFFK
3.5	1390.670135	-0.004187	YRNQESKSSHR
3.2	1390.669678	-0.003730	QEMAIQQLGMR
2.3	1390.655075	0.010873	IHEQDQLYSMK
2.0	1390.676208	-0.010260	AEKSSSTDQK
1.7	1390.669678	-0.003730	CAPASIRLMDNK
1.4	1390.672821	-0.006873	QQLENNLEEFK

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 44409: 1891.878882 from(631.633570,3+) rtinseconds(2138) index(37246)

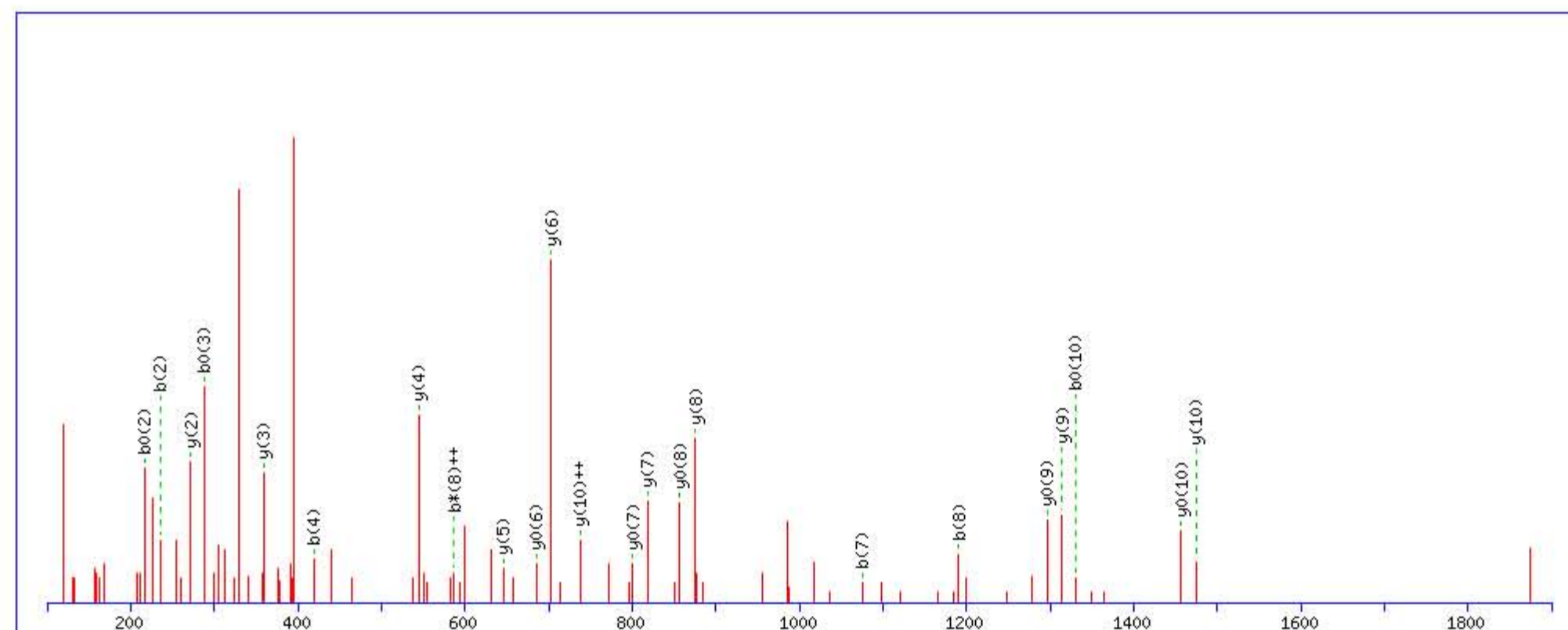
Title: Locus:1.1.1.3164.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1891.870941

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

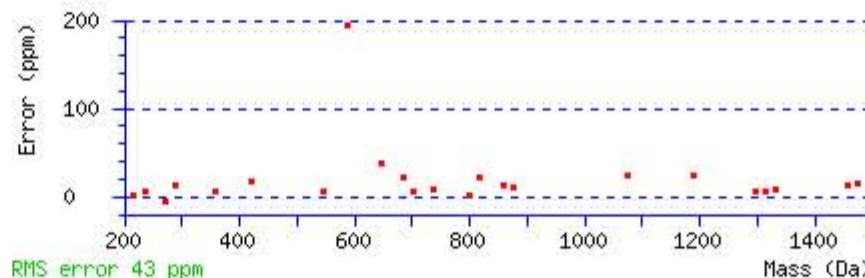
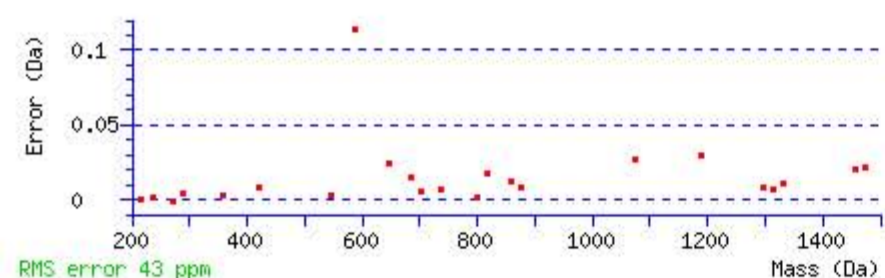
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 39 Expect: 0.0019

Matches : 23/140 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	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
38.7	1891.870941	0.007941	FSAICQGDGTWSPR

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 47664: 2017.031712 from(673.351180,3+) rtinseconds(2070) index(36836)

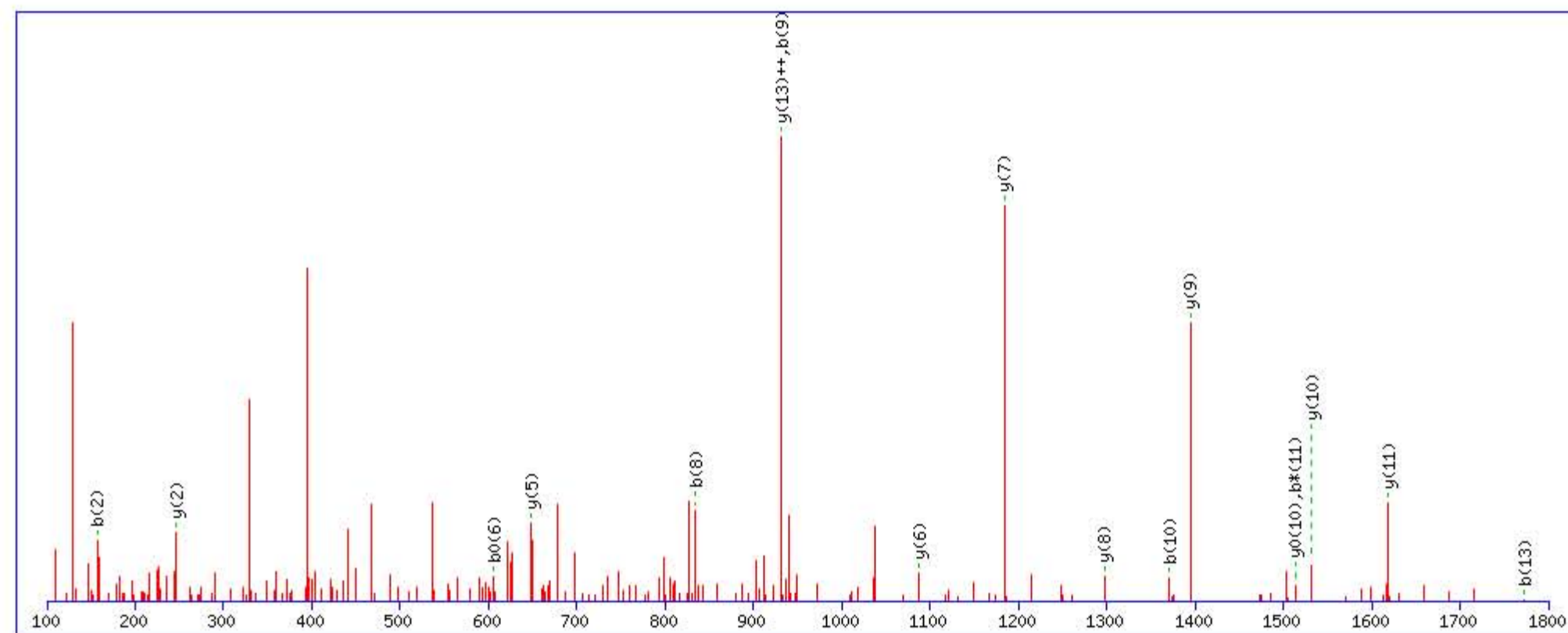
Title: Locus:1.1.1.3140.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2017.027771

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

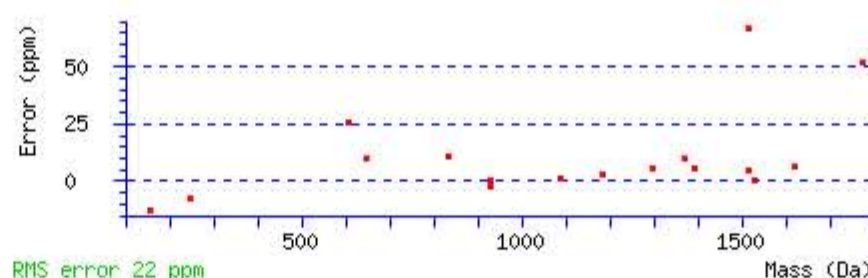
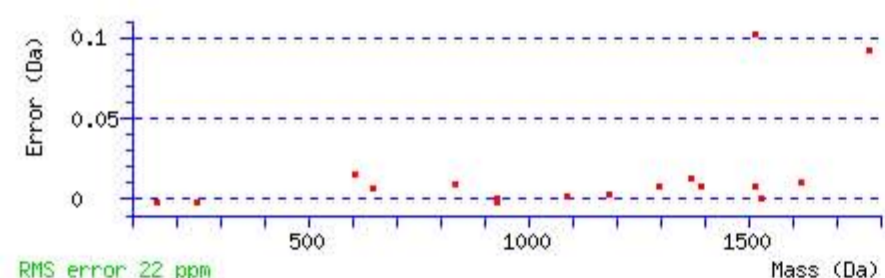
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 34 Expect: 0.013

Matches : 17/136 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							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
33.5	2017.027771	0.003941	GVGWSHPLPQCEIVK

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 50865: 2188.986132 from(730.669320,3+) rtinseconds(1769) index(34880)

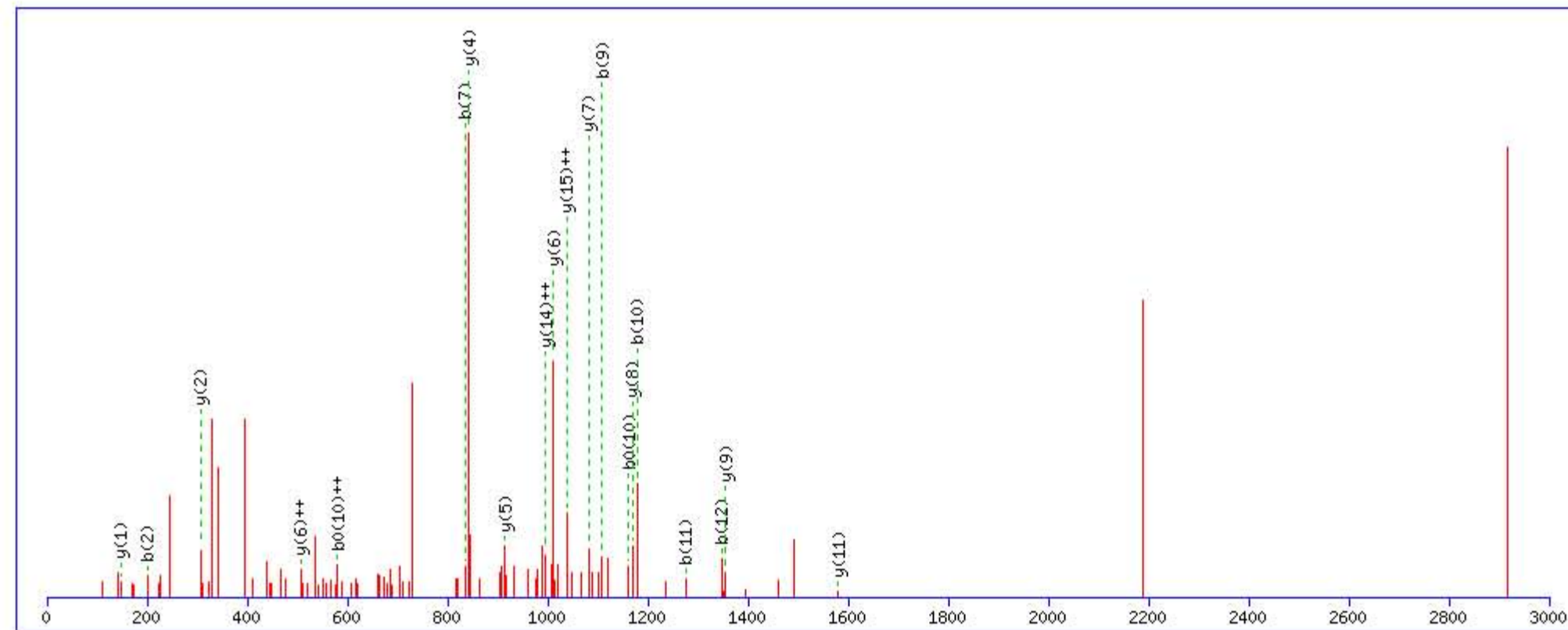
Title: Locus:1.1.1.3035.17 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2188.985626

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

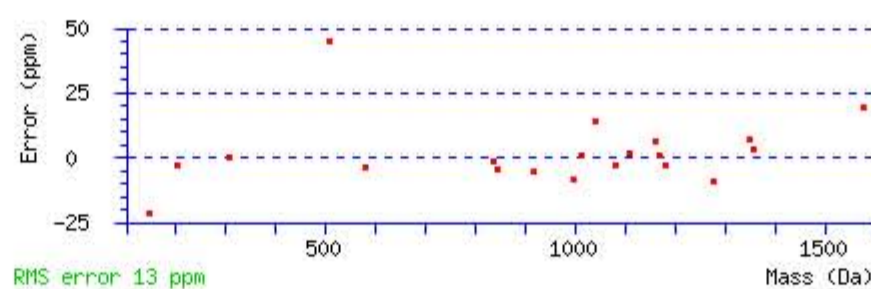
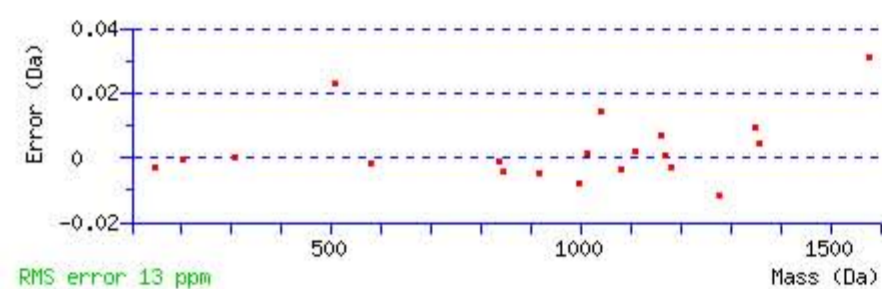
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 31 Expect: 0.008

Matches : 20/138 fragment ions using 54 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							16
2	201.123368	101.065322			183.112803	92.060039	S	2076.908850	1038.958063	2059.882301	1030.444788	2058.898285	1029.952780	15
3	361.154017	181.080647			343.143452	172.075364	C	1989.876822	995.442049	1972.850273	986.928775	1971.866257	986.436767	14
4	448.186045	224.596660			430.175480	215.591378	S	1829.846173	915.426725	1812.819624	906.913450	1811.835608	906.421442	13
5	611.249374	306.128325			593.238809	297.123043	Y	1742.814145	871.910711	1725.787596	863.397436	1724.803580	862.905428	12
6	698.281402	349.644339			680.270837	340.639056	S	1579.750816	790.379046	1562.724267	781.865772	1561.740251	781.373764	11
7	835.340314	418.173795			817.329749	409.168512	H	1492.718788	746.863032	1475.692239	738.349758	1474.708223	737.857750	10
8	1021.419627	511.213452			1003.409062	502.208169	W	1355.659876	678.333576	1338.633327	669.820302	1337.649311	669.328294	9
9	1108.451655	554.729466			1090.441090	545.724183	S	1169.580563	585.293920	1152.554014	576.780645	1151.569998	576.288637	8
10	1179.488769	590.248023			1161.478204	581.242740	A	1082.548535	541.777906	1065.521986	533.264631			7
11	1276.541533	638.774405			1258.530968	629.769122	P	1011.511421	506.259349	994.484872	497.746074			6
12	1347.578647	674.292962			1329.568082	665.287679	A	914.458657	457.732967	897.432108	449.219692			5
13	1444.631411	722.819344			1426.620846	713.814061	P	843.421543	422.214410	826.394994	413.701135			4
14	1883.856737	942.432007	1866.830188	933.918732	1865.846172	933.426724	Q	746.368779	373.688028	729.342230	365.174753			3
15	2043.887386	1022.447331	2026.860837	1013.934057	2025.876821	1013.442049	C	307.143453	154.075365	290.116904	145.562090			2
16							K	147.112804	74.060040	130.086255	65.546766			1



NCBI BLAST search of **LSCSYSHWSAPAPQCK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.9	2188.985626	0.000506	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 53115: 2306.018952 from(769.680260,3+) rtinseconds(2114) index(37103)

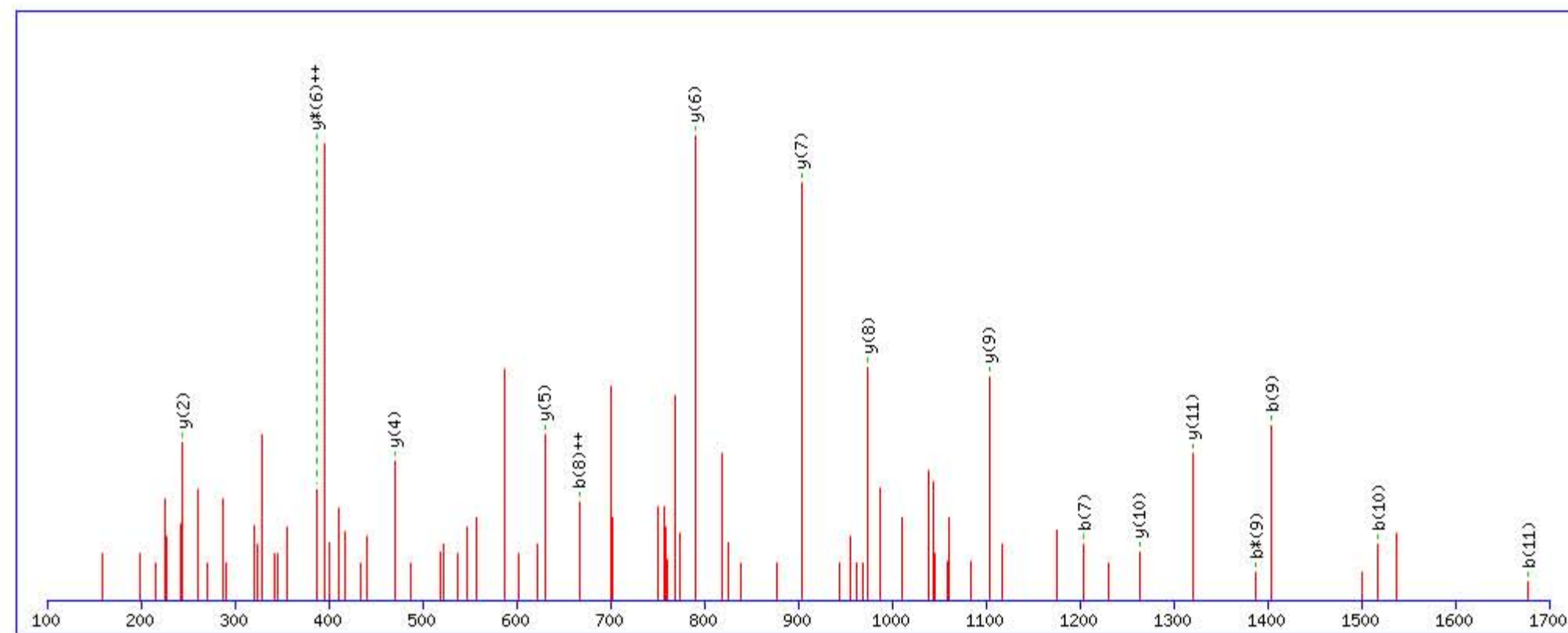
Title: Locus:1.1.1.3155.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2305.999237

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

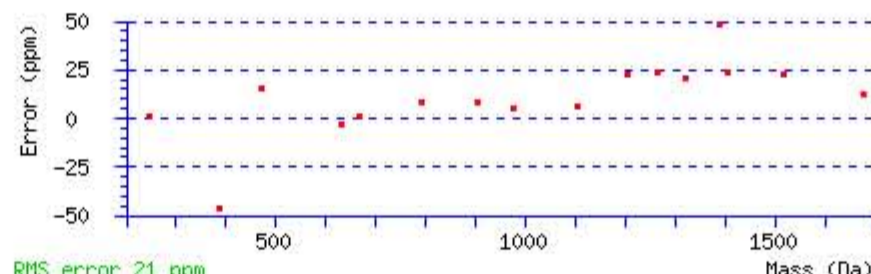
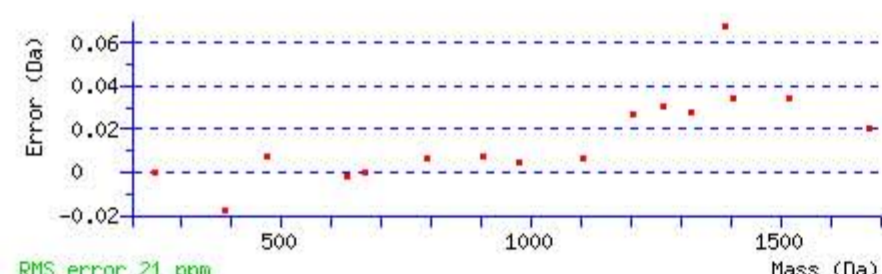
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 47 Expect: 0.00015

Matches : 16/166 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	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	$M_r(\text{calc})$	Delta	Sequence
46.7	2305.999237	0.019715	WTPYQGCEALCCPEPK

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

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 44915: 1919.003468 from(960.509010,2+) rtinseconds(2470) index(39236)

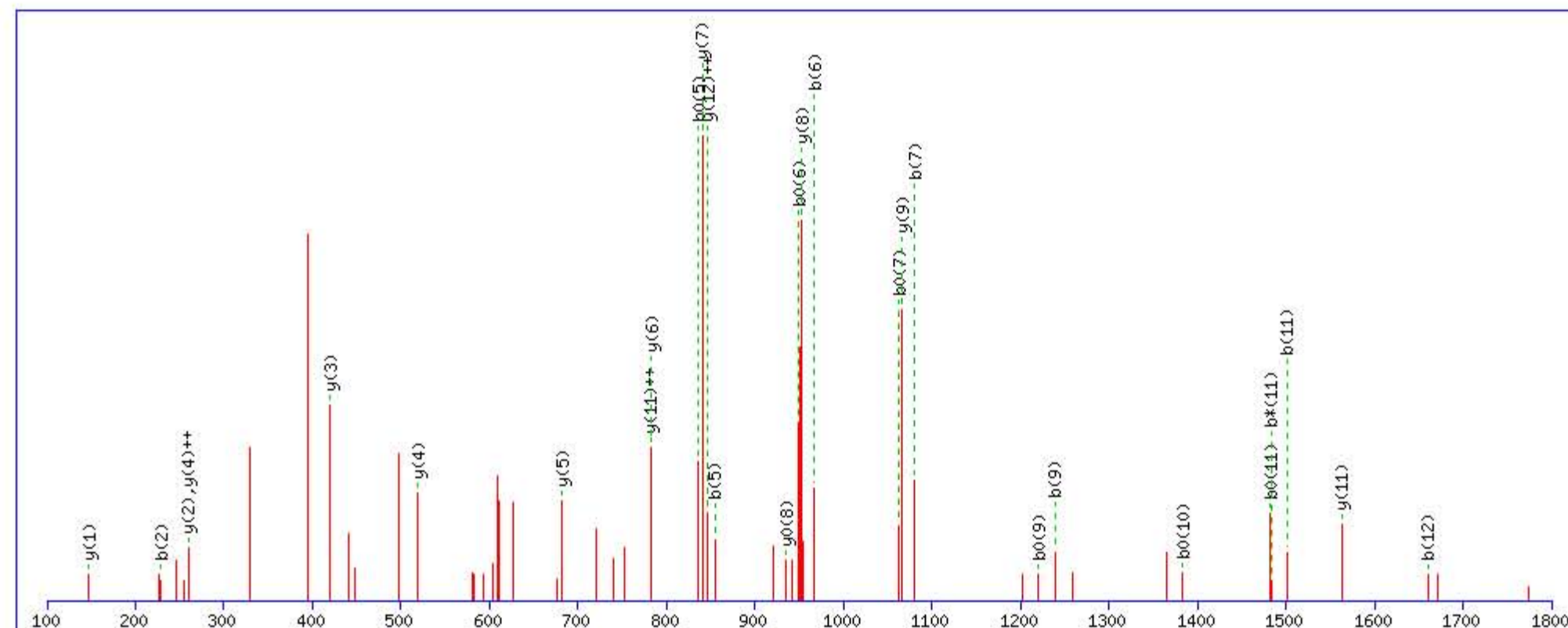
Title: Locus:1.1.1.3279.26 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1918.989639

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

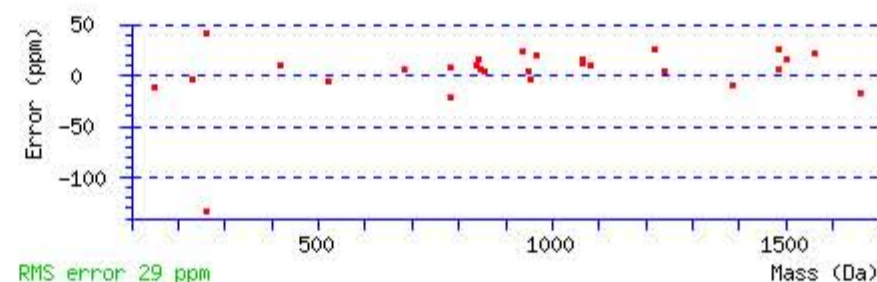
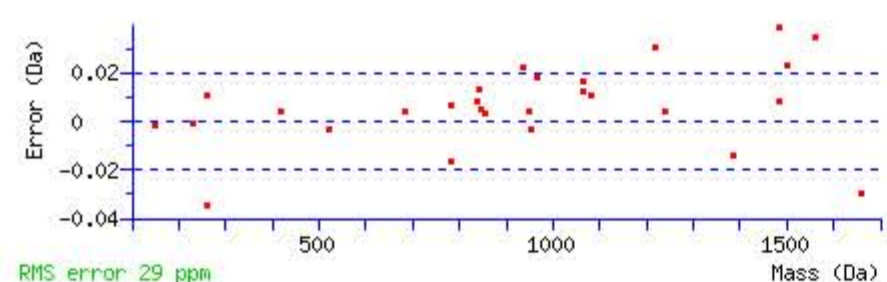
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 56 Expect: 7.2e-005

Matches : 28/138 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	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
55.5	1918.989639	0.013829	EVEGQILGTYVCIK

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

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLCEAMENFMQQLK**

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

Match to Query 48688: 2065.953492 from(689.658440,3+) rtinseconds(3093) index(43559)

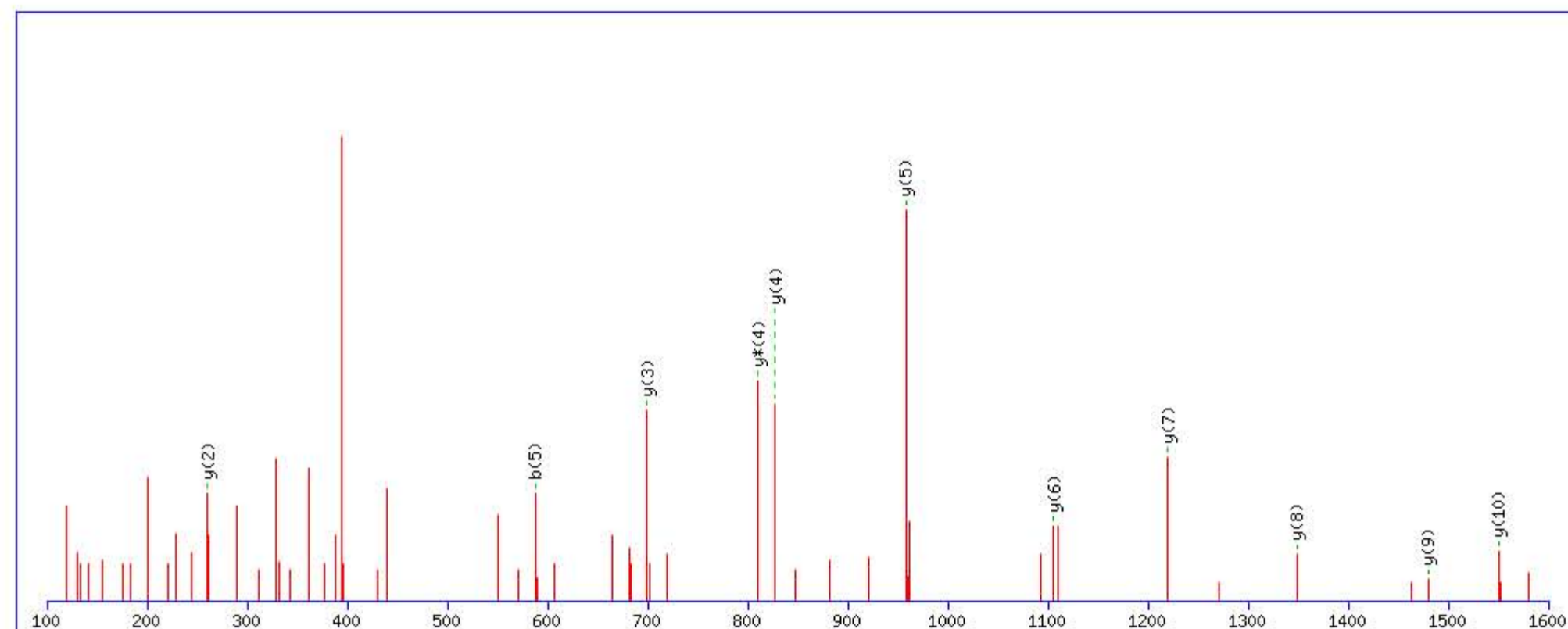
Title: Locus:1.1.1.3493.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2065.945709

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

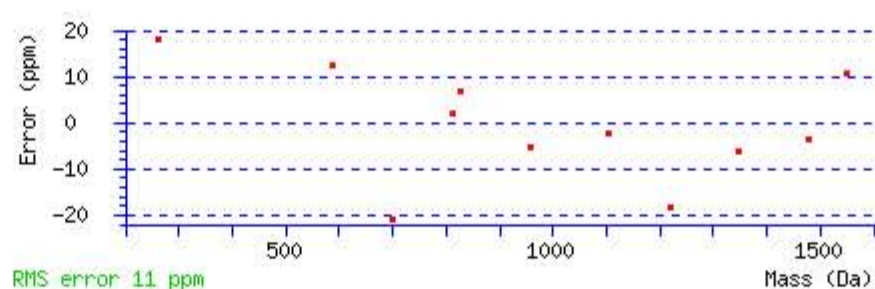
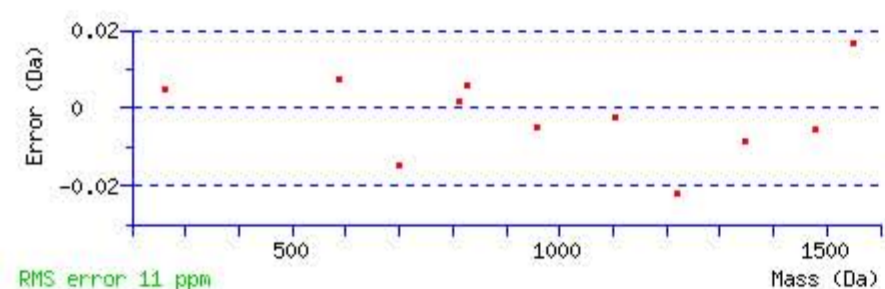
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 65 Expect: 4e-006

Matches : 11/136 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	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
65.3	2065.945709	0.007783	NLCEAMENFMQQLK
50.9	2065.945709	0.007783	NLCEAMENFMQQLK

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

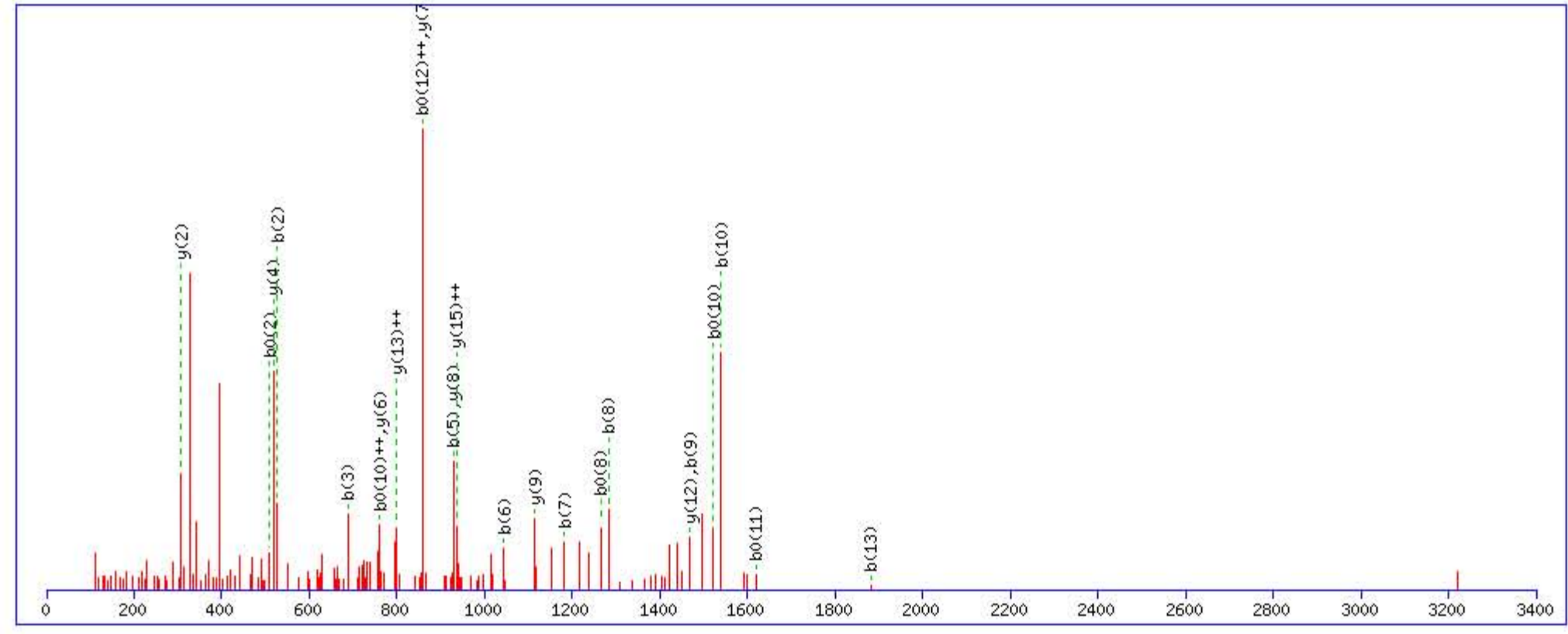
MASCOT Search Results

Peptide View

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

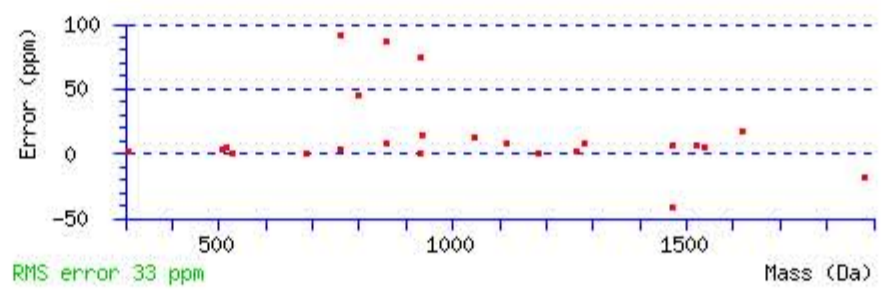
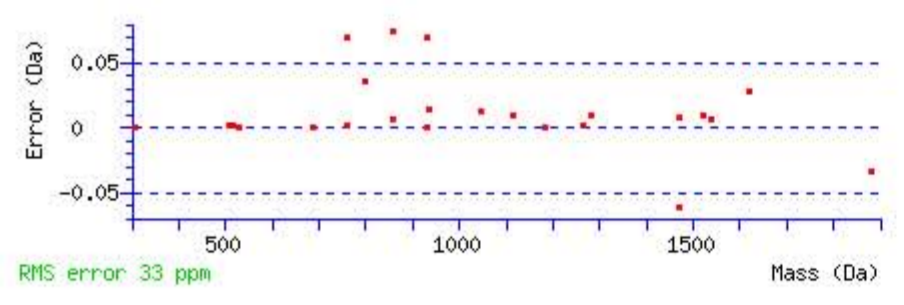
Match to Query 54240: 2396.131002 from(799.717610,3+) rtinseconds(2326) index(38370)
 Title: Locus:1.1.1.3229.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2396.111572
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q2 : Biotin:Thermo-21345 (Q)
 Ions Score: 56 Expect: 5.5e-005
 Matches : 24/172 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							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 **SQCLEDHTWAPFPICK**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.6	2396.111572	0.019430	SQCLEDHTWAPFPICK

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 26446: 1968.958872 from(657.326900,3+) rtinseconds(2305) index(38268)

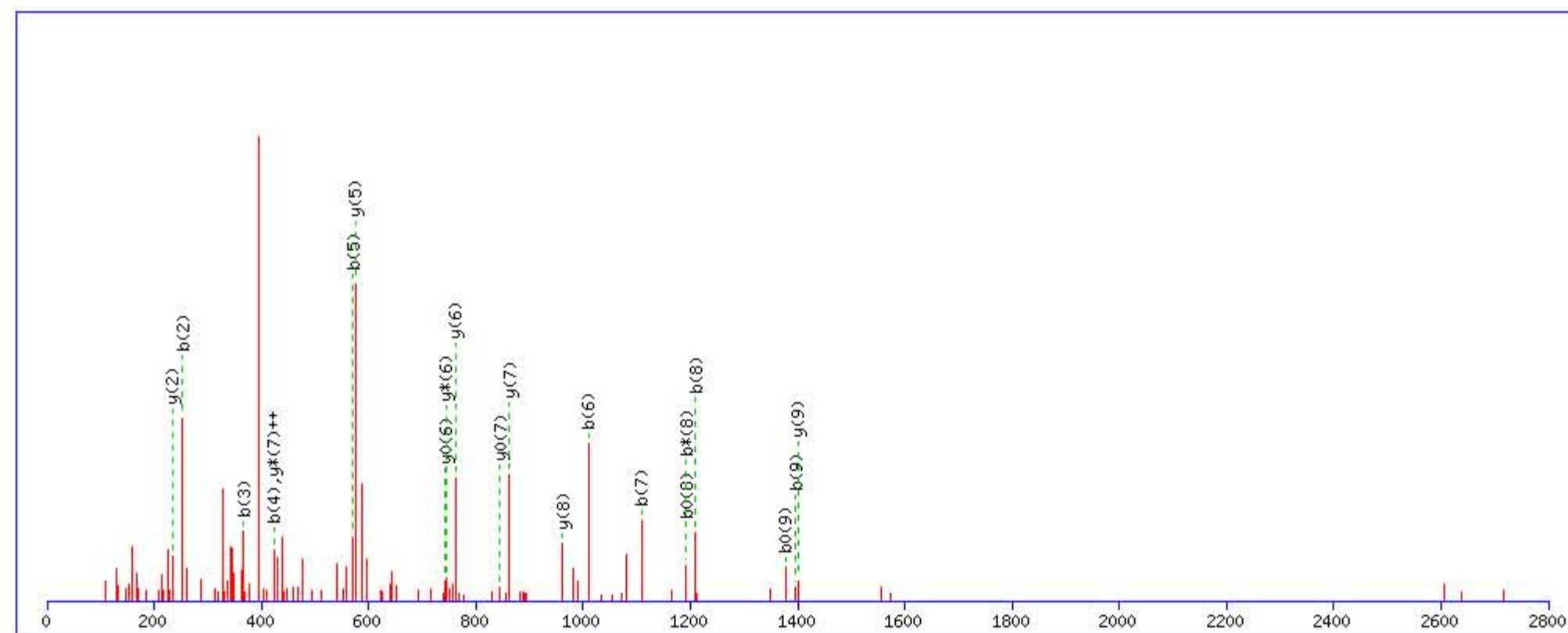
Title: Locus:1.1.1.3222.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1968.940399

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

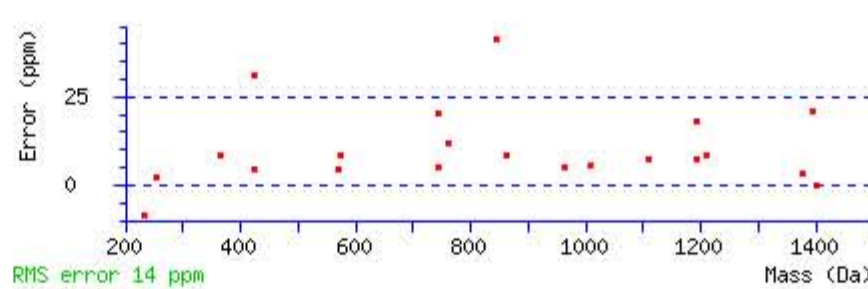
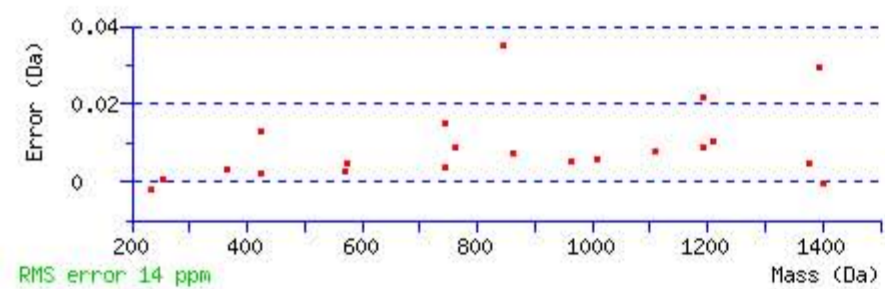
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 38 Expect: 0.0011

Matches : 21/144 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	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
37.9	1968.940399	0.018473	DHLGFQVTWPDESK
6.5	1968.949585	0.009287	EGQMESVEAAMSSKTLKK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SQCTYSNPEGTVVLACDQAQCR**

Found in **CPN2_HUMAN**, Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

Match to Query 60277: 2854.270512 from(952.430780,3+) rtinseconds(2039) index(36632)

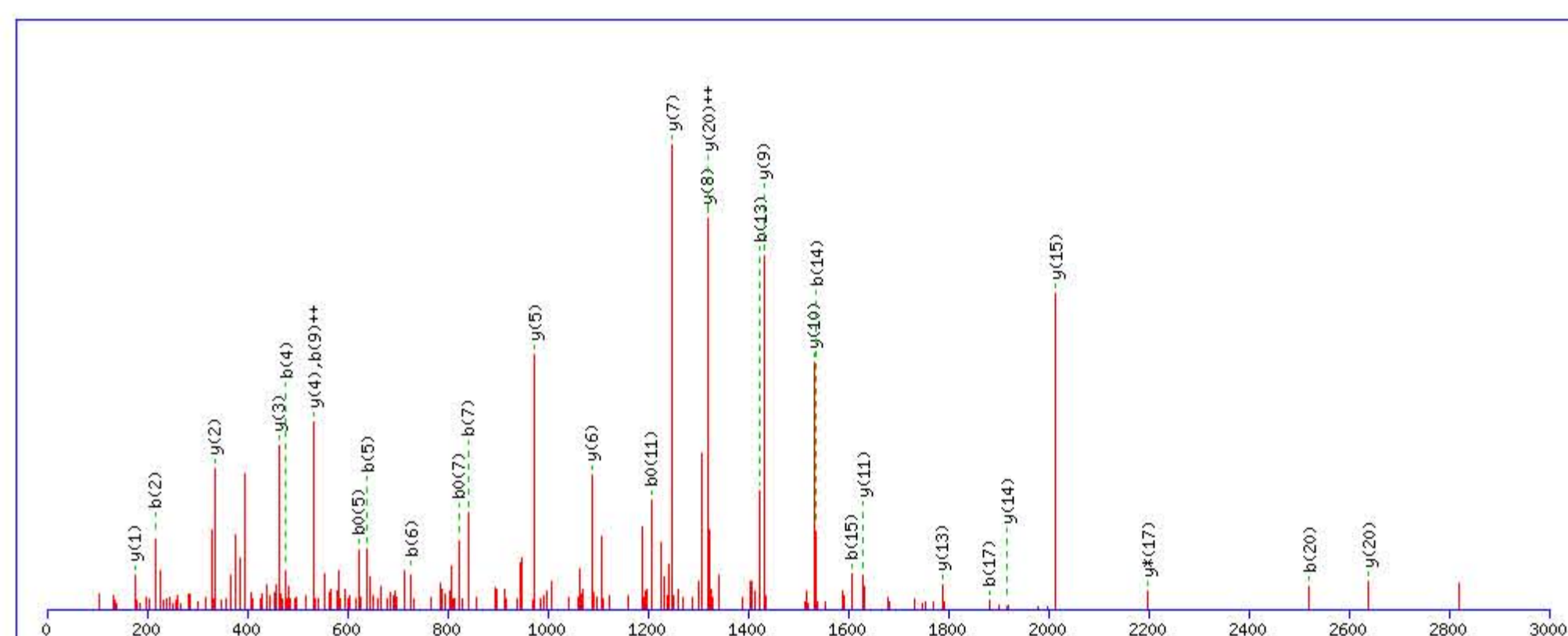
Title: Locus:1.1.1.3129.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2854.250671

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

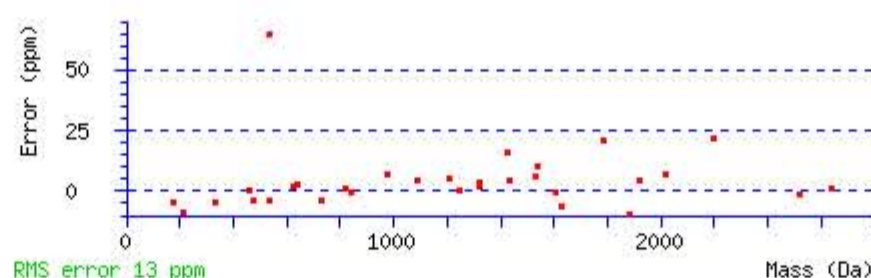
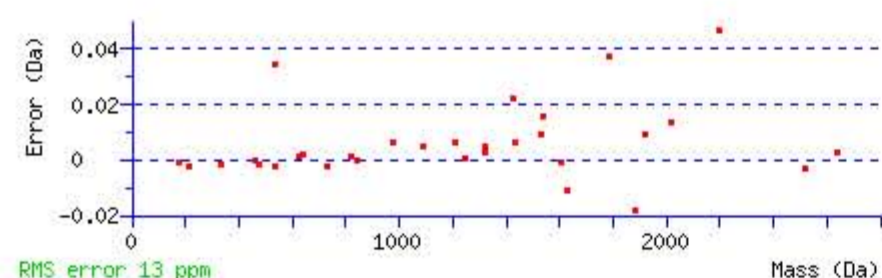
Variable modifications:

Q18 : Biotin:Thermo-21345 (Q)

Ions Score: 111 Expect: 5.1e-011

Matches : 31/240 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							22
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	Q	2768.225907	1384.616591	2751.199358	1376.103317	2750.215342	1375.611309	21
3	376.128531	188.567904	359.101982	180.054629	358.117966	179.562621	C	2640.167329	1320.587302	2623.140780	1312.074028	2622.156764	1311.582020	20
4	477.176210	239.091743	460.149661	230.578469	459.165645	230.086461	T	2480.136680	1240.571978	2463.110131	1232.058703	2462.126115	1231.566695	19
5	640.239539	320.623408	623.212990	312.110133	622.228974	311.618125	Y	2379.089001	1190.048138	2362.062452	1181.534864	2361.078436	1181.042856	18
6	727.271567	364.139422	710.245018	355.626147	709.261002	355.134139	S	2216.025672	1108.516474	2198.999123	1100.003199	2198.015107	1099.511191	17
7	841.314494	421.160885	824.287945	412.647611	823.303929	412.155603	N	2128.993644	1065.000460	2111.967095	1056.487185	2110.983079	1055.995177	16
8	938.367258	469.687267	921.340709	461.173993	920.356693	460.681985	P	2014.950717	1007.978997	1997.924168	999.465722	1996.940152	998.973714	15
9	1067.409851	534.208564	1050.383302	525.695289	1049.399286	525.203281	E	1917.897953	959.452615	1900.871404	950.939340	1899.887388	950.447332	14
10	1124.431315	562.719296	1107.404766	554.206021	1106.420750	553.714013	G	1788.855360	894.931318	1771.828811	886.418044	1770.844795	885.926036	13
11	1225.478994	613.243135	1208.452445	604.729861	1207.468429	604.237853	T	1731.833896	866.420586	1714.807347	857.907312	1713.823331	857.415304	12
12	1324.547408	662.777342	1307.520859	654.264068	1306.536843	653.772060	V	1630.786217	815.896747	1613.759668	807.383472	1612.775652	806.891464	11
13	1423.615822	712.311549	1406.589273	703.798275	1405.605257	703.306267	V	1531.717803	766.362540	1514.691254	757.849265	1513.707238	757.357257	10
14	1536.699886	768.853581	1519.673337	760.340307	1518.689321	759.848299	L	1432.649389	716.828333	1415.622840	708.315058	1414.638824	707.823050	9
15	1607.737000	804.372138	1590.710451	795.858864	1589.726435	795.366856	A	1319.565325	660.286301	1302.538776	651.773026	1301.554760	651.281018	8
16	1767.767649	884.387463	1750.741100	875.874188	1749.757084	875.382180	C	1248.528211	624.767744	1231.501662	616.254469	1230.517646	615.762461	7
17	1882.794592	941.900934	1865.768043	933.387660	1864.784027	932.895652	D	1088.497562	544.752419	1071.471013	536.239145	1070.486997	535.747137	6
18	2322.019918	1161.513597	2304.993369	1153.000322	2304.009353	1152.508314	Q	973.470619	487.238948	956.444070	478.725673			5
19	2393.057032	1197.032154	2376.030483	1188.518879	2375.046467	1188.026872	A	534.245293	267.626285	517.218744	259.113010			4
20	2521.115610	1261.061443	2504.089061	1252.548169	2503.105045	1252.056161	Q	463.208179	232.107727	446.181630	223.594453			3
21	2681.146259	1341.076768	2664.119710	1332.563493	2663.135694	1332.071485	C	335.149601	168.078438	318.123052	159.565164			2
22							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **SQCTYSNPEGTVVLACDQAQCR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
111.4	2854.250671	0.019841	SQCTYSNPEGTVVLACDQAQCR
90.1	2854.250671	0.019841	SQCTYSNPEGTVVLACDQAQCR
9.3	2854.250671	0.019841	SQCTYSNPEGTVVLACDQAQCR

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

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 27036: 1341.673848 from(671.844200,2+) rtinseconds(1599) index(50236)

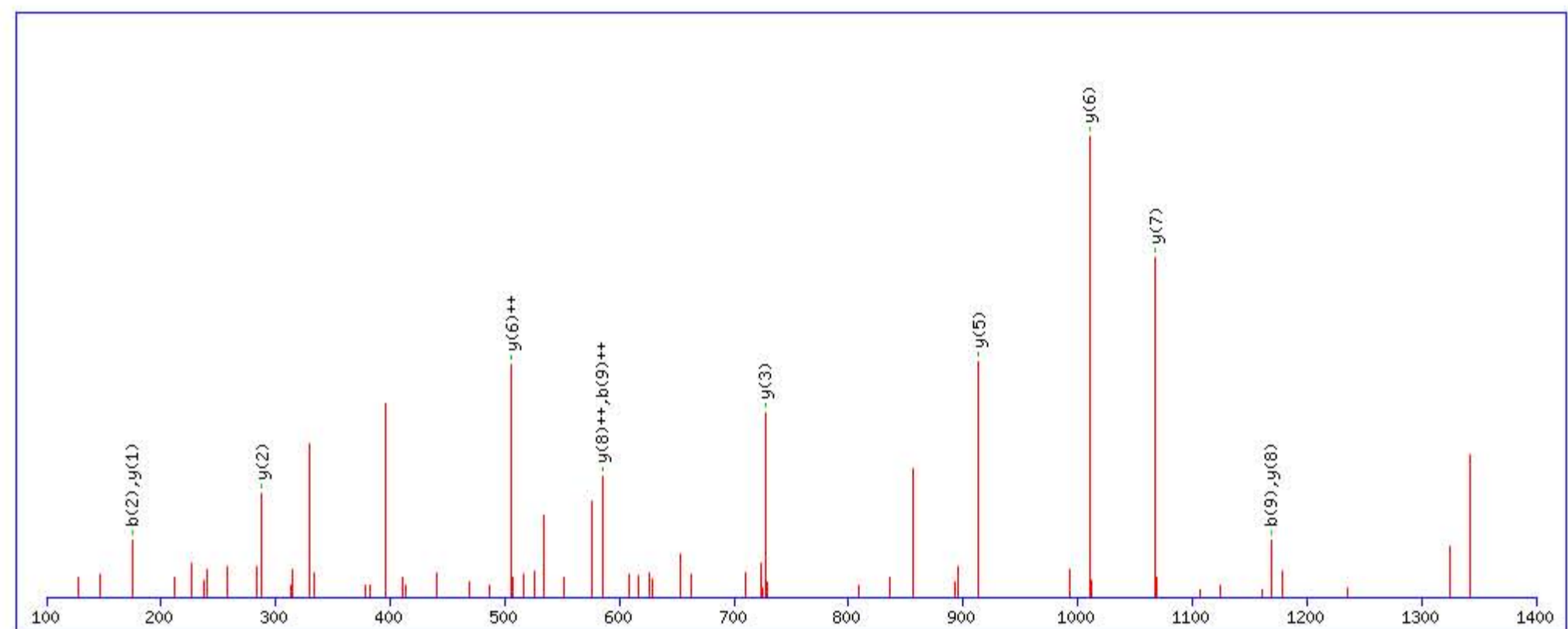
Title: Locus:1.1.1.1172.14 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1341.671082

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

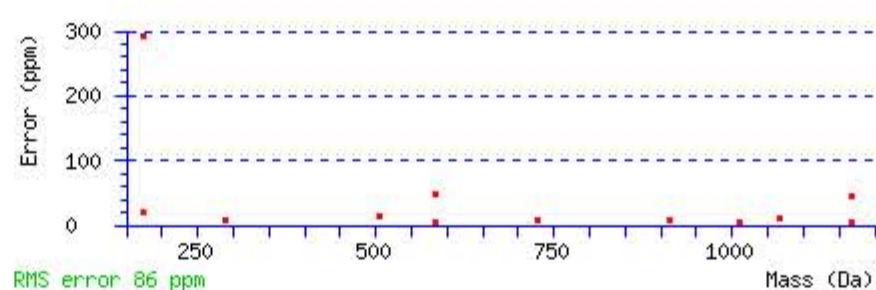
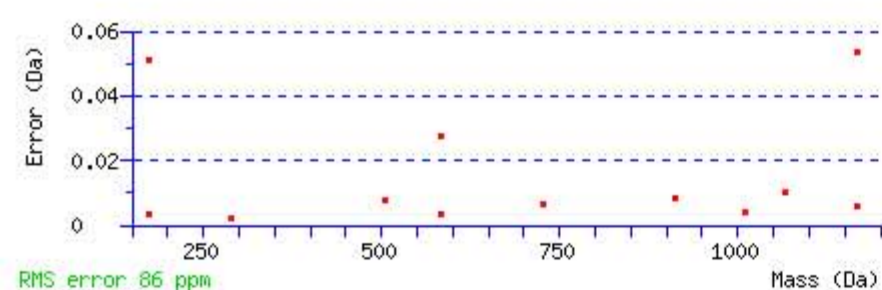
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 67 Expect: 3.7e-006

Matches : 12/88 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
67.2	1341.671082	0.002766	SSTGPGEQLR
14.0	1341.674911	-0.001063	TSPERREPGTGR
13.7	1341.663651	0.010197	ESARDPKPEASR
10.0	1341.663681	0.010167	SSHKDSPRDVSK
9.9	1341.688828	-0.014980	DDAQLSGLPSALR
9.5	1341.682297	-0.008449	ASEQDVRAR
9.5	1341.693512	-0.019664	ASEQERRR
8.6	1341.686325	-0.012477	SMKQLTSHPWK
7.0	1341.653793	0.020055	GFAEHGKQQQGR
6.4	1341.686340	-0.012492	GSGIQWDLR

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

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **NALWHTGDTESQVR**

Found in **COMP_HUMAN**, Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=1 SV=2

Match to Query 45032: 1923.932982 from(642.318270,3+) rtinseconds(1791) index(51457)

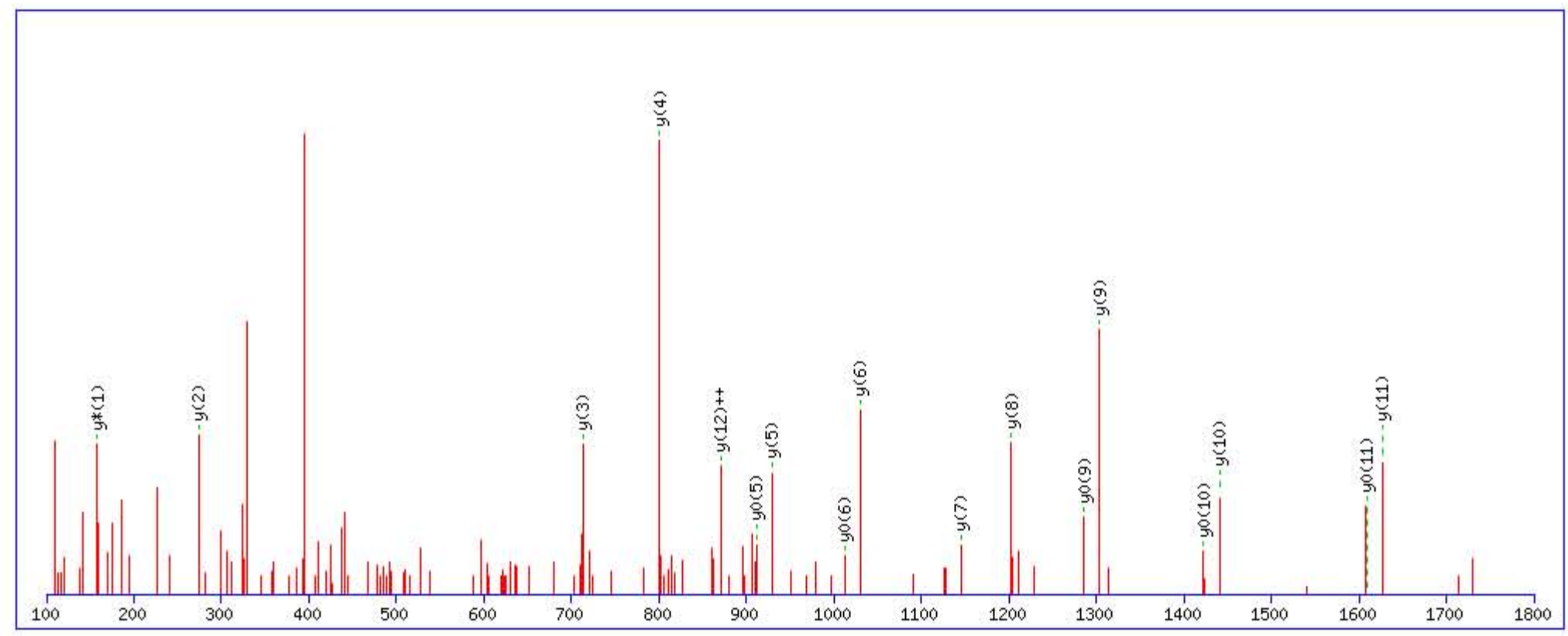
Title: Locus:1.1.1.1239.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1923.926132

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

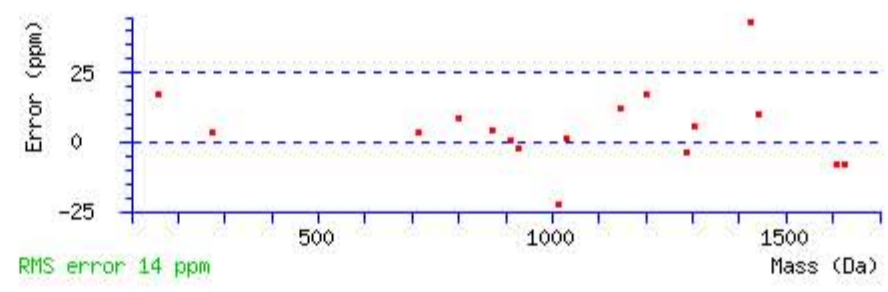
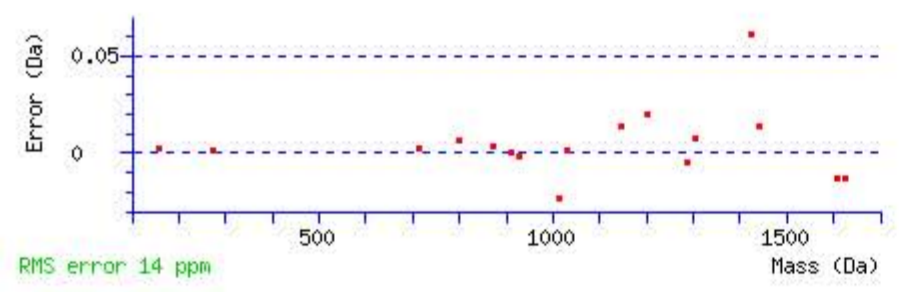
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 58 Expect: 3.7e-005

Matches : 17/140 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	115.050203	58.028740	98.023654	49.515465			N							14
2	186.087317	93.547296	169.060768	85.034022			A	1810.890481	905.948879	1793.863932	897.435604	1792.879916	896.943596	13
3	299.171381	150.089328	282.144832	141.576054			L	1739.853367	870.430322	1722.826818	861.917047	1721.842802	861.425039	12
4	485.250694	243.128985	468.224145	234.615711			W	1626.769303	813.888290	1609.742754	805.375015	1608.758738	804.883007	11
5	622.309606	311.658441	605.283057	303.145167			H	1440.689990	720.848633	1423.663441	712.335359	1422.679425	711.843351	10
6	723.357285	362.182281	706.330736	353.669006	705.346720	353.176998	T	1303.631078	652.319177	1286.604529	643.805903	1285.620513	643.313895	9
7	780.378749	390.693013	763.352200	382.179738	762.368184	381.687730	G	1202.583399	601.795338	1185.556850	593.282063	1184.572834	592.790055	8
8	895.405692	448.206484	878.379143	439.693210	877.395127	439.201202	D	1145.561935	573.284606	1128.535386	564.771331	1127.551370	564.279323	7
9	996.453371	498.730324	979.426822	490.217049	978.442806	489.725041	T	1030.534992	515.771134	1013.508443	507.257860	1012.524427	506.765852	6
10	1125.495964	563.251620	1108.469415	554.738346	1107.485399	554.246337	E	929.487313	465.247295	912.460764	456.734020	911.476748	456.242012	5
11	1212.527992	606.767634	1195.501443	598.254360	1194.517427	597.762352	S	800.444720	400.725998	783.418171	392.212724	782.434155	391.720716	4
12	1651.753318	826.380297	1634.726769	817.867023	1633.742753	817.375015	Q	713.412692	357.209984	696.386143	348.696710			3
13	1750.821732	875.914504	1733.795183	867.401230	1732.811167	866.909222	V	274.187366	137.597321	257.160817	129.084047			2
14							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [NALWHTGDTESQVR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.5	1923.926132	0.006850	NALWHTGDTESQVR

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 43647: 2777.256822 from(926.759550,3+) rtinseconds(2122) index(37166)

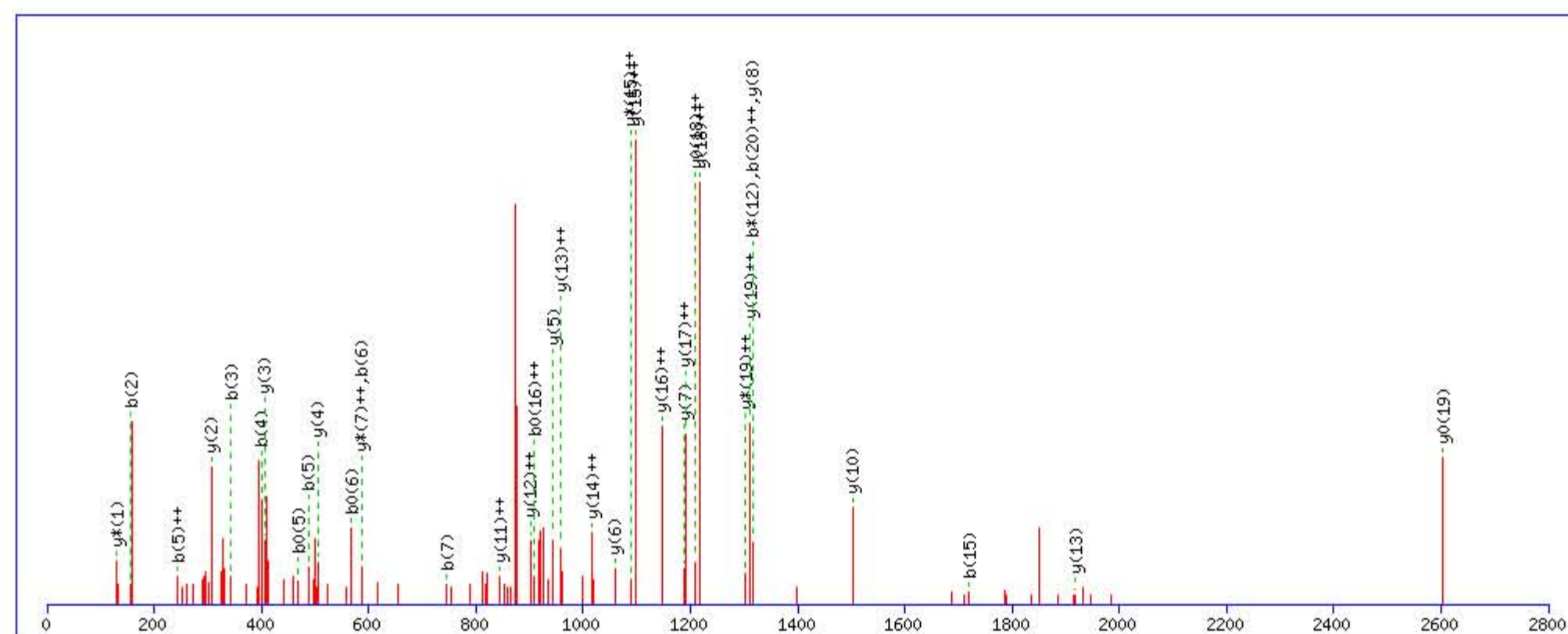
Title: Locus:1.1.1.3158.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2777.224792

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

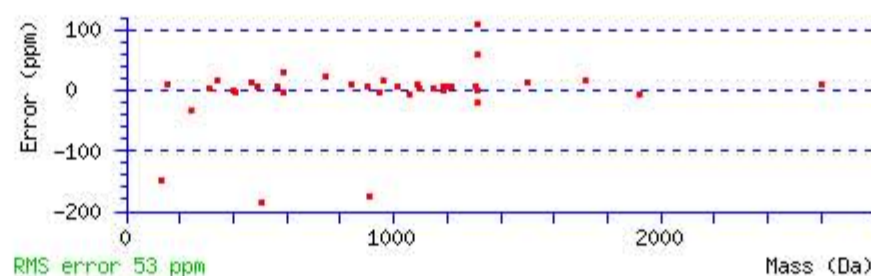
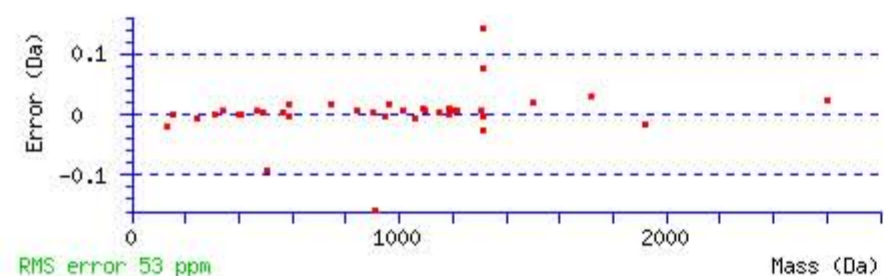
Variable modifications:

Q17 : Biotin:Thermo-21345 (Q)

Ions Score: 35 Expect: 0.0056

Matches : 37/204 fragment ions using 100 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							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



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
34.9	2777.224792	0.032030	GVWGSVCDDNWGEKEDQVVCK

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 57310: 2566.331816 from(642.590230,4+) rtinseconds(1979) index(52716)

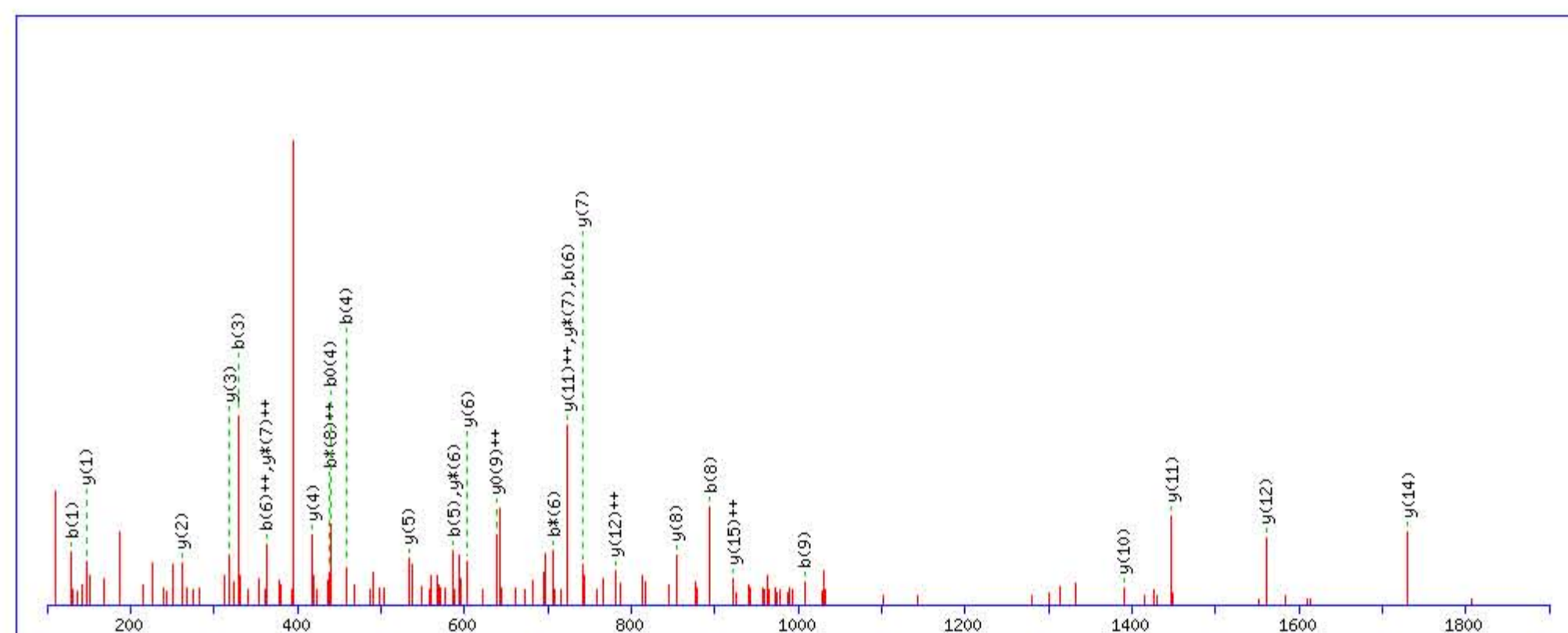
Title: Locus:1.1.1.1304.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2566.321335

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

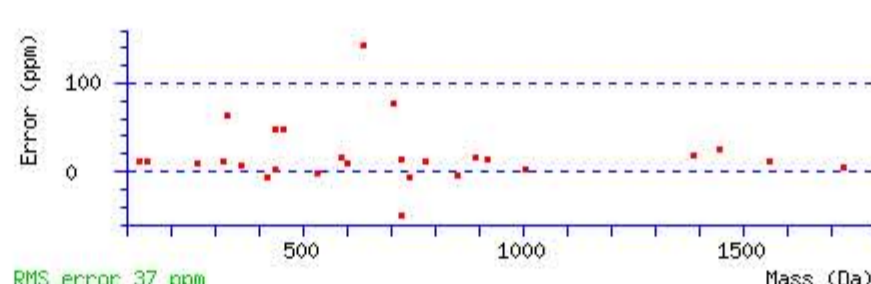
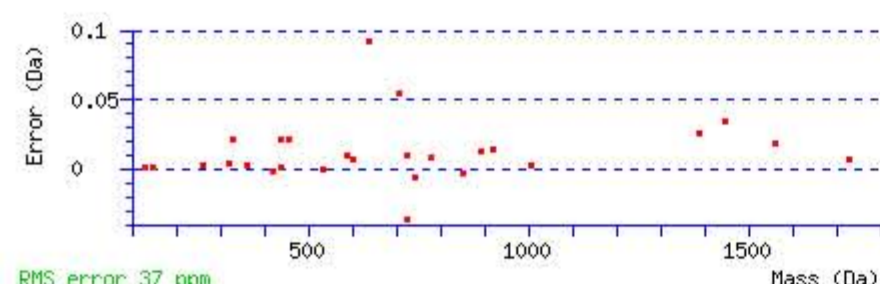
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 7.9e-007

Matches : 30/234 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	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
65.8	2566.321335	0.010481	KAEEEHLGILGPQLHADVGDK
0.7	2566.329437	0.002379	QMHGLRTLNIQCVRITDK

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **ASSIDELFQDR**

Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

Match to Query 40552: 1703.862508 from(852.938530,2+) rtinseconds(2841) index(26710)

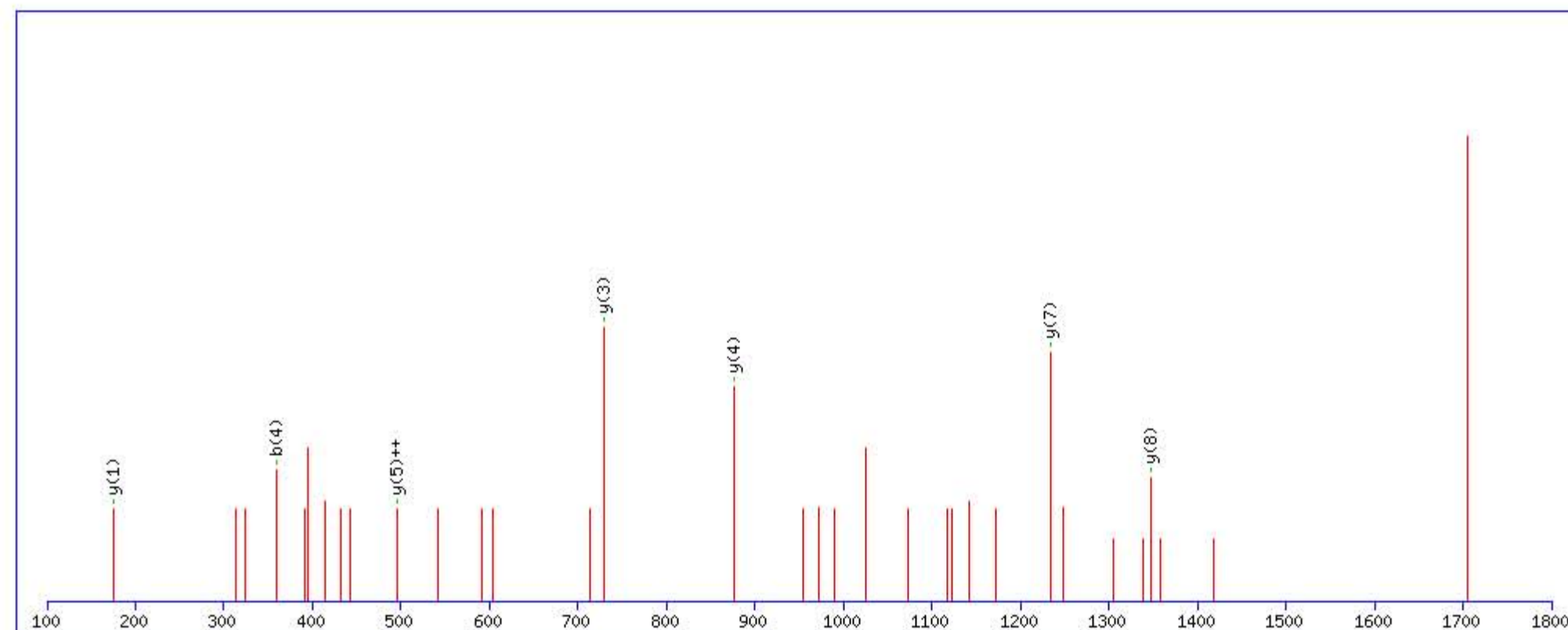
Title: Locus:1.1.1.990.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1703.855240

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

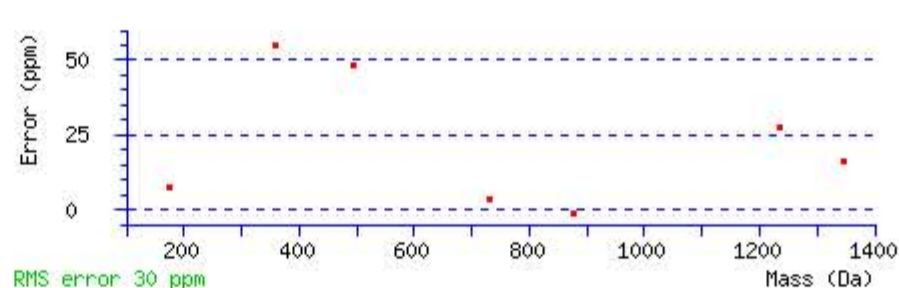
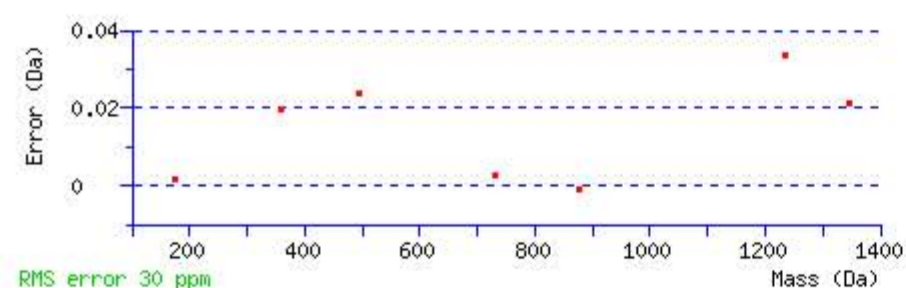
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.0032

Matches : 7/110 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	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 [ASSIDELFQDR](#)

(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	1703.855240	0.007268	ASSIDELFQDR
0.3	1703.877731	-0.015223	AVGMASDIPGLHLPGGGR

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

Peptide View

MS/MS Fragmentation of **RELDES LQVAER**

Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

Match to Query 41759: 1754.894262 from(585.972030,3+) rtinseconds(1753) index(34789)

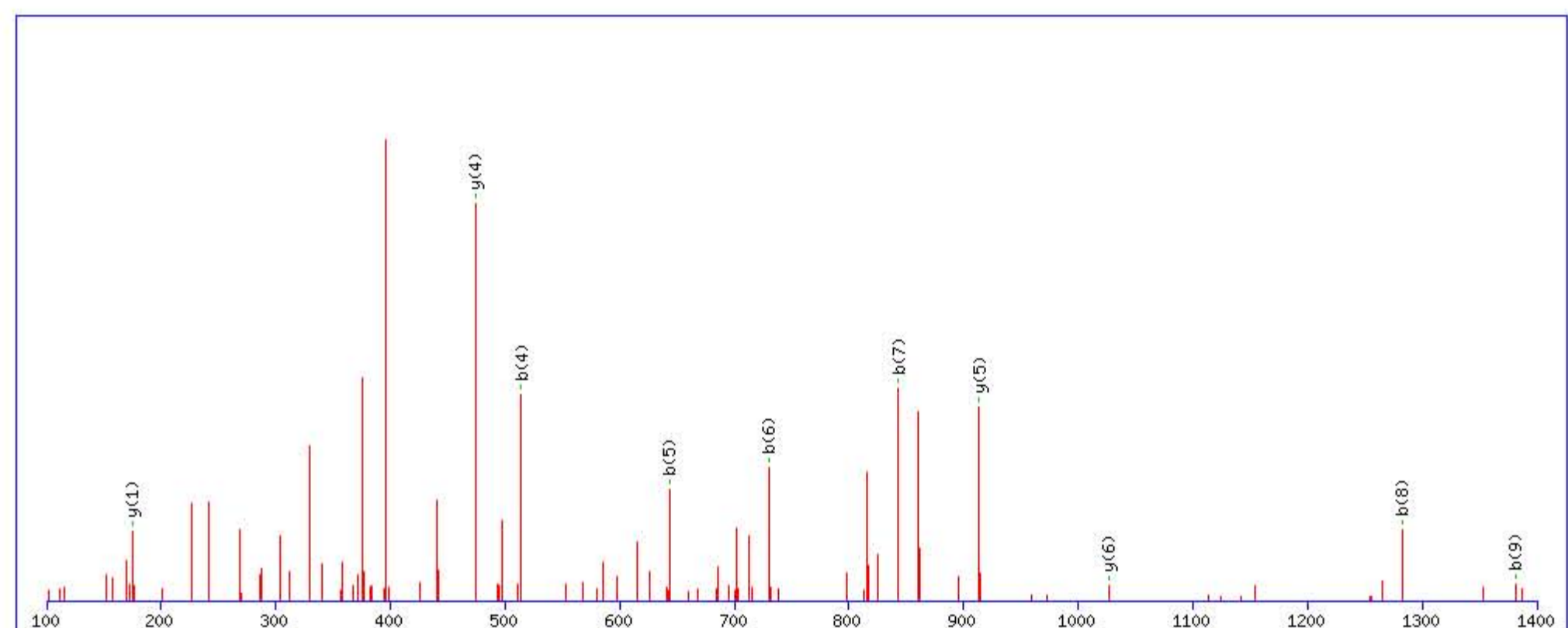
Title: Locus:1.1.1.3030.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\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): 1754.898483

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

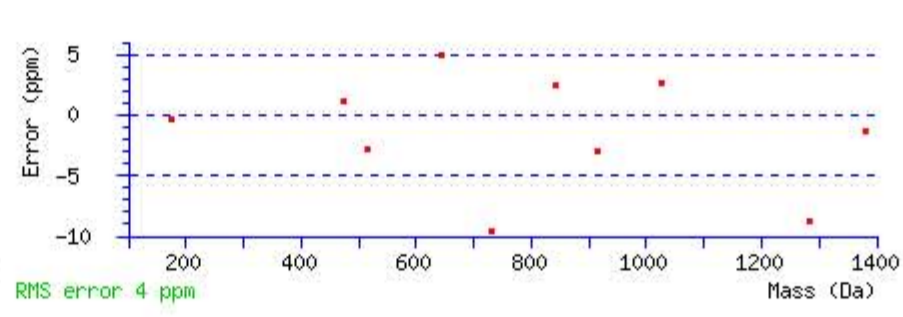
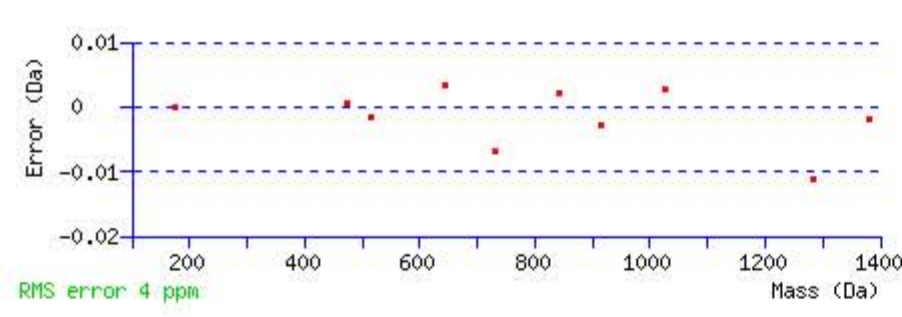
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 42 Expect: 0.00052

Matches : 10/128 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	157.108387	79.057831	140.081838	70.544557			R							12
2	286.150980	143.579128	269.124431	135.065854	268.140415	134.573846	E	1599.804684	800.405980	1582.778135	791.892706	1581.794119	791.400698	11
3	399.235044	200.121160	382.208495	191.607886	381.224479	191.115878	L	1470.762091	735.884684	1453.735542	727.371409	1452.751526	726.879401	10
4	514.261987	257.634632	497.235438	249.121357	496.251422	248.629349	D	1357.678027	679.342652	1340.651478	670.829377	1339.667462	670.337369	9
5	643.304580	322.155928	626.278031	313.642654	625.294015	313.150646	E	1242.651084	621.829180	1225.624535	613.315906	1224.640519	612.823898	8
6	730.336608	365.671942	713.310059	357.158668	712.326043	356.666660	S	1113.608491	557.307884	1096.581942	548.794609	1095.597926	548.302601	7
7	843.420672	422.213974	826.394123	413.700700	825.410107	413.208692	L	1026.576463	513.791870	1009.549914	505.278595	1008.565898	504.786587	6
8	1282.645998	641.826637	1265.619449	633.313363	1264.635433	632.821355	Q	913.492399	457.249838	896.465850	448.736563	895.481834	448.244555	5
9	1381.714412	691.360844	1364.687863	682.847570	1363.703847	682.355562	V	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
10	1452.751526	726.879401	1435.724977	718.366127	1434.740961	717.874119	A	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
11	1581.794119	791.400698	1564.767570	782.887423	1563.783554	782.395415	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
12							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **RELDES LQVAER**

(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	1754.898483	-0.004221	RELDES LQVAER
6.8	1754.873306	0.020956	EREQKEIEAMHSLR
4.1	1754.880737	0.013525	QQLLACAGVEAER
3.7	1754.898483	-0.004221	AEAQGKQEVESLR
2.3	1754.898483	-0.004221	RLEESDVLQEAR
1.8	1754.917130	-0.022868	LCVTIQEANQLR
1.4	1754.898483	-0.004221	AEAQGKQEVESLR
0.7	1754.896011	-0.001749	FCSPHQSLLSIR
0.4	1754.898514	-0.004252	DQGSPTLSANVSLR

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 48789: 2073.006368 from(1037.510460,2+) rtinseconds(1835) index(51777)

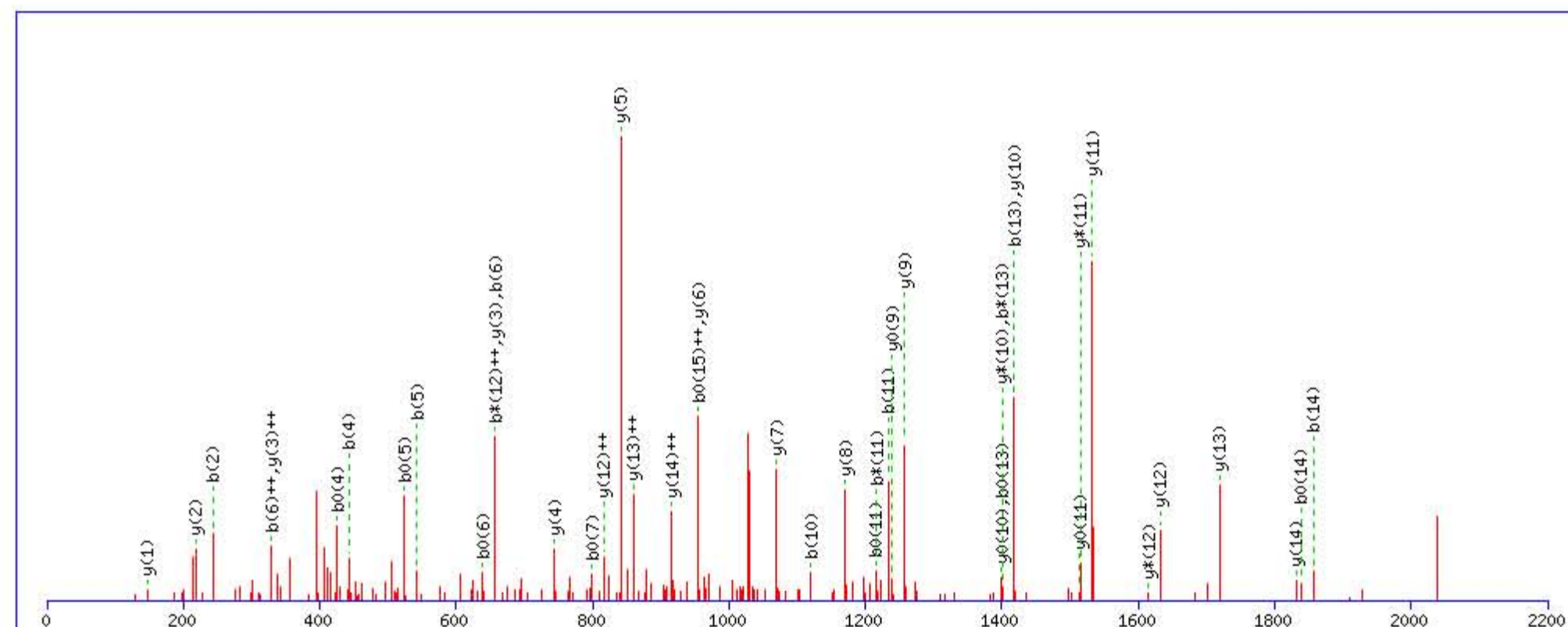
Title: Locus:1.1.1.1254.26 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2072.987061

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

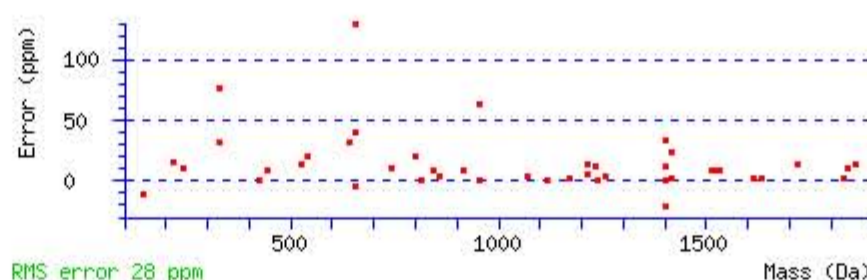
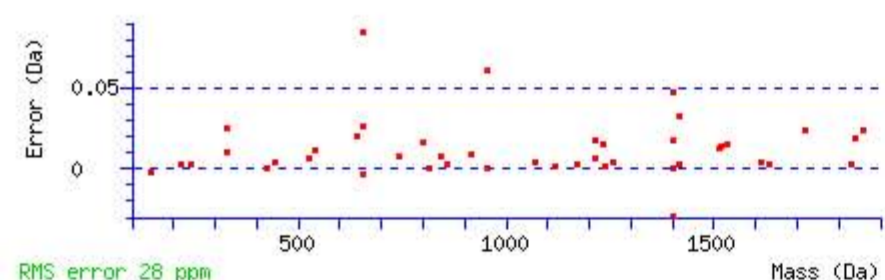
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 119 Expect: 2.5e-011

Matches : 44/156 fragment ions using 52 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							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
119.1	2072.987061	0.019307	EILSVDCSTNNPSQAK
5.7	2073.031265	-0.024897	YMEHEERPKALNDLGKK
5.0	2073.029984	-0.023616	LQDDSVETVTSIEQAK
2.5	2072.994492	0.011876	ELVKSGLGADGVCMTFMK
1.0	2073.016708	-0.010340	EGQIIKVVYGDKDADGFYR
0.3	2072.994904	0.011464	MQDPNADTEWNDILRKK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **QQTHMLDVMQDHF**SR

Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

Match to Query 50711: 2183.004096 from(546.758300,4+) rtinseconds(2009) index(36443)

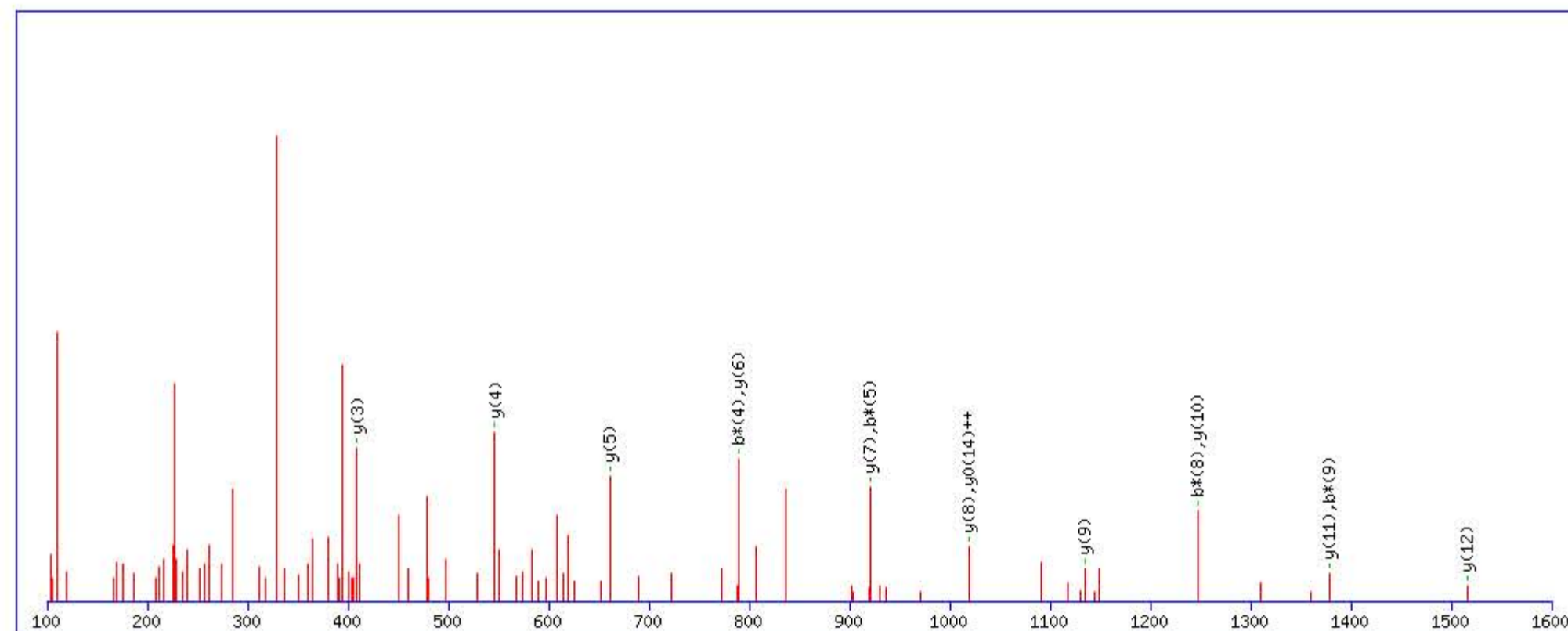
Title: Locus:1.1.1.3119.4 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2183.007446

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

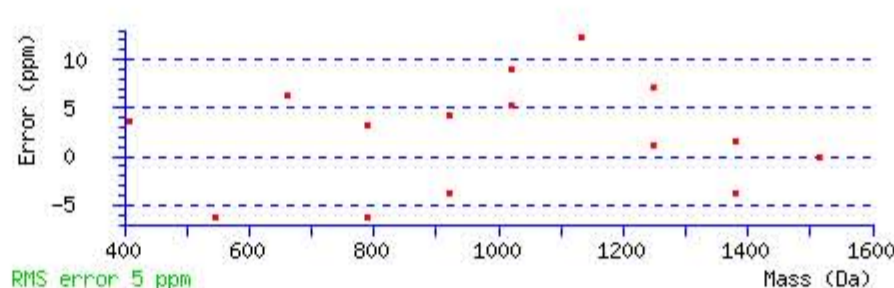
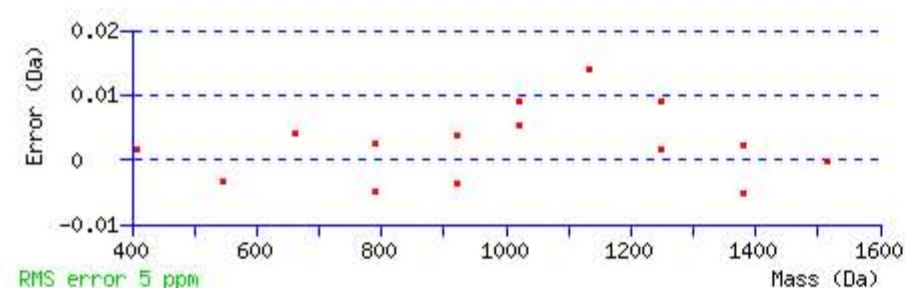
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 77 Expect: 2.7e-007

Matches : 15/162 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							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 **QQTHMLDVMQDHF**SR

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
76.5	2183.007446	-0.003350	QQTHMLDVMQDHF SR
76.5	2183.007446	-0.003350	QQTHMLDVMQDHF SR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **QQTHMLDVMQDHF^{SR}**

Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

Match to Query 50713: 2183.012176 from(546.760320,4+) rtinseconds(1981) index(21586)

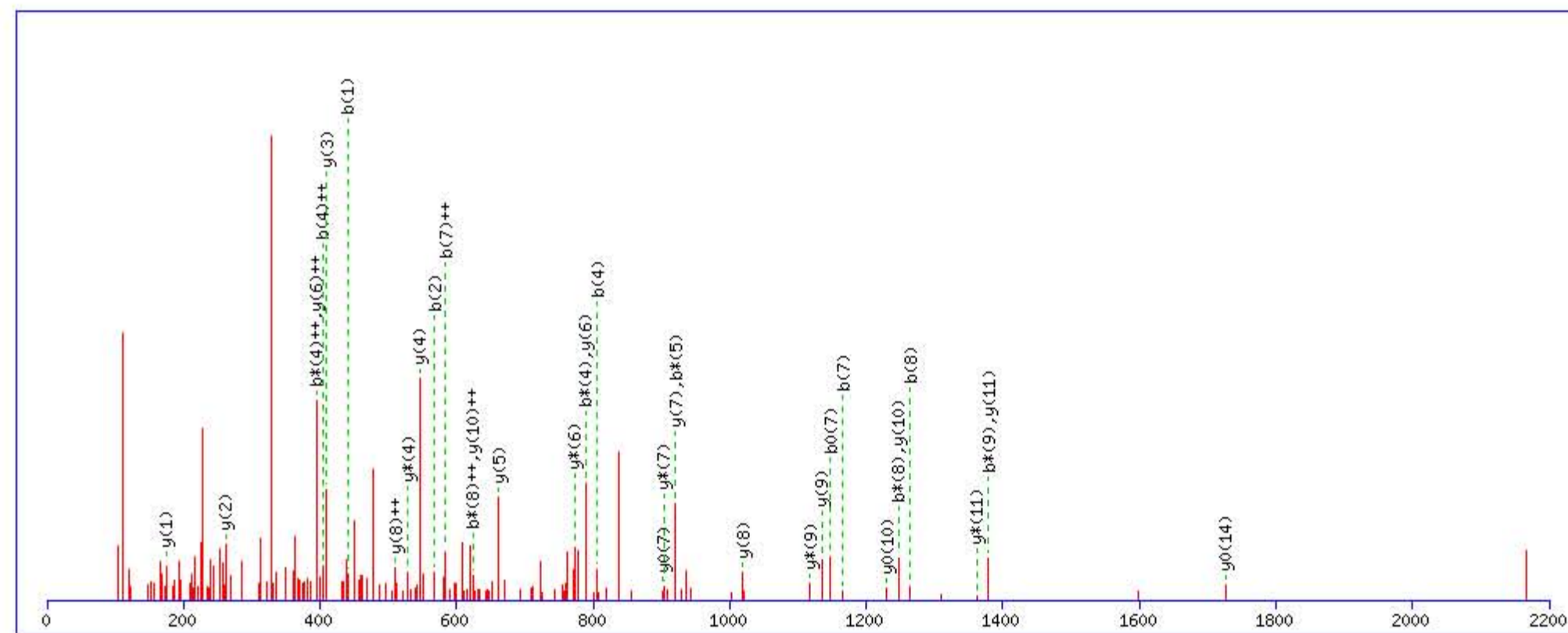
Title: Locus:1.1.1.692.3 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2183.007446

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

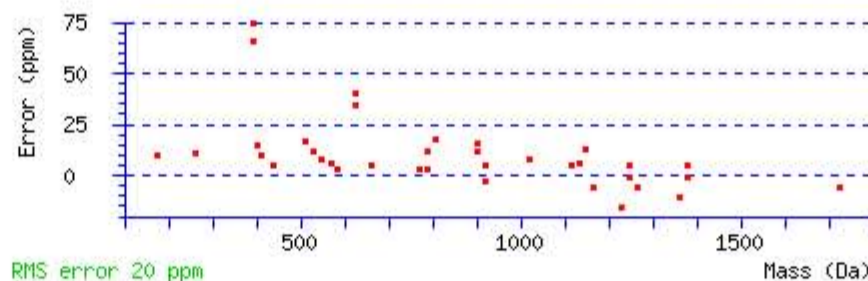
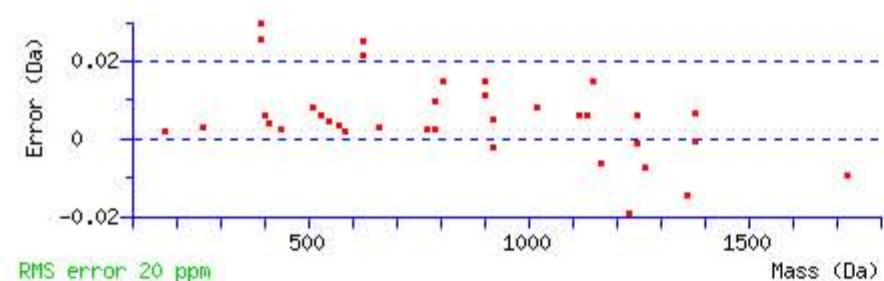
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 53 Expect: 6.7e-005

Matches : 36/162 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	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 **QQTHMLDVMQDHF^{SR}**

(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	2183.007446	0.004730	QQTHMLDVMQDHF^{SR}
50.5	2183.007446	0.004730	QQTHMLDVMQDHF^{SR}

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

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 21478: 1145.612008 from(573.813280,2+) rtinseconds(1448) index(49162)

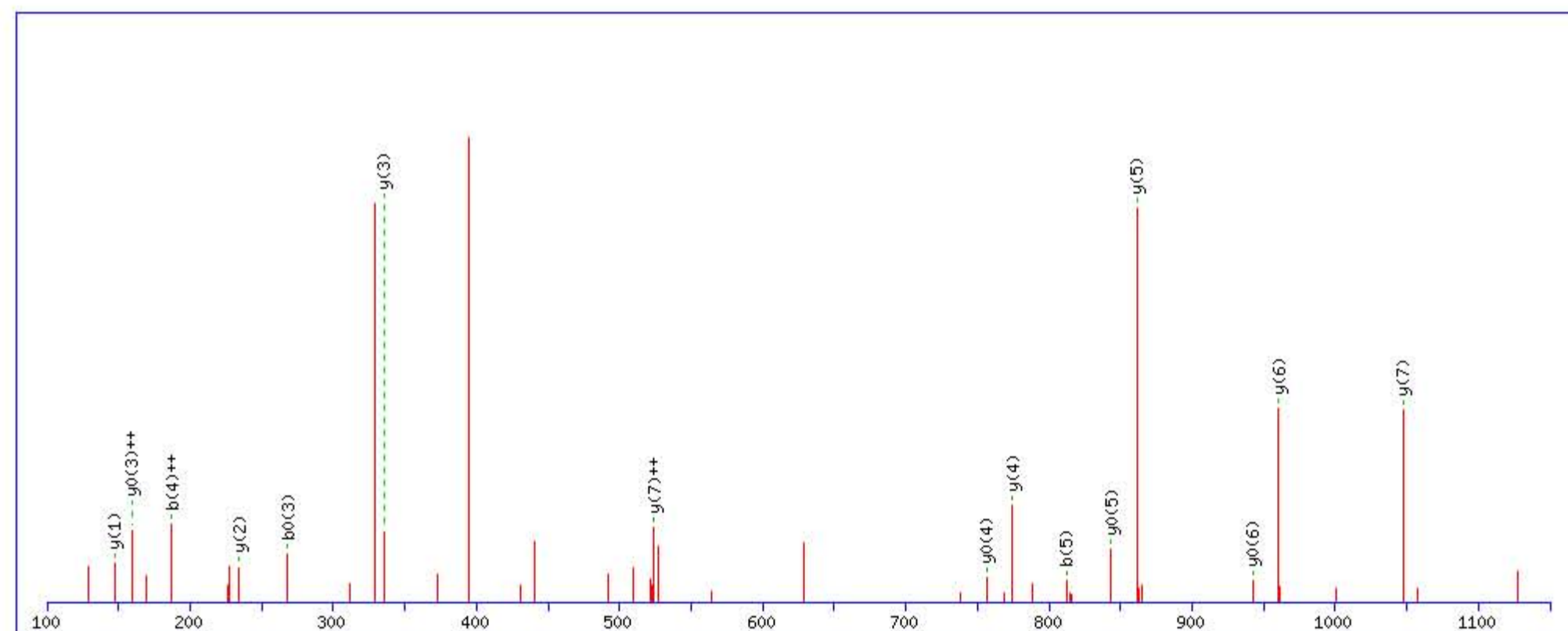
Title: Locus:1.1.1.1119.24 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1145.611450

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

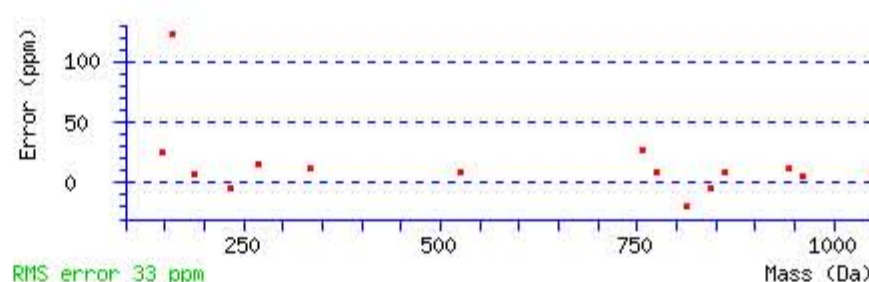
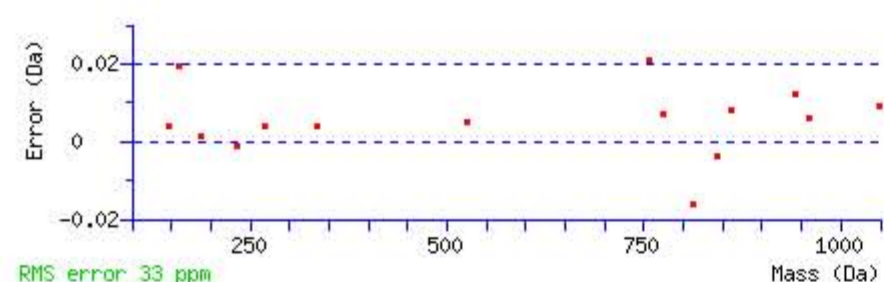
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 0.00027

Matches : 16/72 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							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
46.5	1145.611450	0.000558	VSVSQTSK
8.0	1145.611420	0.000588	KSIMVQSPEK
6.7	1145.622650	-0.010642	VDNAMSRLK
3.9	1145.629196	-0.017188	GEVLGLSSSLGK
3.9	1145.629181	-0.017173	VAKEVVEASSK
3.7	1145.604034	0.007974	STPSSPSLRK
3.3	1145.623337	-0.011329	WVDGGKPLFK
2.8	1145.608047	0.003961	WTKEKTEPK
2.2	1145.622650	-0.010642	VSMDLRANLK
1.1	1145.629166	-0.017158	EDKLEAVKSK

MASCOT Mascot Search Results

Peptide View

MS/MS Fragmentation of **SALVLQYLR**

Found in **FA9_HUMAN**, Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2

Match to Query 29293: 1372.803028 from(687.408790,2+) rtinseconds(2436) index(55616)

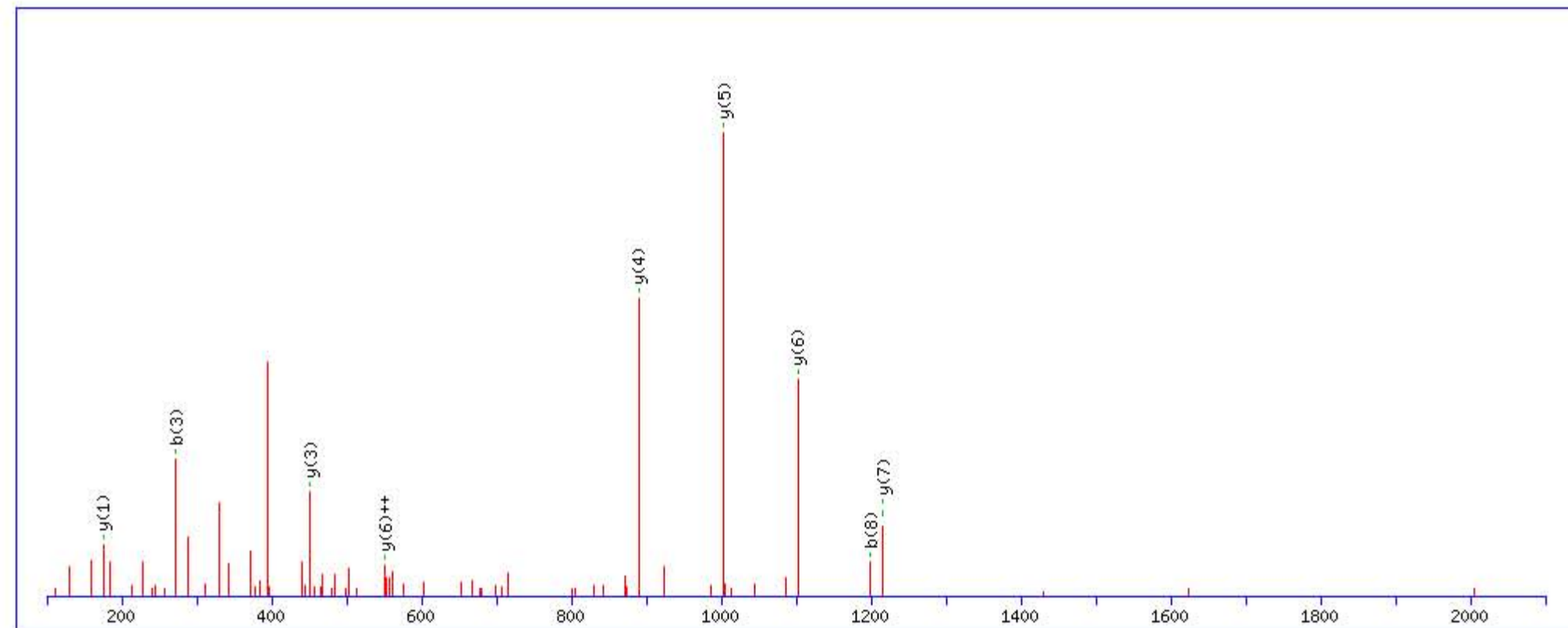
Title: Locus:1.1.1.1463.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1372.790054

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

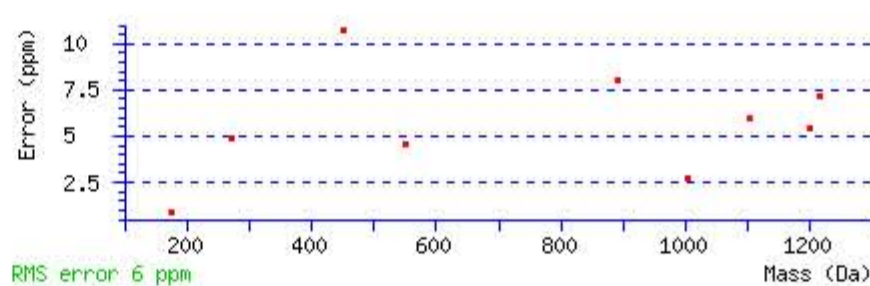
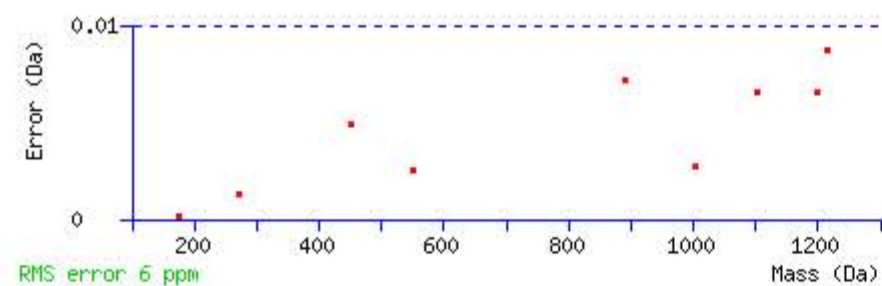
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 47 Expect: 0.00015

Matches : 9/70 fragment ions using 12 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	88.039304	44.523290			70.028739	35.518008	S					9
2	159.076418	80.041847			141.065853	71.036564	A	1286.765327	643.886301	1269.738778	635.373027	8
3	272.160482	136.583879			254.149917	127.578597	L	1215.728213	608.367744	1198.701664	599.854470	7
4	371.228896	186.118086			353.218331	177.112804	V	1102.644149	551.825713	1085.617600	543.312438	6
5	484.312960	242.660118			466.302395	233.654836	L	1003.575735	502.291505	986.549186	493.778231	5
6	923.538286	462.272781	906.511737	453.759507	905.527721	453.267499	Q	890.491671	445.749473	873.465122	437.236199	4
7	1086.601615	543.804446	1069.575066	535.291171	1068.591050	534.799163	Y	451.266345	226.136810	434.239796	217.623536	3
8	1199.685679	600.346477	1182.659130	591.833203	1181.675114	591.341195	L	288.203016	144.605146	271.176467	136.091871	2
9							R	175.118952	88.063114	158.092403	79.549839	1



NCBI BLAST search of **SALVLQYLR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
47.2	1372.790054	0.012974	SALVLQYLR
8.1	1372.782669	0.020359	LSNKFNSVIPVR
7.0	1372.790039	0.012989	KELQILYR
1.1	1372.801270	0.001758	ALKMPYRILPR
0.6	1372.797913	0.005115	LRLLSGYLWPR

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 55964: 2474.215896 from(619.561250,4+) rtinseconds(1653) index(50592)

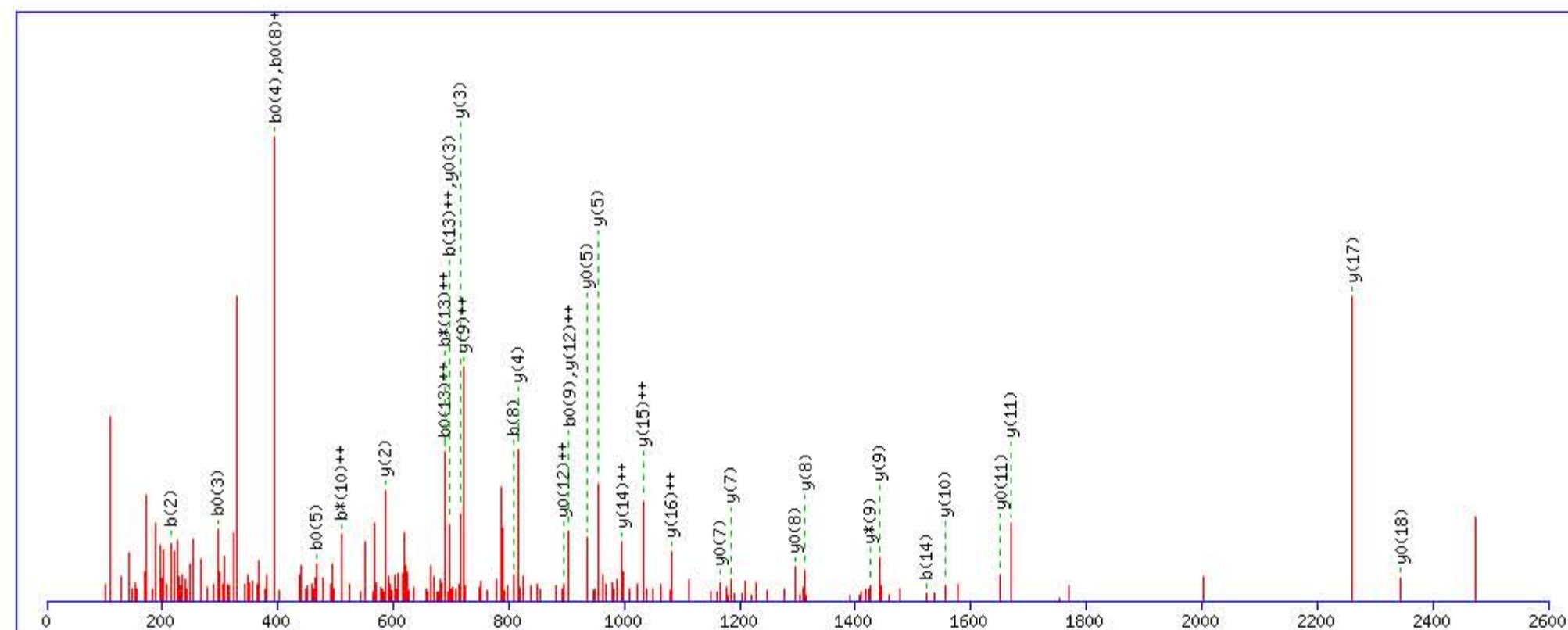
Title: Locus:1.1.1.1191.8 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2474.211121

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

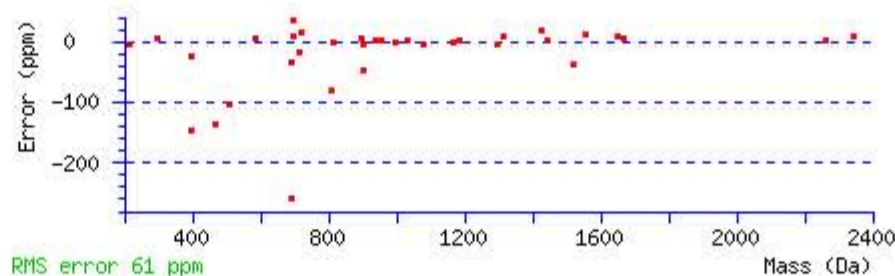
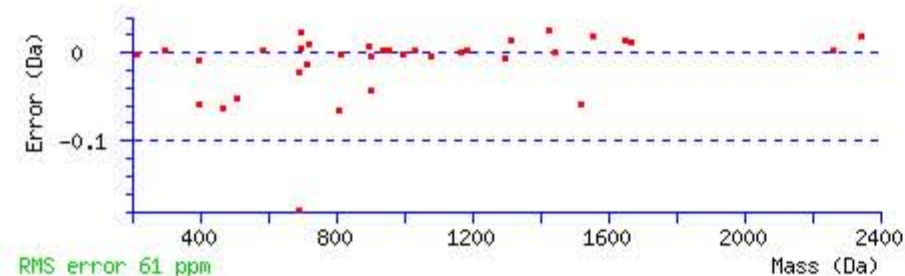
Variable modifications:

Q18 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.0012

Matches : 35/194 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	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
43.3	2474.211121	0.004775	ITVVAGEHNIEETEHTEQK

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

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **SQHLDNFSNQIGK**

Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

Match to Query 42681: 1797.889002 from(600.303610,3+) rtinseconds(1796) index(51491)

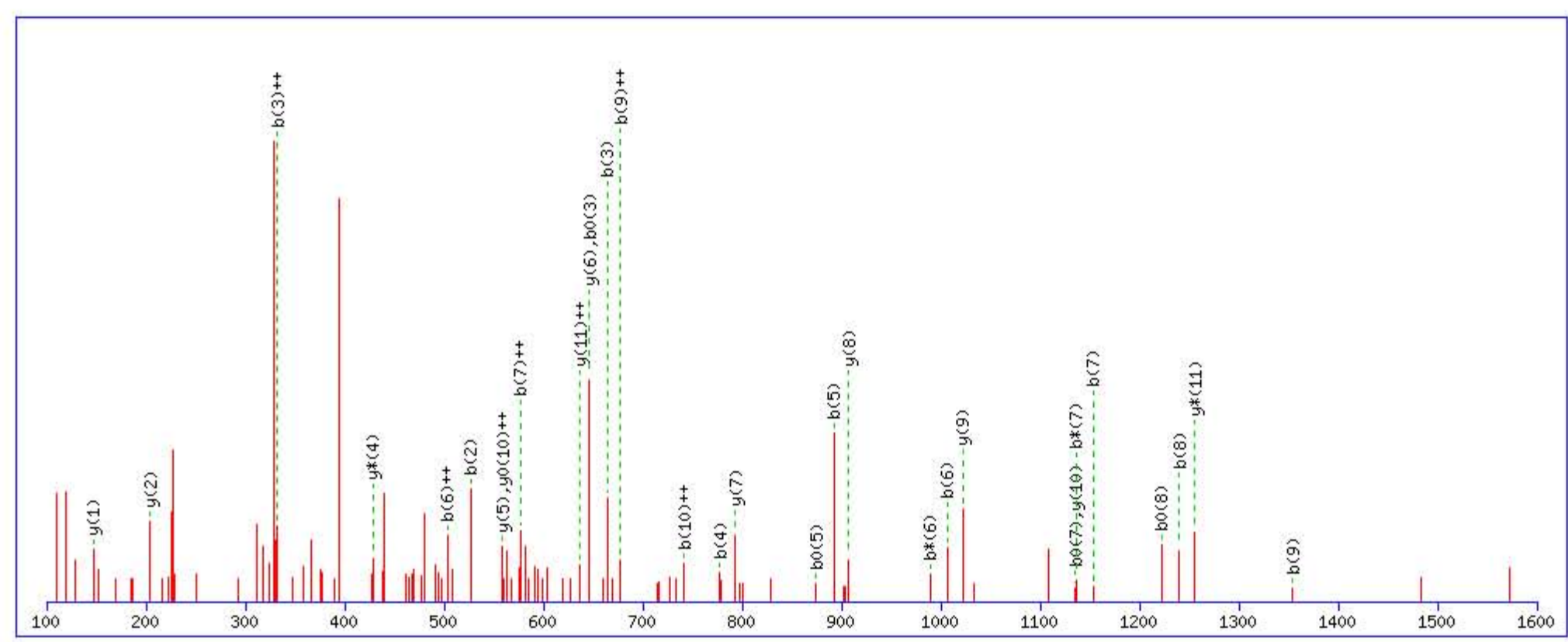
Title: Locus:1.1.1.1241.4 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1797.883194

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

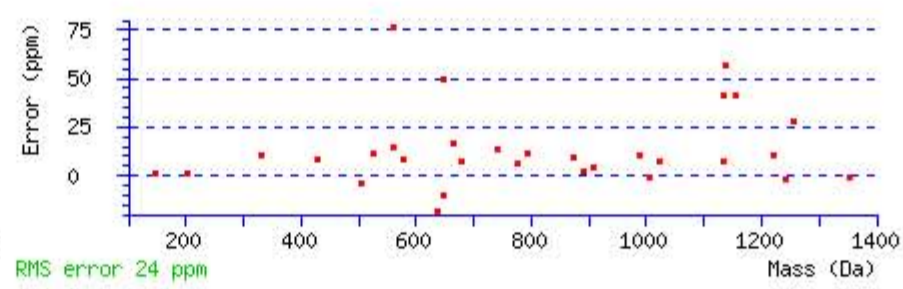
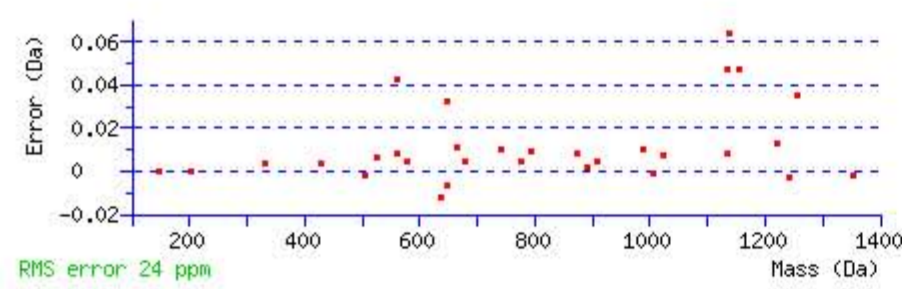
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 48 Expect: 0.00041

Matches : 31/132 fragment ions using 46 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							13
2	527.264630	264.135953	510.238081	255.622679	509.254065	255.130671	Q	1711.858451	856.432863	1694.831902	847.919589	1693.847886	847.427581	12
3	664.323542	332.665409	647.296993	324.152134	646.312977	323.660126	H	1272.633125	636.820200	1255.606576	628.306926	1254.622560	627.814918	11
4	777.407606	389.207441	760.381057	380.694166	759.397041	380.202159	L	1135.574213	568.290744	1118.547664	559.777470	1117.563648	559.285462	10
5	892.434549	446.720913	875.408000	438.207638	874.423984	437.715630	D	1022.490149	511.748712	1005.463600	503.235438	1004.479584	502.743430	9
6	1006.477476	503.742376	989.450927	495.229101	988.466911	494.737093	N	907.463206	454.235241	890.436657	445.721966	889.452641	445.229958	8
7	1153.545890	577.276583	1136.519341	568.763308	1135.535325	568.271300	F	793.420279	397.213777	776.393730	388.700503	775.409714	388.208495	7
8	1240.577918	620.792597	1223.551369	612.279323	1222.567353	611.787314	S	646.351865	323.679570	629.325316	315.166296	628.341300	314.674288	6
9	1354.620845	677.814060	1337.594296	669.300786	1336.610280	668.808778	N	559.319837	280.163556	542.293288	271.650282			5
10	1482.679423	741.843349	1465.652874	733.330075	1464.668858	732.838067	Q	445.276910	223.142093	428.250361	214.628818			4
11	1595.763487	798.385381	1578.736938	789.872107	1577.752922	789.380099	I	317.218332	159.112804	300.191783	150.599529			3
12	1652.784951	826.896113	1635.758402	818.382839	1634.774386	817.890831	G	204.134268	102.570772	187.107719	94.057497			2
13							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **SQHLDNFSNQIGK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.6	1797.883194	0.005808	SQHLDNFSNQIGK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **MPMGLSTGIISDSQIK**

Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

Match to Query 46222: 1988.032482 from(663.684770,3+) rtinseconds(2496) index(55899)

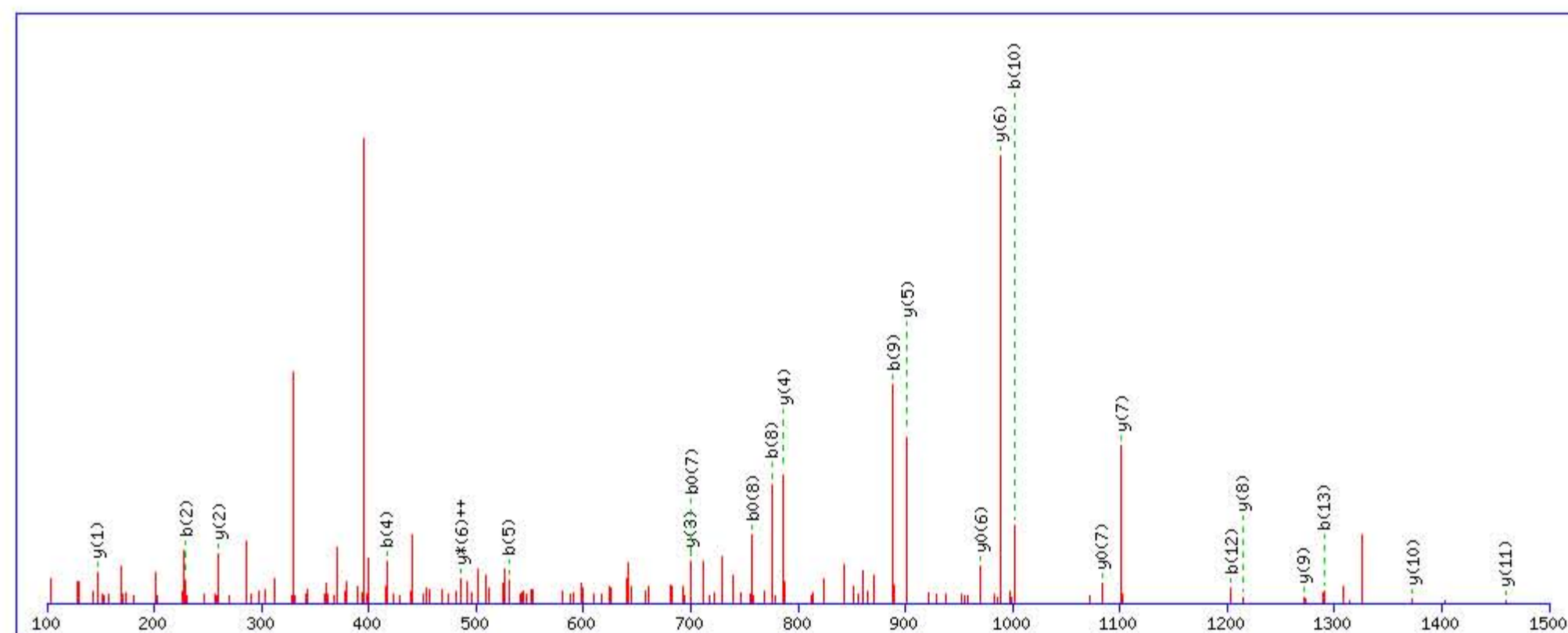
Title: Locus:1.1.1.1484.4 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1988.014465

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

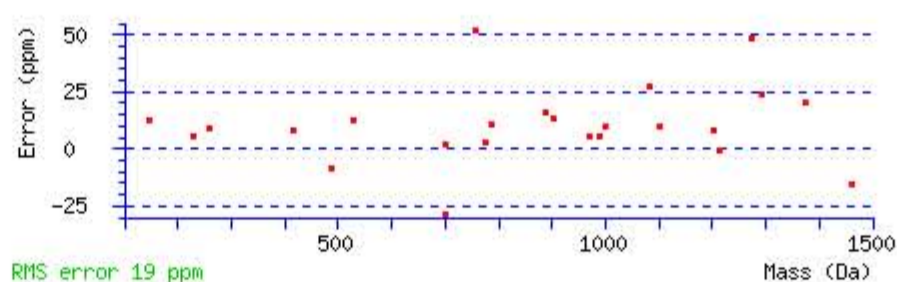
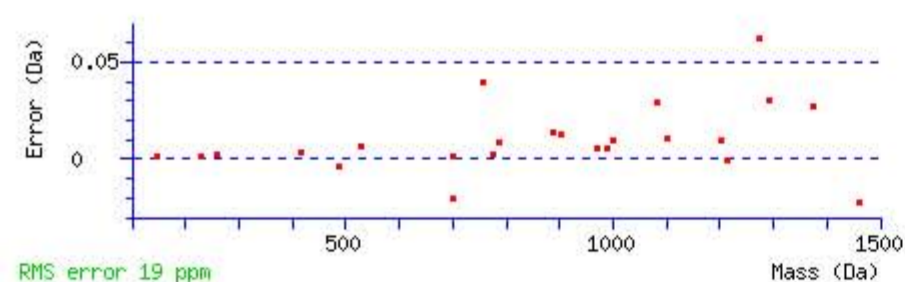
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 59 Expect: 5.8e-006

Matches : 24/138 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	132.047761	66.527518					M							16
2	229.100525	115.053900					P	1857.981269	929.494273	1840.954720	920.980998	1839.970704	920.488990	15
3	360.141010	180.574143					M	1760.928505	880.967891	1743.901956	872.454616	1742.917940	871.962608	14
4	417.162474	209.084875					G	1629.888020	815.447648	1612.861471	806.934374	1611.877455	806.442366	13
5	530.246538	265.626907					L	1572.866556	786.936916	1555.840007	778.423642	1554.855991	777.931634	12
6	617.278566	309.142921			599.268001	300.137638	S	1459.782492	730.394884	1442.755943	721.881610	1441.771927	721.389602	11
7	718.326245	359.666761			700.315680	350.661478	T	1372.750464	686.878870	1355.723915	678.365596	1354.739899	677.873588	10
8	775.347709	388.177493			757.337144	379.172210	G	1271.702785	636.355031	1254.676236	627.841756	1253.692220	627.349748	9
9	888.431773	444.719525			870.421208	435.714242	I	1214.681321	607.844299	1197.654772	599.331024	1196.670756	598.839016	8
10	1001.515837	501.261557			983.505272	492.256274	I	1101.597257	551.302267	1084.570708	542.788992	1083.586692	542.296984	7
11	1088.547865	544.777571			1070.537300	535.772288	S	988.513193	494.760235	971.486644	486.246960	970.502628	485.754952	6
12	1203.574808	602.291042			1185.564243	593.285760	D	901.481165	451.244221	884.454616	442.730946	883.470600	442.238938	5
13	1290.606836	645.807056			1272.596271	636.801774	S	786.454222	393.730749	769.427673	385.217475	768.443657	384.725467	4
14	1729.832162	865.419719	1712.805613	856.906445	1711.821597	856.414437	Q	699.422194	350.214735	682.395645	341.701461			3
15	1842.916226	921.961751	1825.889677	913.448477	1824.905661	912.956469	I	260.196868	130.602072	243.170319	122.088797			2
16							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **MPMGLSTGIISDSQIK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.1	1988.014465	0.018017	MPMGLSTGIISDSQIK
3.3	1988.051331	-0.018849	MTHKLVFLEDGTSQVRK

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

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 51132: 2205.098172 from(736.040000,3+) rtinseconds(2786) index(57735)

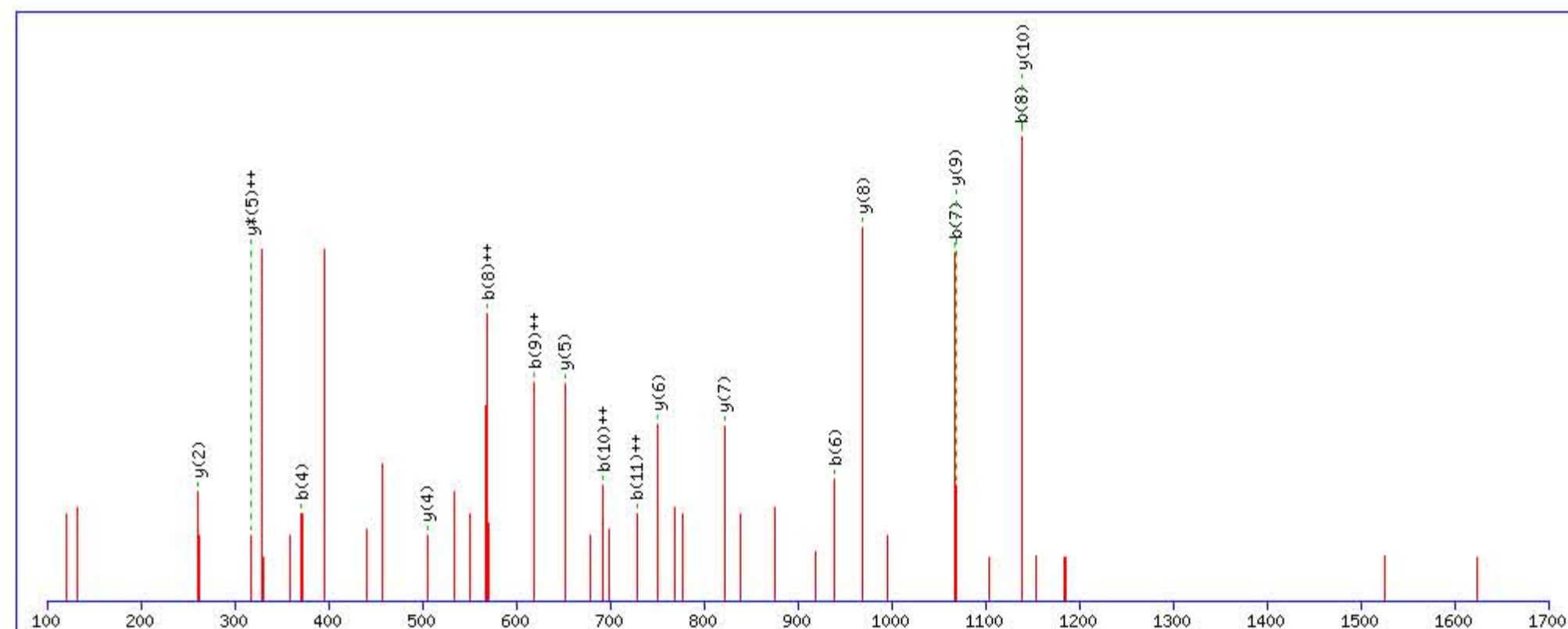
Title: Locus:1.1.1.1584.15 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2205.077591

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

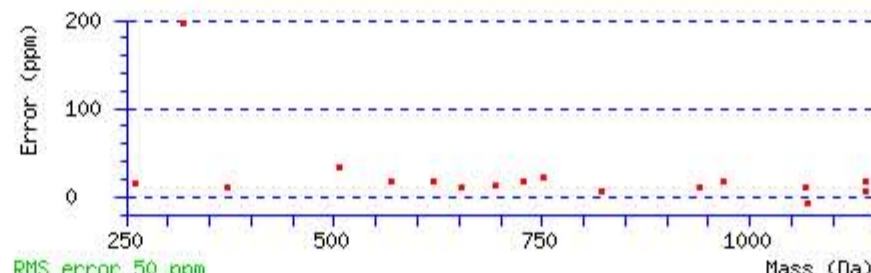
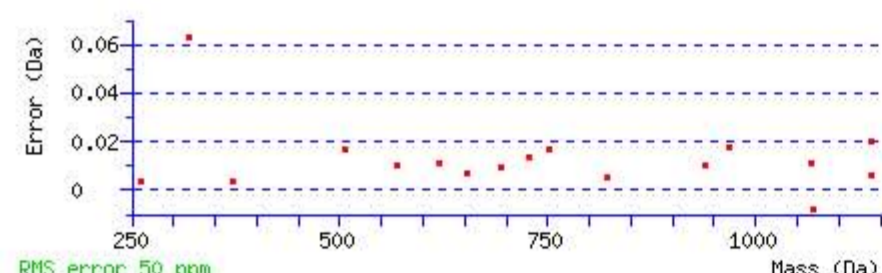
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 38 Expect: 0.00039

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



NCBI BLAST search of **AADIEQQAVFAVFDENK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.3	2205.077591	0.020581	AADIEQQAVFAVFDENK
36.6	2205.077591	0.020581	AADIEQQAVFAVFDENK
1.9	2205.129929	-0.031757	YPGRNGAQMMVHIVFKVAR
0.8	2205.107452	-0.009280	TNLQFMGQAFKSIHEK

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 23316: 1200.600788 from(601.307670,2+) rtinseconds(1450) index(49182)

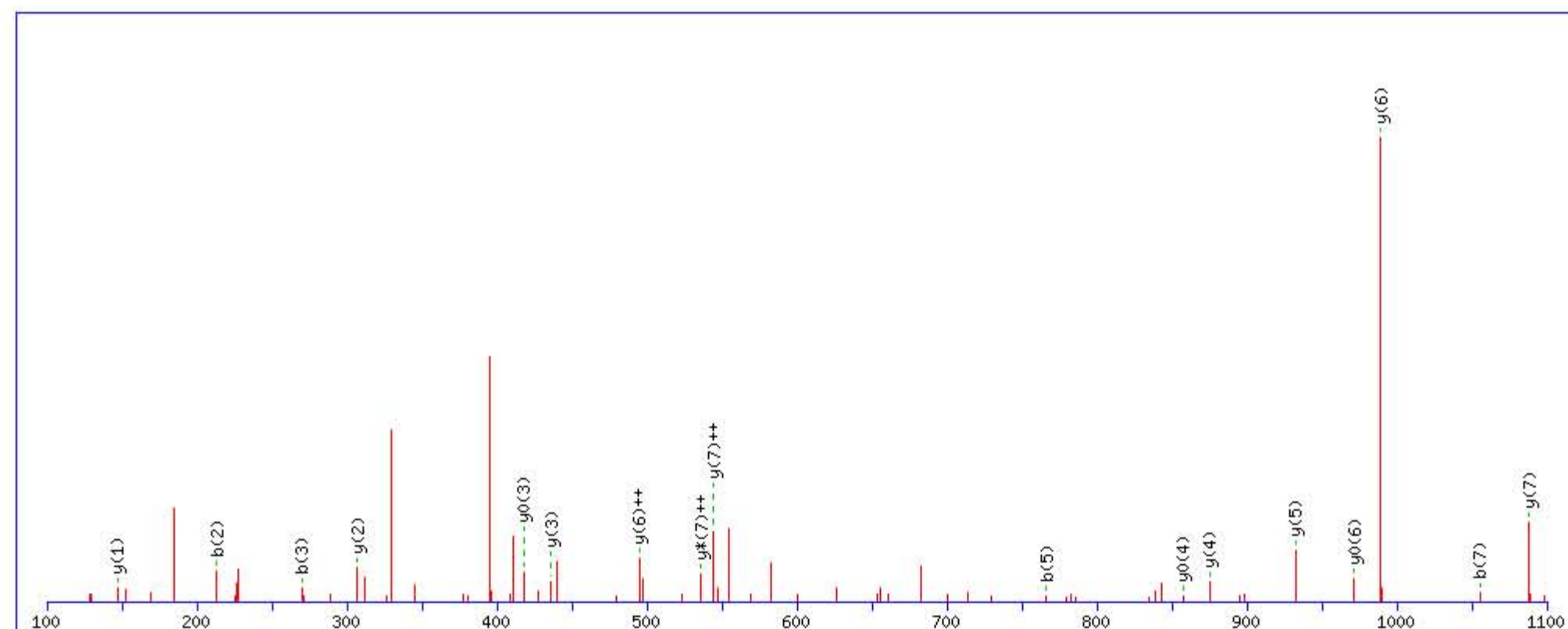
Title: Locus:1.1.1.1120.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1200.599503

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

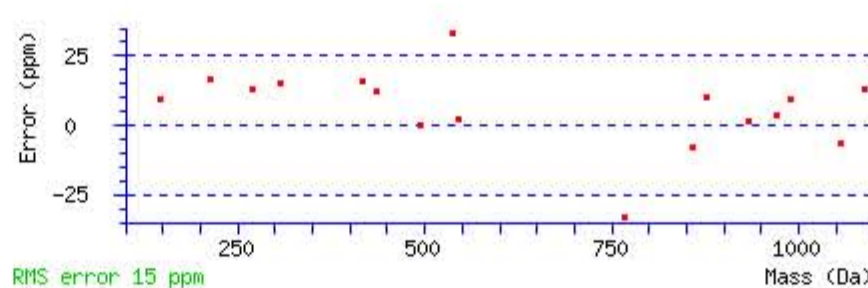
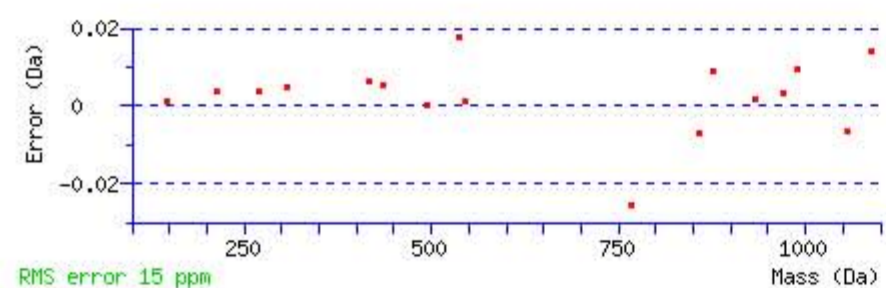
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.0039

Matches : 17/62 fragment ions using 48 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					I							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
29.7	1200.599503	0.001285	IVGGQECK
3.7	1200.598587	0.002201	ILADLEENR
3.3	1200.599503	0.001285	LIQGDGCK
0.5	1200.596100	0.004688	LVKMYDNR
0.1	1200.599487	0.001301	LLNDQCK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **DWAESTLMTQK**

Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

Match to Query 37931: 1619.779988 from(810.897270,2+) rtinseconds(2304) index(54875)

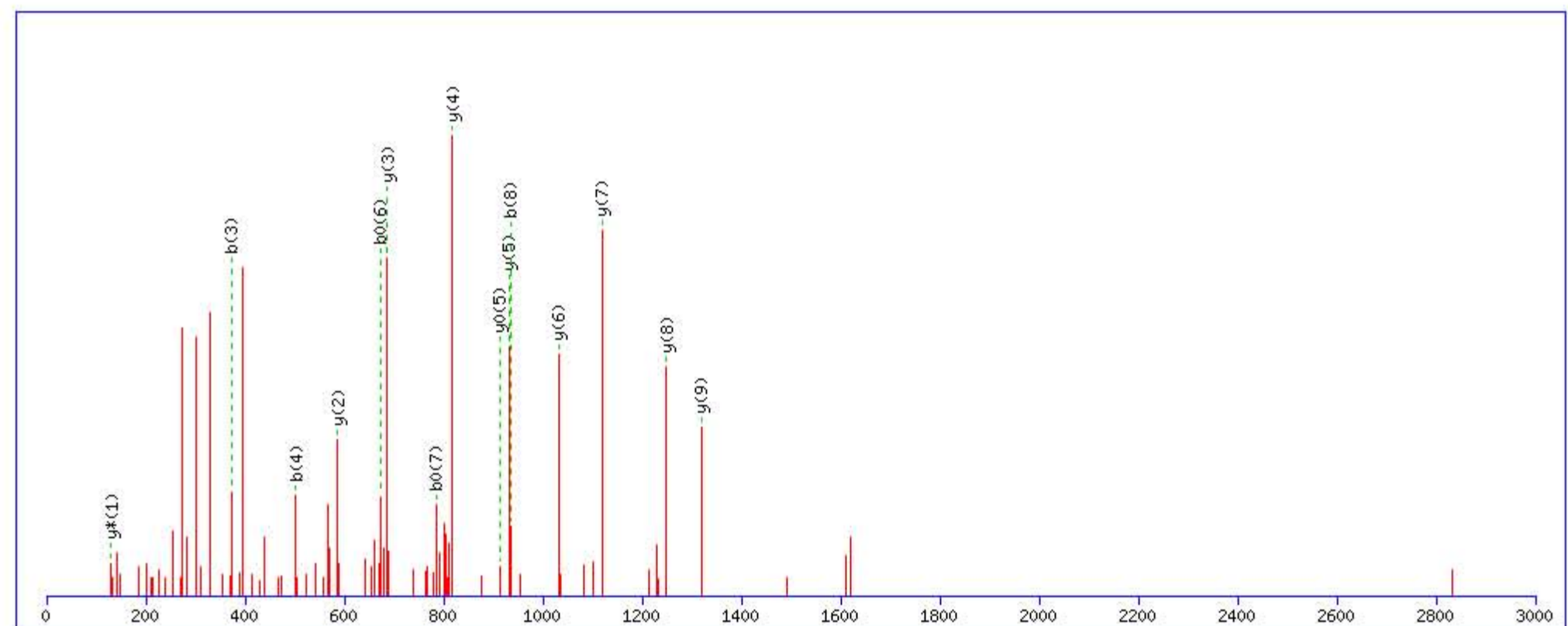
Title: Locus:1.1.1.1417.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1619.768738

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

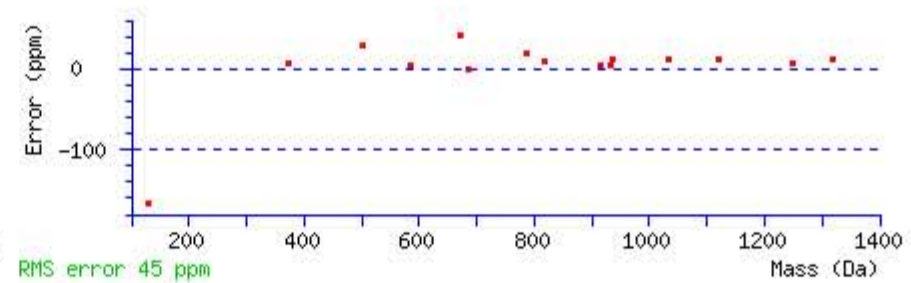
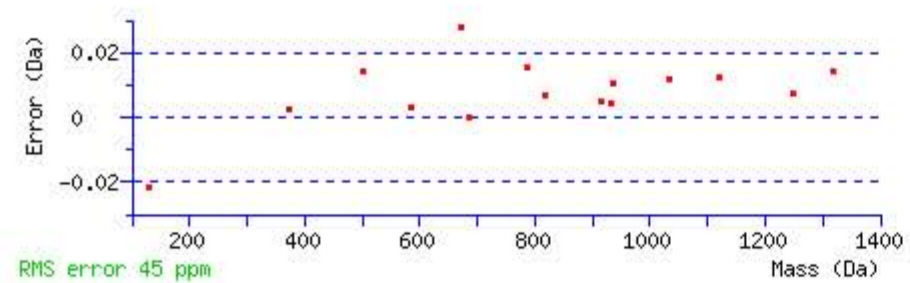
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 52 Expect: 0.00012

Matches : 15/98 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	116.034219	58.520748			98.023654	49.515465	D							11
2	302.113532	151.560404			284.102967	142.555122	W	1505.749085	753.378180	1488.722536	744.864906	1487.738520	744.372898	10
3	373.150646	187.078961			355.140081	178.073679	A	1319.669772	660.338524	1302.643223	651.825250	1301.659207	651.333241	9
4	502.193239	251.600258			484.182674	242.594975	E	1248.632658	624.819967	1231.606109	616.306693	1230.622093	615.814685	8
5	589.225267	295.116272			571.214702	286.110989	S	1119.590065	560.298671	1102.563516	551.785396	1101.579500	551.293388	7
6	690.272946	345.640111			672.262381	336.634829	T	1032.558037	516.782657	1015.531488	508.269382	1014.547472	507.777374	6
7	803.357010	402.182143			785.346445	393.176861	L	931.510358	466.258817	914.483809	457.745543	913.499793	457.253535	5
8	934.397495	467.702386			916.386930	458.697103	M	818.426294	409.716785	801.399745	401.203510	800.415729	400.711502	4
9	1035.445174	518.226225			1017.434609	509.220942	T	687.385809	344.196543	670.359260	335.683268	669.375244	335.191260	3
10	1474.670500	737.838888	1457.643951	729.325614	1456.659935	728.833605	Q	586.338130	293.672703	569.311581	285.159429			2
11							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [DWAESTLMTQK](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.0	1619.768738	0.011250	DWAESTLMTQK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **QEDACQGDSSGGPHVTR**

Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

Match to Query 47758: 2023.888212 from(675.636680,3+) rtinseconds(1339) index(48484)

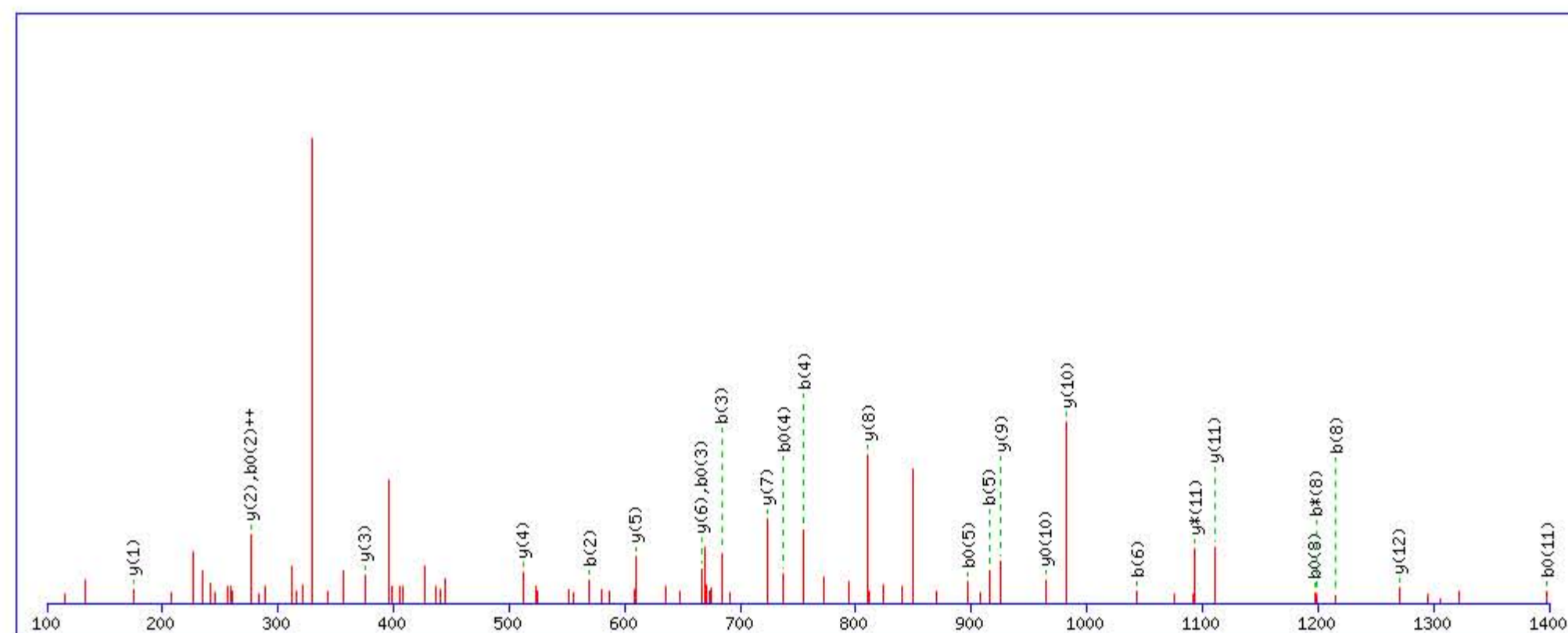
Title: Locus:1.1.1.1081.24 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2023.884033

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

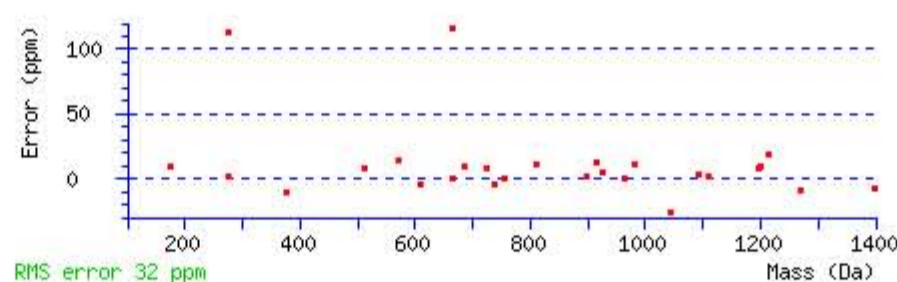
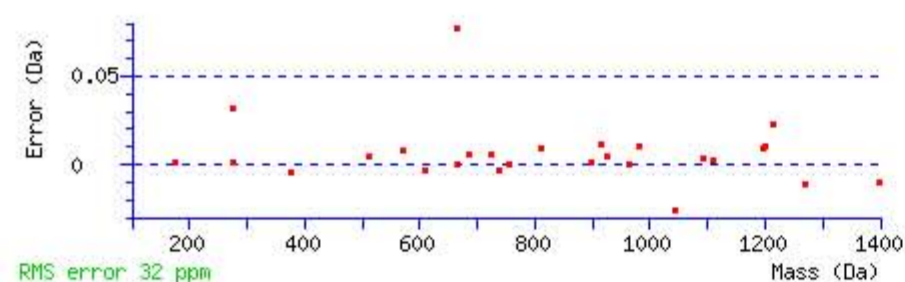
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 71 Expect: 4.4e-007

Matches : 27/176 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							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 **QEDACQGDSSGGPHVTR**

(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	2023.884033	0.004179	QEDACQGDSSGGPHVTR
41.7	2023.884033	0.004179	QEDACQGDSSGGPHVTR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **YKDGDCETSPCQNQGK**

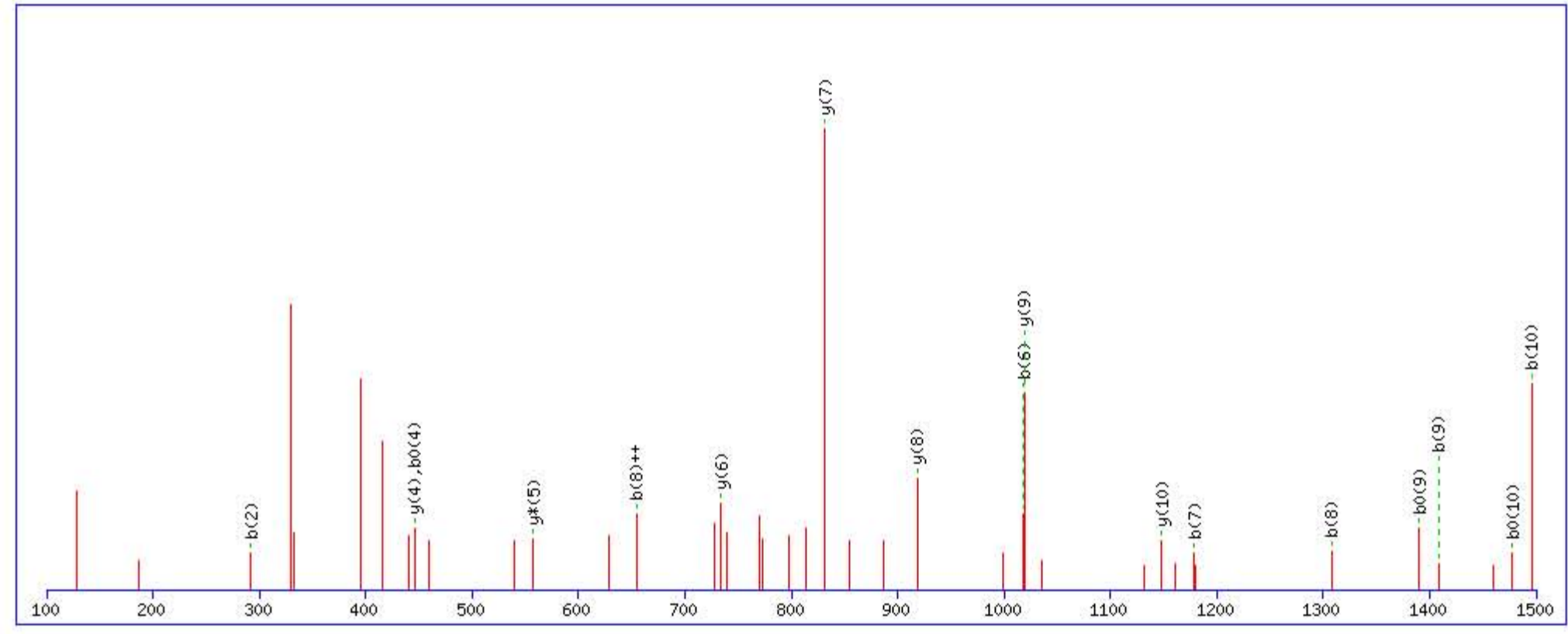
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

Match to Query 53442: 2324.989452 from(776.003760,3+) rtinseconds(1308) index(48295)
 Title: Locus:1.1.1.1070.17 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

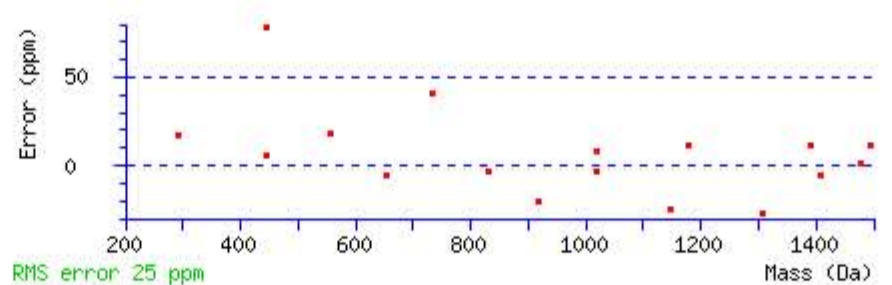
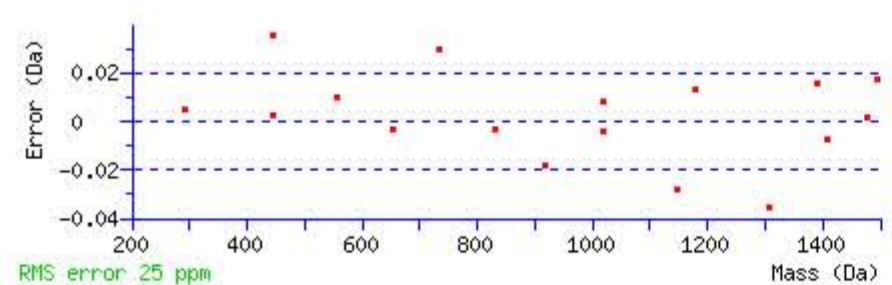
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2324.982407
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q6 : Biotin:Thermo-21345 (Q)
 Ions Score: 37 Expect: 0.00055
 Matches : 17/172 fragment ions using 25 most intense peaks [\(help\)](#)

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



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

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
37.0	2324.982407	0.007045	YKDGDCETSPCQNQGK

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 19749: 1115.555988 from(558.785270,2+) rtinseconds(1362) index(64812)

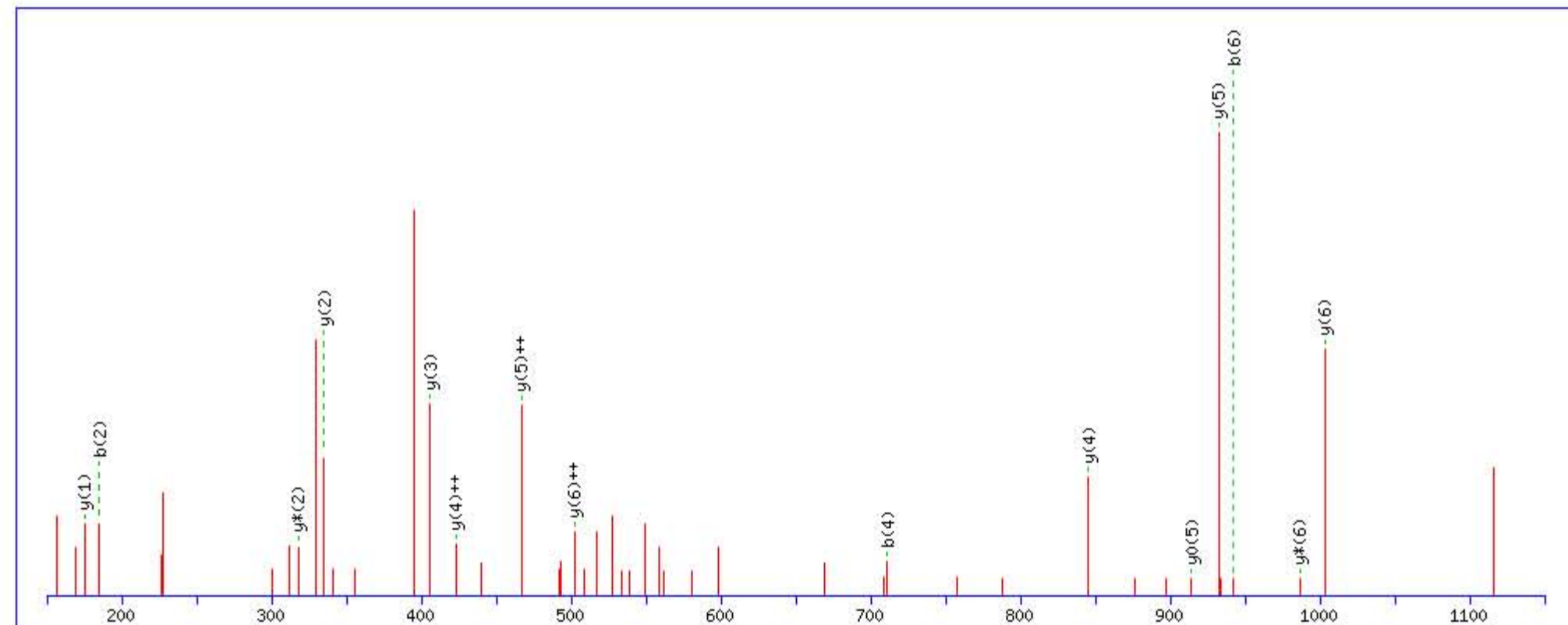
Title: Locus:1.1.1.1411.21 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1115.557953

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

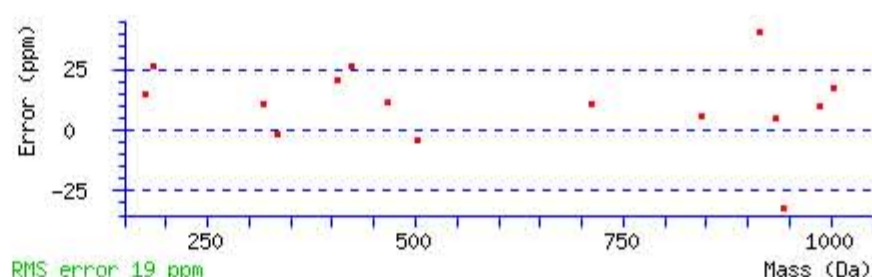
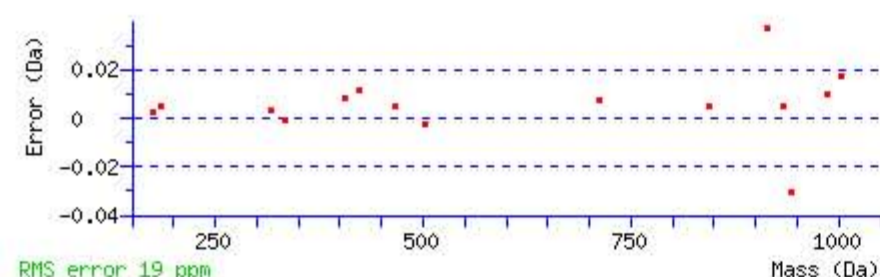
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 31 Expect: 0.0083

Matches : 15/54 fragment ions using 32 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b*	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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
31.4	1115.557953	-0.001965	LASQACR
8.7	1115.543350	0.012638	SFCYISALR
5.1	1115.539352	0.016636	ACLTSGTPGPR
4.8	1115.550552	0.005436	LAAGSRCPER
2.0	1115.543350	0.012638	LEYKFCTR
1.9	1115.539322	0.016666	QSAQESR
0.6	1115.546722	0.009266	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 21799: 1155.602148 from(578.808350,2+) rtinseconds(1376) index(17578)

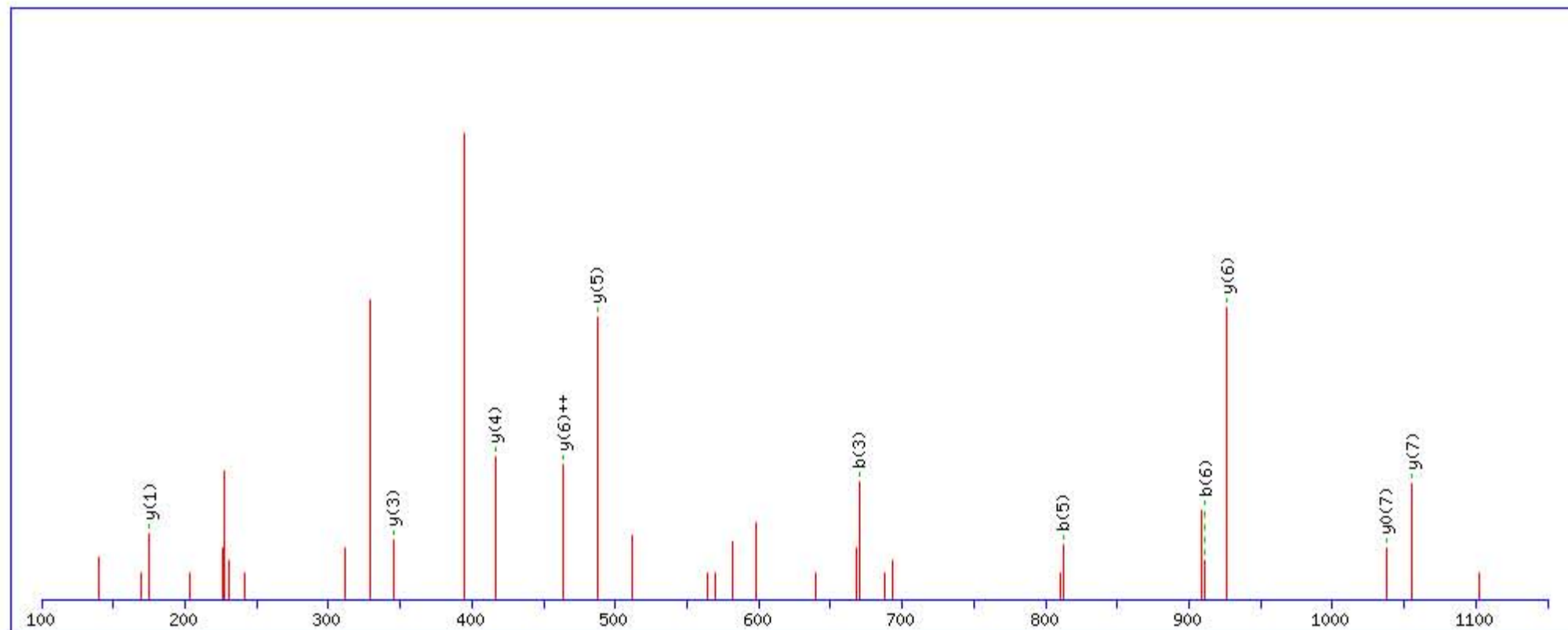
Title: Locus:1.1.1.481.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1155.607010

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

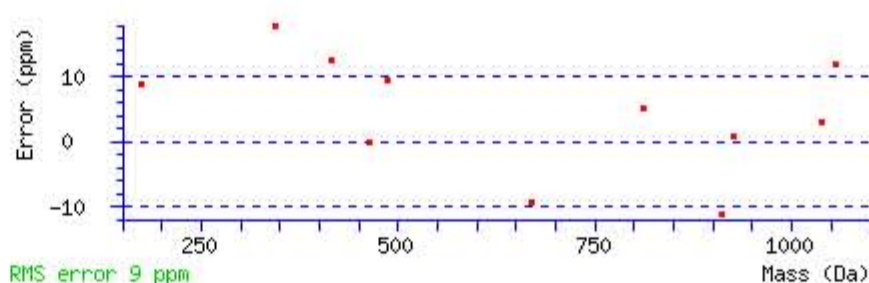
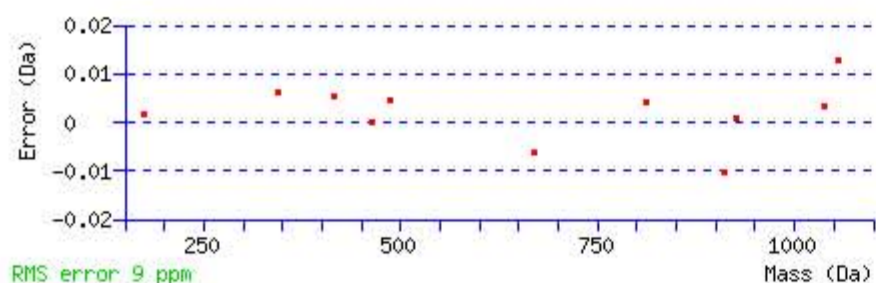
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.016

Matches : 11/68 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
27.6	1155.607010	-0.004862	TEQAAVAR
8.3	1155.588394	0.013754	VEQIEAGTPGR
5.2	1155.588379	0.013769	TEVPLAENQR

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **CFEPQLLR**

Found in **FA12_HUMAN**, Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3

Match to Query 29275: 1372.699228 from(687.356890,2+) rtinseconds(2199) index(69965)

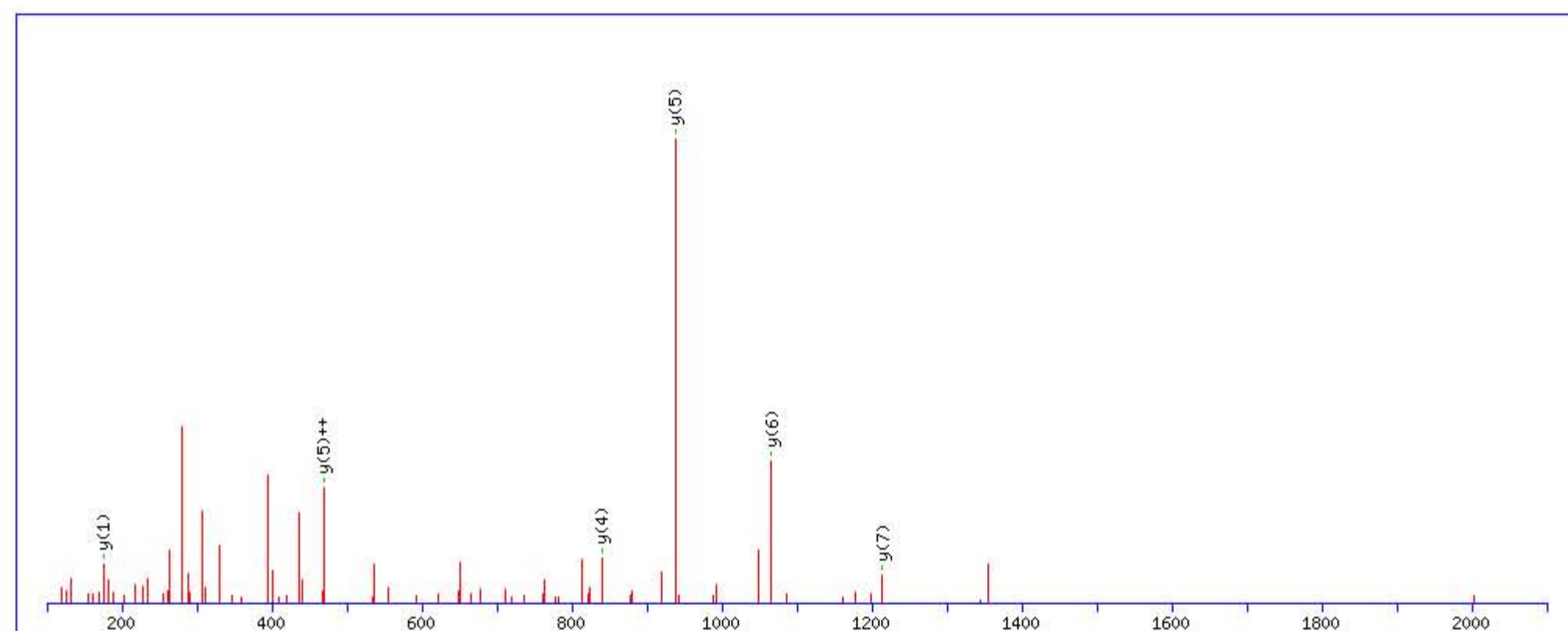
Title: Locus:1.1.1.1703.13 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1372.699539

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

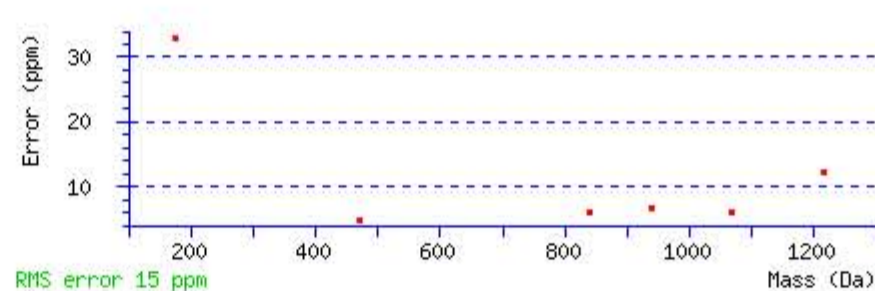
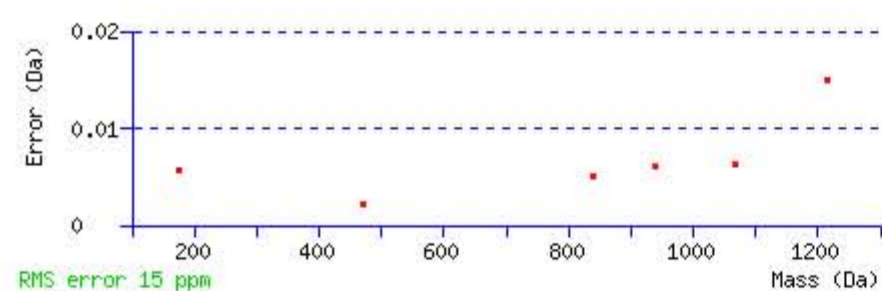
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 29 Expect: 0.0079

Matches : 6/62 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	161.037925	81.022600					C							8
2	308.106339	154.556807					F	1213.676177	607.341726	1196.649628	598.828452	1195.665612	598.336444	7
3	437.148932	219.078104			419.138367	210.072822	E	1066.607763	533.807519	1049.581214	525.294245	1048.597198	524.802237	6
4	534.201696	267.604486			516.191131	258.599204	P	937.565170	469.286223	920.538621	460.772948			5
5	973.427022	487.217149	956.400473	478.703875	955.416457	478.211867	Q	840.512406	420.759841	823.485857	412.246566			4
6	1086.511086	543.759181	1069.484537	535.245907	1068.500521	534.753898	L	401.287080	201.147178	384.260531	192.633903			3
7	1199.595150	600.301213	1182.568601	591.787939	1181.584585	591.295930	L	288.203016	144.605146	271.176467	136.091871			2
8							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **CFEPQLLR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.4	1372.699539	-0.000311	CFEPQLLR
6.6	1372.710770	-0.011542	QPRMLDFR
0.8	1372.717331	-0.018103	QGLPVVMPVFDR
0.1	1372.703369	-0.004141	NPPKQEGHR

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

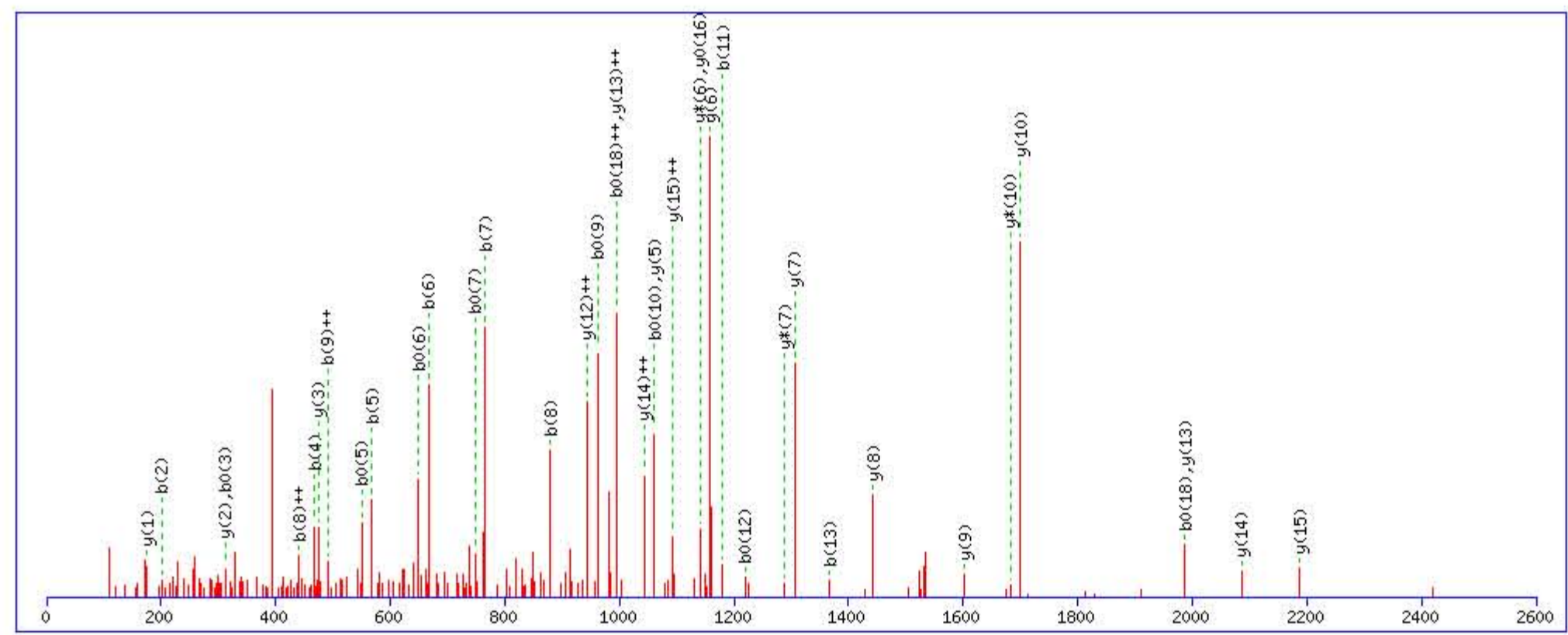
MASCOT Mascot Search Results

Peptide View

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

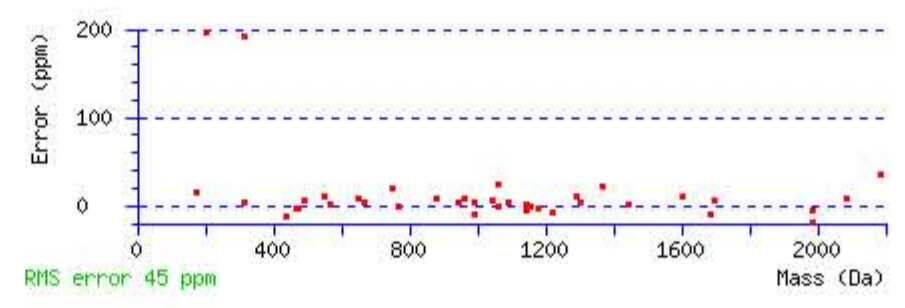
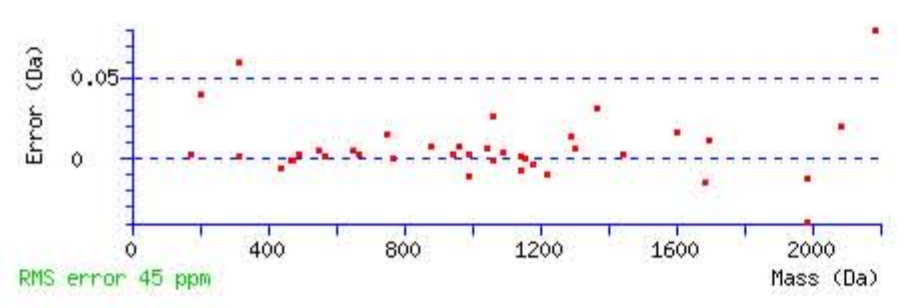
Match to Query 62135: 3064.482096 from(767.127800,4+) rtinseconds(2143) index(69615)
 Title: Locus:1.1.1.1683.17 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 3064.468796
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q20 : Biotin:Thermo-21345 (Q)
 Ions Score: 66 Expect: 6.7e-006
 Matches : 39/204 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	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 [AEHTVVLTVTGEPCHFPPQYHR](#)
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.6	3064.468796	0.013300	AEHTVVLTVTGEPCHFPPQYHR

MASCOT 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 23368: 1203.569848 from(602.792200,2+) rtinseconds(1465) index(65613)

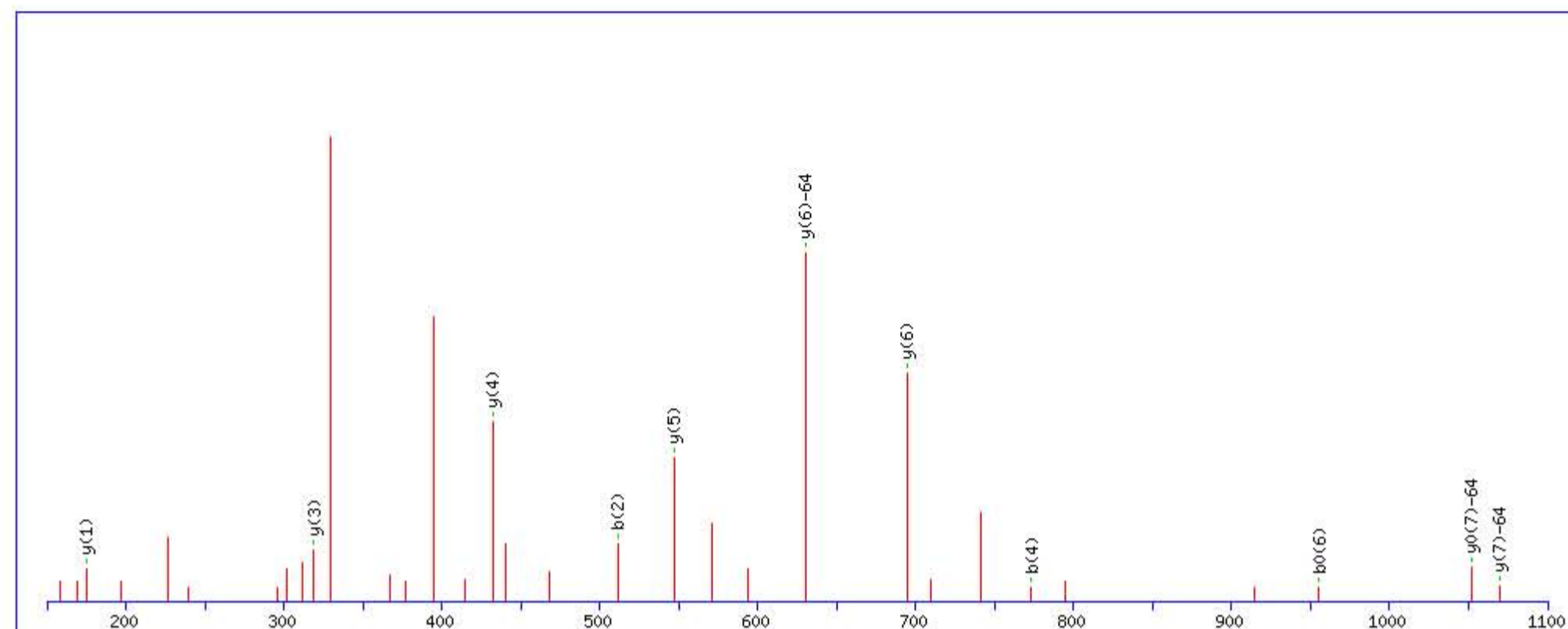
Title: Locus:1.1.1.1447.21 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1203.574005

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

Variable modifications:

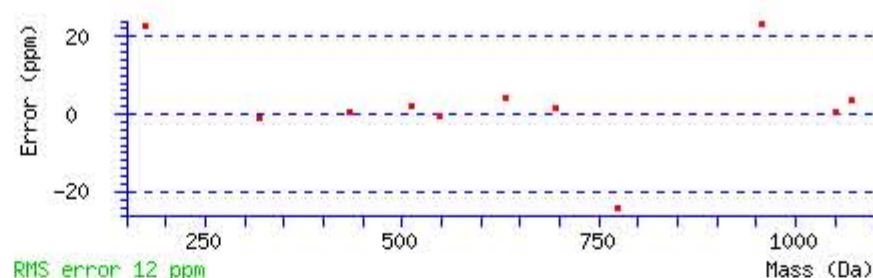
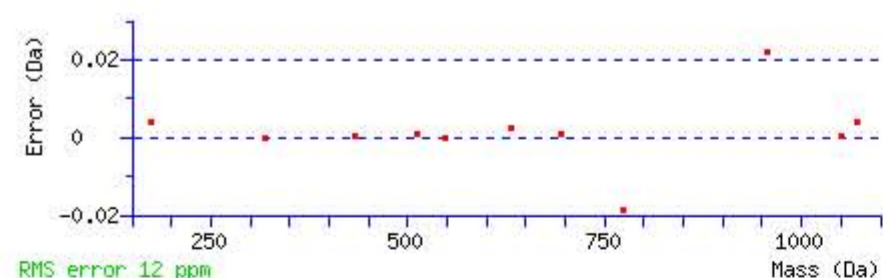
Q2 : Biotin:Thermo-21345 (Q)

M3 : Oxidation (M), with neutral losses 63.998285 (shown in table), 0.000000

Ions Score: 33 Expect: 0.0018

Matches : 11/112 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	72.044390	36.525833					A							8
2	511.269716	256.138496	494.243167	247.625221			Q	1069.545892	535.276584	1052.519343	526.763310	1051.535327	526.271302	7
3	594.306831	297.657054	577.280282	289.143779			M	630.320566	315.663921	613.294017	307.150646	612.310001	306.658639	6
4	709.333774	355.170525	692.307225	346.657250	691.323209	346.165242	D	547.283451	274.145364	530.256902	265.632089	529.272886	265.140081	5
5	822.417838	411.712557	805.391289	403.199282	804.407273	402.707274	L	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	4
6	909.449866	455.228571	892.423317	446.715296	891.439301	446.223288	S	319.172444	160.089860	302.145895	151.576585	301.161879	151.084577	3
7	966.471330	483.739303	949.444781	475.226028	948.460765	474.734020	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
32.8	1203.574005	-0.004157	AQMDLSGR
3.5	1203.577820	-0.007972	EAQQRQAAMR

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

MASCOT 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 32782: 1461.654748 from(731.834650,2+) rtinseconds(1458) index(2602)

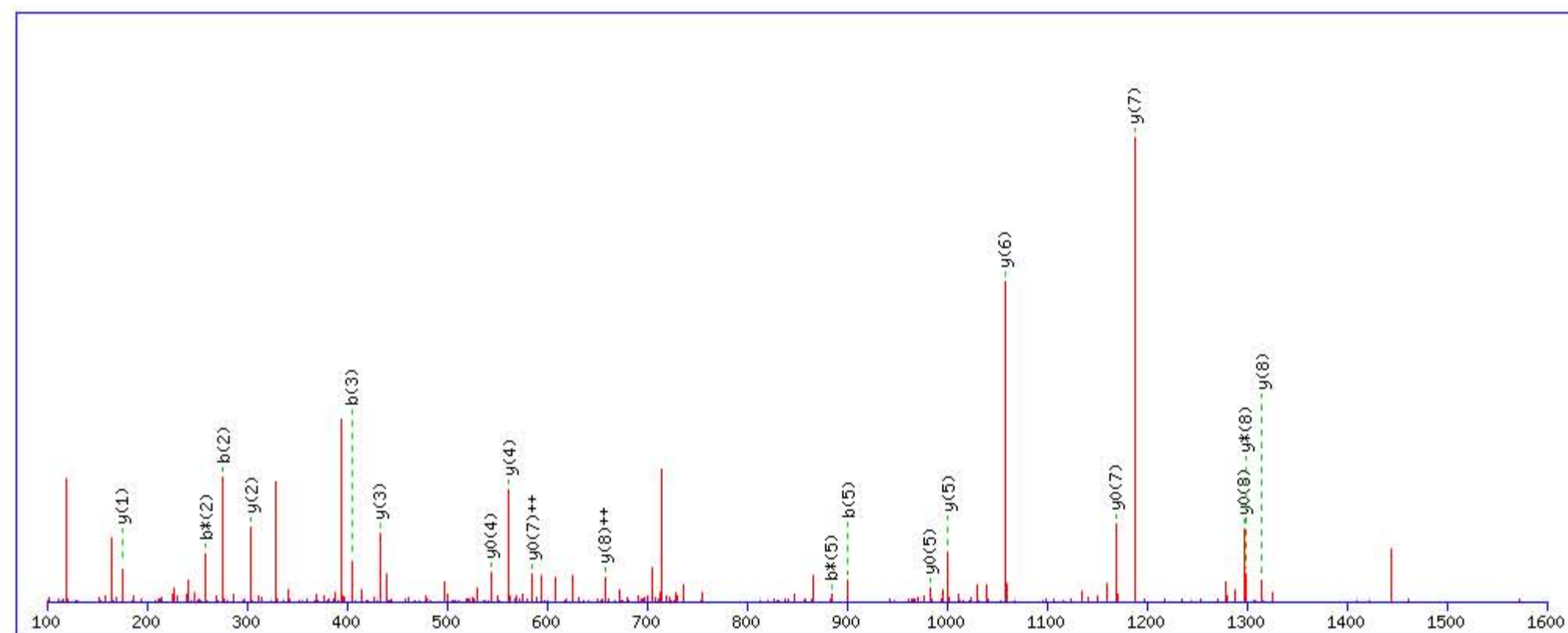
Title: Locus:1.1.1.1316.26 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1461.655807

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

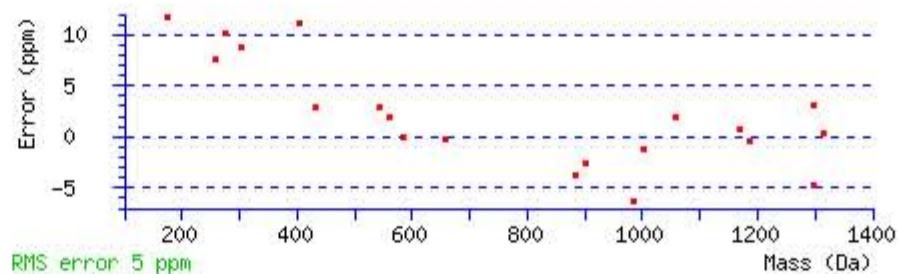
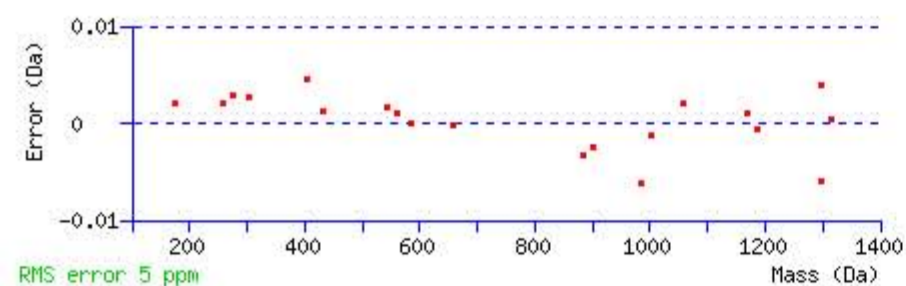
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.00037

Matches : 20/88 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							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
42.8	1461.655807	-0.001059	FQEGQEEER
11.2	1461.640564	0.014184	NSGTQSDGEEK
7.8	1461.648392	0.006356	HREELSDYEER
7.2	1461.655807	-0.001059	FQEGQEEER
6.3	1461.640564	0.014184	VMTDVAGNPEEER
2.3	1461.637161	0.017587	ESELQWQEEER

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 42023: 1766.908528 from(884.461540,2+) rtinseconds(1962) index(68494)

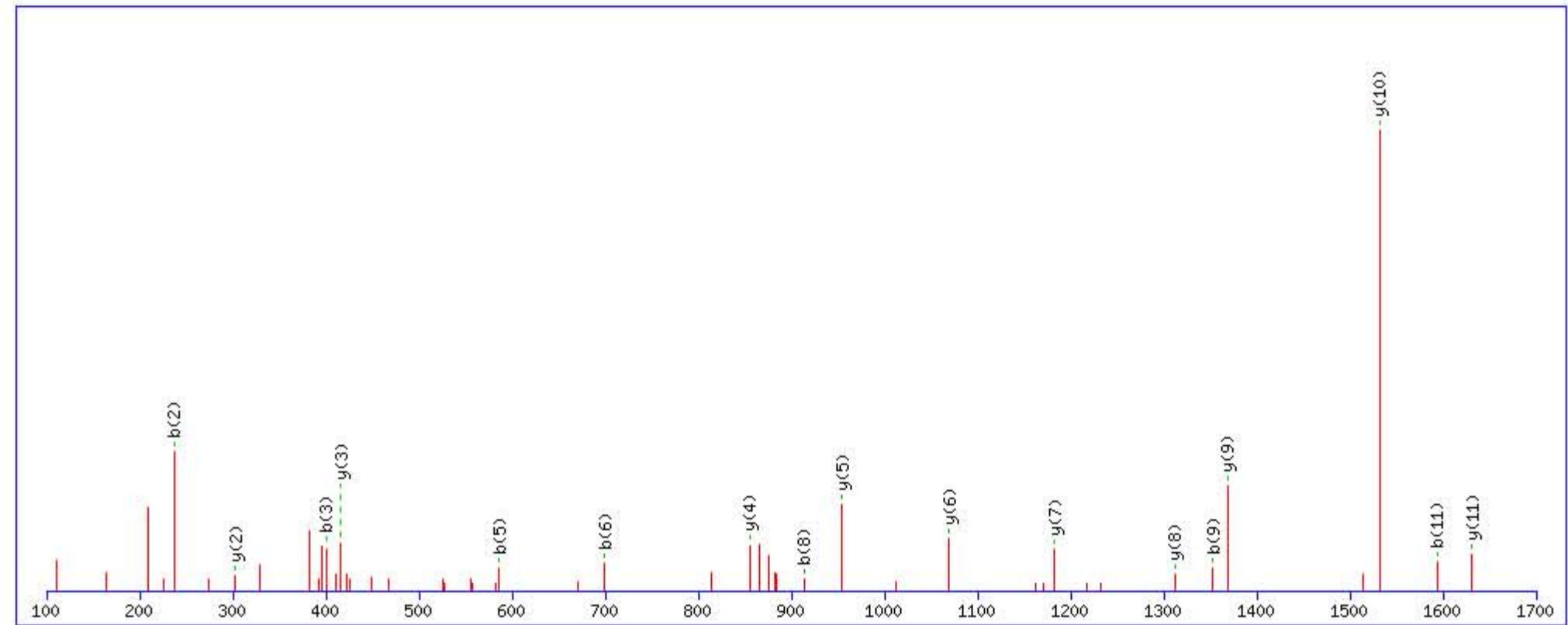
Title: Locus:1.1.1.1620.25 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1766.913773

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

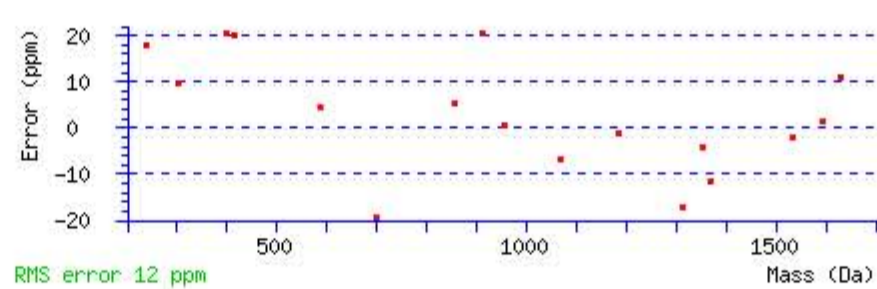
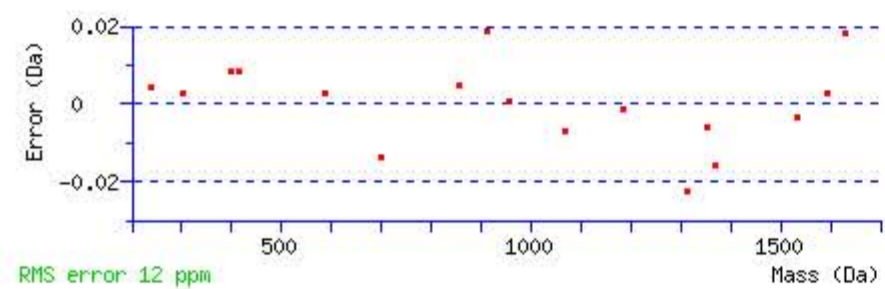
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 64 Expect: 4.3e-006

Matches : 17/98 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	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
63.6	1766.913773	-0.005245	HVYGELDVQIQR
42.0	1766.913773	-0.005245	HVYGELDVQIQR
5.1	1766.888596	0.019932	NQDDRELWPRK
4.8	1766.888138	0.020390	IMQNGTILYTMR

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 42205: 1772.818908 from(887.416730,2+) rtinseconds(1835) index(20548)

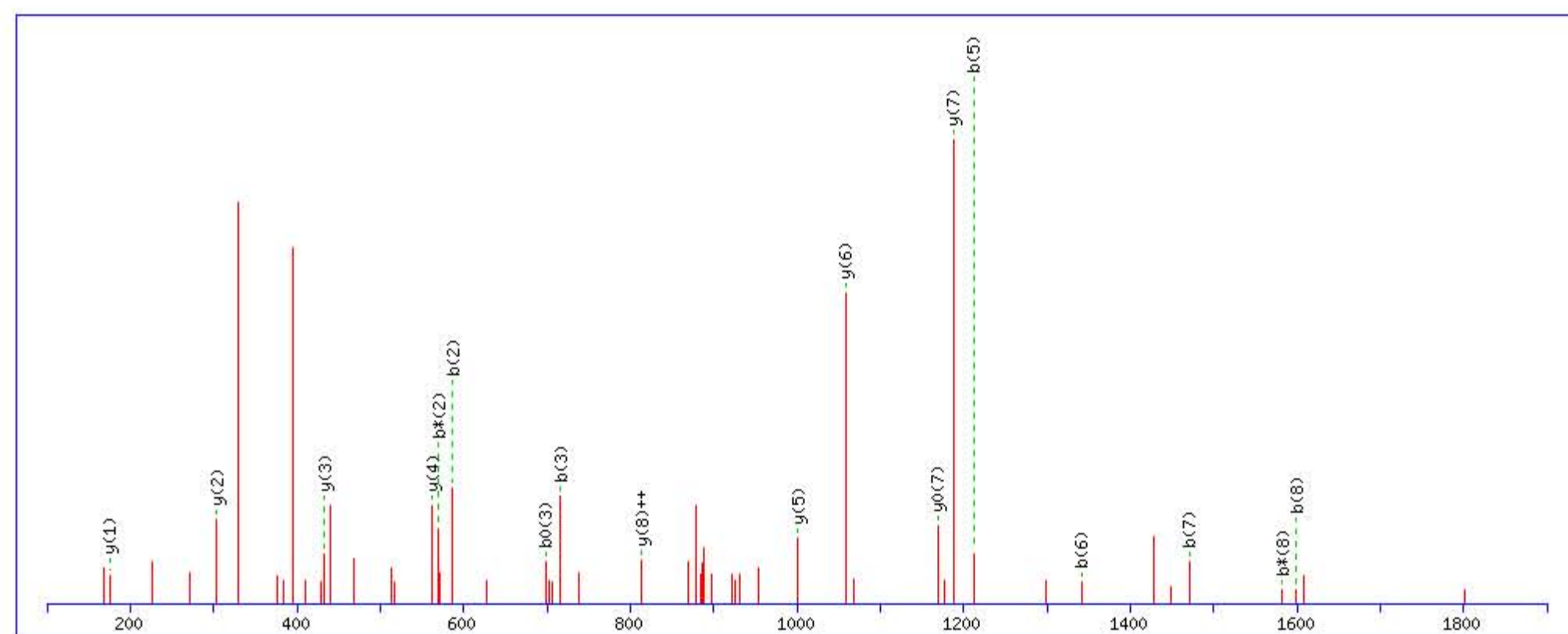
Title: Locus:1.1.1.641.15 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1772.822556

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

Variable modifications:

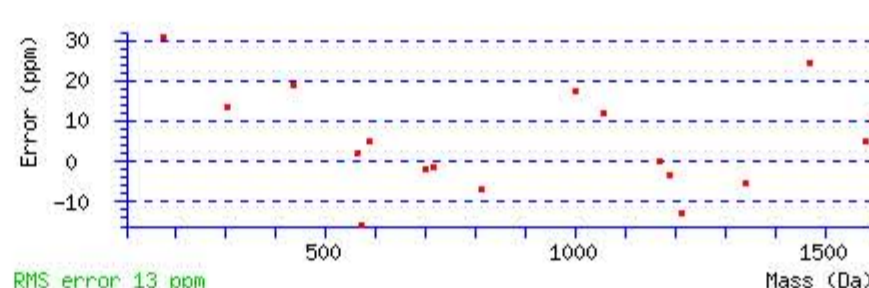
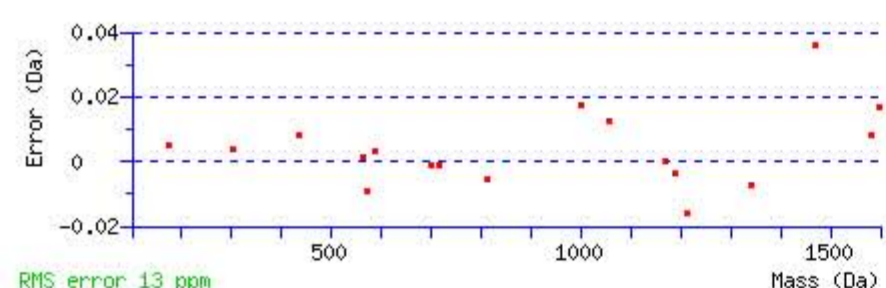
Q2 : Biotin:Thermo-21345 (Q)

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.01

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	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
33.4	1772.803909	0.014999	ESELQWQEEER
33.1	1772.822556	-0.003648	FQEGQEEER
11.1	1772.829727	-0.010819	QEEEEAMRRER
9.5	1772.803909	0.014999	ESELQWQEEER
5.3	1772.798752	0.020156	HISSCMRWPGHYSR
3.7	1772.811798	0.007110	YQTTPPHQNFEDLER
3.3	1772.803909	0.014999	DMASPNWSILPEEER
3.1	1772.828873	-0.009965	QAEQEATVAREEQER
3.0	1772.819901	-0.000993	CGKSFSQSCHLVAHR
1.3	1772.836288	-0.017380	ADGSLTGGGLEAAAMAPER

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GTYPVPIVSELQSGK**

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

Match to Query 46450: 1998.091152 from(667.037660,3+) rtinseconds(2770) index(73343)

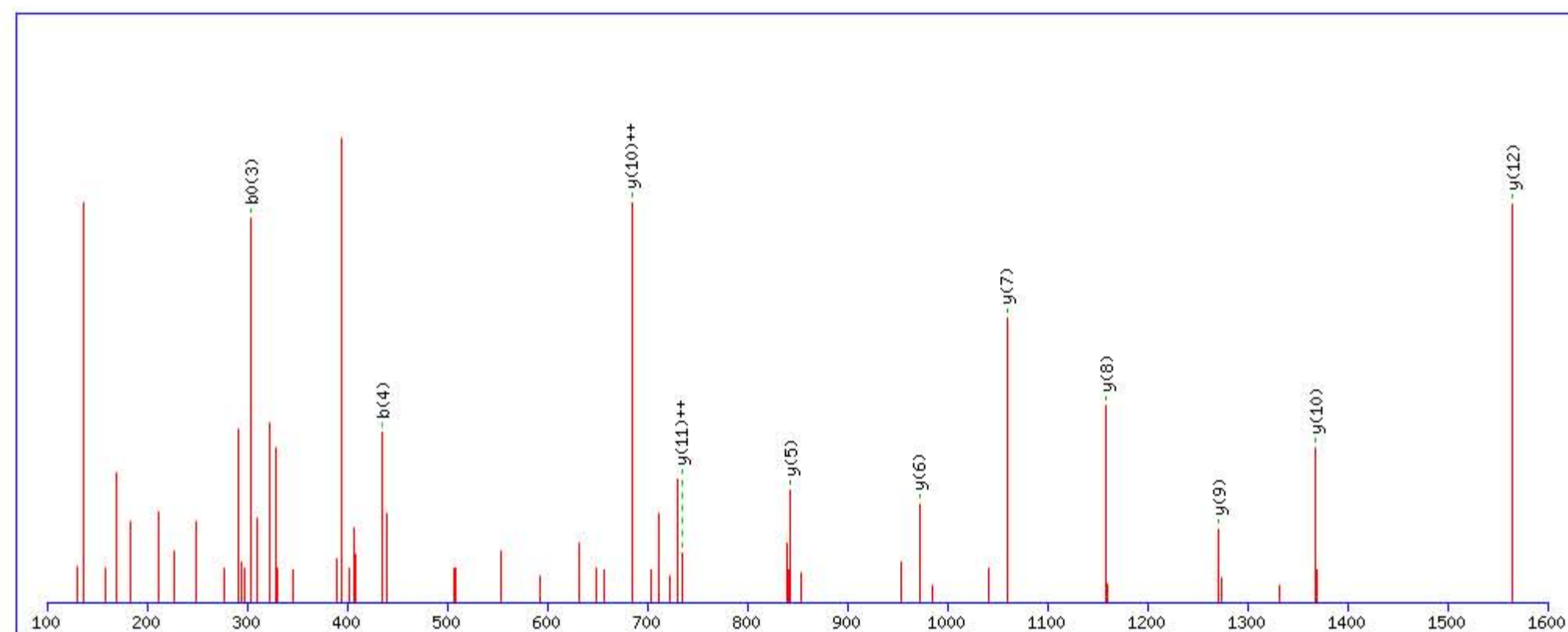
Title: Locus:1.1.1.1901.8 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1998.085983

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

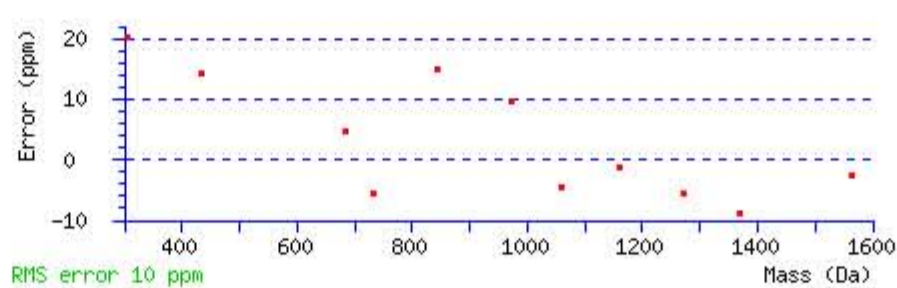
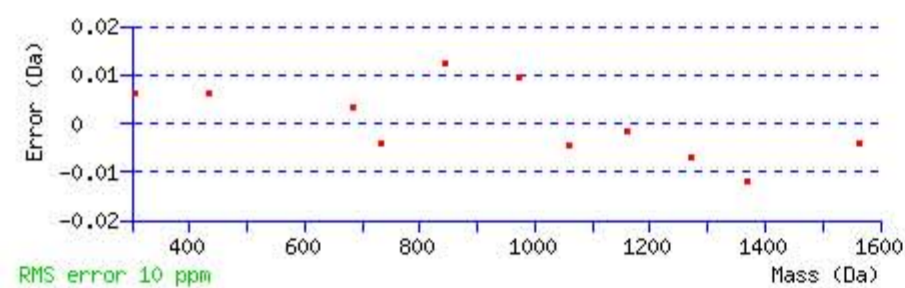
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 52 Expect: 2.1e-005

Matches : 11/150 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							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 **GTYPVPIVSELQSGK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.6	1998.085983	0.005169	GTYPVPIVSELQSGK
1.7	1998.099731	-0.008579	GDEVVVELVENGKKVTVGK
0.5	1998.076065	0.015087	LQKYSTKPGSYIFR

MASCOT Search Results

Peptide View

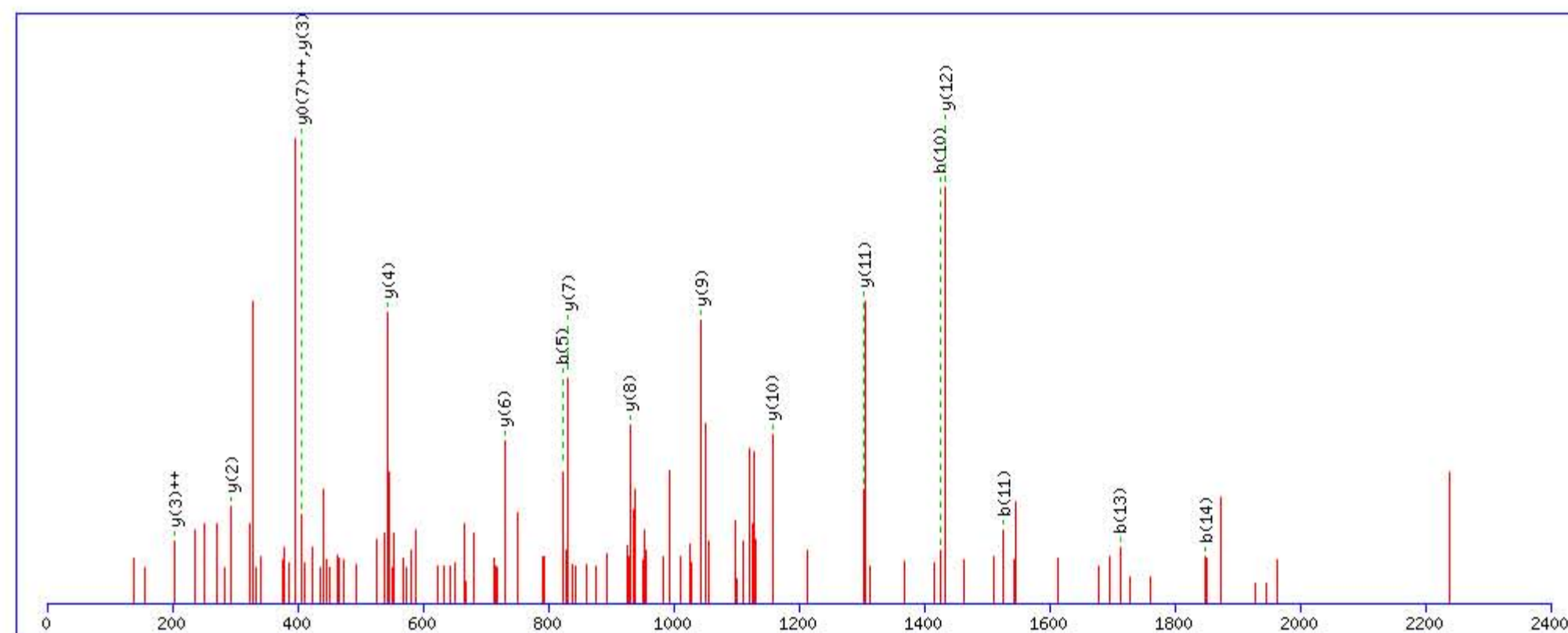
MS/MS Fragmentation of **GVNLQEFLNVTSVHLFK**
 Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

Match to Query 52075: 2255.224988 from(1128.619770,2+) rtinseconds(3004) index(27831)
 Title: Locus:1.1.1.1045.22 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

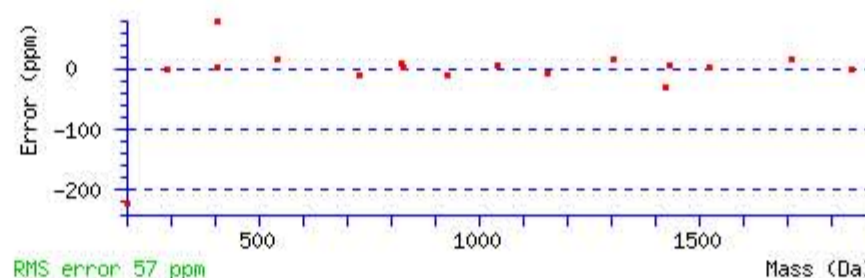
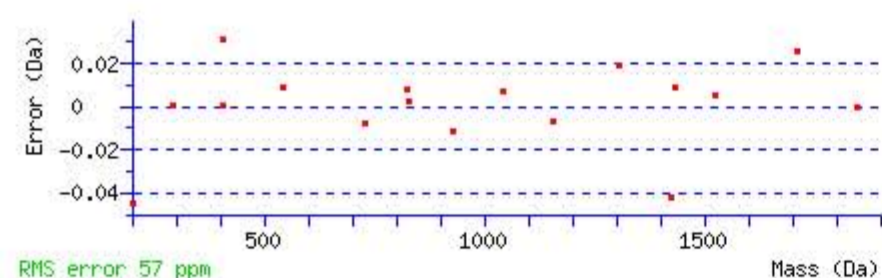
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2255.213654
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q5 : Biotin:Thermo-21345 (Q)
 Ions Score: 44 Expect: 0.00073
 Matches : 17/168 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	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	$M_r(\text{calc})$:	Delta	Sequence
44.1	2255.213654	0.011334	GVNLQEFLNVTSVHLFK

Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVPPNNSNAEEDDLPTVELQGVVPR**

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

Match to Query 60940: 2912.478912 from(971.833580,3+) rtinseconds(2568) index(24846)

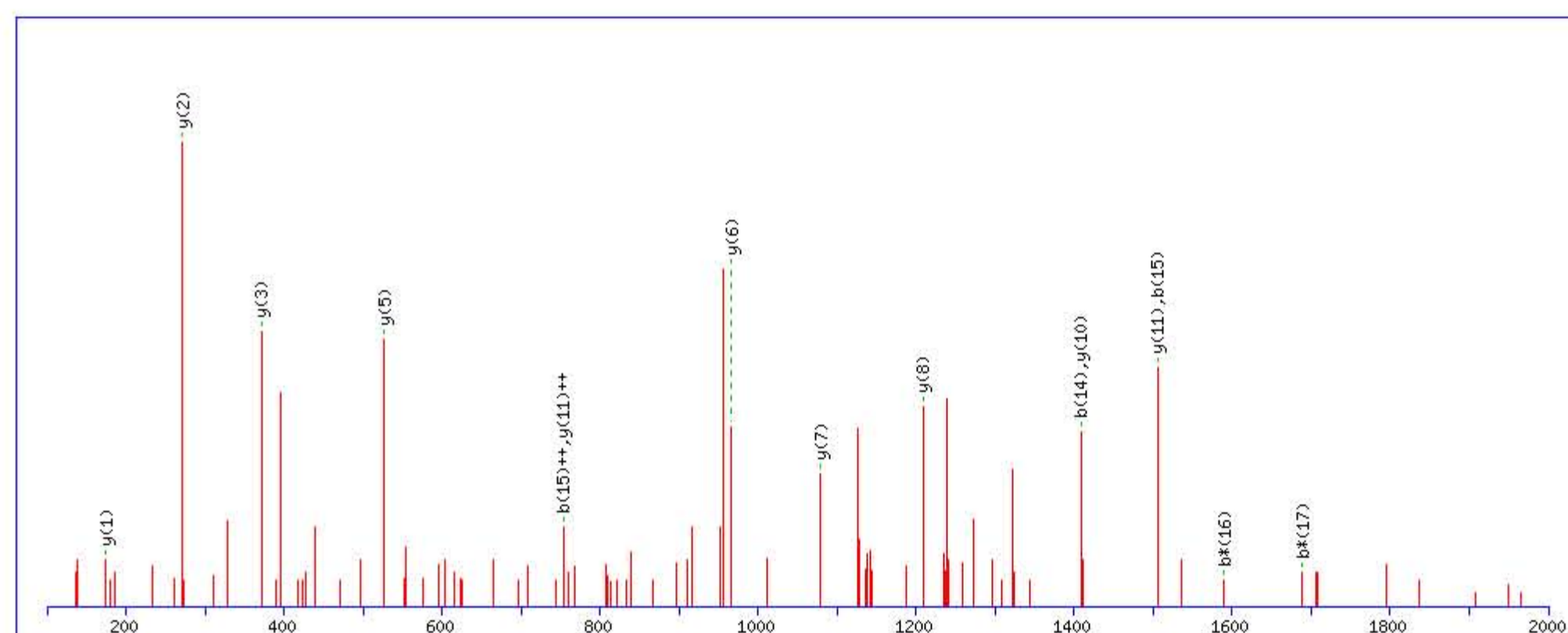
Title: Locus:1.1.1.896.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2912.470200

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

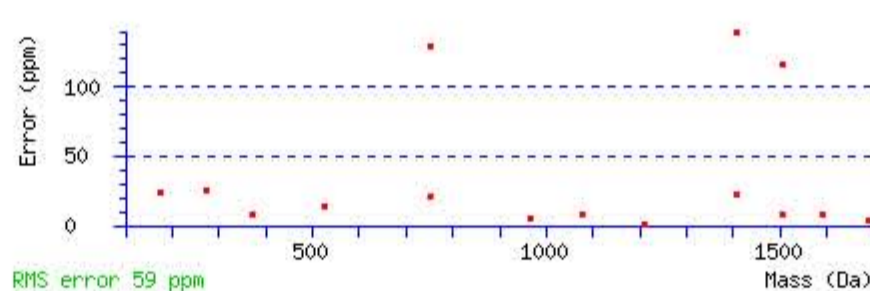
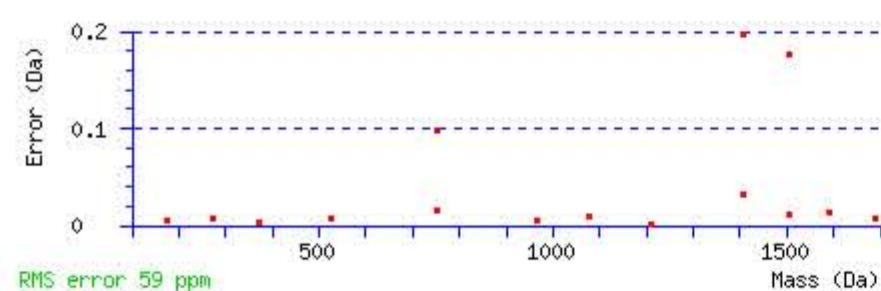
Variable modifications:

Q20 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.081

Matches : 15/254 fragment ions using 37 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.044390	36.525833					A							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 [AVPPNNSNAEEDDLPTVELQGVVPR](#)
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
25.8	2912.470200	0.008712	AVPPNNSNAEEDDLPTVELQGVVPR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AIGEMDNQVSQLTSELK**

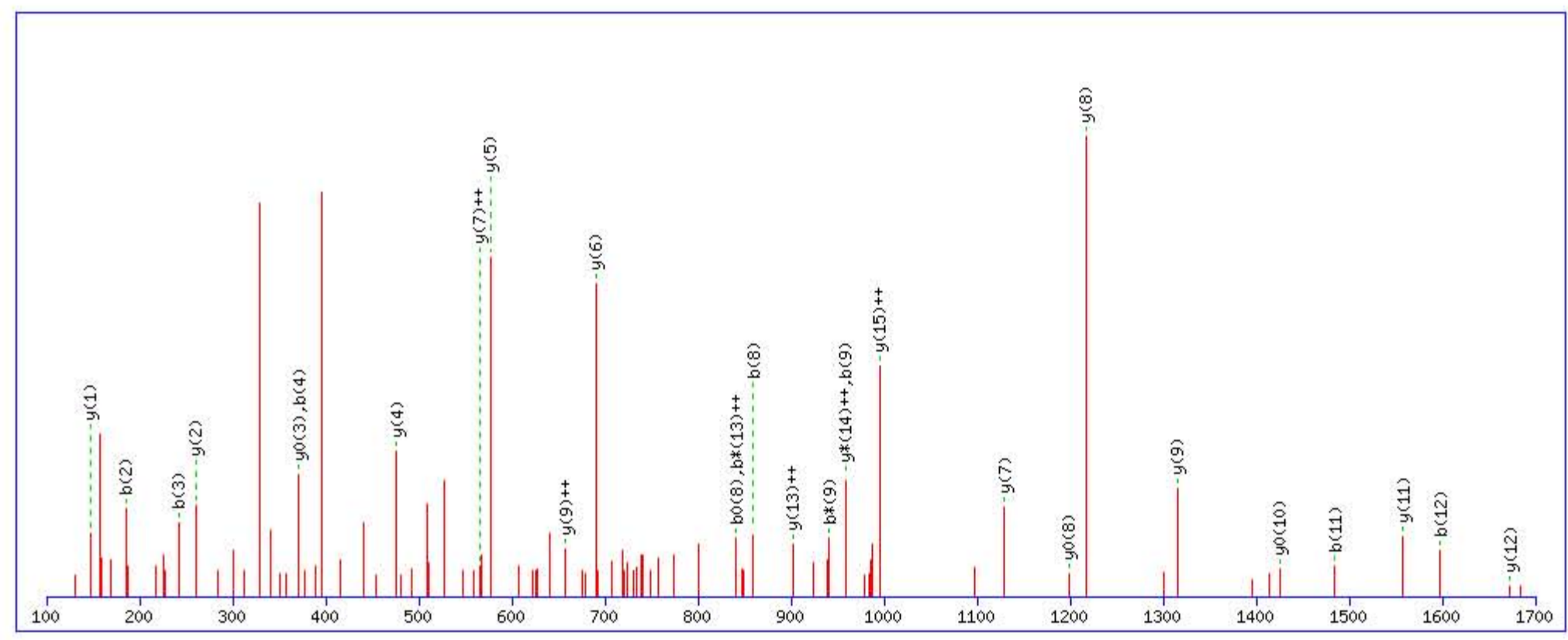
Found in **COL11_HUMAN**, Collectin-11 OS=Homo sapiens GN=COLEC11 PE=1 SV=1

Match to Query 50526: 2173.094622 from(725.372150,3+) rtinseconds(2436) index(55618)
 Title: Locus:1.1.1.1463.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

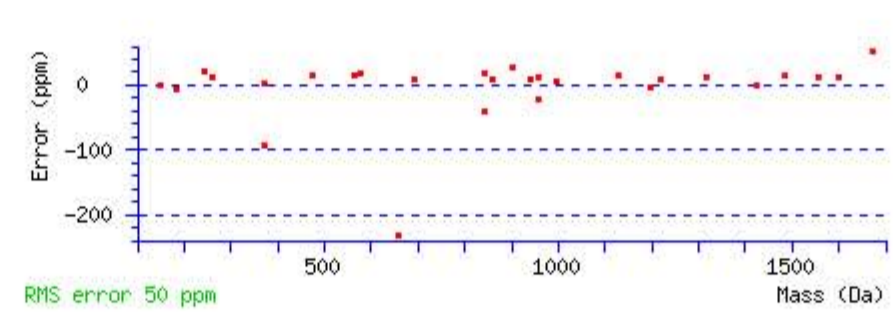
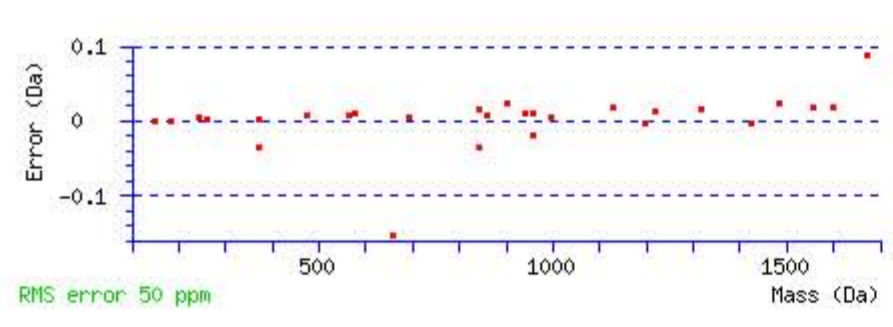
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2173.075867
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q11 : Biotin:Thermo-21345 (Q)
 Ions Score: 64 Expect: 1.2e-005
 Matches : 28/170 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	72.044390	36.525833					A							17
2	185.128454	93.067865					I	2103.046054	1052.026665	2086.019505	1043.513390	2085.035489	1043.021382	16
3	242.149918	121.578597					G	1989.961990	995.484633	1972.935441	986.971359	1971.951425	986.479351	15
4	371.192511	186.099894			353.181946	177.094611	E	1932.940526	966.973901	1915.913977	958.460627	1914.929961	957.968619	14
5	502.232996	251.620136			484.222431	242.614854	M	1803.897933	902.452605	1786.871384	893.939330	1785.887368	893.447322	13
6	617.259939	309.133608			599.249374	300.128325	D	1672.857448	836.932362	1655.830899	828.419088	1654.846883	827.927080	12
7	731.302866	366.155071	714.276317	357.641797	713.292301	357.149789	N	1557.830505	779.418891	1540.803956	770.905616	1539.819940	770.413608	11
8	859.361444	430.184360	842.334895	421.671086	841.350879	421.179078	Q	1443.787578	722.397427	1426.761029	713.884153	1425.777013	713.392145	10
9	958.429858	479.718567	941.403309	471.205292	940.419293	470.713284	V	1315.729000	658.368138	1298.702451	649.854864	1297.718435	649.362856	9
10	1045.461886	523.234581	1028.435337	514.721307	1027.451321	514.229299	S	1216.660586	608.833931	1199.634037	600.320657	1198.650021	599.828649	8
11	1484.687212	742.847244	1467.660663	734.333970	1466.676647	733.841962	Q	1129.628558	565.317917	1112.602009	556.804643	1111.617993	556.312635	7
12	1597.771276	799.389276	1580.744727	790.876002	1579.760711	790.383993	L	690.403232	345.705254	673.376683	337.191980	672.392667	336.699972	6
13	1698.818955	849.913116	1681.792406	841.399841	1680.808390	840.907833	T	577.319168	289.163222	560.292619	280.649948	559.308603	280.157940	5
14	1785.850983	893.429130	1768.824434	884.915855	1767.840418	884.423847	S	476.271489	238.639383	459.244940	230.126108	458.260924	229.634100	4
15	1914.893576	957.950426	1897.867027	949.437152	1896.883011	948.945144	E	389.239461	195.123369	372.212912	186.610094	371.228896	186.118086	3
16	2027.977640	1014.492458	2010.951091	1005.979184	2009.967075	1005.487176	L	260.196868	130.602072	243.170319	122.088798			2
17							K	147.112804	74.060040	130.086255	65.546766			1



NCBI BLAST search of **AIGEMDNQVSQLTSELK**
 (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	2173.075867	0.018755	AIGEMDNQVSQLTSELK
28.5	2173.075867	0.018755	AIGEMDNQVSQLTSELK

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 44249: 1876.851852 from(626.624560,3+) rtinseconds(1938) index(35986)

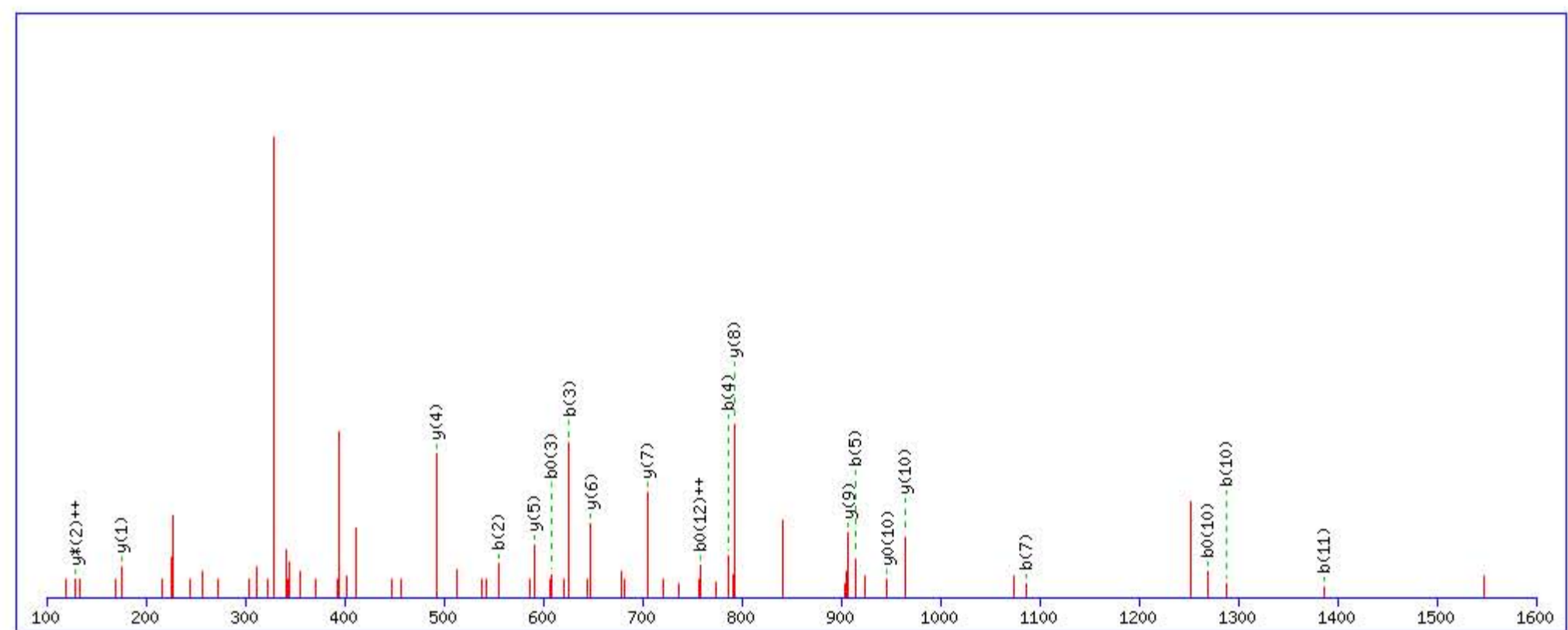
Title: Locus:1.1.1.3094.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1876.856033

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

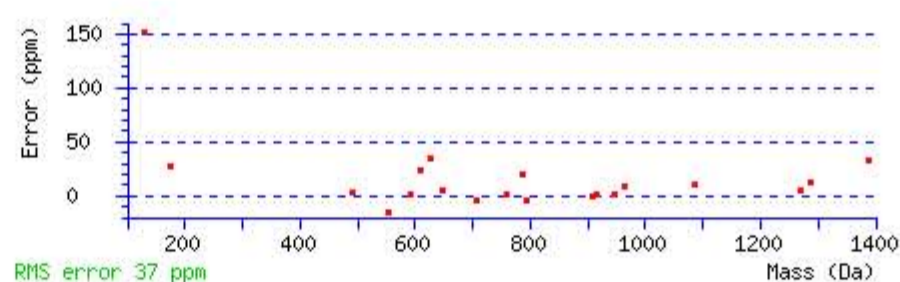
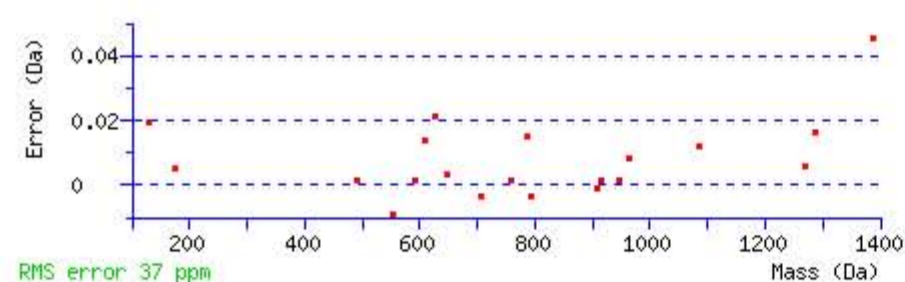
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 54 Expect: 8.7e-006

Matches : 20/152 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	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
54.1	1876.856033	-0.004181	QDACQGDSGGVFAVR
43.1	1876.856033	-0.004181	QDACQGDSGGVFAVR
0.1	1876.855820	-0.003968	QRAGSSGGRGECDISGAGR

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 50315: 2167.026388 from(1084.520470,2+) rtinseconds(2163) index(37411)

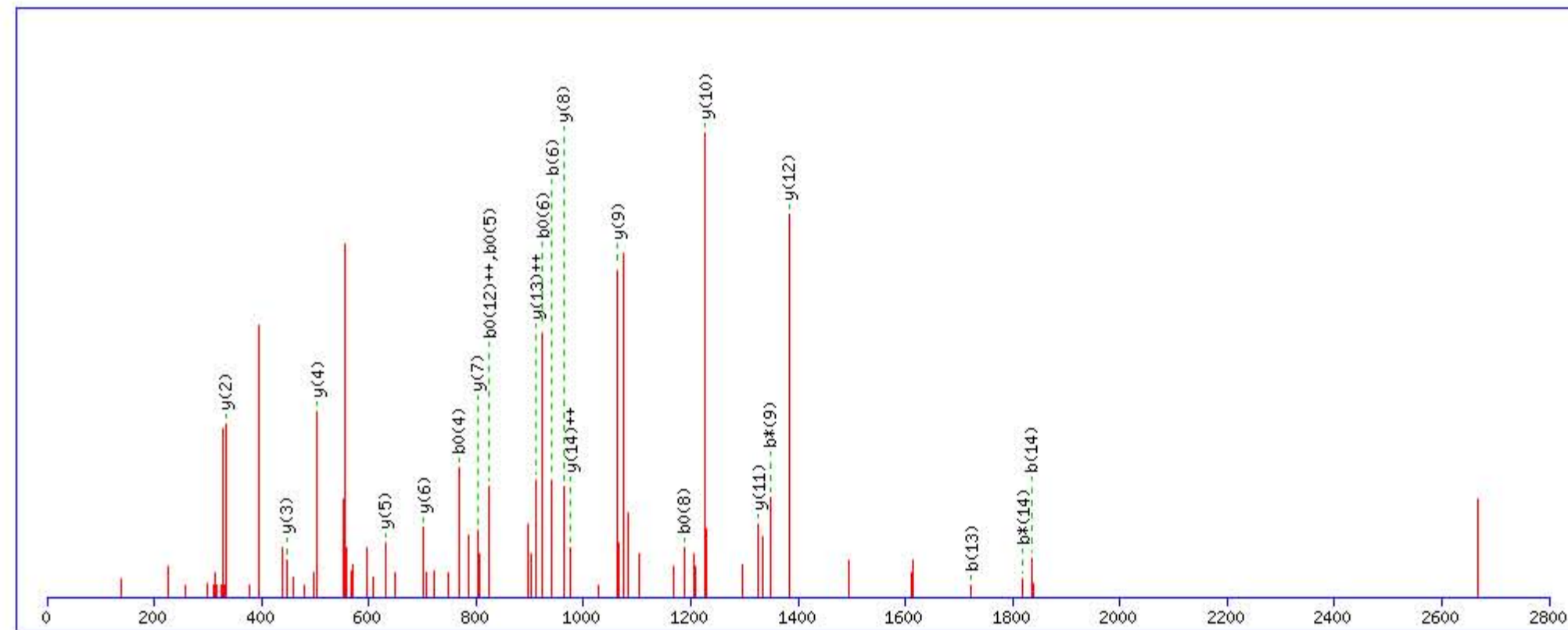
Title: Locus:1.1.1.3172.26 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2167.007813

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

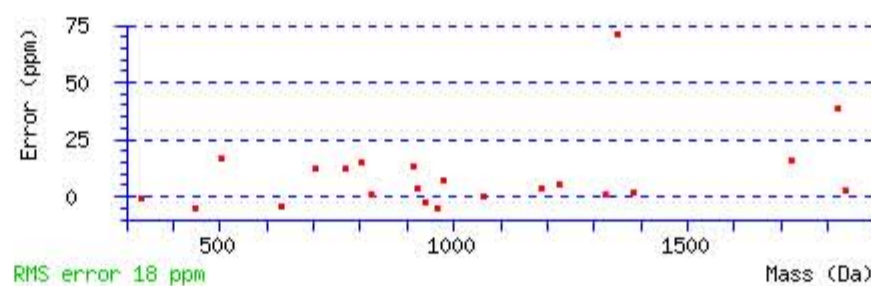
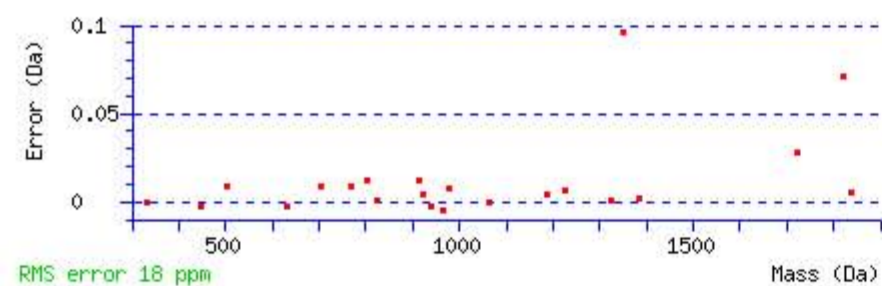
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 62 Expect: 1.2e-005

Matches : 23/162 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	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	$M_r(\text{calc})$	Delta	Sequence
62.0	2167.007813	0.018576	ESEQGVYTCTAQGIWK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SNALDIIFQTDLTGQK**

Found in **C1S_HUMAN**, Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1

Match to Query 48811: 2074.100688 from(1038.057620,2+) rtinseconds(2891) index(58620)

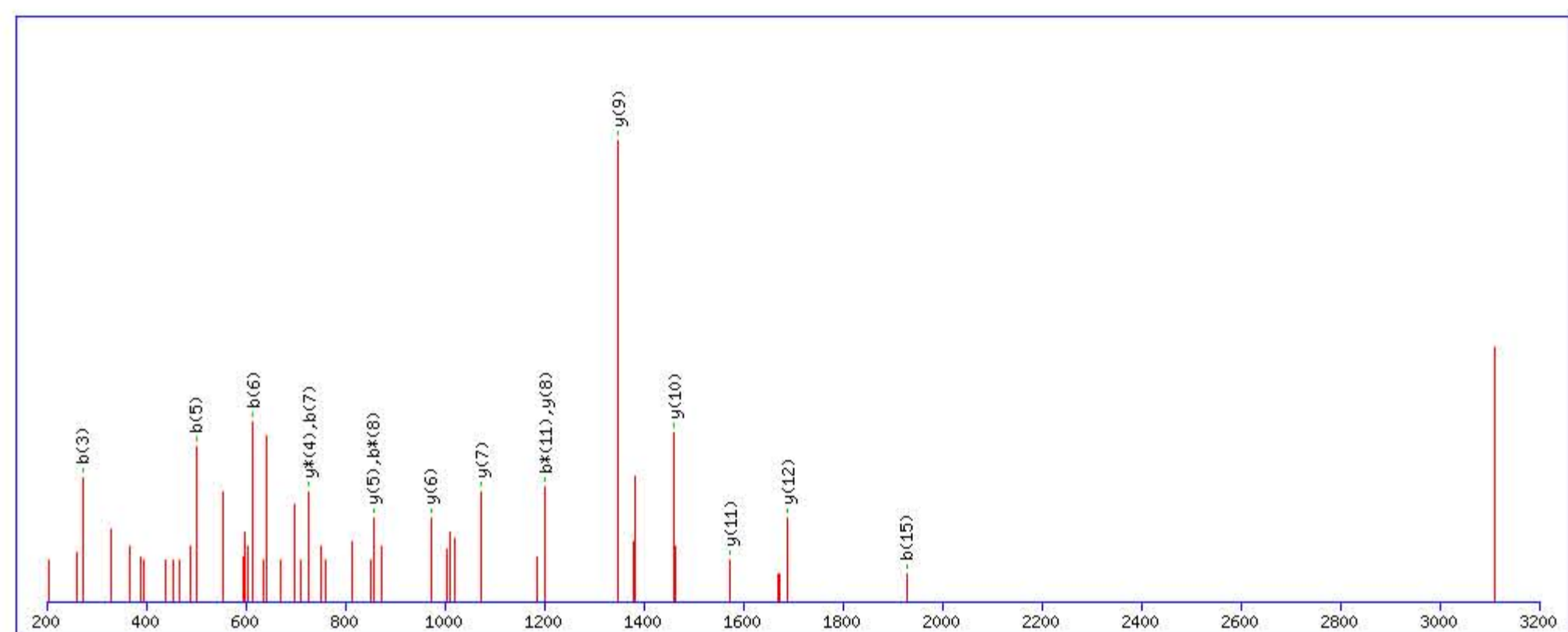
Title: Locus:1.1.1.1619.25 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2074.076874

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

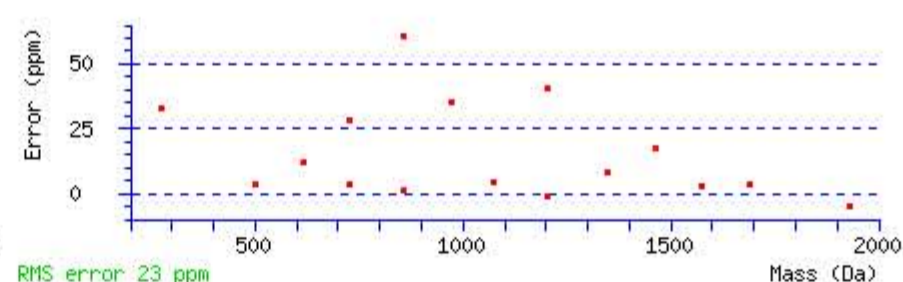
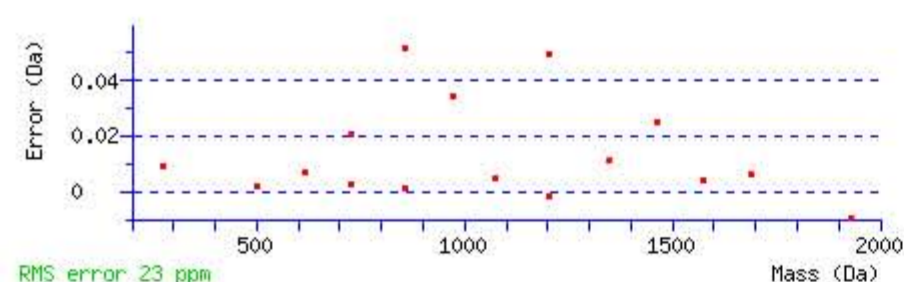
Variable modifications:

Q15 : Biotin:Thermo-21345 (Q)

Ions Score: 69 Expect: 2.5e-006

Matches : 16/172 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	202.082231	101.544753	185.055682	93.031479	184.071666	92.539471	N	1988.052127	994.529702	1971.025578	986.016427	1970.041562	985.524419	15
3	273.119345	137.063311	256.092796	128.550036	255.108780	128.058028	A	1874.009200	937.508238	1856.982651	928.994964	1855.998635	928.502956	14
4	386.203409	193.605343	369.176860	185.092068	368.192844	184.600060	L	1802.972086	901.989681	1785.945537	893.476407	1784.961521	892.984399	13
5	501.230352	251.118814	484.203803	242.605540	483.219787	242.113532	D	1689.888022	845.447649	1672.861473	836.934375	1671.877457	836.442367	12
6	614.314416	307.660846	597.287867	299.147572	596.303851	298.655564	I	1574.861079	787.934178	1557.834530	779.420903	1556.850514	778.928895	11
7	727.398480	364.202878	710.371931	355.689604	709.387915	355.197596	I	1461.777015	731.392146	1444.750466	722.878871	1443.766450	722.386863	10
8	874.466894	437.737085	857.440345	429.223811	856.456329	428.731803	F	1348.692951	674.850114	1331.666402	666.336839	1330.682386	665.844831	9
9	1002.525472	501.766374	985.498923	493.253100	984.514907	492.761092	Q	1201.624537	601.315907	1184.597988	592.802632	1183.613972	592.310624	8
10	1103.573151	552.290214	1086.546602	543.776939	1085.562586	543.284931	T	1073.565959	537.286618	1056.539410	528.773343	1055.555394	528.281335	7
11	1218.600094	609.803685	1201.573545	601.290411	1200.589529	600.798403	D	972.518280	486.762778	955.491731	478.249504	954.507715	477.757496	6
12	1331.684158	666.345717	1314.657609	657.832443	1313.673593	657.340435	L	857.491337	429.249307	840.464788	420.736032	839.480772	420.244024	5
13	1432.731837	716.869557	1415.705288	708.356282	1414.721272	707.864274	T	744.407273	372.707275	727.380724	364.194000	726.396708	363.701992	4
14	1489.753301	745.380289	1472.726752	736.867014	1471.742736	736.375006	G	643.359594	322.183435	626.333045	313.670161			3
15	1928.978627	964.992952	1911.952078	956.479677	1910.968062	955.987669	Q	586.338130	293.672703	569.311581	285.159429			2
16							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **SNALDIIFQTDLTGQK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.8	2074.076874	0.023814	SNALDIIFQTDLTGQK
38.8	2074.076874	0.023814	SNALDIIFQTDLTGQK
8.5	2074.088104	0.012584	SKGLVQNIDQLYSGGGK
1.8	2074.076813	0.023875	LEEELREKQAYVEK
1.6	2074.110535	-0.009847	QNPSLPAARGLNELQR
0.5	2074.111420	-0.010732	VFVGFLLFPWALMLLSYR
0.3	2074.126923	-0.026235	IEALKATAASLSSRIESEAK
0.2	2074.100662	0.000026	DYKIQNHGHRVLQR
0.2	2074.081589	0.019099	GTMGNHLLTNPVLQPR
0.2	2074.118423	-0.017735	VRETRHLWVGNLPEVNR

MASCOT 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 19739: 1114.600588 from(558.307570,2+) rtinseconds(1507) index(33332)

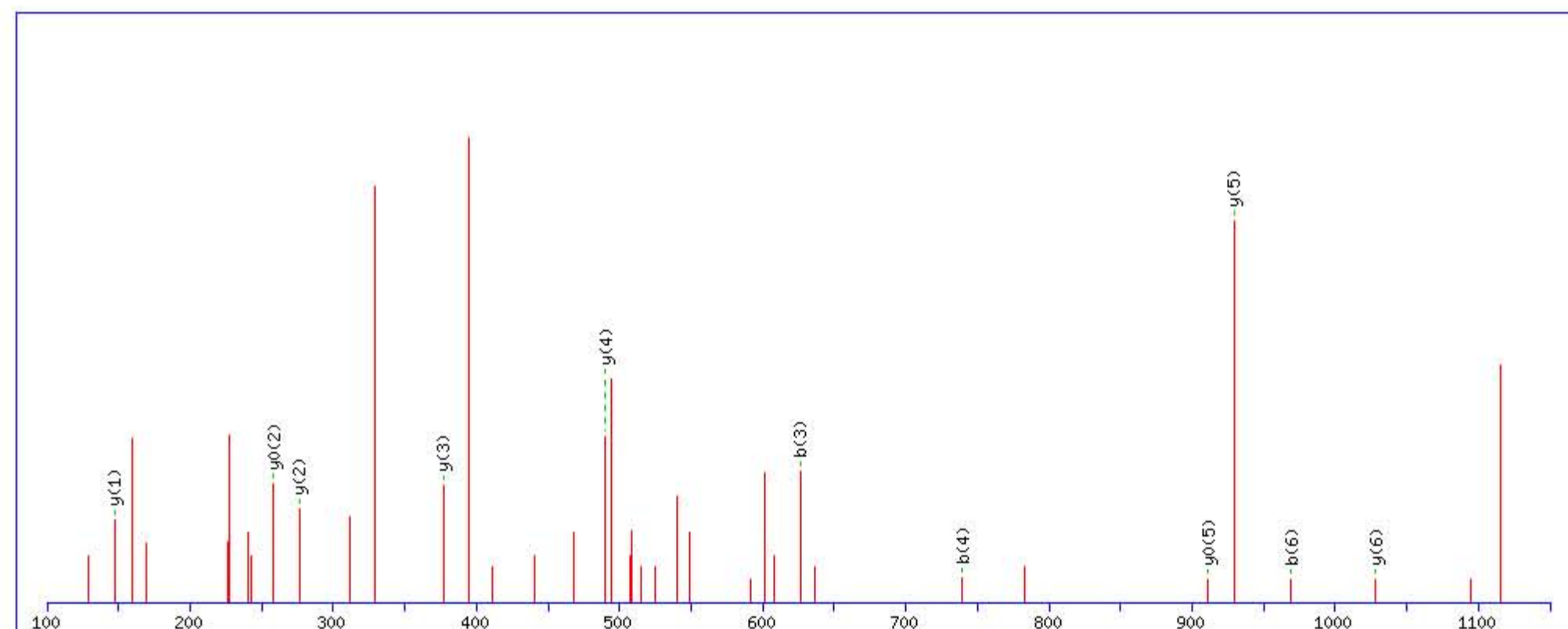
Title: Locus:1.1.1.2944.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1114.605621

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

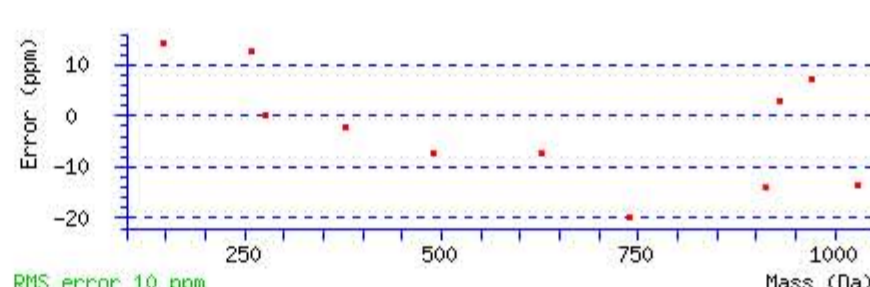
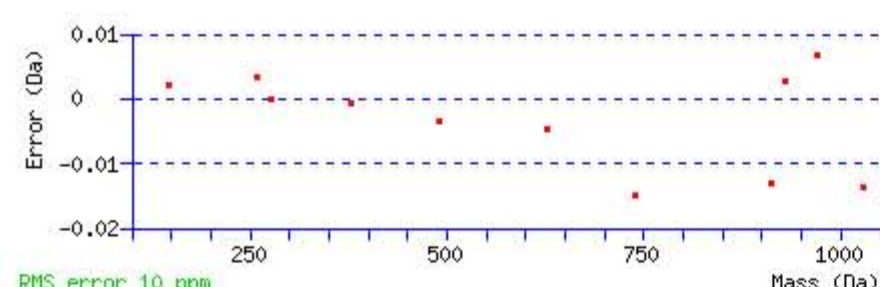
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.0051

Matches : 11/66 fragment ions using 23 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							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
33.4	1114.605621	-0.005033	SVQLTEK
8.5	1114.591690	0.008898	ASVHSMISRK
6.9	1114.613480	-0.012892	SVFAKHGLEK
4.6	1114.584503	0.016085	DAQVFPK
3.4	1114.598236	0.002352	SAVITSLDPGR
2.7	1114.598190	0.002398	QEQAALKLAK

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 23267: 1197.613508 from(599.814030,2+) rtinseconds(1591) index(33866)

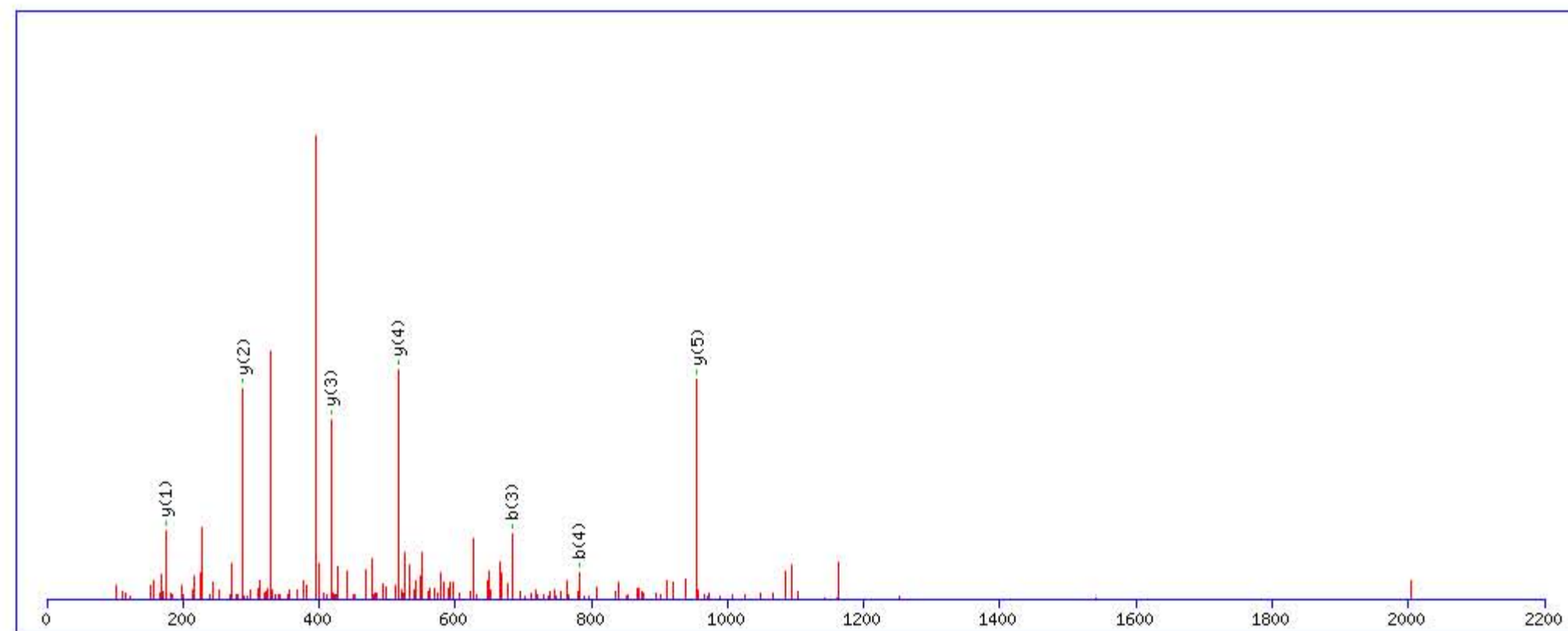
Title: Locus:1.1.1.2973.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1197.617569

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

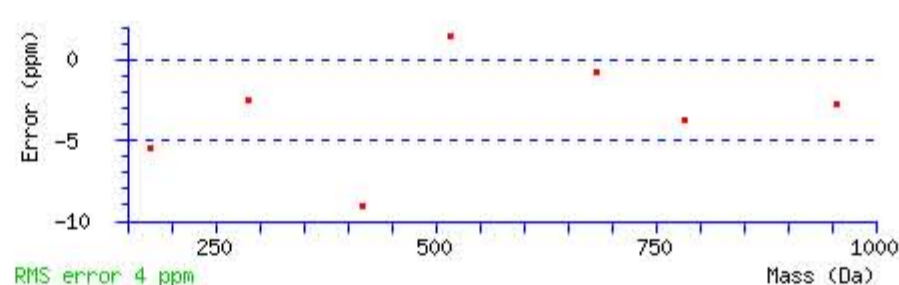
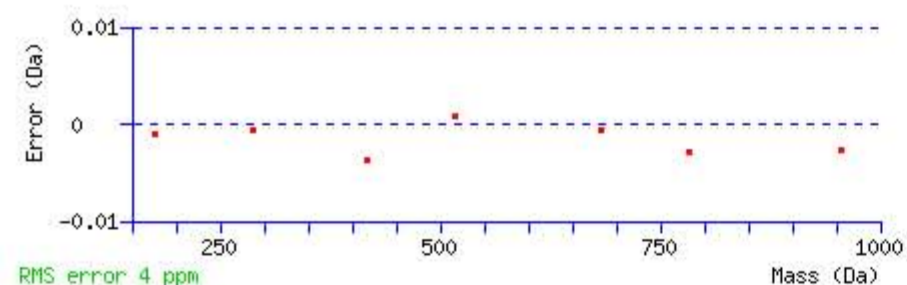
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.0032

Matches : 7/66 fragment ions using 11 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.050203	58.028740	98.023654	49.515465			N							7
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	E	1084.581942	542.794609	1067.555393	534.281335	1066.571377	533.789327	6
3	683.318122	342.162699	666.291573	333.649425	665.307557	333.157417	Q	955.539349	478.273313	938.512800	469.760038	937.528784	469.268030	5
4	782.386536	391.696906	765.359987	383.183632	764.375971	382.691624	V	516.314023	258.660650	499.287474	250.147375	498.303458	249.655367	4
5	911.429129	456.218203	894.402580	447.704928	893.418564	447.212920	E	417.245609	209.126443	400.219060	200.613168	399.235044	200.121160	3
6	1024.513193	512.760235	1007.486644	504.246960	1006.502628	503.754952	I	288.203016	144.605146	271.176467	136.091872			2
7							R	175.118952	88.063114	158.092403	79.549840			1



NCBI BLAST search of [NEQVEIR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.9	1197.617569	-0.004061	NEQVEIR
8.8	1197.617569	-0.004061	NQEDLLR
8.8	1197.598953	0.014555	QDNLPDIEVR
8.4	1197.617569	-0.004061	QEVNELR
8.2	1197.598938	0.014570	AAQEGDLPCLR
8.0	1197.617569	-0.004061	LQDNELR
7.6	1197.598953	0.014555	EISPGSGPGEIR
6.0	1197.621399	-0.007891	EKHSTQAKNR
3.9	1197.628815	-0.015307	QLSMQVHALR
2.8	1197.598953	0.014555	VDNQPEELVR

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

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **TGLQEVEVK**

Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

Match to Query 26450: 1312.705908 from(657.360230,2+) rtinseconds(1814) index(35116)

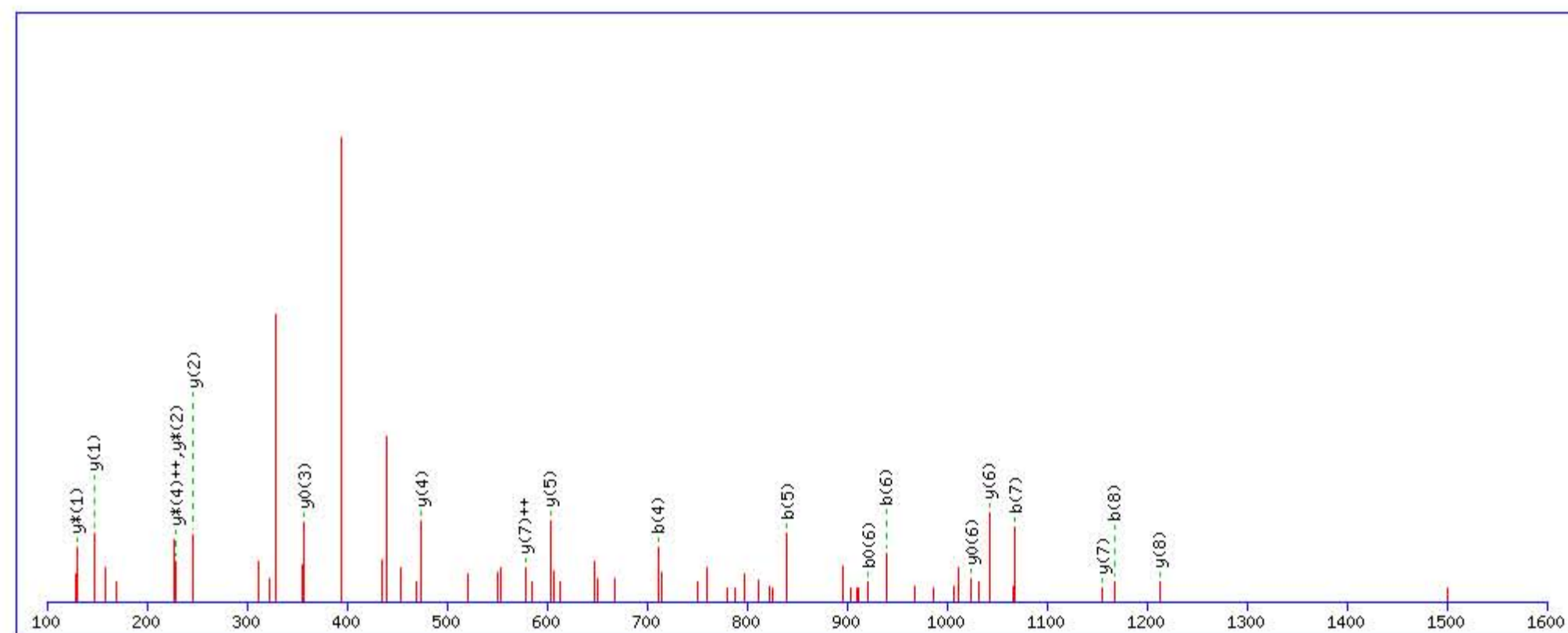
Title: Locus:1.1.1.3051.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1312.706070

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

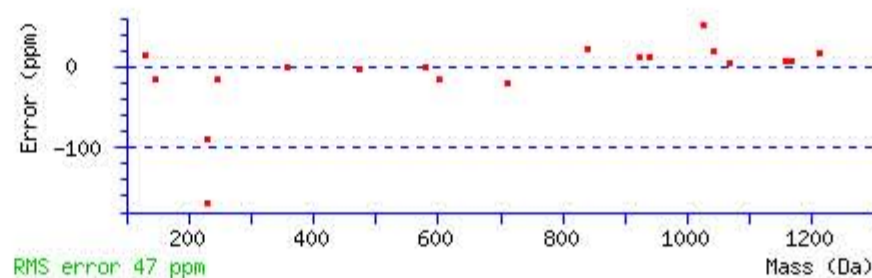
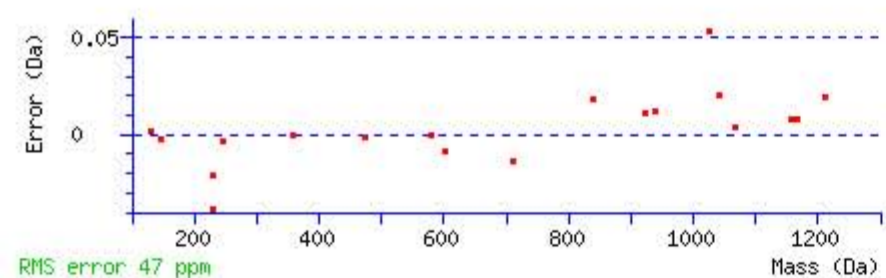
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 39 Expect: 0.002

Matches : 19/86 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							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
39.2	1312.706070	-0.000162	TGLQEVEVK
9.8	1312.699524	0.006384	TIMHLMINNVK
5.9	1312.692139	0.013769	DRQSQIQK
2.4	1312.688766	0.017142	HKVHTGEKSYK
1.3	1312.706055	-0.000147	QSAEEVIVK
1.1	1312.691422	0.014486	YKELYLEEVK

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 31271: 1420.793088 from(711.403820,2+) rtinseconds(1980) index(36296)

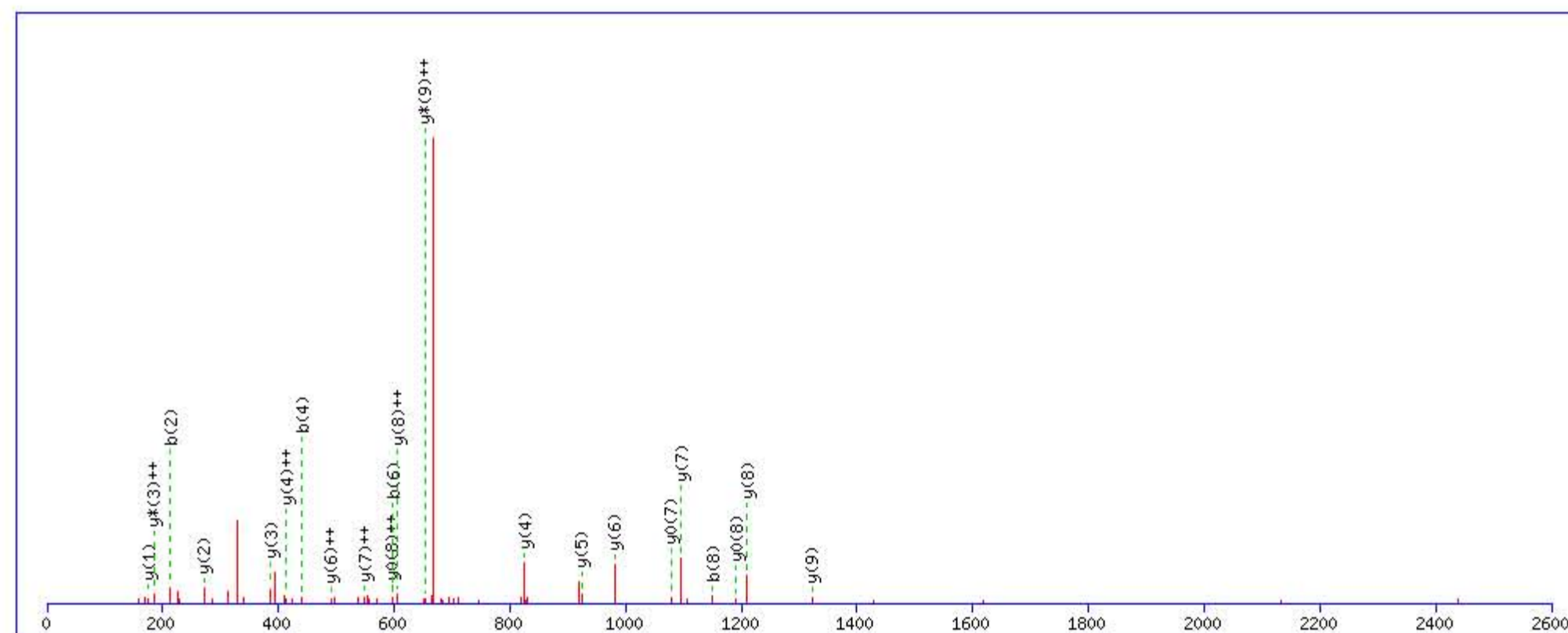
Title: Locus:1.1.1.3109.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1420.786057

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

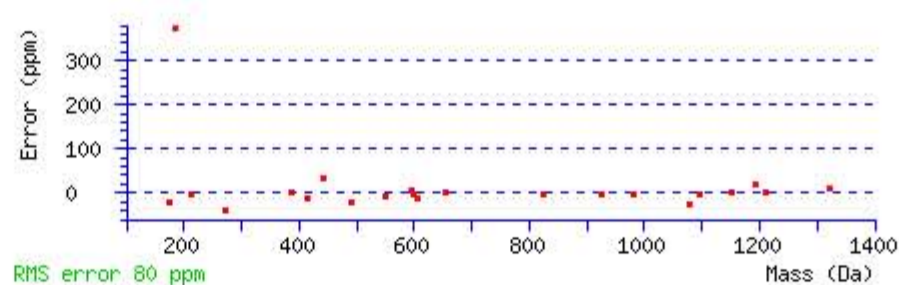
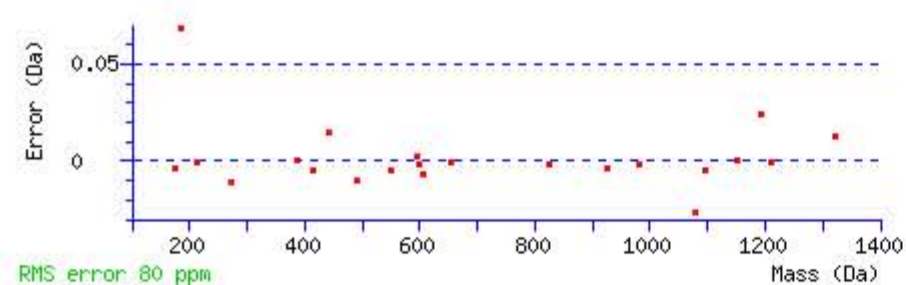
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 8.7e-005

Matches : 22/78 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	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
45.6	1420.786057	0.007031	VLLDGVQNPR
2.3	1420.811172	-0.018084	KQKQLEILFMK
1.7	1420.801315	-0.008227	VLQPFLTHR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **HQQTVTIPPK**

Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

Match to Query 32710: 1458.791502 from(487.271110,3+) rtinseconds(1614) index(33955)

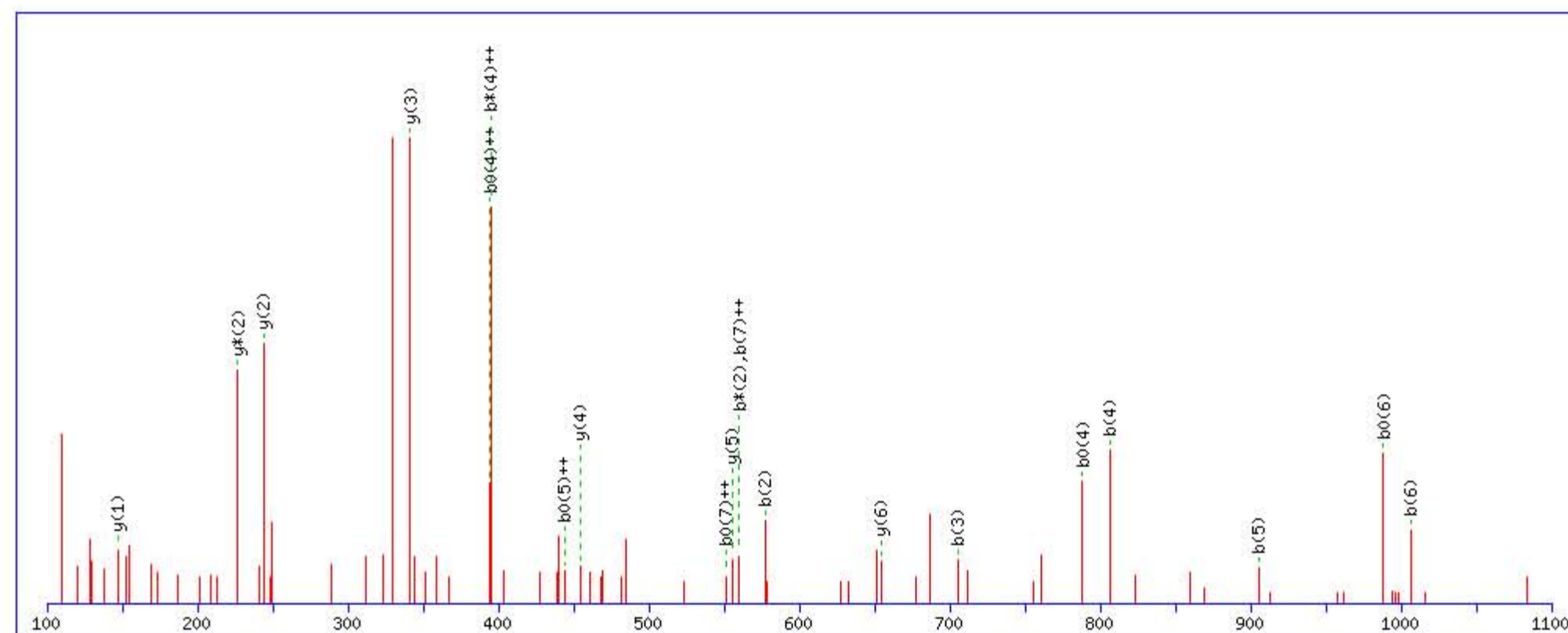
Title: Locus:1.1.1.2981.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1458.801712

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

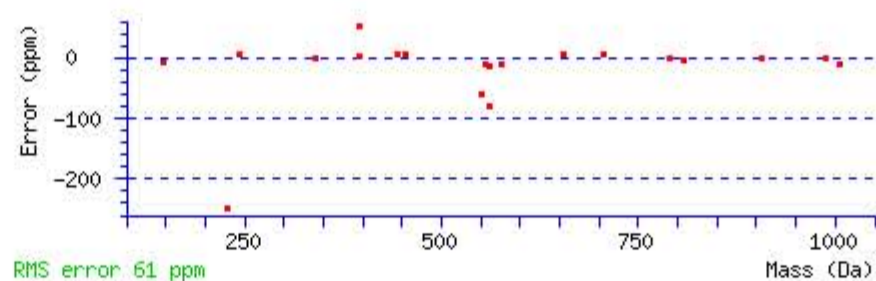
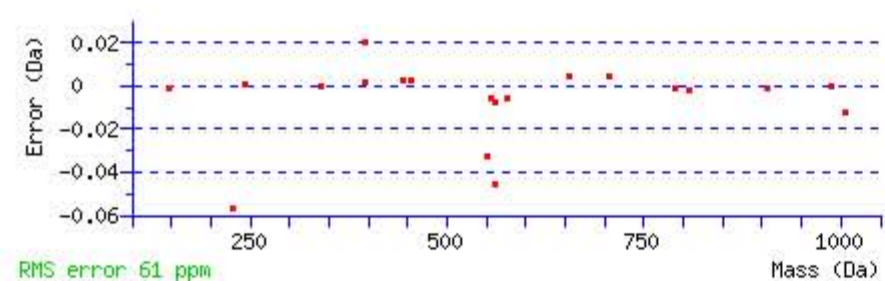
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 32 Expect: 0.0019

Matches : 20/92 fragment ions using 38 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	138.066188	69.536732					H							10
2	577.291514	289.149395	560.264965	280.636121			Q	1322.750072	661.878674	1305.723523	653.365400	1304.739507	652.873392	9
3	705.350092	353.178684	688.323543	344.665410			Q	883.524746	442.266011	866.498197	433.752737	865.514181	433.260729	8
4	806.397771	403.702524	789.371222	395.189249	788.387206	394.697241	T	755.466168	378.236722	738.439619	369.723448	737.455603	369.231440	7
5	905.466185	453.236731	888.439636	444.723456	887.455620	444.231448	V	654.418489	327.712883	637.391940	319.199608	636.407924	318.707600	6
6	1006.513864	503.760570	989.487315	495.247296	988.503299	494.755288	T	555.350075	278.178676	538.323526	269.665401	537.339510	269.173393	5
7	1119.597928	560.302602	1102.571379	551.789328	1101.587363	551.297319	I	454.302396	227.654836	437.275847	219.141561			4
8	1216.650692	608.828984	1199.624143	600.315710	1198.640127	599.823701	P	341.218332	171.112804	324.191783	162.599530			3
9	1313.703456	657.355366	1296.676907	648.842092	1295.692891	648.350083	P	244.165568	122.586422	227.139019	114.073148			2
10							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [HQQTVTIPPK](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.7	1458.801712	-0.010210	HQQTVTIPPK
29.4	1458.801712	-0.010210	HQQTVTIPPK
2.8	1458.776535	0.014967	QHPADKLPSR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **HQQTVTIPPK**

Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

Match to Query 32728: 1458.795732 from(487.272520,3+) rtinseconds(1545) index(33581)

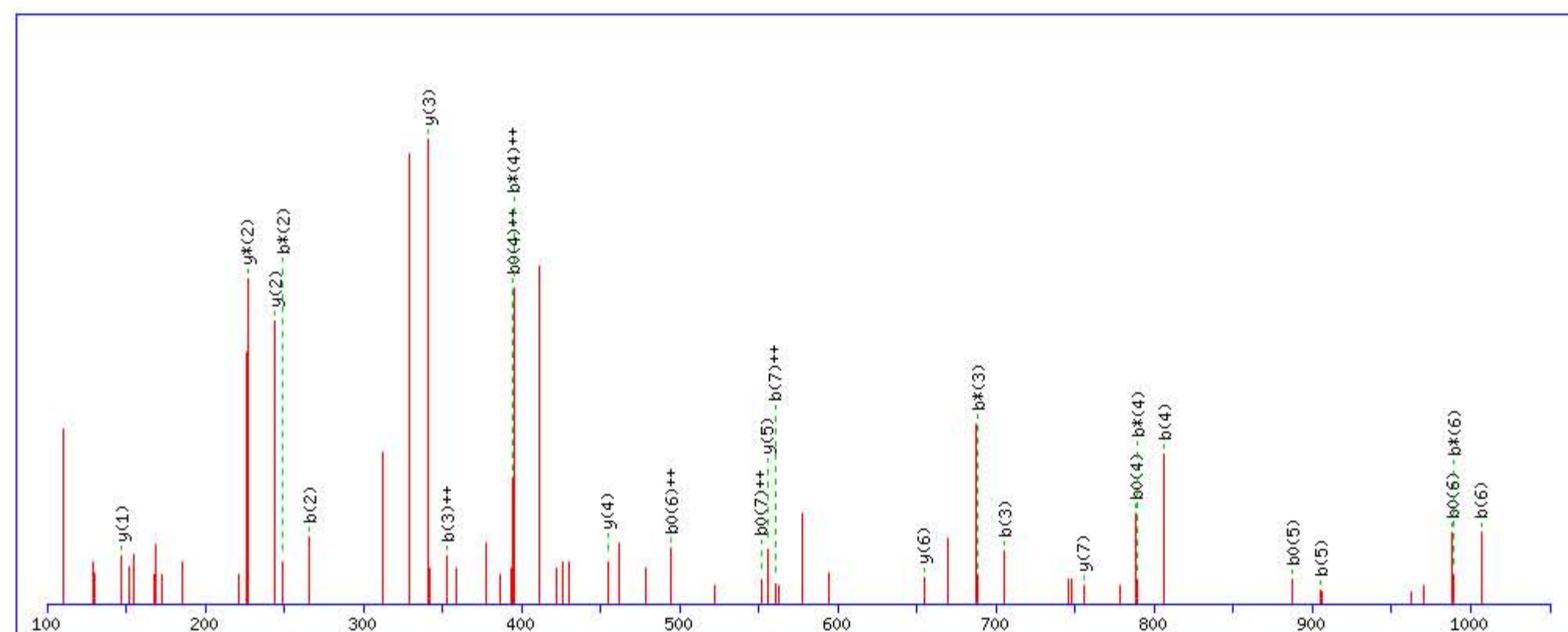
Title: Locus:1.1.1.2957.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf.5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1458.801712

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

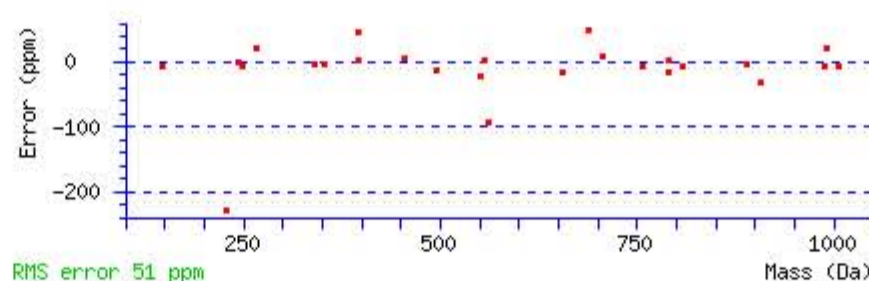
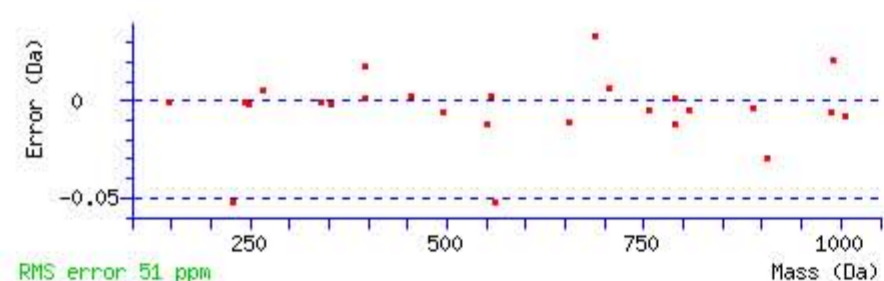
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.023

Matches : 26/92 fragment ions using 54 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	138.066188	69.536732					H							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



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	$M_r(\text{calc})$:	Delta	Sequence
29.8	1458.801712	-0.005980	HQQTVTIPPK
28.9	1458.801712	-0.005980	HQQTVTIPPK

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 37178: 1599.760392 from(534.260740,3+) rtinseconds(1516) index(33398)

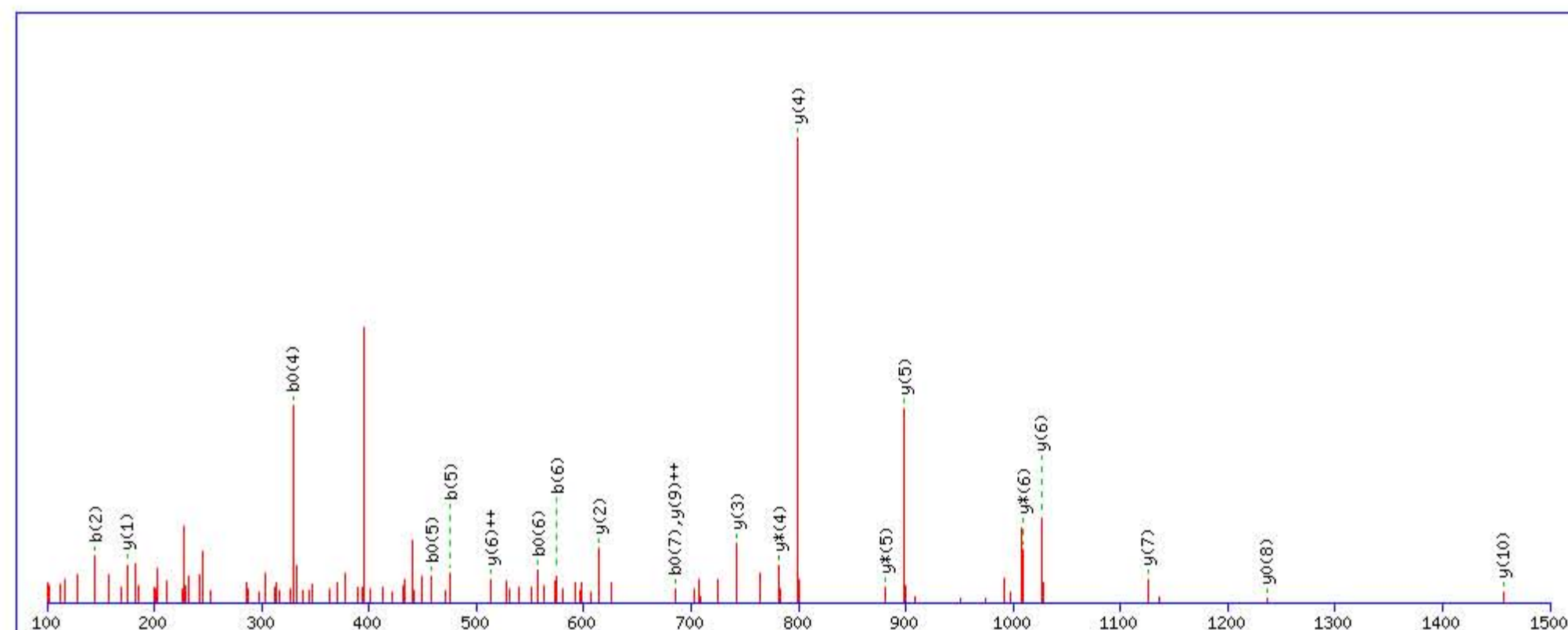
Title: Locus:1.1.1.2947.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1599.767517

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

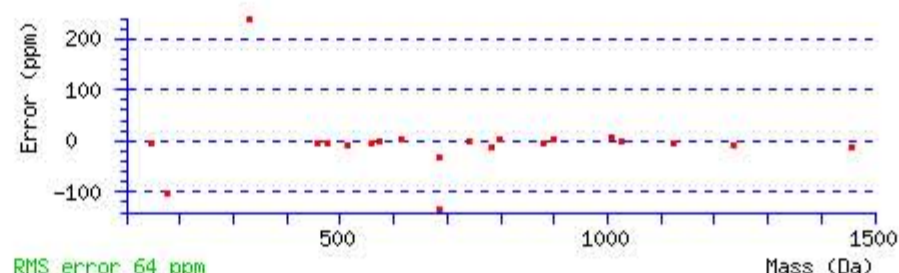
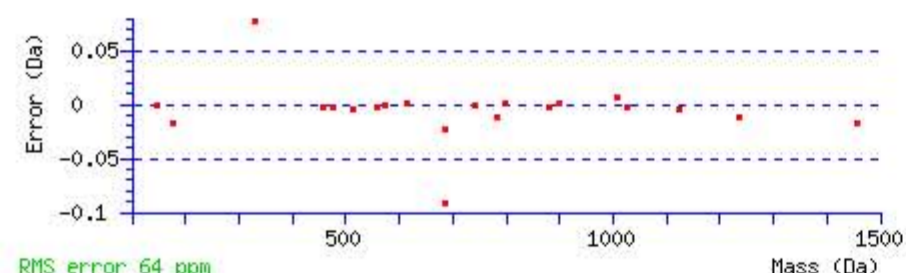
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 48 Expect: 0.00023

Matches : 21/106 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	88.039304	44.523290			70.028739	35.518008	S							12
2	145.060768	73.034022			127.050203	64.028740	G	1513.742754	757.375015	1496.716205	748.861741	1495.732189	748.369733	11
3	232.092796	116.550036			214.082231	107.544753	S	1456.721290	728.864283	1439.694741	720.351009	1438.710725	719.859001	10
4	347.119739	174.063507			329.109174	165.058225	D	1369.689262	685.348269	1352.662713	676.834995	1351.678697	676.342987	9
5	476.162332	238.584804			458.151767	229.579522	E	1254.662319	627.834798	1237.635770	619.321523	1236.651754	618.829515	8
6	575.230746	288.119011			557.220181	279.113729	V	1125.619726	563.313501	1108.593177	554.800227			7
7	703.289324	352.148300	686.262775	343.635026	685.278759	343.143018	Q	1026.551312	513.779294	1009.524763	505.266020			6
8	802.357738	401.682507	785.331189	393.169233	784.347173	392.677225	V	898.492734	449.750005	881.466185	441.236731			5
9	859.379202	430.193239	842.352653	421.679965	841.368637	421.187957	G	799.424320	400.215798	782.397771	391.702524			4
10	987.437780	494.222528	970.411231	485.709254	969.427215	485.217246	Q	742.402856	371.705066	725.376307	363.191792			3
11	1426.663106	713.835191	1409.636557	705.321917	1408.652541	704.829909	Q	614.344278	307.675777	597.317729	299.162503			2
12							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **SGSDEVQVGQQR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.9	1599.767517	-0.007125	SGSDEVQVGQQR
36.8	1599.767517	-0.007125	SGSDEVQVGQQR
12.5	1599.767517	-0.007125	SGSDEVQVGQQR

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 37179: 1599.767148 from(800.890850,2+) rtinseconds(1500) index(33277)

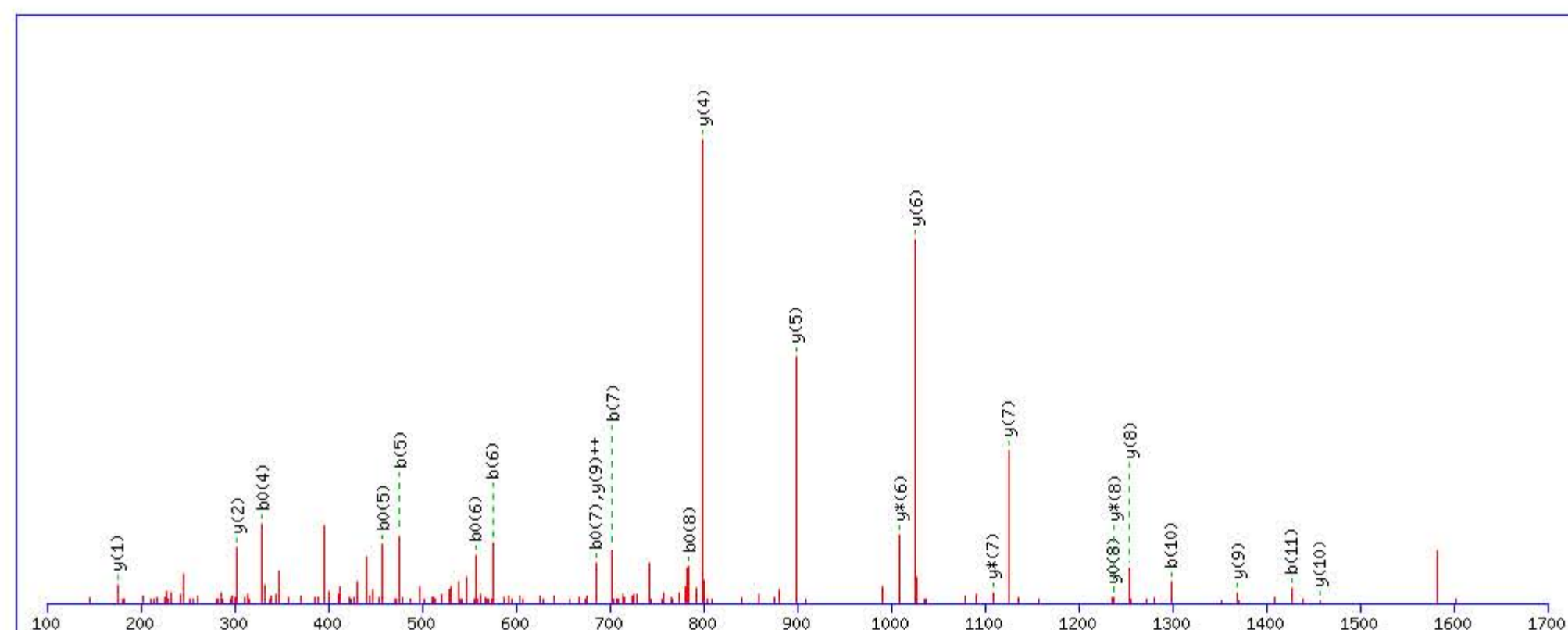
Title: Locus:1.1.1.2941.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1599.767517

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

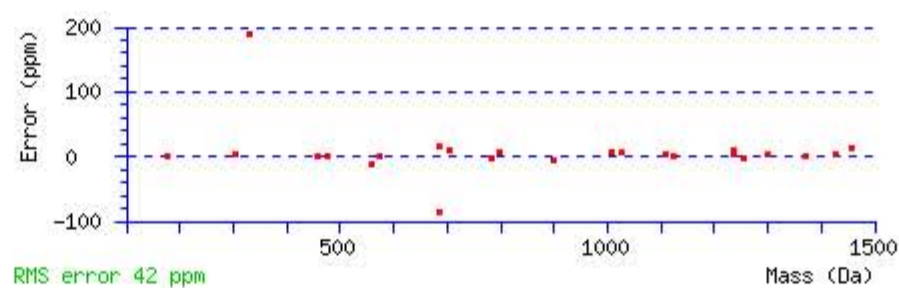
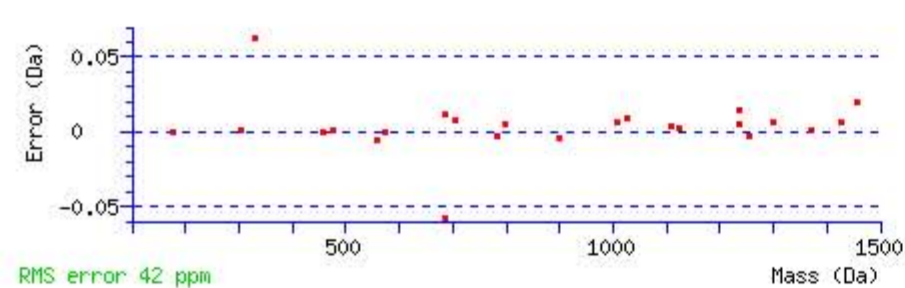
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 81 Expect: 1.3e-007

Matches : 24/106 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	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
80.7	1599.767517	-0.000369	SGSDEVQVGQQR
64.9	1599.767517	-0.000369	SGSDEVQVGQQR
44.1	1599.767517	-0.000369	SGSDEVQVGQQR
8.1	1599.767471	-0.000323	AMNAANLNIPPSDTR
7.8	1599.767502	-0.000354	LHMLSSVDLNGQDR
5.5	1599.779388	-0.012240	RFPDFSYITQNGR
4.4	1599.774872	-0.007724	MAKEAIFQDTMRK
3.3	1599.789291	-0.022143	DPVFEITGAPGNVER
1.6	1599.753769	0.013379	ASTFSCIMQKWGGK
1.1	1599.771515	-0.004367	YVTSAPMPEPQAPGR

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **KQELSEAEQATR**

Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

Match to Query 40430: 1699.850652 from(567.624160,3+) rtinseconds(1373) index(32379)

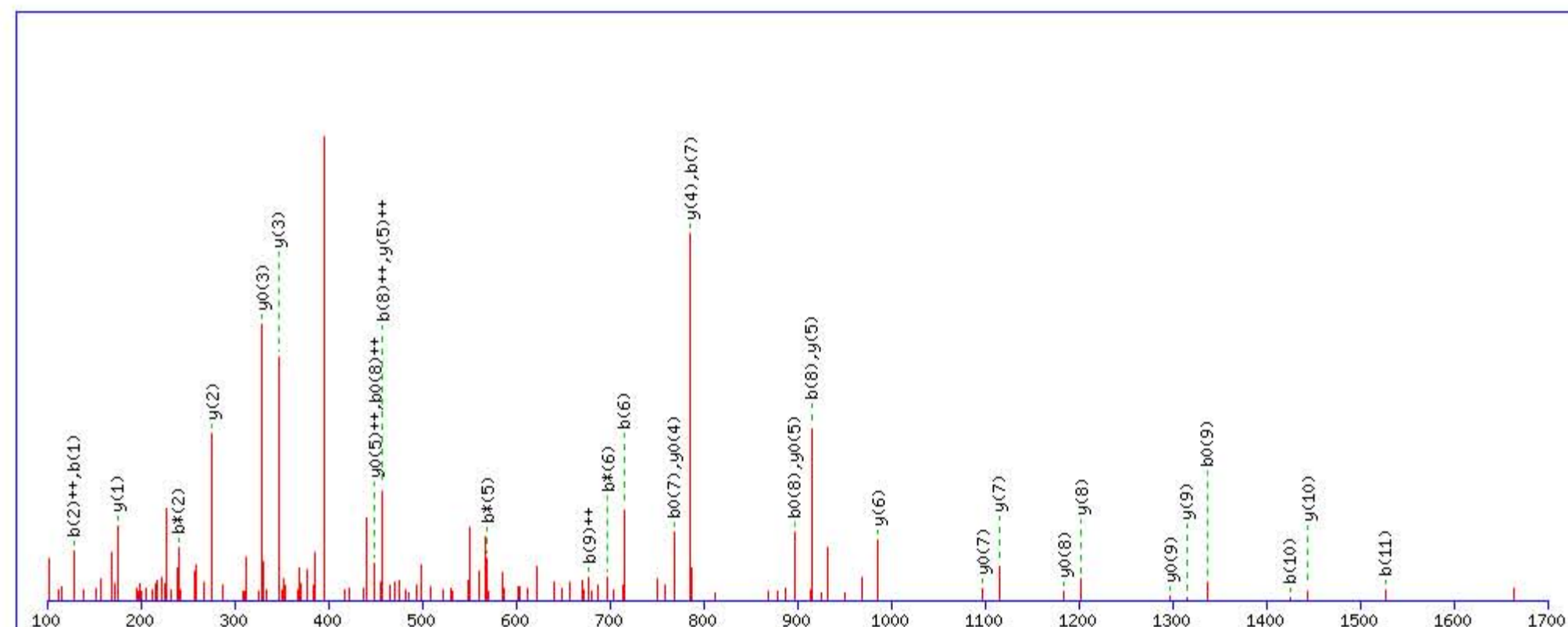
Title: Locus:1.1.1.2897.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1699.856277

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

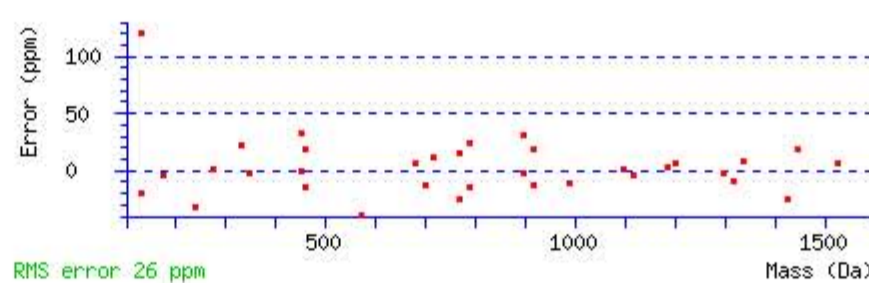
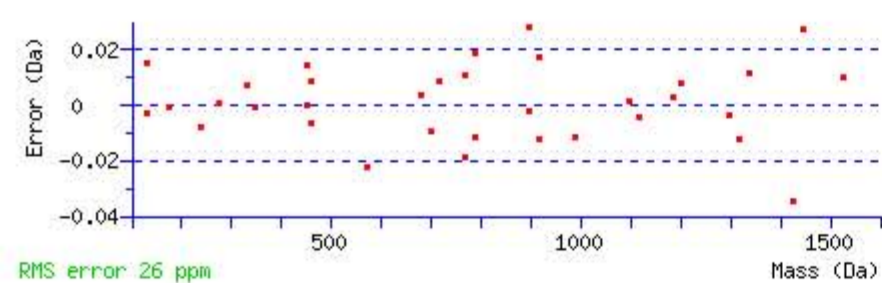
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 75 Expect: 9.2e-007

Matches : 34/126 fragment ions using 39 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.102239	65.054757	112.075690	56.541483			K							12
2	257.160817	129.084047	240.134268	120.570772			Q	1572.768634	786.887955	1555.742085	778.374681	1554.758069	777.882673	11
3	386.203410	193.605343	369.176861	185.092069	368.192845	184.600061	E	1444.710056	722.858666	1427.683507	714.345392	1426.699491	713.853384	10
4	499.287474	250.147375	482.260925	241.634101	481.276909	241.142093	L	1315.667463	658.337370	1298.640914	649.824095	1297.656898	649.332087	9
5	586.319502	293.663389	569.292953	285.150115	568.308937	284.658107	S	1202.583399	601.795338	1185.556850	593.282063	1184.572834	592.790055	8
6	715.362095	358.184686	698.335546	349.671411	697.351530	349.179403	E	1115.551371	558.279324	1098.524822	549.766049	1097.540806	549.274041	7
7	786.399209	393.703243	769.372660	385.189968	768.388644	384.697960	A	986.508778	493.758027	969.482229	485.244753	968.498213	484.752745	6
8	915.441802	458.224539	898.415253	449.711265	897.431237	449.219257	E	915.471664	458.239470	898.445115	449.726196	897.461099	449.234188	5
9	1354.667128	677.837202	1337.640579	669.323928	1336.656563	668.831920	Q	786.429071	393.718174	769.402522	385.204899	768.418506	384.712891	4
10	1425.704242	713.355759	1408.677693	704.842485	1407.693677	704.350477	A	347.203745	174.105510	330.177196	165.592236	329.193180	165.100228	3
11	1526.751921	763.879599	1509.725372	755.366324	1508.741356	754.874316	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
12							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **KQELSEAEQATR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.7	1699.856277	-0.005625	KQELSEAEQATR
20.0	1699.856277	-0.005625	KQELSEAEQATR
11.2	1699.849792	0.000860	QEMRTTQLGPGR
10.6	1699.843735	0.006917	QFNRQRGVSHAMGGR
10.3	1699.874039	-0.023387	KEISVNDLNESSIPR
7.3	1699.843063	0.007589	GKVSEGIDFVHHYGR
7.2	1699.874924	-0.024272	SQGMLALSISPNR
6.1	1699.845932	0.004720	QAMQEQLSK
5.3	1699.848907	0.001745	TQATERVNSQPVNEK
4.7	1699.845932	0.004720	QAMQEQLSK

MASCOT 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 42140: 1769.958912 from(590.993580,3+) rtinseconds(1927) index(35891)

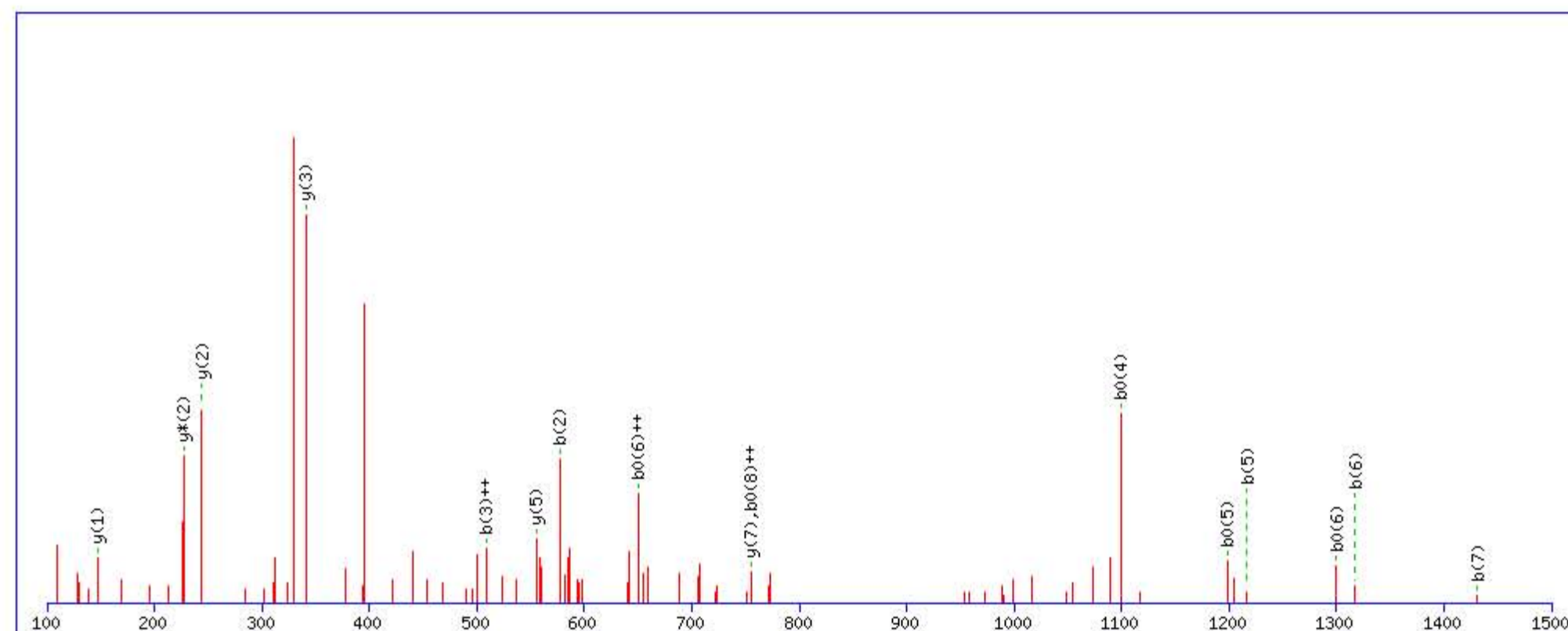
Title: Locus:1.1.1.3090.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1769.968460

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

Variable modifications:

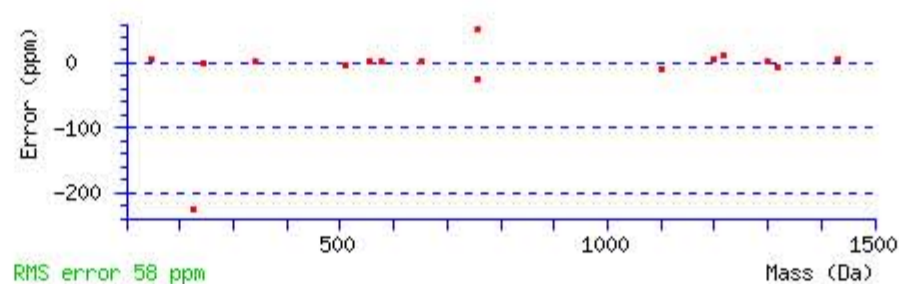
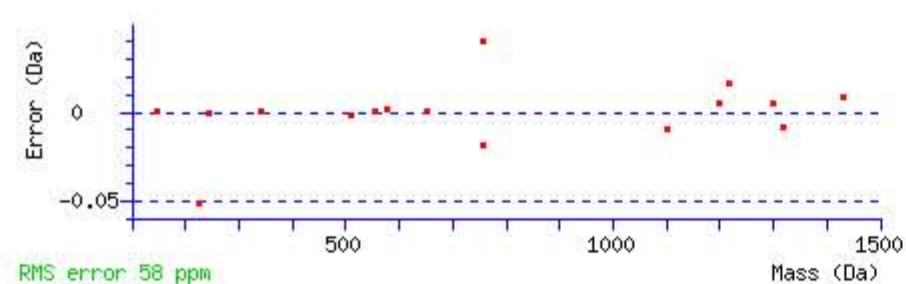
Q2 : Biotin:Thermo-21345 (Q)

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.018

Matches : 16/92 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	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
27.3	1769.968460	-0.009548	HQQTVTIPPK
8.4	1769.961029	-0.002117	WMLSRDRASTLPLPK
1.8	1769.976303	-0.017391	VIQVWFQNARAK
1.8	1769.976303	-0.017391	VLQVWFQNARAK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **QGGLSVVTMYHAK**

Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

Match to Query 43143: 1817.912832 from(606.978220,3+) rtinseconds(1823) index(35167)

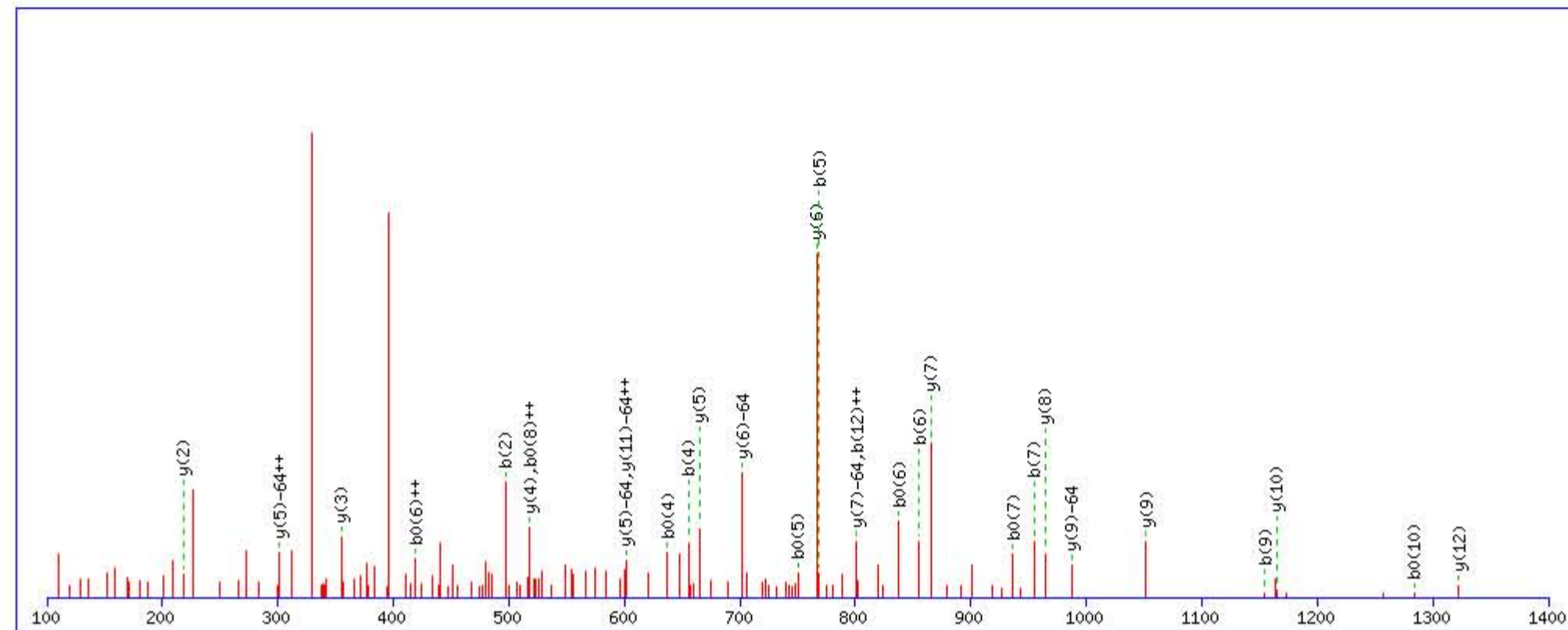
Title: Locus:1.1.1.3054.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1817.916824

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

Variable modifications:

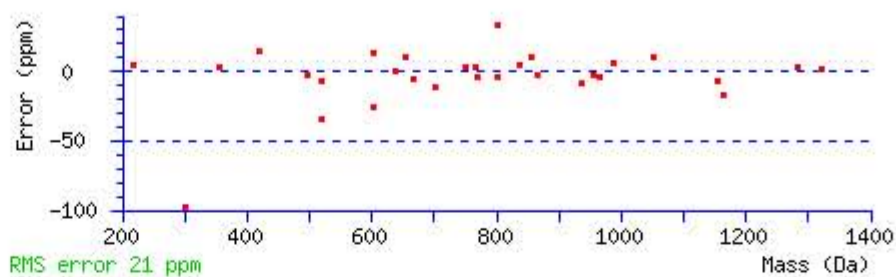
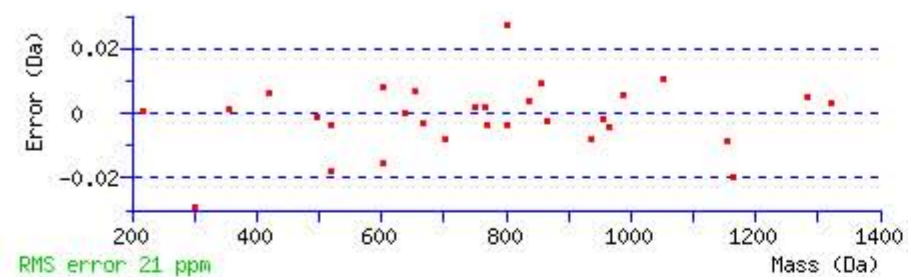
Q2 : Biotin:Thermo-21345 (Q)

M10 : Oxidation (M), with neutral losses 0.000000 (shown in table), 63.998285

Ions Score: 63 Expect: 1.5e-005

Matches : 30/214 fragment ions using 44 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							14
2	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 [QGGLSVVTMYHAK](#)

(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	1817.916824	-0.003992	QGGLSVVTMYHAK

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 44786: 1910.934492 from(637.985440,3+) rtinseconds(1903) index(35690)

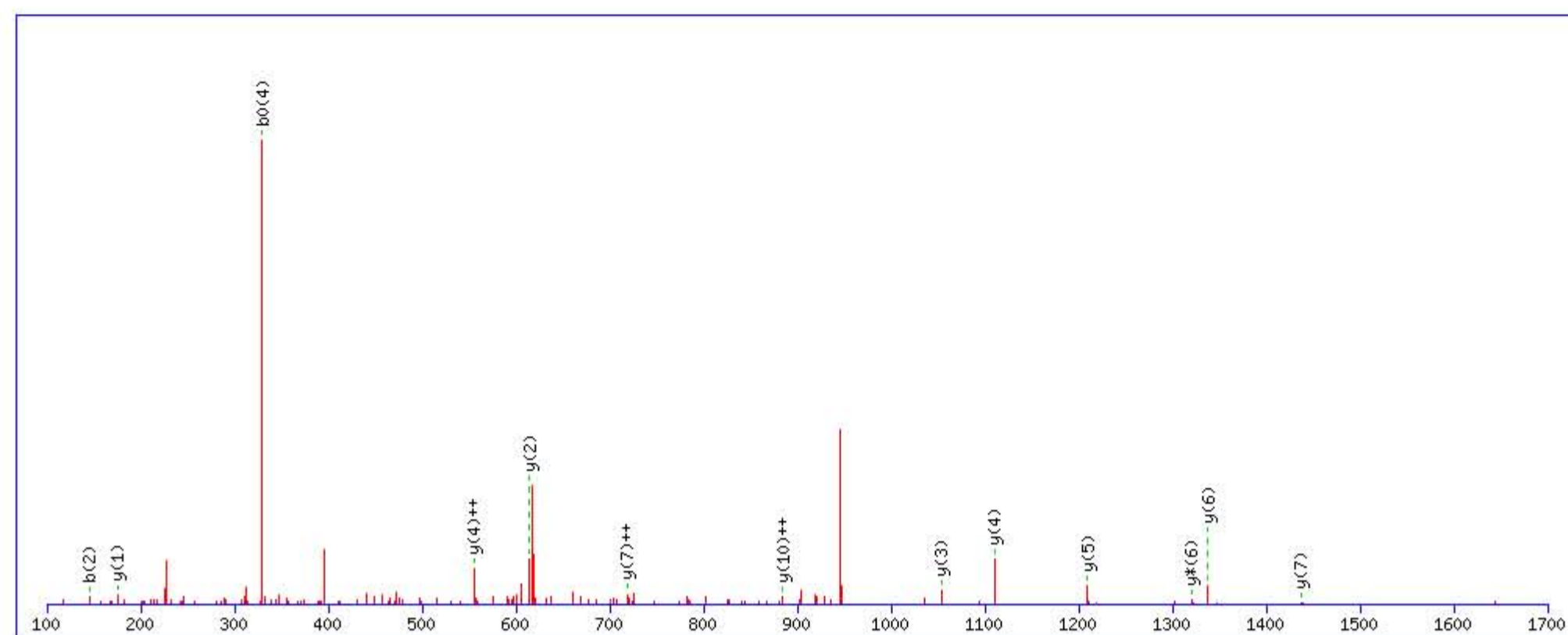
Title: Locus:1.1.1.3082.17 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1910.934265

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

Variable modifications:

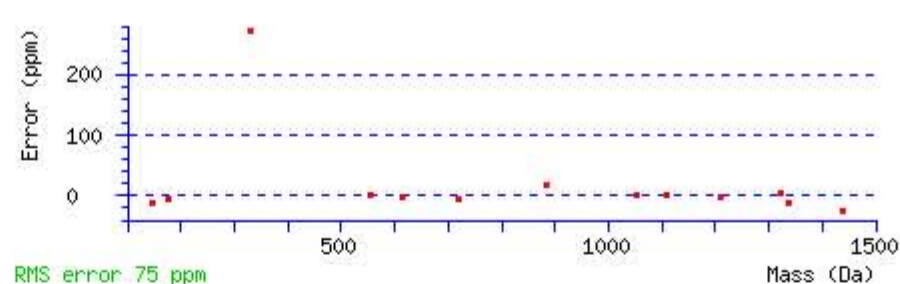
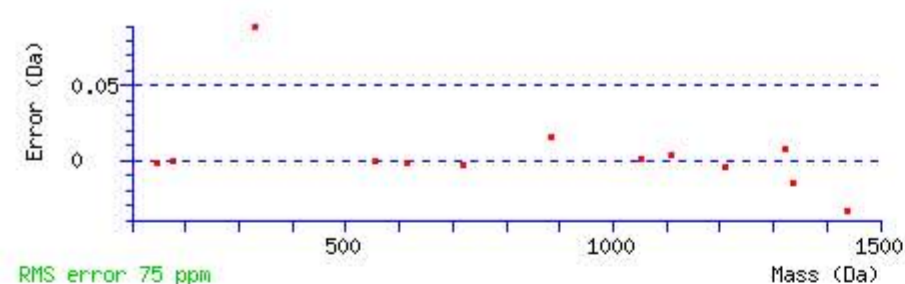
Q10 : Biotin:Thermo-21345 (Q)

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.0054

Matches : 13/106 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	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
26.8	1910.934265	0.000227	SGSDEVQVGQQR
11.3	1910.934265	0.000227	SGSDEVQVGQQR
4.2	1910.934265	0.000227	SGSDEVQVGQQR
2.5	1910.960709	-0.026217	VGAPAWREAAQAMAR
0.5	1910.958542	-0.024050	TDDYGRDLSSVQILLTK

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 44788: 1910.954128 from(956.484340,2+) rtinseconds(1867) index(35386)

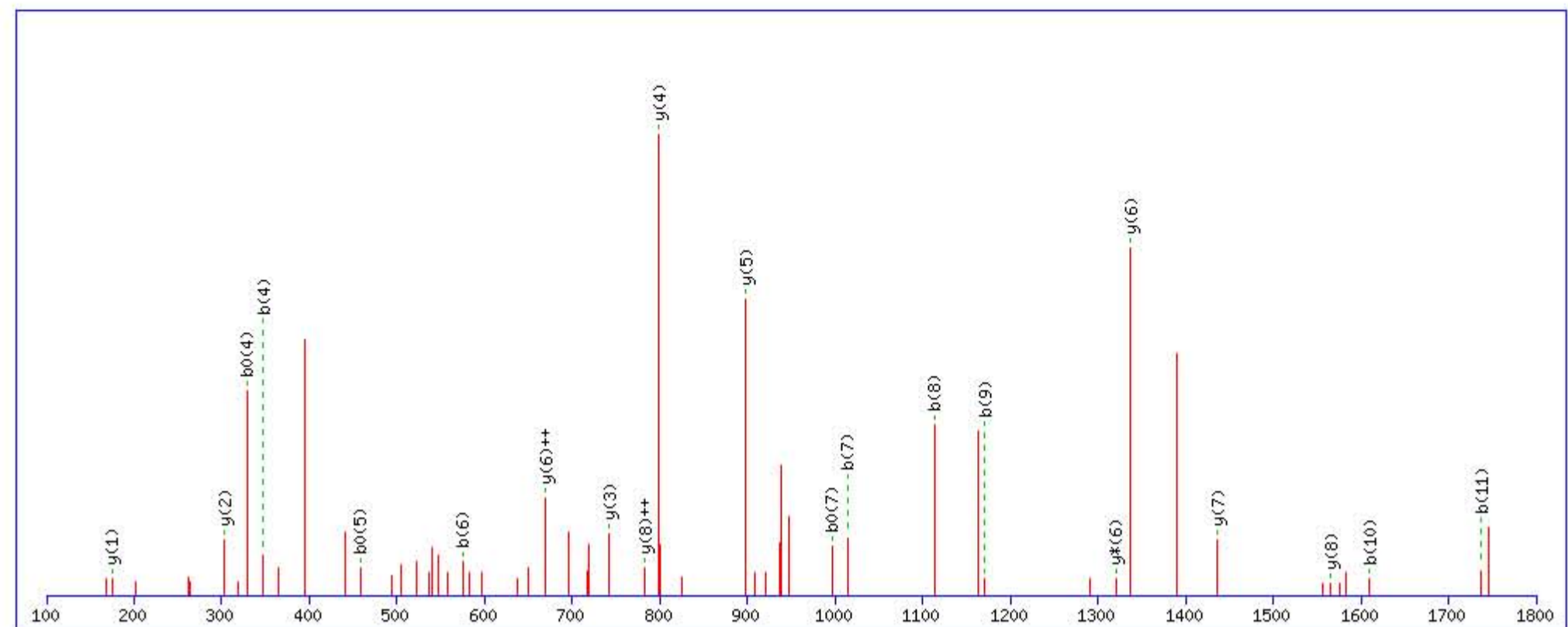
Title: Locus:1.1.1.3069.26 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1910.934265

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

Variable modifications:

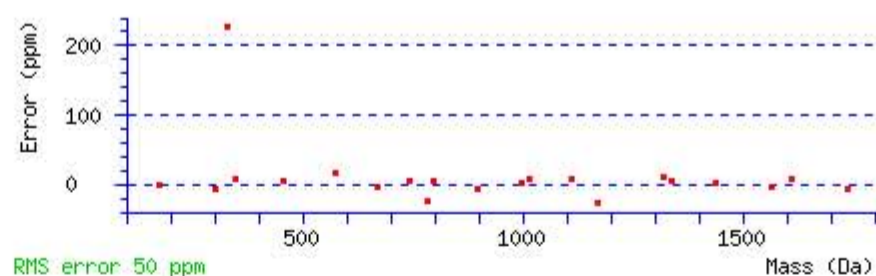
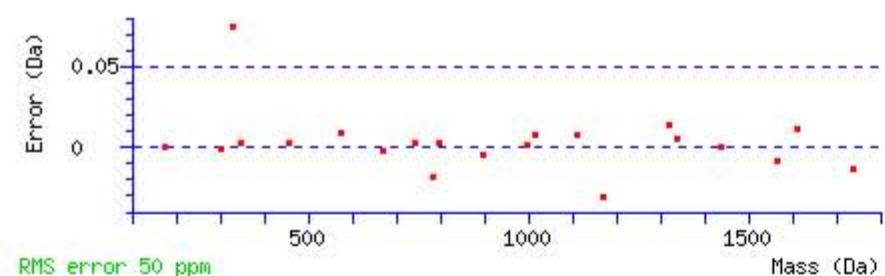
Q7 : Biotin:Thermo-21345 (Q)

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 42 Expect: 0.0029

Matches : 21/106 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							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
41.5	1910.934265	0.019863	SGSDEVQVGQQR
30.8	1910.934265	0.019863	SGSDEVQVGQQR
13.5	1910.938263	0.015865	YVTSAPMPEPQAPGR
5.7	1910.934265	0.019863	SGSDEVQVGQQR
5.5	1910.938721	0.015407	QEA EGLALDSPWHRFR
1.5	1910.930725	0.023403	AGSGGLGGGAGGGQGAGAGQGAALR
0.1	1910.956024	-0.001896	DFQPVREQIPEDK
0.0	1910.971970	-0.017842	KAPMGTARFGHHMAVLR

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 49190: 2098.140102 from(700.387310,3+) rtinseconds(2328) index(38382)

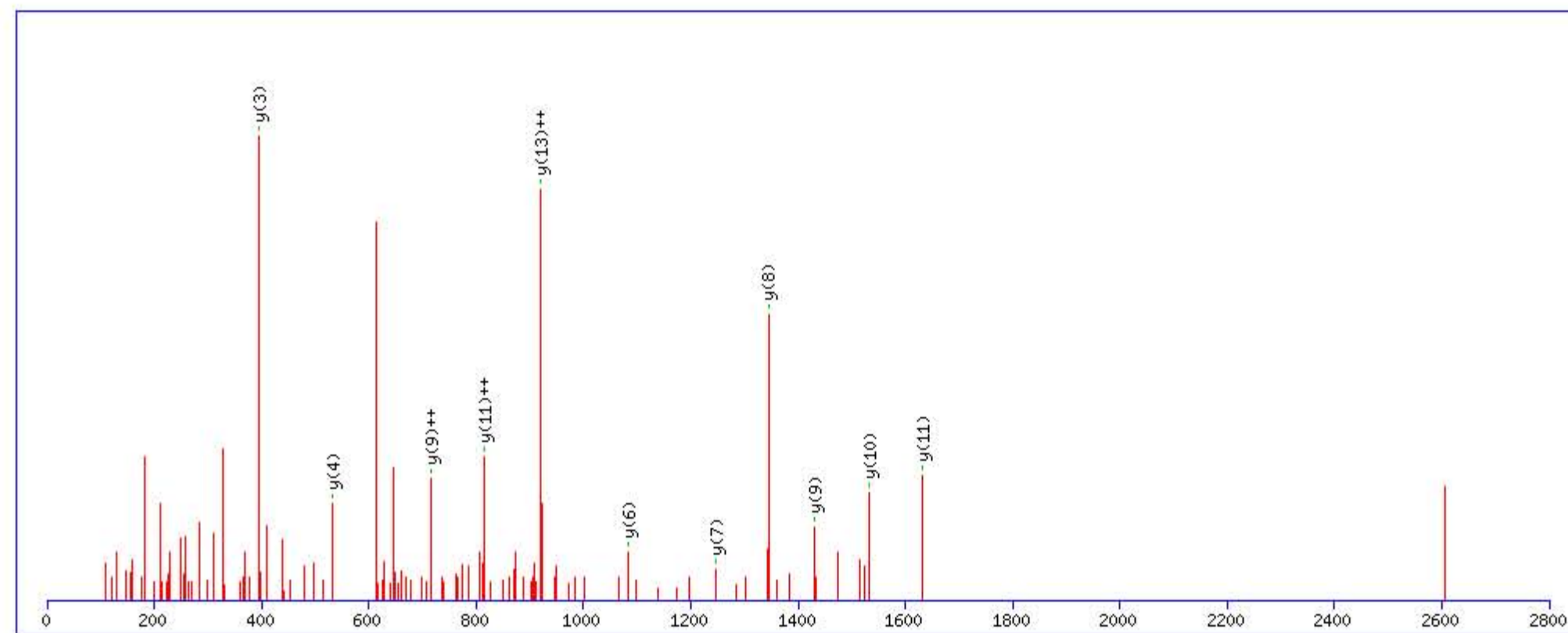
Title: Locus:1.1.1.3230.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2098.128525

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

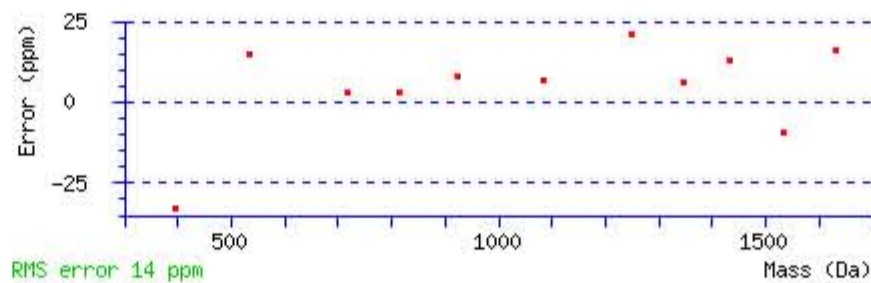
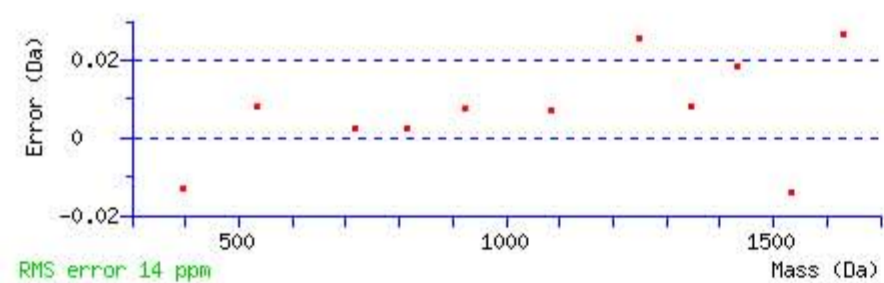
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 55 Expect: 5.5e-005

Matches : 11/158 fragment ions using 16 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							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
55.3	2098.128525	0.011577	SGIPIVTSPYQIHFTK

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

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 51086: 2201.231736 from(551.315210,4+) rtinseconds(1880) index(35492)

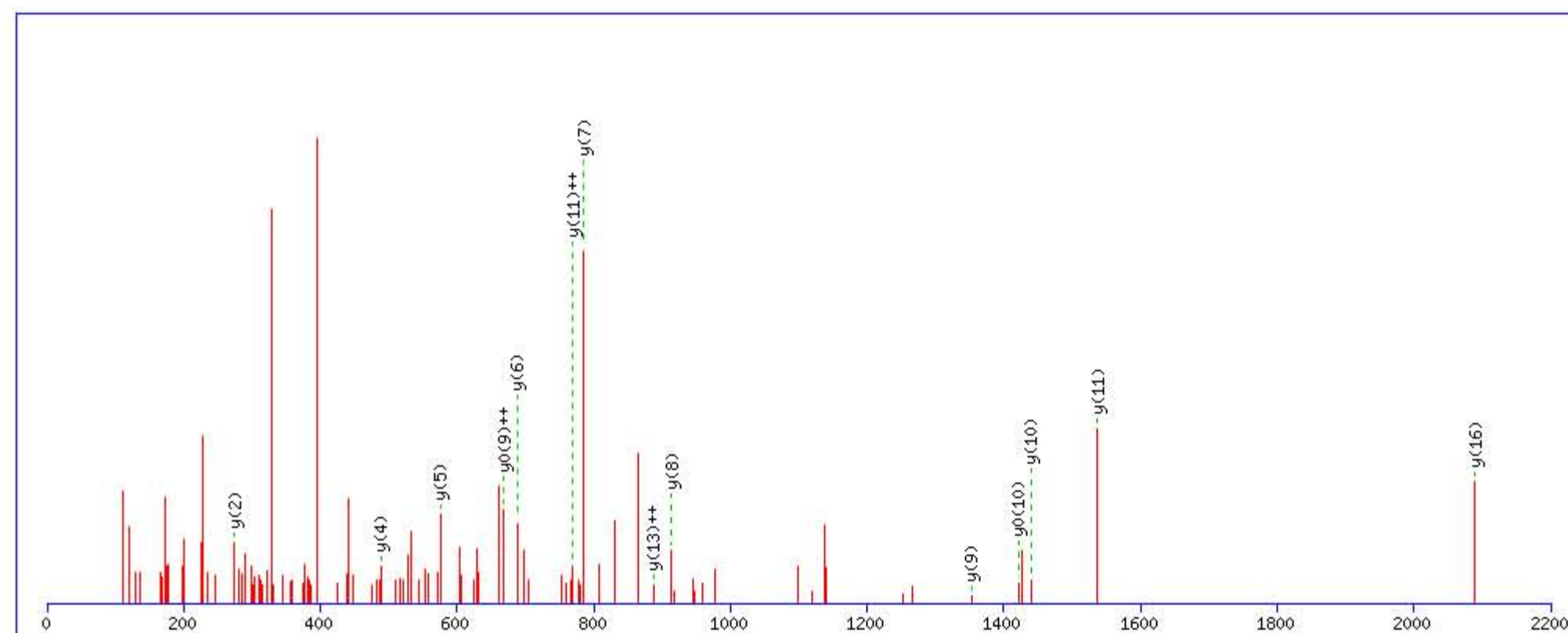
Title: Locus:1.1.1.3074.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2201.235428

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

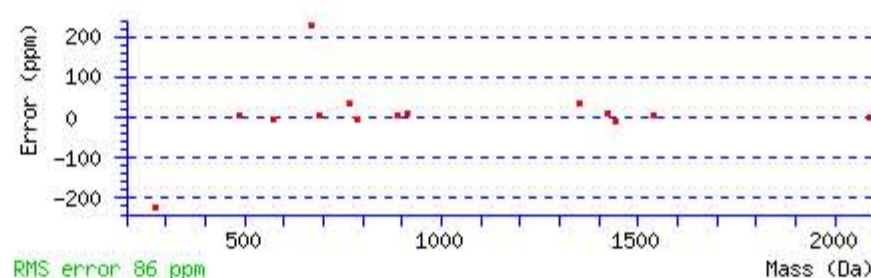
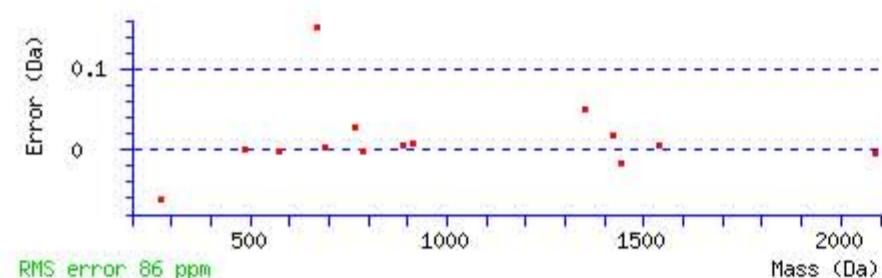
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 39 Expect: 0.0012

Matches : 14/180 fragment ions using 40 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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
38.7	2201.235428	-0.003692	LSINTHPSQKPLSITVR

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

MASCOT Search Results

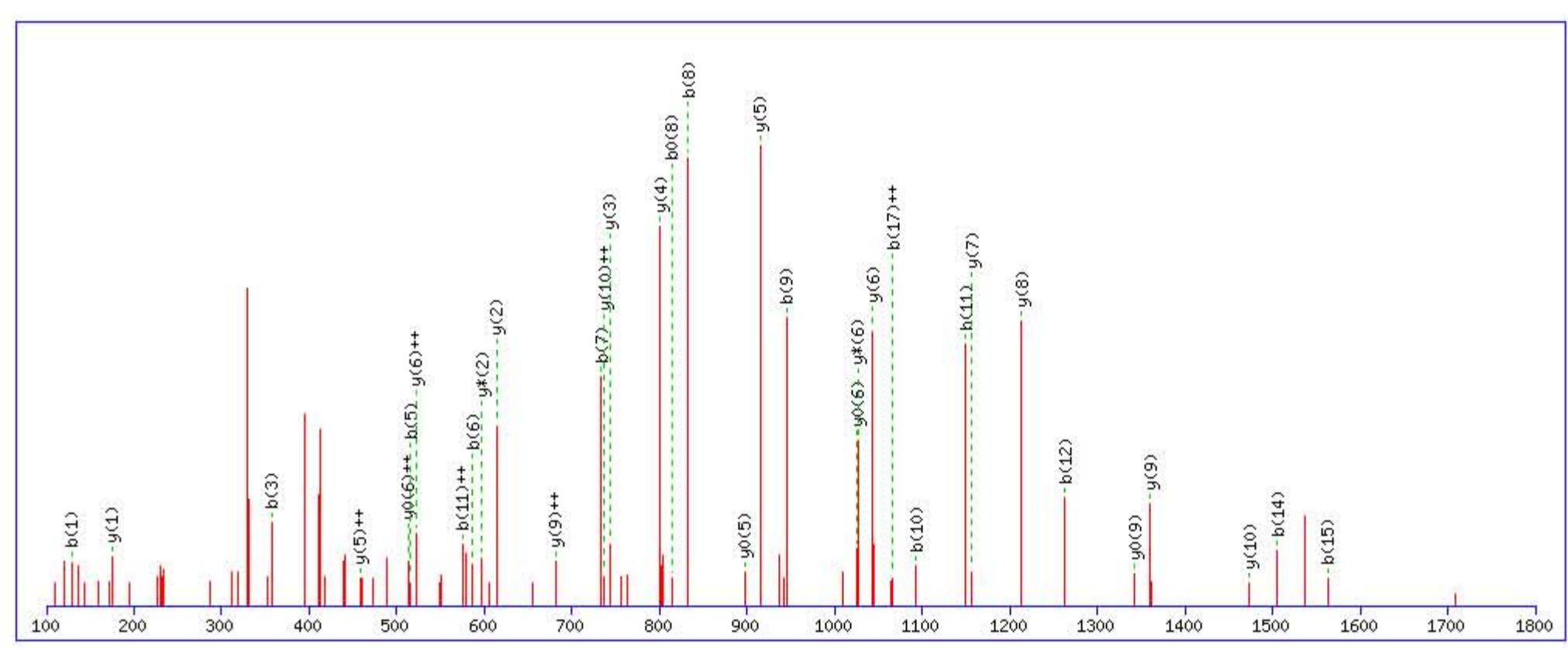
Peptide View

MS/MS Fragmentation of **KVEGTAFVIFGIQDGEQR**

Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

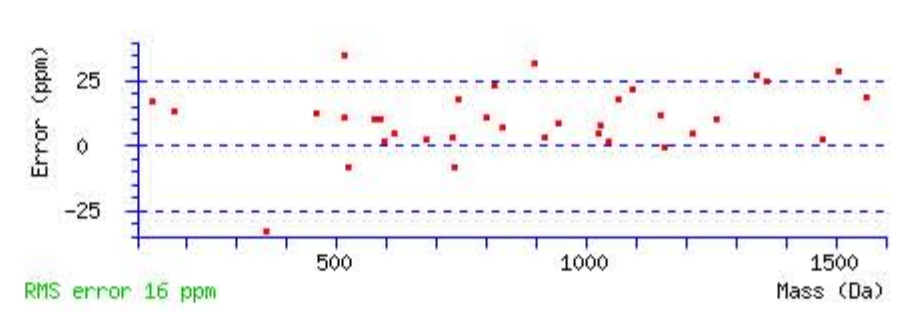
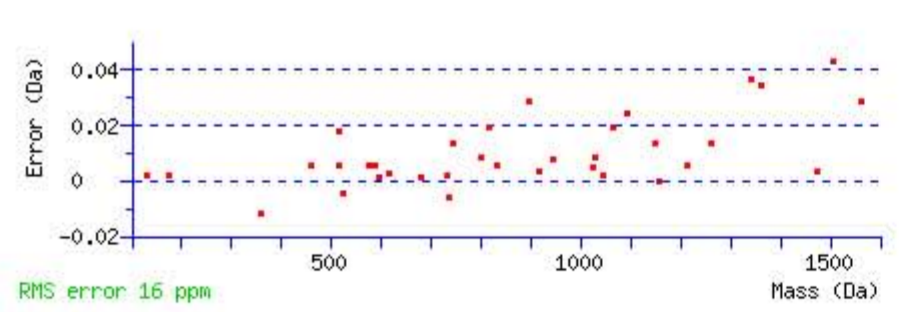
Match to Query 53078: 2304.216672 from(769.079500,3+) rtinseconds(2464) index(39183)
 Title: Locus:1.1.1.3277.14 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2304.193649
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q17 : Biotin:Thermo-21345 (Q)
 Ions Score: 61 Expect: 1.9e-005
 Matches : 35/196 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	129.102239	65.054757	112.075690	56.541483			K							18
2	228.170653	114.588965	211.144104	106.075690			V	2177.105954	1089.056615	2160.079405	1080.543340	2159.095389	1080.051332	17
3	357.213246	179.110261	340.186697	170.596987	339.202681	170.104979	E	2078.037540	1039.522408	2061.010991	1031.009133	2060.026975	1030.517125	16
4	414.234710	207.620993	397.208161	199.107719	396.224145	198.615711	G	1948.994947	975.001111	1931.968398	966.487837	1930.984382	965.995829	15
5	515.282389	258.144833	498.255840	249.631558	497.271824	249.139550	T	1891.973483	946.490380	1874.946934	937.977105	1873.962918	937.485097	14
6	586.319503	293.663390	569.292954	285.150115	568.308938	284.658107	A	1790.925804	895.966540	1773.899255	887.453265	1772.915239	886.961257	13
7	733.387917	367.197597	716.361368	358.684322	715.377352	358.192314	F	1719.888690	860.447983	1702.862141	851.934709	1701.878125	851.442701	12
8	832.456331	416.731804	815.429782	408.218529	814.445766	407.726521	V	1572.820276	786.913776	1555.793727	778.400502	1554.809711	777.908493	11
9	945.540395	473.273836	928.513846	464.760561	927.529830	464.268553	I	1473.751862	737.379569	1456.725313	728.866294	1455.741297	728.374286	10
10	1092.608809	546.808043	1075.582260	538.294768	1074.598244	537.802760	F	1360.667798	680.837537	1343.641249	672.324263	1342.657233	671.832254	9
11	1149.630273	575.318775	1132.603724	566.805500	1131.619708	566.313492	G	1213.599384	607.303330	1196.572835	598.790055	1195.588819	598.298047	8
12	1262.714337	631.860806	1245.687788	623.347532	1244.703772	622.855524	I	1156.577920	578.792598	1139.551371	570.279324	1138.567355	569.787315	7
13	1390.772915	695.890095	1373.746366	687.376821	1372.762350	686.884813	Q	1043.493856	522.250566	1026.467307	513.737292	1025.483291	513.245284	6
14	1505.799858	753.403567	1488.773309	744.890292	1487.789293	744.398284	D	915.435278	458.221277	898.408729	449.708003	897.424713	449.215995	5
15	1562.821322	781.914299	1545.794773	773.401024	1544.810757	772.909016	G	800.408335	400.707806	783.381786	392.194531	782.397770	391.702523	4
16	1691.863915	846.435595	1674.837366	837.922321	1673.853350	837.430313	E	743.386871	372.197074	726.360322	363.683799	725.376306	363.191791	3
17	2131.089241	1066.048258	2114.062692	1057.534984	2113.078676	1057.042976	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 [KVEGTAFVIFGIQDGEQR](#)
 (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	2304.193649	0.023023	KVEGTAFVIFGIQDGEQR
31.4	2304.193649	0.023023	KVEGTAFVIFGIQDGEQR

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 55503: 2457.243072 from(820.088300,3+) rtinseconds(2571) index(39898)

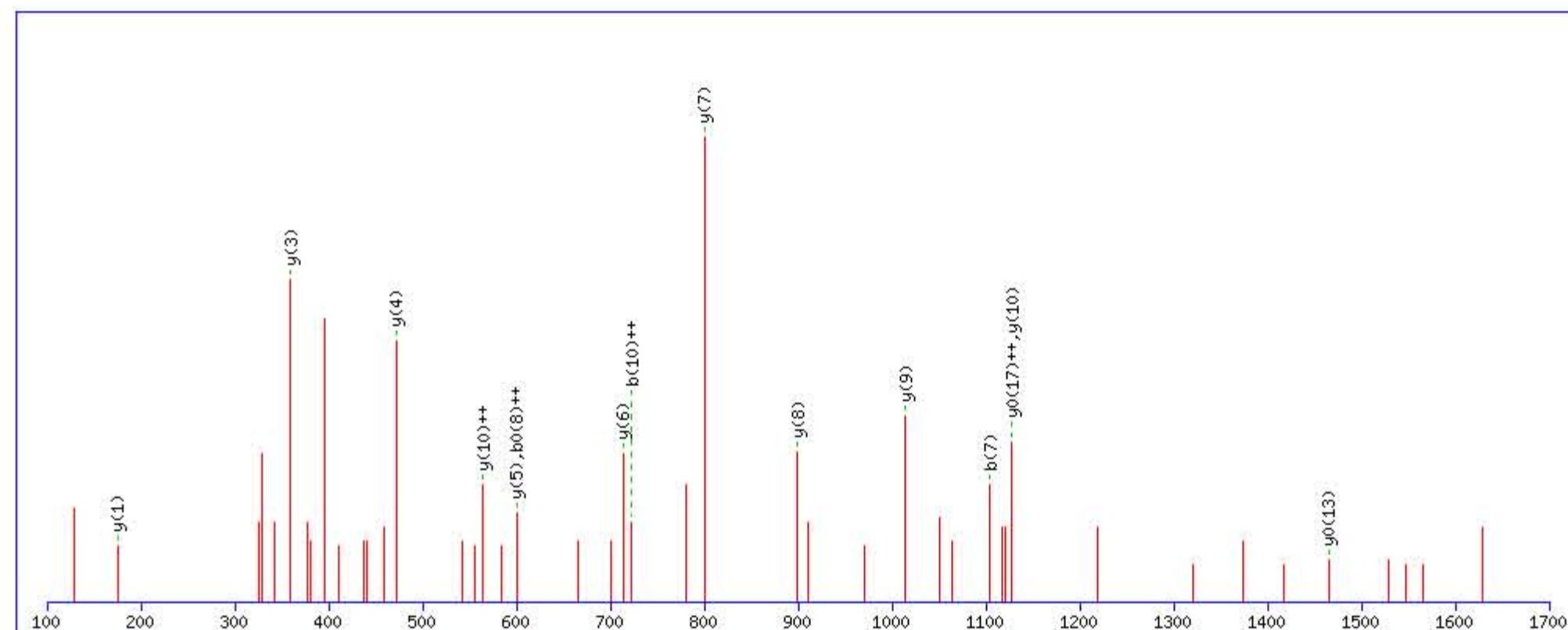
Title: Locus:1.1.1.3314.21 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2457.232193

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

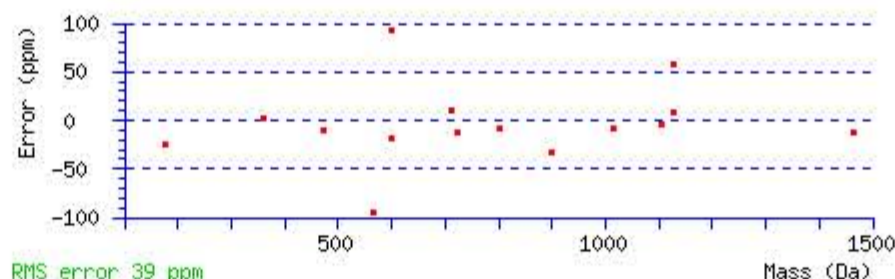
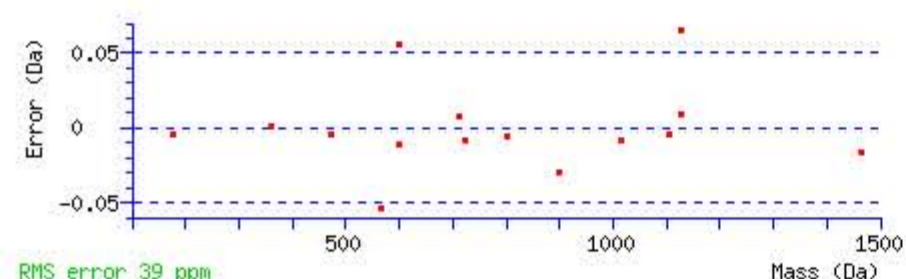
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 38 Expect: 0.0013

Matches : 15/204 fragment ions using 27 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.034219	58.520748			98.023654	49.515465	D							19
2	187.071333	94.039304			169.060768	85.034022	A	2343.212542	1172.109909	2326.185993	1163.596634	2325.201977	1163.104626	18
3	284.124097	142.565686			266.113532	133.560404	P	2272.175428	1136.591352	2255.148879	1128.078077	2254.164863	1127.586069	17
4	399.151040	200.079158			381.140475	191.073875	D	2175.122664	1088.064970	2158.096115	1079.551695	2157.112099	1079.059687	16
5	536.209952	268.608614			518.199387	259.603332	H	2060.095721	1030.551498	2043.069172	1022.038224	2042.085156	1021.546216	15
6	975.435278	488.221277	958.408729	479.708003	957.424713	479.215995	Q	1923.036809	962.022043	1906.010260	953.508768	1905.026244	953.016760	14
7	1104.477871	552.742574	1087.451322	544.229299	1086.467306	543.737291	E	1483.811483	742.409380	1466.784934	733.896105	1465.800918	733.404097	13
8	1217.561935	609.284606	1200.535386	600.771331	1199.551370	600.279323	L	1354.768890	677.888083	1337.742341	669.374809	1336.758325	668.882801	12
9	1331.604862	666.306069	1314.578313	657.792795	1313.594297	657.300786	N	1241.684826	621.346051	1224.658277	612.832777	1223.674261	612.340769	11
10	1444.688926	722.848101	1427.662377	714.334826	1426.678361	713.842818	L	1127.641899	564.324588	1110.615350	555.811313	1109.631334	555.319305	10
11	1559.715869	780.361572	1542.689320	771.848298	1541.705304	771.356290	D	1014.557835	507.782556	997.531286	499.269281	996.547270	498.777273	9
12	1658.784283	829.895780	1641.757734	821.382505	1640.773718	820.890497	V	899.530892	450.269084	882.504343	441.755810	881.520327	441.263802	8
13	1745.816311	873.411794	1728.789762	864.898519	1727.805746	864.406511	S	800.462478	400.734877	783.435929	392.221603	782.451913	391.729595	7
14	1858.900375	929.953825	1841.873826	921.440551	1840.889810	920.948543	L	713.430450	357.218863	696.403901	348.705589	695.419885	348.213581	6
15	1986.958953	993.983115	1969.932404	985.469840	1968.948388	984.977832	Q	600.346386	300.676831	583.319837	292.163557	582.335821	291.671549	5
16	2100.043017	1050.525146	2083.016468	1042.011872	2082.032452	1041.519864	L	472.287808	236.647542	455.261259	228.134268	454.277243	227.642260	4
17	2197.095781	1099.051528	2180.069232	1090.538254	2179.085216	1090.046246	P	359.203744	180.105510	342.177195	171.592236	341.193179	171.100228	3
18	2284.127809	1142.567542	2267.101260	1134.054268	2266.117244	1133.562260	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
19							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [DAPDHQELNLDVSLQLPSR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.5	2457.232193	0.010879	DAPDHQELNLDVSLQLPSR
7.1	2457.278442	-0.035370	EPVSNVTAEGMEALTKILAEIR
1.5	2457.243423	-0.000351	TGLSDAFMILNPSDPVPESTR
0.4	2457.232193	0.010879	DAPDHQELNLDVSLQLPSR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **ILLQGPVAQMTEDAVDAER**

Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

Match to Query 55784: 2467.260642 from(823.427490,3+) rtinseconds(2676) index(40595)

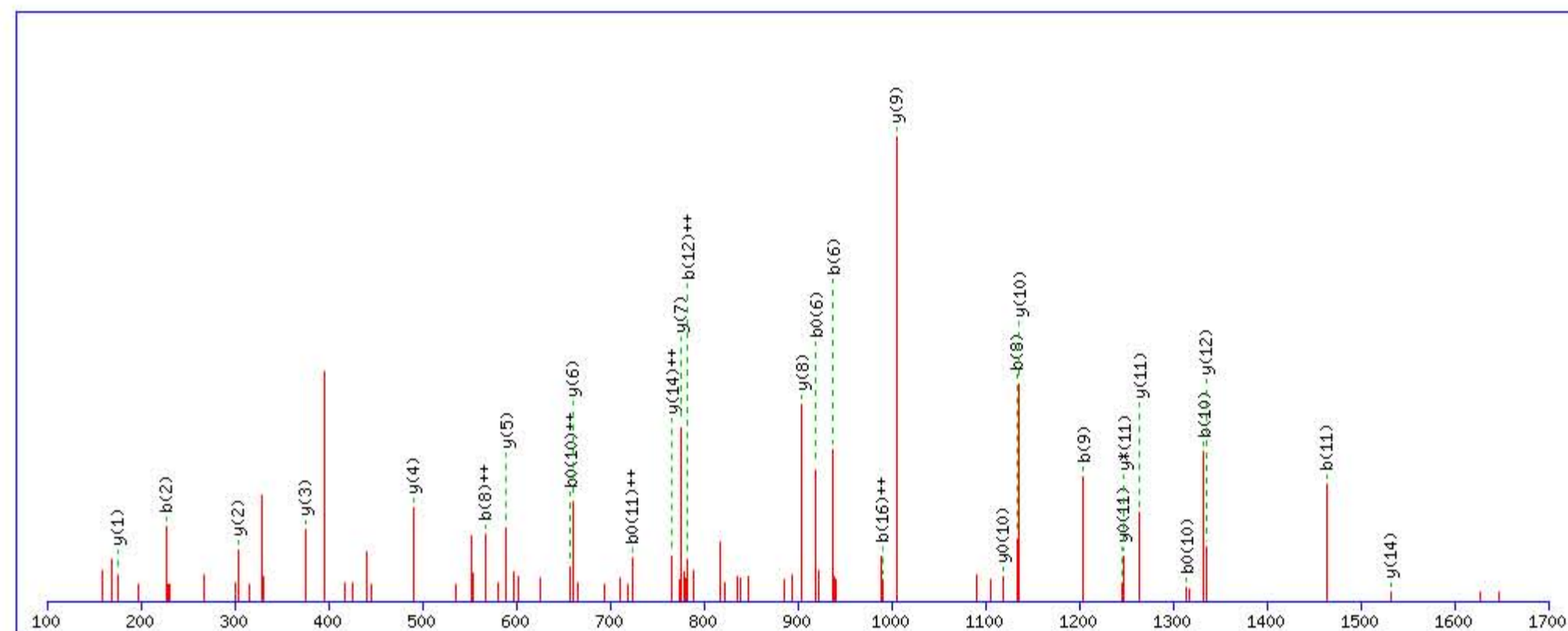
Title: Locus:1.1.1.3350.22 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2467.245071

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

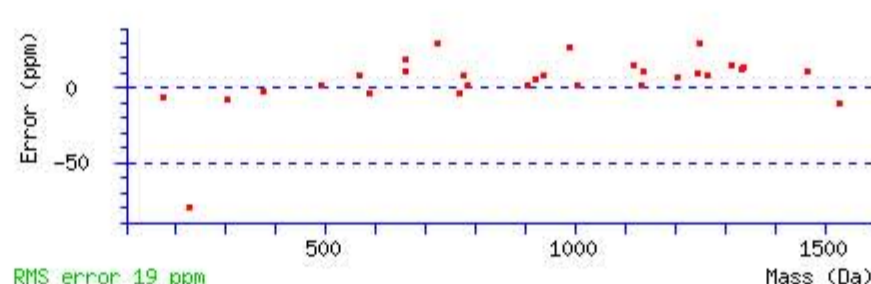
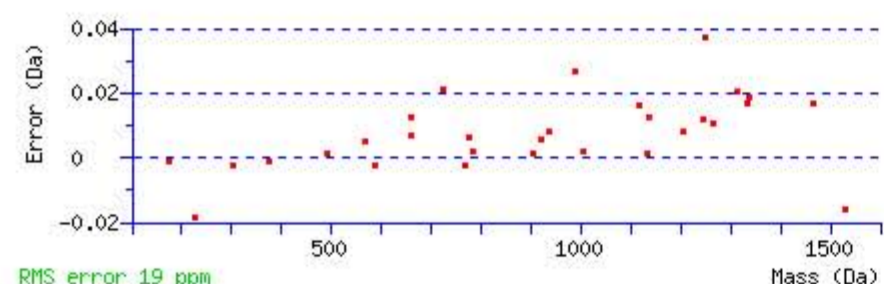
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 80 Expect: 3.3e-007

Matches : 30/210 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							20
2	227.175404	114.091340					L	2355.168297	1178.087786	2338.141748	1169.574512	2337.157732	1169.082504	19
3	340.259468	170.633372					L	2242.084233	1121.545754	2225.057684	1113.032480	2224.073668	1112.540472	18
4	779.484794	390.246035	762.458245	381.732760			Q	2129.000169	1065.003722	2111.973620	1056.490448	2110.989604	1055.998440	17
5	836.506258	418.756767	819.479709	410.243493			G	1689.774843	845.391060	1672.748294	836.877785	1671.764278	836.385777	16
6	937.553937	469.280607	920.527388	460.767332	919.543372	460.275324	T	1632.753379	816.880328	1615.726830	808.367053	1614.742814	807.875045	15
7	1034.606701	517.806988	1017.580152	509.293714	1016.596136	508.801706	P	1531.705700	766.356488	1514.679151	757.843214	1513.695135	757.351206	14
8	1133.675115	567.341196	1116.648566	558.827921	1115.664550	558.335913	V	1434.652936	717.830106	1417.626387	709.316832	1416.642371	708.824824	13
9	1204.712229	602.859753	1187.685680	594.346478	1186.701664	593.854470	A	1335.584522	668.295899	1318.557973	659.782625	1317.573957	659.290617	12
10	1332.770807	666.889042	1315.744258	658.375767	1314.760242	657.883759	Q	1264.547408	632.777342	1247.520859	624.264068	1246.536843	623.772060	11
11	1463.811292	732.409284	1446.784743	723.896010	1445.800727	723.404002	M	1136.488830	568.748053	1119.462281	560.234779	1118.478265	559.742771	10
12	1564.858971	782.933124	1547.832422	774.419849	1546.848406	773.927841	T	1005.448345	503.227811	988.421796	494.714536	987.437780	494.222528	9
13	1693.901564	847.454420	1676.875015	838.941146	1675.890999	838.449138	E	904.400666	452.703971	887.374117	444.190697	886.390101	443.698689	8
14	1808.928507	904.967892	1791.901958	896.454617	1790.917942	895.962609	D	775.358073	388.182675	758.331524	379.669400	757.347508	379.177392	7
15	1879.965621	940.486449	1862.939072	931.973174	1861.955056	931.481166	A	660.331130	330.669203	643.304581	322.155929	642.320565	321.663921	6
16	1979.034035	990.020656	1962.007486	981.507381	1961.023470	981.015373	V	589.294016	295.150646	572.267467	286.637372	571.283451	286.145364	5
17	2094.060978	1047.534127	2077.034429	1039.020852	2076.050413	1038.528844	D	490.225602	245.616439	473.199053	237.103165	472.215037	236.611157	4
18	2165.098092	1083.052684	2148.071543	1074.539409	2147.087527	1074.047402	A	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
19	2294.140685	1147.573981	2277.114136	1139.060706	2276.130120	1138.568698	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
20							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [ILLQGPVAQMTEDAVDAER](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
79.6	2467.245071	0.015571	ILLQGPVAQMTEDAVDAER
54.1	2467.245071	0.015571	ILLQGPVAQMTEDAVDAER

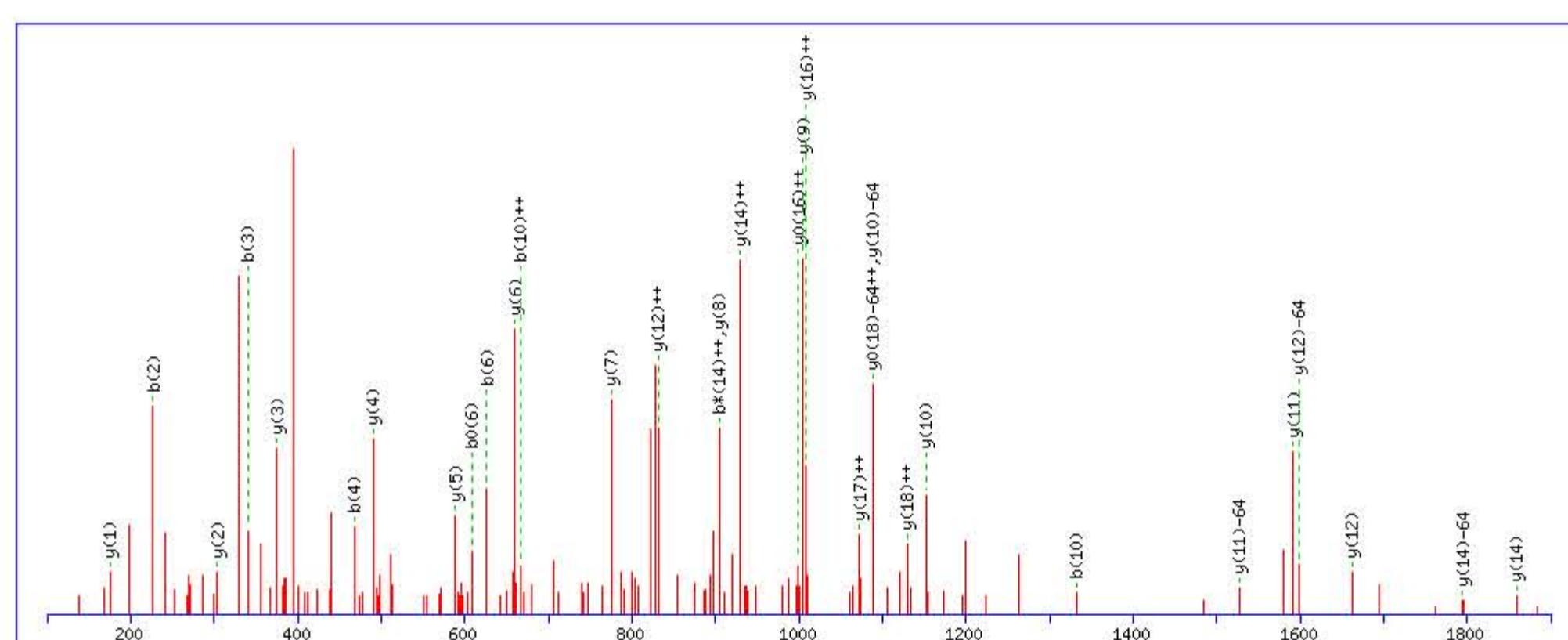
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **ILLQGTPVAQMTEDAVER**
 Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

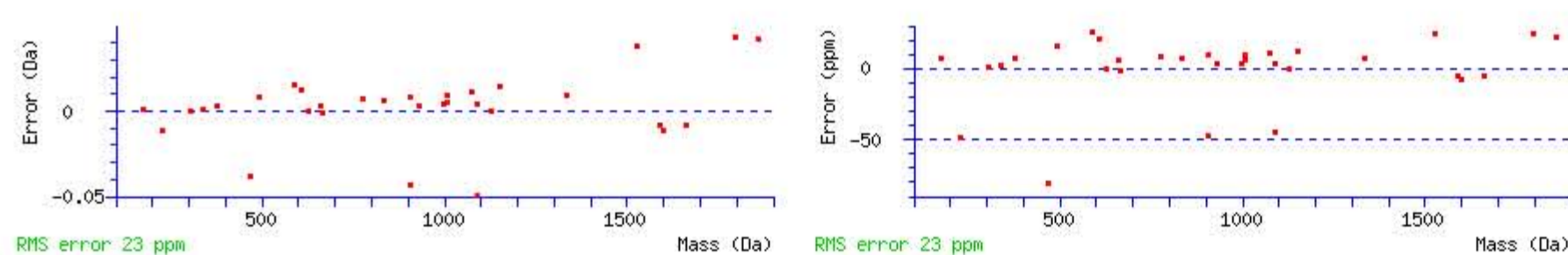
Match to Query 56191: 2483.252112 from(828.757980,3+) rtinseconds(2234) index(37885)
 Title: Locus:1.1.1.3197.22 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 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: 81 Expect: 2.4e-007
 Matches : 32/324 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					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 [ILLQGTPVAQMTEDAVER](#)
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.0	2483.239990	0.012122	ILLQGTPVAQMTEDAVER
33.8	2483.239990	0.012122	ILLQGTPVAQMTEDAVER

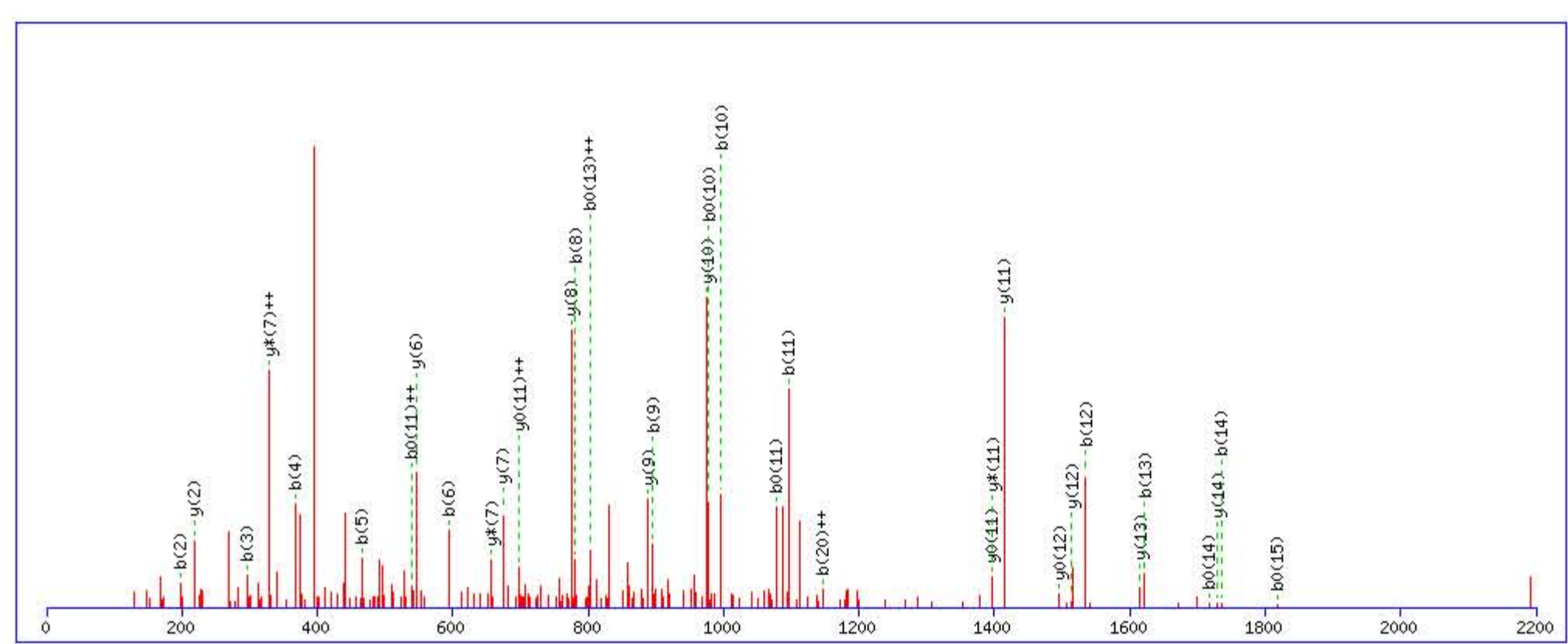
MASCOT Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPVAVQGEDTVQSLTQGDGVAK**
 Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

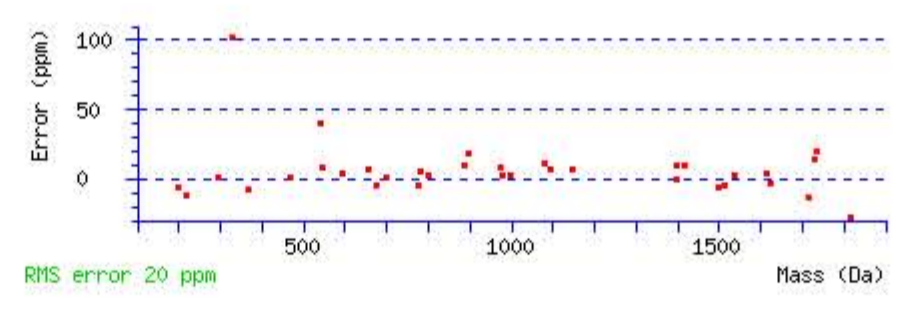
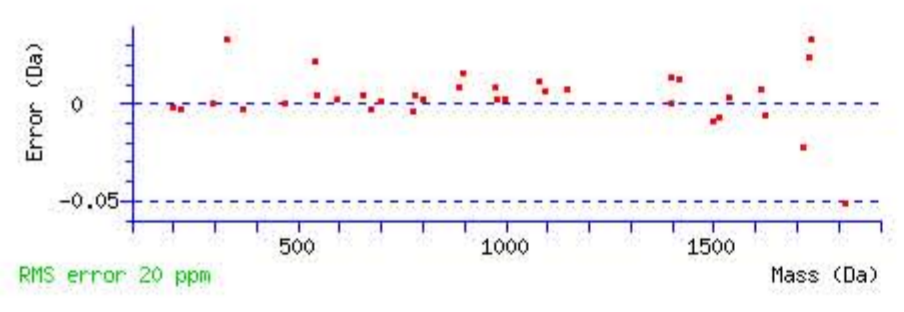
Match to Query 56831: 2508.305142 from(837.108990,3+) rtinseconds(2220) index(37789)
 Title: Locus:1.1.1.3192.24 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2508.289429
 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 : 35/220 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	100.075690	50.541483					V							22
2	197.128454	99.067865					P	2410.228255	1205.617765	2393.201706	1197.104491	2392.217690	1196.612483	21
3	296.196868	148.602072					V	2313.175491	1157.091383	2296.148942	1148.578109	2295.164926	1148.086101	20
4	367.233982	184.120629					A	2214.107077	1107.557176	2197.080528	1099.043902	2196.096512	1098.551894	19
5	466.302396	233.654836					V	2143.069963	1072.038619	2126.043414	1063.525345	2125.059398	1063.033337	18
6	594.360974	297.684125	577.334425	289.170851			Q	2044.001549	1022.504413	2026.975000	1013.991138	2025.990984	1013.499130	17
7	651.382438	326.194857	634.355889	317.681583			G	1915.942971	958.475124	1898.916422	949.961849	1897.932406	949.469841	16
8	780.425031	390.716154	763.398482	382.202879	762.414466	381.710871	E	1858.921507	929.964391	1841.894958	921.451117	1840.910942	920.959109	15
9	895.451974	448.229625	878.425425	439.716351	877.441409	439.224343	D	1729.878914	865.443095	1712.852365	856.929821	1711.868349	856.437812	14
10	996.499653	498.753465	979.473104	490.240190	978.489088	489.748182	T	1614.851971	807.929623	1597.825422	799.416349	1596.841406	798.924341	13
11	1095.568067	548.287672	1078.541518	539.774397	1077.557502	539.282389	V	1513.804292	757.405784	1496.777743	748.892510	1495.793727	748.400502	12
12	1534.793393	767.900335	1517.766844	759.387060	1516.782828	758.895052	Q	1414.735878	707.871577	1397.709329	699.358303	1396.725313	698.866294	11
13	1621.825421	811.416349	1604.798872	802.903074	1603.814856	802.411066	S	975.510552	488.258914	958.484003	479.745639	957.499987	479.253631	10
14	1734.909485	867.958381	1717.882936	859.445106	1716.898920	858.953098	L	888.478524	444.742900	871.451975	436.229625	870.467959	435.737617	9
15	1835.957164	918.482220	1818.930615	909.968946	1817.946599	909.476938	T	775.394460	388.200868	758.367911	379.687593	757.383895	379.195585	8
16	1964.015742	982.511509	1946.989193	973.998235	1946.005177	973.506227	Q	674.346781	337.677029	657.320232	329.163754	656.336216	328.671746	7
17	2021.037206	1011.022241	2004.010657	1002.508967	2003.026641	1002.016959	G	546.288203	273.647739	529.261654	265.134465	528.277638	264.642457	6
18	2136.064149	1068.535712	2119.037600	1060.022438	2118.053584	1059.530430	D	489.266739	245.137007	472.240190	236.623733	471.256174	236.131725	5
19	2193.085613	1097.046444	2176.059064	1088.533170	2175.075048	1088.041162	G	374.239796	187.623536	357.213247	179.110261			4
20	2292.154027	1146.580651	2275.127478	1138.067377	2274.143462	1137.575369	V	317.218332	159.112804	300.191783	150.599530			3
21	2363.191141	1182.099208	2346.164592	1173.585934	2345.180576	1173.093926	A	218.149918	109.578597	201.123369	101.065323			2
22							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

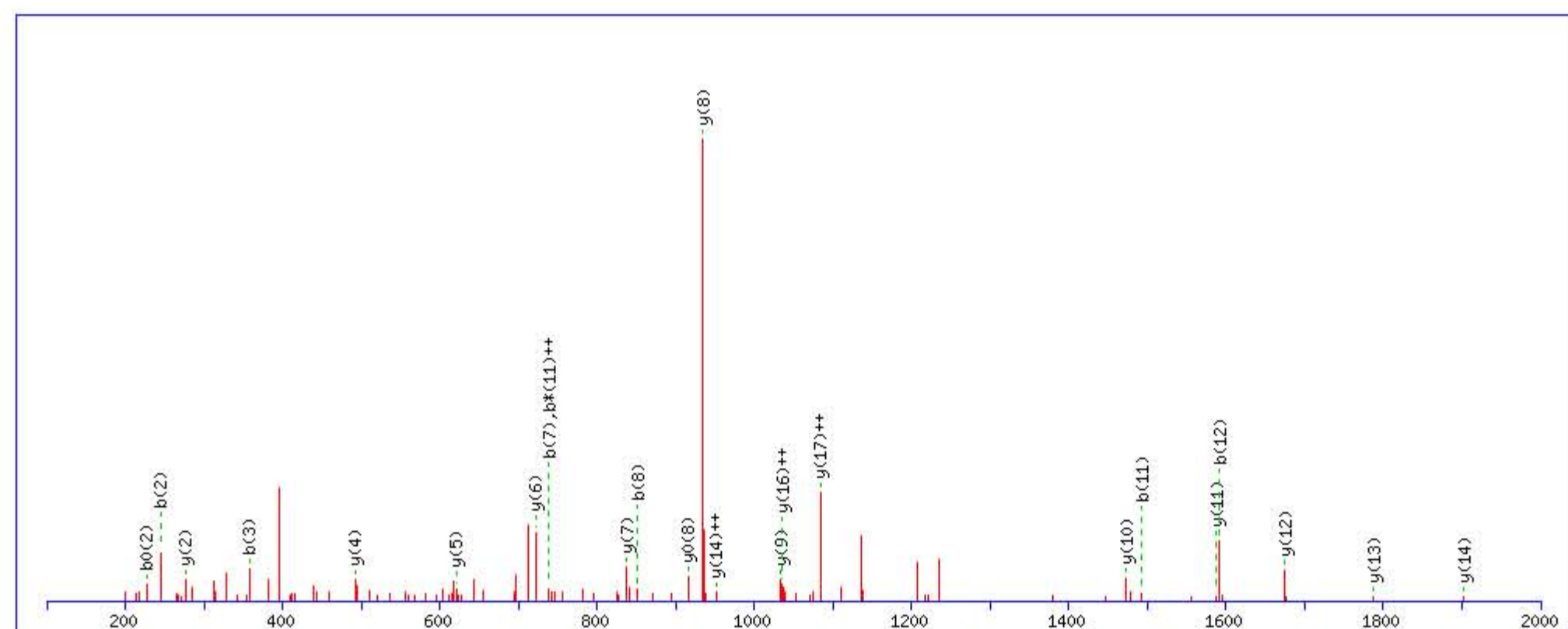
Score	$M_r(\text{calc})$:	Delta	Sequence
82.8	2508.289429	0.015713	VPVAVQGEDTVQSLTQGDGVAK
48.5	2508.289429	0.015713	VPVAVQGEDTVQSLTQGDGVAK
31.3	2508.289429	0.015713	VPVAVQGEDTVQSLTQGDGVAK

Peptide View

MS/MS Fragmentation of **EDIPPADLSDQVPDTESETR**
 Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

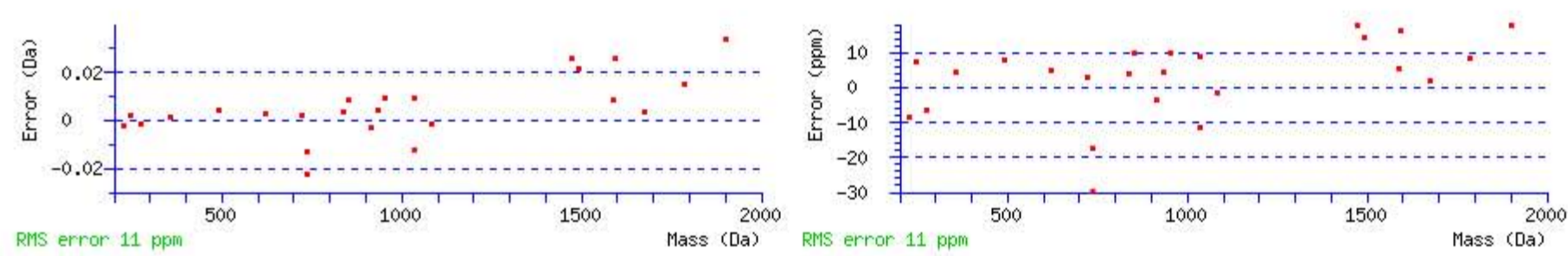
Match to Query 57007: 2524.176792 from(842.399540,3+) rtinseconds(2096) index(37001)
 Title: Locus:1.1.1.3149.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2524.163910
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q11 : Biotin:Thermo-21345 (Q)
 Ions Score: 54 Expect: 6.4e-005
 Matches : 24/206 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	130.049869	65.528572			112.039304	56.523290	E							20
2	245.076812	123.042044			227.066247	114.036762	D	2396.128598	1198.567937	2379.102049	1190.054662	2378.118033	1189.562654	19
3	358.160876	179.584076			340.150311	170.578794	I	2281.101655	1141.054465	2264.075106	1132.541191	2263.091090	1132.049183	18
4	455.213640	228.110458			437.203075	219.105176	P	2168.017591	1084.512433	2150.991042	1075.999159	2150.007026	1075.507151	17
5	552.266404	276.636840			534.255839	267.631558	P	2070.964827	1035.986051	2053.938278	1027.472777	2052.954262	1026.980769	16
6	623.303518	312.155397			605.292953	303.150115	A	1973.912063	987.459670	1956.885514	978.946395	1955.901498	978.454387	15
7	738.330461	369.668869			720.319896	360.663586	D	1902.874949	951.941113	1885.848400	943.427838	1884.864384	942.935830	14
8	851.414525	426.210901			833.403960	417.205618	L	1787.848006	894.427641	1770.821457	885.914367	1769.837441	885.422359	13
9	938.446553	469.726915			920.435988	460.721632	S	1674.763942	837.885609	1657.737393	829.372335	1656.753377	828.880327	12
10	1053.473496	527.240386			1035.462931	518.235104	D	1587.731914	794.369595	1570.705365	785.856321	1569.721349	785.364313	11
11	1492.698822	746.853049	1475.672273	738.339775	1474.688257	737.847767	Q	1472.704971	736.856124	1455.678422	728.342849	1454.694406	727.850841	10
12	1591.767236	796.387256	1574.740687	787.873982	1573.756671	787.381974	V	1033.479645	517.243461	1016.453096	508.730186	1015.469080	508.238178	9
13	1688.820000	844.913638	1671.793451	836.400364	1670.809435	835.908356	P	934.411231	467.709254	917.384682	459.195979	916.400666	458.703971	8
14	1803.846943	902.427110	1786.820394	893.913835	1785.836378	893.421827	D	837.358467	419.182872	820.331918	410.669597	819.347902	410.177589	7
15	1904.894622	952.950949	1887.868073	944.437675	1886.884057	943.945667	T	722.331524	361.669400	705.304975	353.156125	704.320959	352.664117	6
16	2033.937215	1017.472246	2016.910666	1008.958971	2015.926650	1008.466963	E	621.283845	311.145560	604.257296	302.632286	603.273280	302.140278	5
17	2120.969243	1060.988259	2103.942694	1052.474985	2102.958678	1051.982977	S	492.241252	246.624264	475.214703	238.110989	474.230687	237.618981	4
18	2250.011836	1125.509556	2232.985287	1116.996281	2232.001271	1116.504274	E	405.209224	203.108250	388.182675	194.594975	387.198659	194.102967	3
19	2351.059515	1176.033395	2334.032966	1167.520121	2333.048950	1167.028113	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
20							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.6	2524.163910	0.012882	EDIPPADLSDQVPDTESETR

MASCOT Search Results

Peptide View

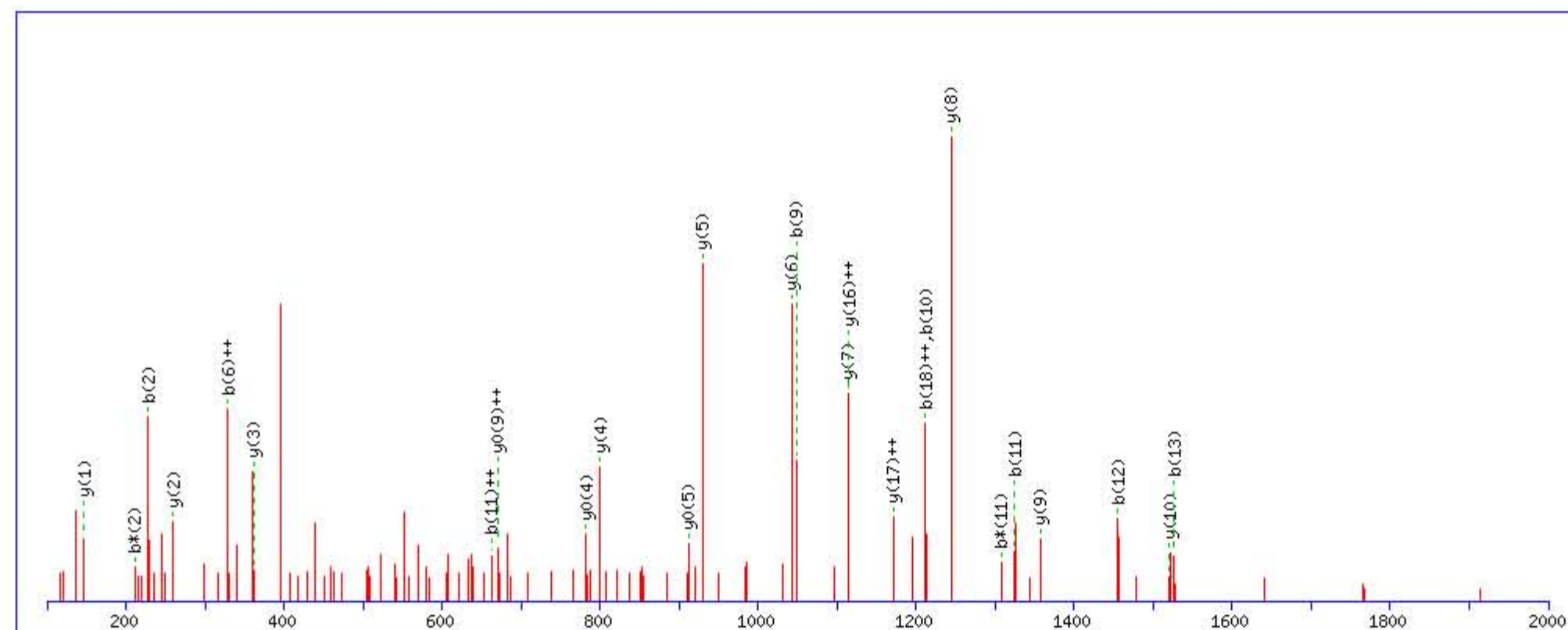
MS/MS Fragmentation of **VQLSNDFDEYIMAIEQTIK**
 Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

Match to Query 57316: 2567.276352 from(856.766060,3+) rtinseconds(3246) index(44662)
 Title: Locus:1.1.1.3544.21 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

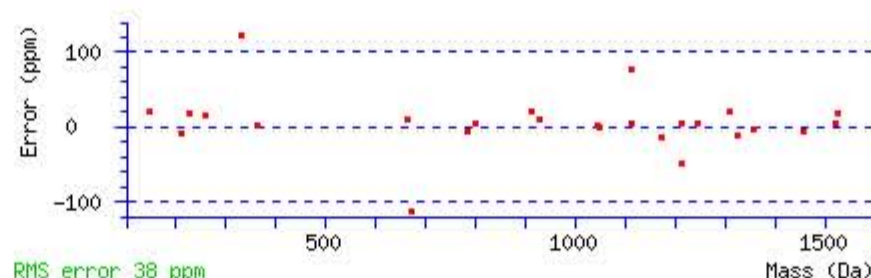
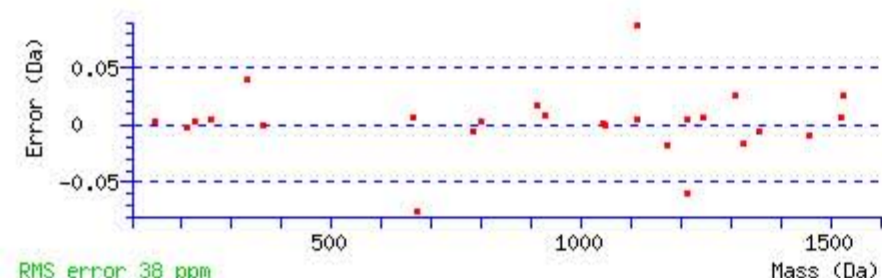
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2567.265121
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q16 : Biotin:Thermo-21345 (Q)
 Ions Score: 35 Expect: 0.0098
 Matches : 26/204 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							19
2	228.134268	114.570772	211.107719	106.057498			Q	2469.204012	1235.105644	2452.177463	1226.592369	2451.193447	1226.100361	18
3	341.218332	171.112804	324.191783	162.599530			L	2341.145434	1171.076355	2324.118885	1162.563080	2323.134869	1162.071072	17
4	428.250360	214.628818	411.223811	206.115544	410.239795	205.623536	S	2228.061370	1114.534323	2211.034821	1106.021048	2210.050805	1105.529040	16
5	542.293287	271.650282	525.266738	263.137007	524.282722	262.644999	N	2141.029342	1071.018309	2124.002793	1062.505034	2123.018777	1062.013026	15
6	657.320230	329.163753	640.293681	320.650479	639.309665	320.158471	D	2026.986415	1013.996845	2009.959866	1005.483571	2008.975850	1004.991563	14
7	804.388644	402.697960	787.362095	394.184686	786.378079	393.692678	F	1911.959472	956.483374	1894.932923	947.970099	1893.948907	947.478091	13
8	919.415587	460.211432	902.389038	451.698157	901.405022	451.206149	D	1764.891058	882.949167	1747.864509	874.435893	1746.880493	873.943884	12
9	1048.458180	524.732728	1031.431631	516.219453	1030.447615	515.727445	E	1649.864115	825.435695	1632.837566	816.922421	1631.853550	816.430413	11
10	1211.521509	606.264392	1194.494960	597.751118	1193.510944	597.259110	Y	1520.821522	760.914399	1503.794973	752.401125	1502.810957	751.909116	10
11	1324.605573	662.806424	1307.579024	654.293150	1306.595008	653.801142	I	1357.758193	679.382734	1340.731644	670.869460	1339.747628	670.377452	9
12	1455.646058	728.326667	1438.619509	719.813392	1437.635493	719.321384	M	1244.674129	622.840703	1227.647580	614.327428	1226.663564	613.835420	8
13	1526.683172	763.845224	1509.656623	755.331949	1508.672607	754.839941	A	1113.633644	557.320460	1096.607095	548.807186	1095.623079	548.315178	7
14	1639.767236	820.387256	1622.740687	811.873981	1621.756671	811.381973	I	1042.596530	521.801903	1025.569981	513.288629	1024.585965	512.796621	6
15	1768.809829	884.908552	1751.783280	876.395278	1750.799264	875.903270	E	929.512466	465.259871	912.485917	456.746597	911.501901	456.254589	5
16	2208.035155	1104.521215	2191.008606	1096.007941	2190.024590	1095.515933	Q	800.469873	400.738575	783.443324	392.225300	782.459308	391.733292	4
17	2309.082834	1155.045055	2292.056285	1146.531780	2291.072269	1146.039772	T	361.244547	181.125911	344.217998	172.612637	343.233982	172.120629	3
18	2422.166898	1211.587087	2405.140349	1203.073812	2404.156333	1202.581804	I	260.196868	130.602072	243.170319	122.088798			2
19							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.5	2567.265121	0.011231	VQLSNDFDEYIMAIEQTIK

Mascot Search Results

Peptide View

MS/MS Fragmentation of **QKPDGVFQEDAPVIHQEMIGGLR**

Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

Match to Query 60616: 2874.463176 from(719.623070,4+) rtinseconds(2217) index(37760)

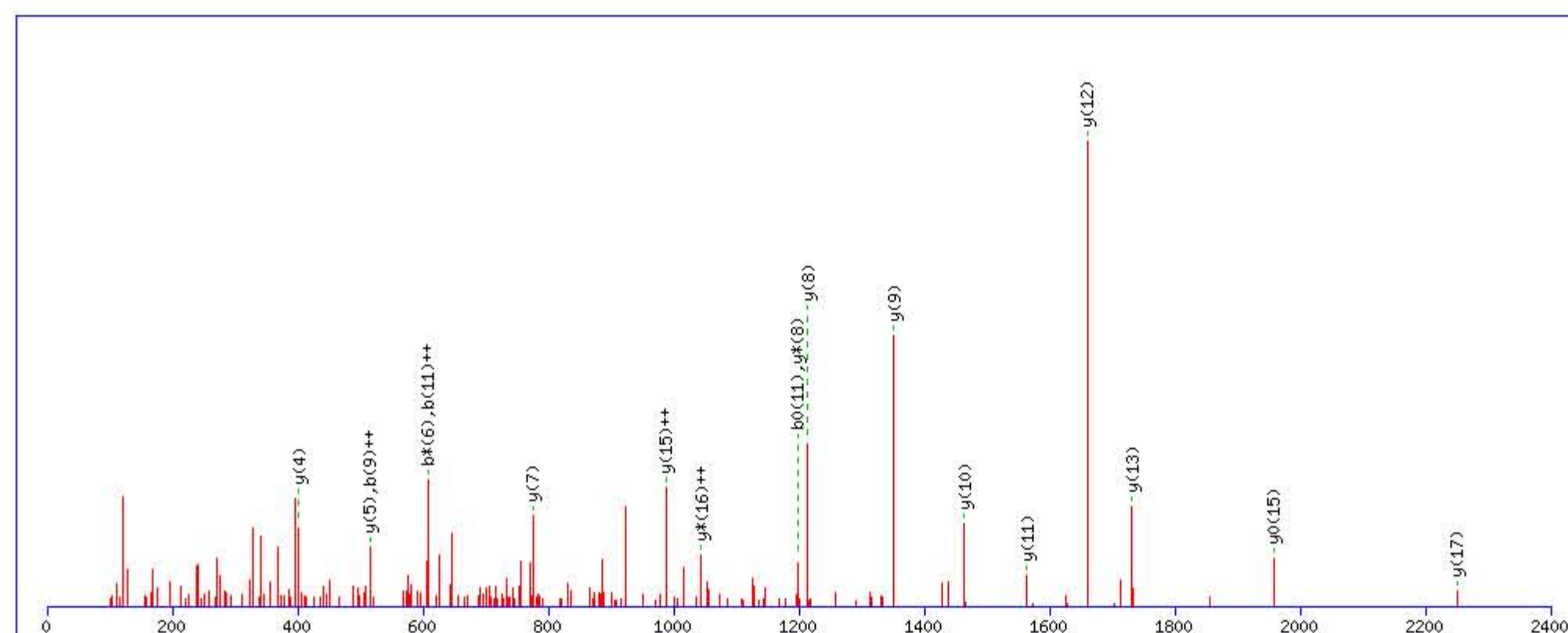
Title: Locus:1.1.1.3191.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2874.452057

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

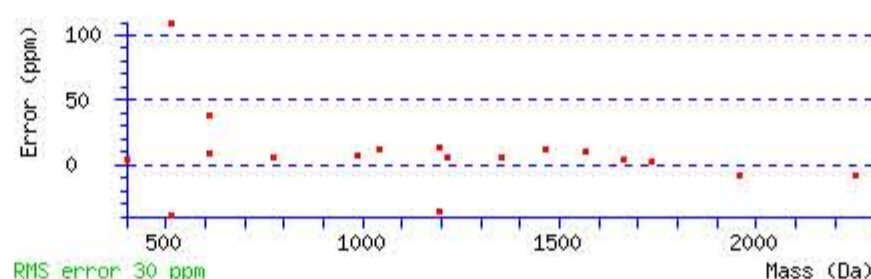
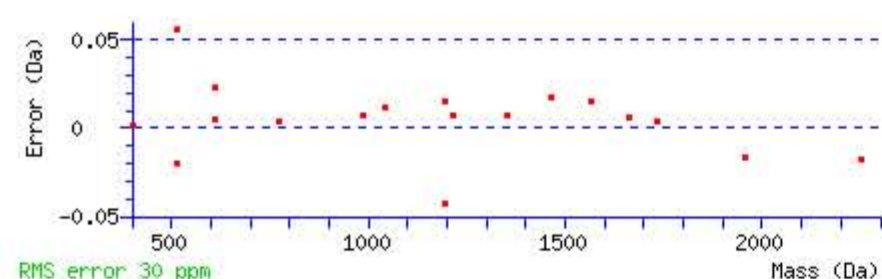
Variable modifications:

Q16 : Biotin:Thermo-21345 (Q)

Ions Score: 68 Expect: 4.3e-006

Matches : 18/246 fragment ions using 20 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.065854	65.036565	112.039305	56.523291			Q							23
2	257.160817	129.084047	240.134268	120.570772			K	2747.400756	1374.204016	2730.374207	1365.690741	2729.390191	1365.198733	22
3	354.213581	177.610429	337.187032	169.097154			P	2619.305793	1310.156534	2602.279244	1301.643260	2601.295228	1301.151252	21
4	469.240524	235.123900	452.213975	226.610626	451.229959	226.118618	D	2522.253029	1261.630152	2505.226480	1253.116878	2504.242464	1252.624870	20
5	526.261988	263.634632	509.235439	255.121358	508.251423	254.629350	G	2407.226086	1204.116681	2390.199537	1195.603406	2389.215521	1195.111398	19
6	625.330402	313.168839	608.303853	304.655565	607.319837	304.163557	V	2350.204622	1175.605949	2333.178073	1167.092674	2332.194057	1166.600666	18
7	772.398816	386.703046	755.372267	378.189772	754.388251	377.697764	F	2251.136208	1126.071742	2234.109659	1117.558467	2233.125643	1117.066459	17
8	900.457394	450.732335	883.430845	442.219061	882.446829	441.727053	Q	2104.067794	1052.537535	2087.041245	1044.024260	2086.057229	1043.532252	16
9	1029.499987	515.253631	1012.473438	506.740357	1011.489422	506.248349	E	1976.009216	988.508246	1958.982667	979.994972	1957.998651	979.502964	15
10	1144.526930	572.767103	1127.500381	564.253829	1126.516365	563.761821	D	1846.966623	923.986950	1829.940074	915.473675	1828.956058	914.981667	14
11	1215.564044	608.285660	1198.537495	599.772386	1197.553479	599.280377	A	1731.939680	866.473478	1714.913131	857.960204	1713.929115	857.468196	13
12	1312.616808	656.812042	1295.590259	648.298768	1294.606243	647.806760	P	1660.902566	830.954921	1643.876017	822.441647	1642.892001	821.949639	12
13	1411.685222	706.346249	1394.658673	697.832975	1393.674657	697.340967	V	1563.849802	782.428539	1546.823253	773.915265	1545.839237	773.423257	11
14	1524.769286	762.888281	1507.742737	754.375007	1506.758721	753.882998	I	1464.781388	732.894332	1447.754839	724.381058	1446.770823	723.889050	10
15	1661.828198	831.417737	1644.801649	822.904463	1643.817633	822.412454	H	1351.697324	676.352300	1334.670775	667.839026	1333.686759	667.347018	9
16	2101.053524	1051.030400	2084.026975	1042.517125	2083.042959	1042.025117	Q	1214.638412	607.822844	1197.611863	599.309570	1196.627847	598.817562	8
17	2230.096117	1115.551696	2213.069568	1107.038422	2212.085552	1106.546414	E	775.413086	388.210181	758.386537	379.696907	757.402521	379.204899	7
18	2361.136602	1181.071939	2344.110053	1172.558664	2343.126037	1172.066656	M	646.370493	323.688885	629.343944	315.175610			6
19	2474.220666	1237.613971	2457.194117	1229.100696	2456.210101	1228.608689	I	515.330008	258.168642	498.303459	249.655368			5
20	2531.242130	1266.124703	2514.215581	1257.611428	2513.231565	1257.119420	G	402.245944	201.626610	385.219395	193.113335			4
21	2588.263594	1294.635435	2571.237045	1286.122160	2570.253029	1285.630152	G	345.224480	173.115878	328.197931	164.602603			3
22	2701.347658	1351.177467	2684.321109	1342.664192	2683.337093	1342.172185	L	288.203016	144.605146	271.176467	136.091872			2
23							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **QKPDGVFQEDAPVIHQEMIGGLR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.3	2874.452057	0.011119	QKPDGVFQEDAPVIHQEMIGGLR
6.5	2874.452057	0.011119	QKPDGVFQEDAPVIHQEMIGGLR

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

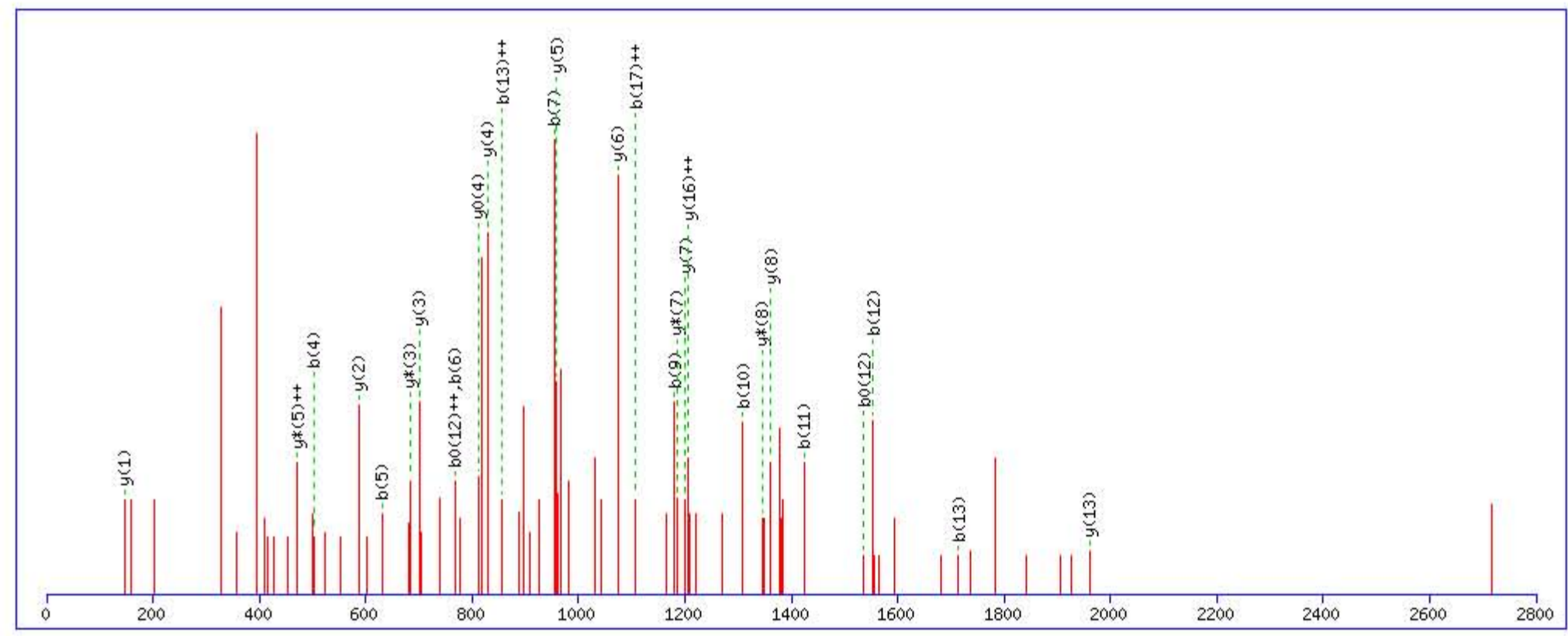
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **DTWVEHWPEEDECQDEENQK**
 Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

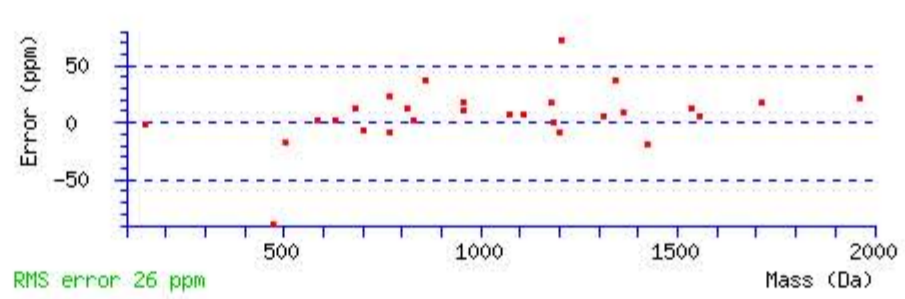
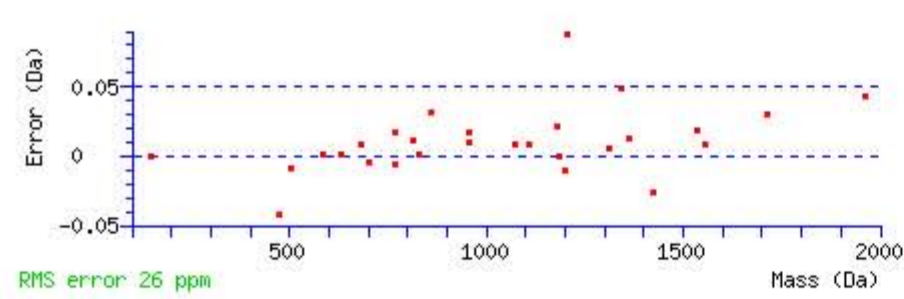
Match to Query 60968: 2913.206682 from(972.076170,3+) rtinseconds(2114) index(37109)
 Title: Locus:1.1.1.3155.26 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2913.185776
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q19 : Biotin:Thermo-21345 (Q)
 Ions Score: 47 Expect: 3.4e-005
 Matches : 28/196 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							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	$M_r(\text{calc})$:	Delta	Sequence
46.8	2913.185776	0.020906	DTWVEHWPEEDECQDEENQK
17.9	2913.185776	0.020906	DTWVEHWPEEDECQDEENQK

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQAGLQR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 17300: 1039.555588 from(520.785070,2+) rtinseconds(1467) index(49286)

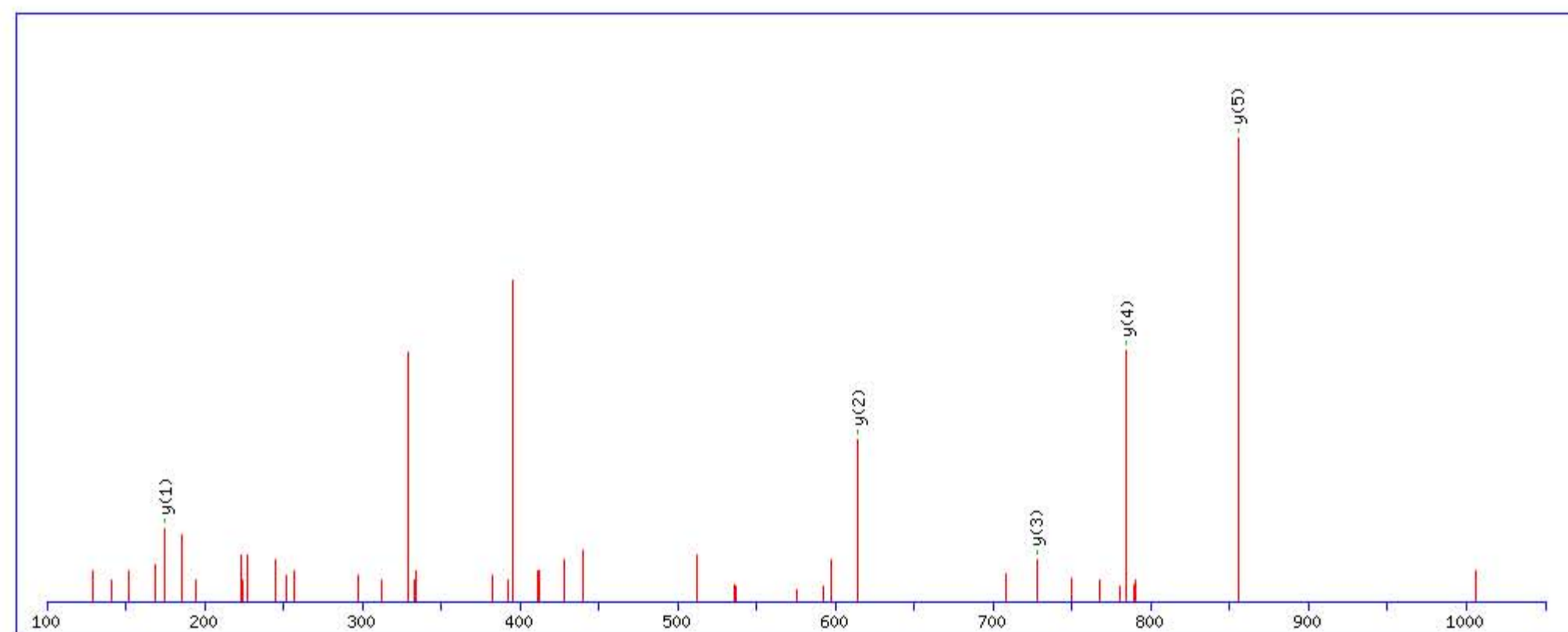
Title: Locus:1.1.1.1126.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1039.559677

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

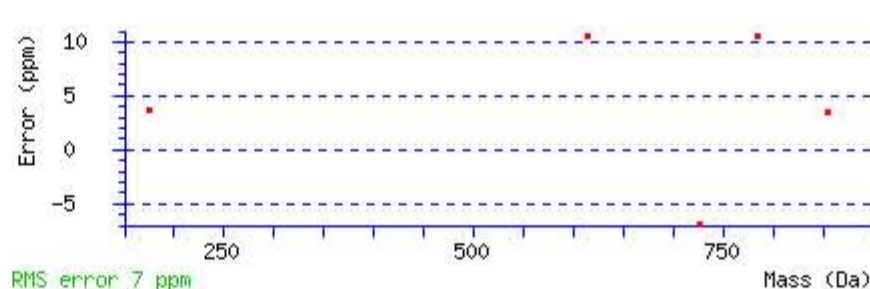
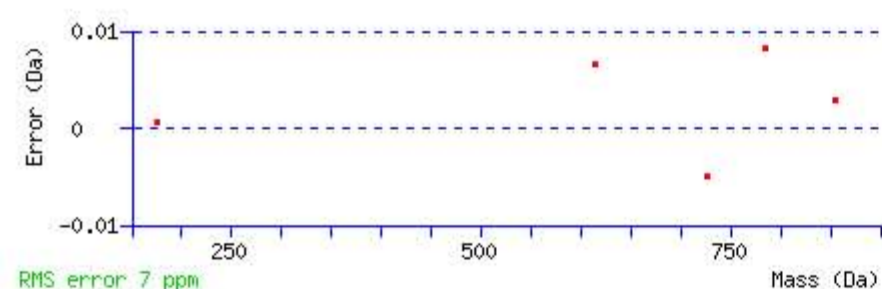
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 34 Expect: 0.0068

Matches : 5/46 fragment ions using 9 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ^{*++}	Seq.	y	y ⁺⁺	y ⁺	y ^{*++}	#
1	58.028740	29.518008			G					7
2	186.087318	93.547297	169.060769	85.034023	Q	983.545498	492.276387	966.518949	483.763113	6
3	257.124432	129.065854	240.097883	120.552580	A	855.486920	428.247098	838.460371	419.733824	5
4	314.145896	157.576586	297.119347	149.063312	G	784.449806	392.728541	767.423257	384.215267	4
5	427.229960	214.118618	410.203411	205.605344	L	727.428342	364.217809	710.401793	355.704535	3
6	866.455286	433.731281	849.428737	425.218007	Q	614.344278	307.675777	597.317729	299.162503	2
7					R	175.118952	88.063114	158.092403	79.549840	1



NCBI BLAST search of [GQAGLQR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.5	1039.559677	-0.004089	GQAGLQR
19.5	1039.559677	-0.004089	GQQIQR
9.5	1039.559677	-0.004089	KGGPSQR
7.8	1039.541061	0.014527	GQGDLLQPGR
5.5	1039.552277	0.003311	QRAALDGGPR
5.2	1039.548431	0.007157	SPEIQR
3.2	1039.541046	0.014542	NATTAPNPVR
1.8	1039.563522	-0.007934	ARRGGDGVPR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GLESQTK**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 18125: 1072.558368 from(537.286460,2+) rtinseconds(1491) index(49479)

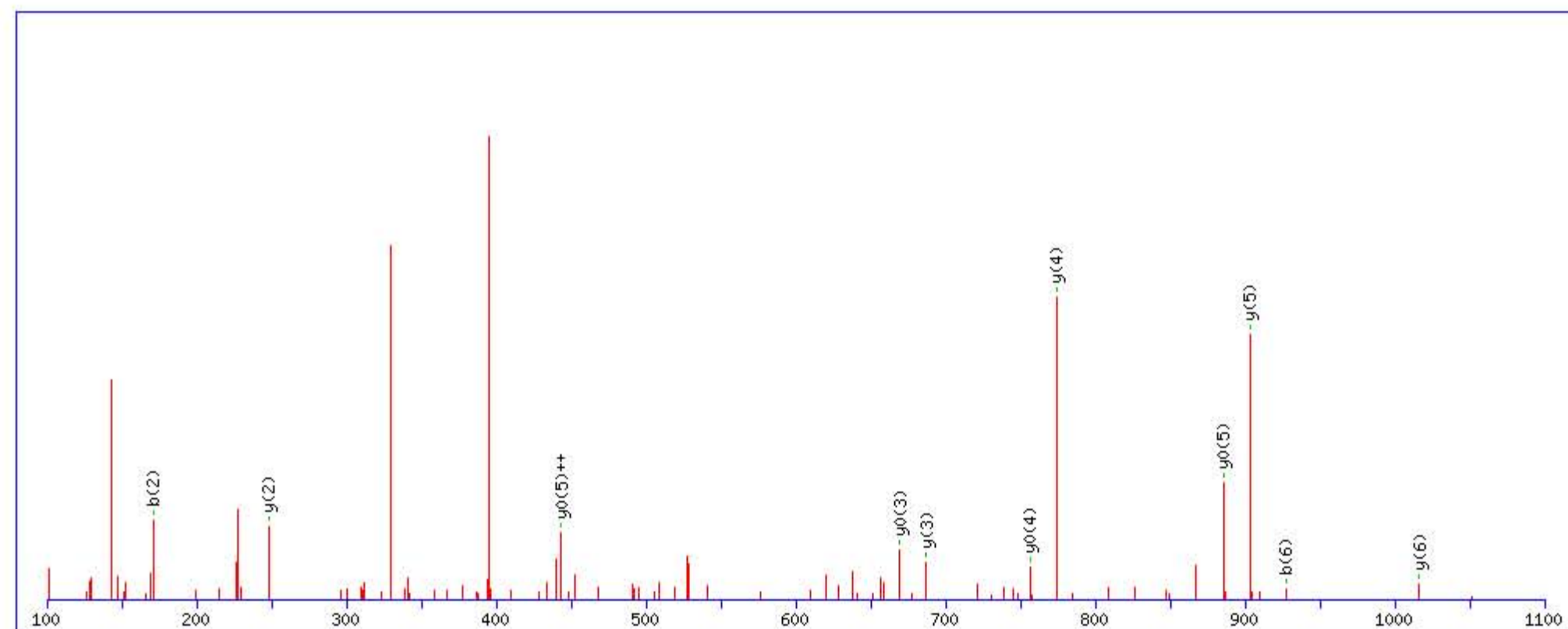
Title: Locus:1.1.1.1134.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1072.558670

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

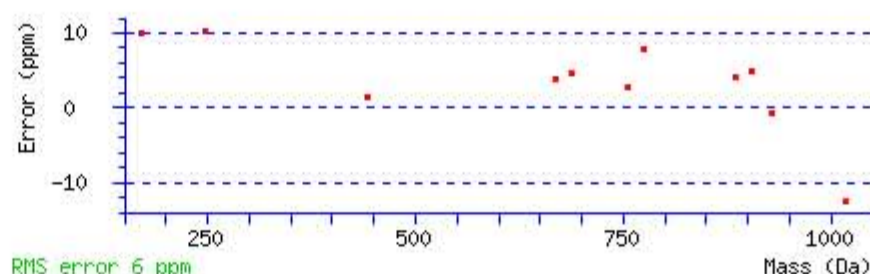
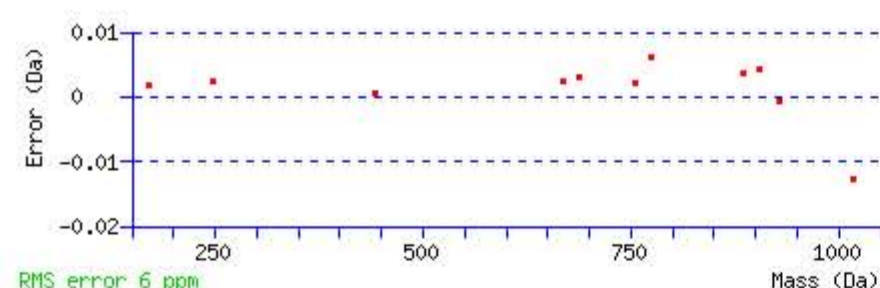
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 29 Expect: 0.011

Matches : 11/58 fragment ions using 20 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b*	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							7
2	171.112804	86.060040					L	1016.544494	508.775885	999.517945	500.262611	998.533929	499.770603	6
3	300.155397	150.581336			282.144832	141.576054	E	903.460430	452.233853	886.433881	443.720579	885.449865	443.228571	5
4	387.187425	194.097351			369.176860	185.092068	S	774.417837	387.712557	757.391288	379.199282	756.407272	378.707274	4
5	826.412751	413.710014	809.386202	405.196739	808.402186	404.704731	Q	687.385809	344.196543	670.359260	335.683268	669.375244	335.191260	3
6	927.460430	464.233853	910.433881	455.720579	909.449865	455.228571	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
7							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **GLESQTK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
29.2	1072.558670	-0.000302	GLESQTK
7.9	1072.558670	-0.000302	QSEGLTK
7.2	1072.558670	-0.000302	LGECPAVLSK
7.0	1072.551254	0.007114	KEAPRDETK
3.8	1072.551285	0.007083	GPRTTEPSTK
0.4	1072.566559	-0.008191	VQIHFGGSTK
0.3	1072.544739	0.013629	LGEPQARMR

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 23594: 1212.574068 from(607.294310,2+) rtinseconds(1319) index(48351)

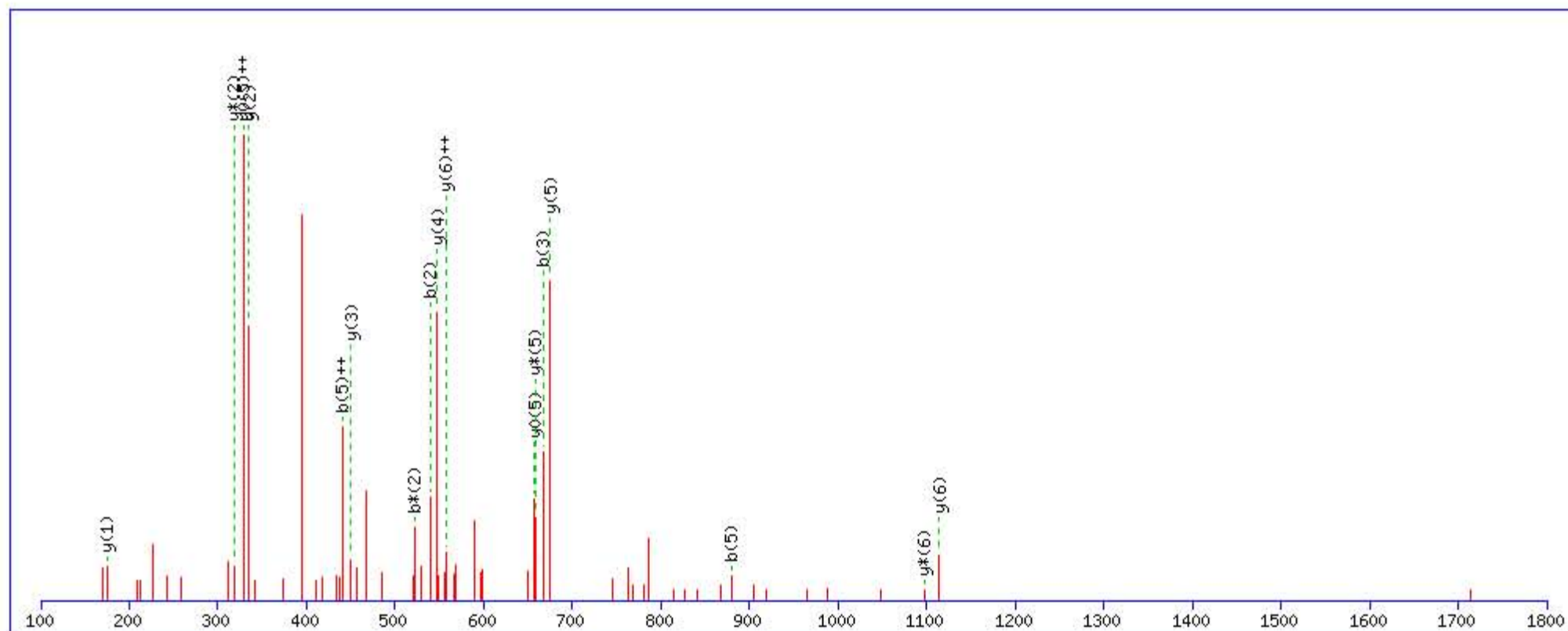
Title: Locus:1.1.1.1074.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1212.574356

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

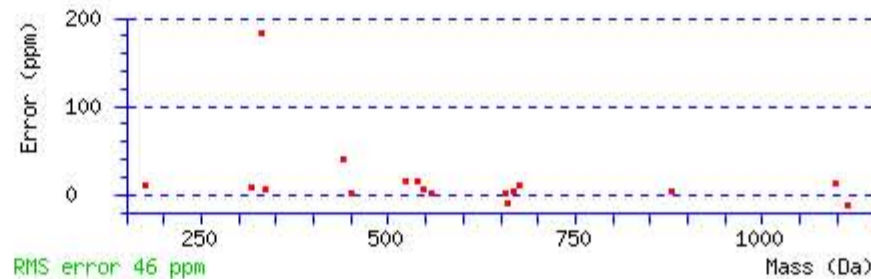
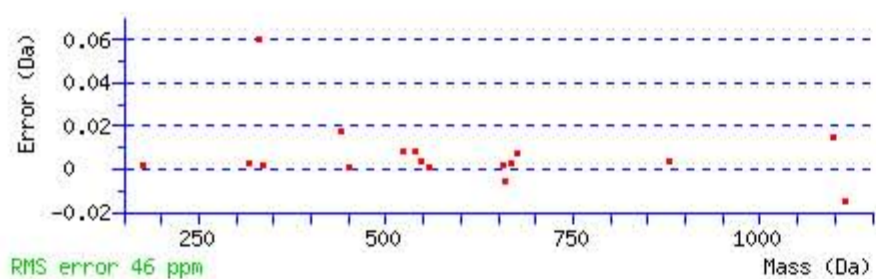
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.0052

Matches : 17/58 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	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
29.6	1212.574356	-0.000288	VQQPDCR
12.6	1212.574356	-0.000288	VQQPDCR
5.2	1212.592102	-0.018034	VQEDQQR

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 25584: 1279.667348 from(640.840950,2+) rtinseconds(2022) index(53086)

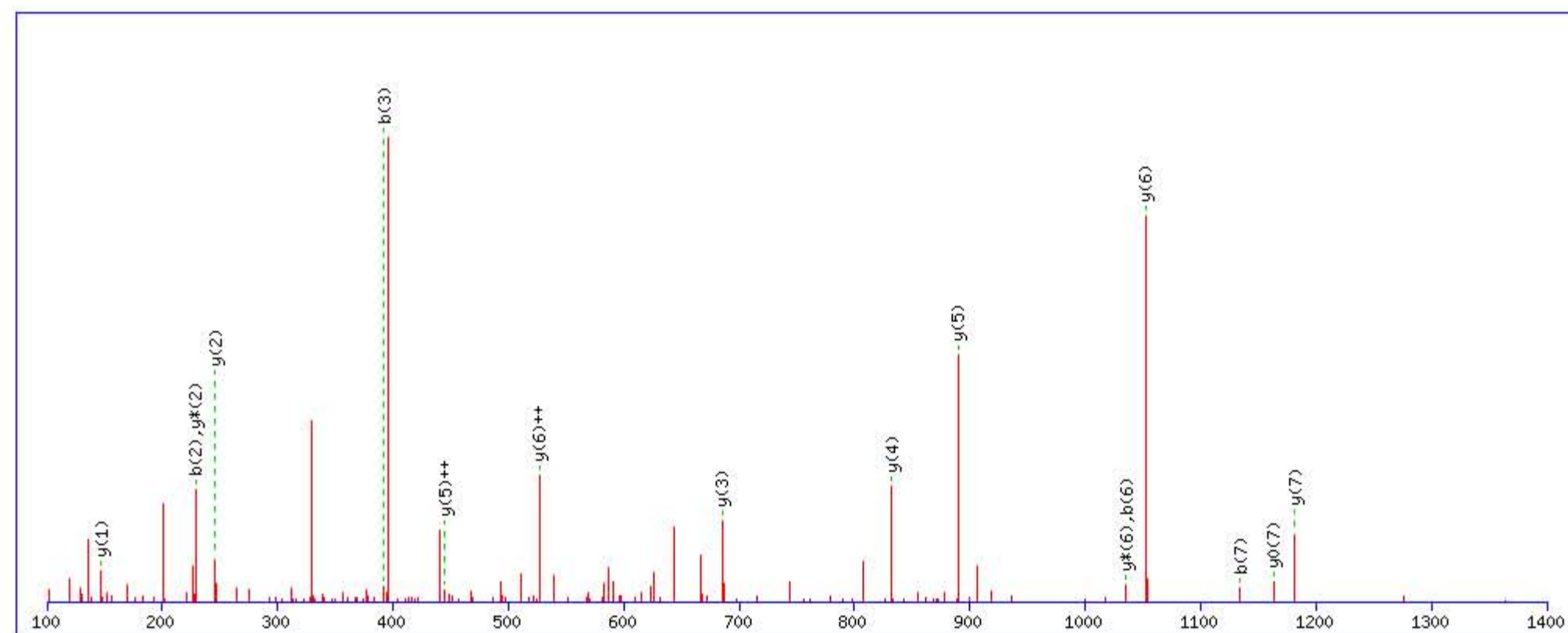
Title: Locus:1.1.1.1319.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1279.663483

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

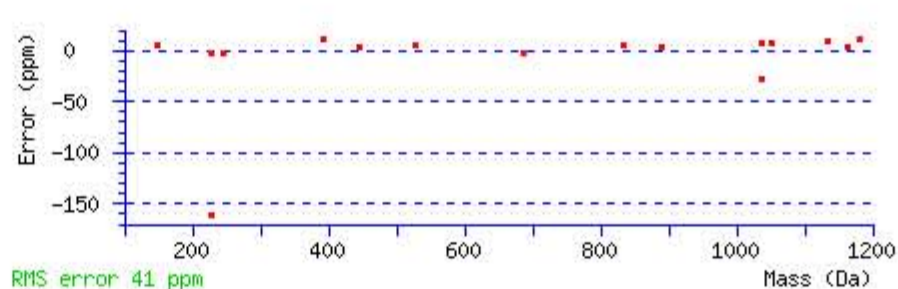
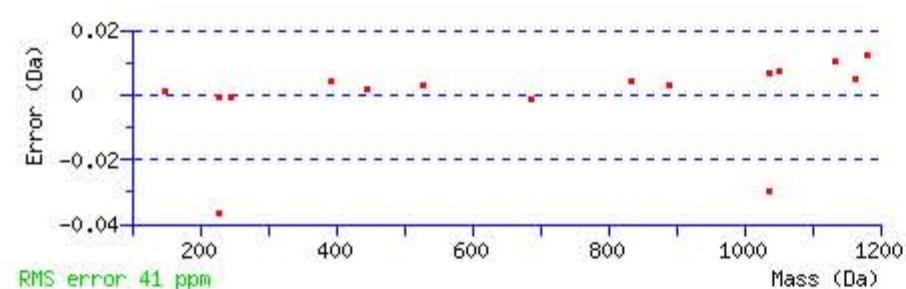
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.0029

Matches : 16/60 fragment ions using 34 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483					V							8
2	229.118283	115.062780			211.107718	106.057497	E	1181.602344	591.304810	1164.575795	582.791536	1163.591779	582.299528	7
3	392.181612	196.594444			374.171047	187.589162	Y	1052.559751	526.783514	1035.533202	518.270239			6
4	449.203076	225.105176			431.192511	216.099894	G	889.496422	445.251849	872.469873	436.738575			5
5	596.271490	298.639383			578.260925	289.634101	F	832.474958	416.741117	815.448409	408.227843			4
6	1035.496816	518.252046	1018.470267	509.738772	1017.486251	509.246764	Q	685.406544	343.206910	668.379995	334.693636			3
7	1134.565230	567.786253	1117.538681	559.272979	1116.554665	558.780971	V	246.181218	123.594247	229.154669	115.080973			2
8							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **VEYGFQVK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.1	1279.663483	0.003865	VEYGFQVK
5.9	1279.681229	-0.013881	EVTVKEWYVK
5.9	1279.663483	0.003865	QFVGYLDK
5.7	1279.659470	0.007878	VCSFGKQVVEK
4.0	1279.677216	-0.009868	VFKTEDTQGKK
3.8	1279.684601	-0.017253	MSASAVFILDVK
2.0	1279.666824	0.000524	VKEWSLMIMK

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVEEQESR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 25907: 1285.634328 from(643.824440,2+) rtinseconds(1393) index(48807)

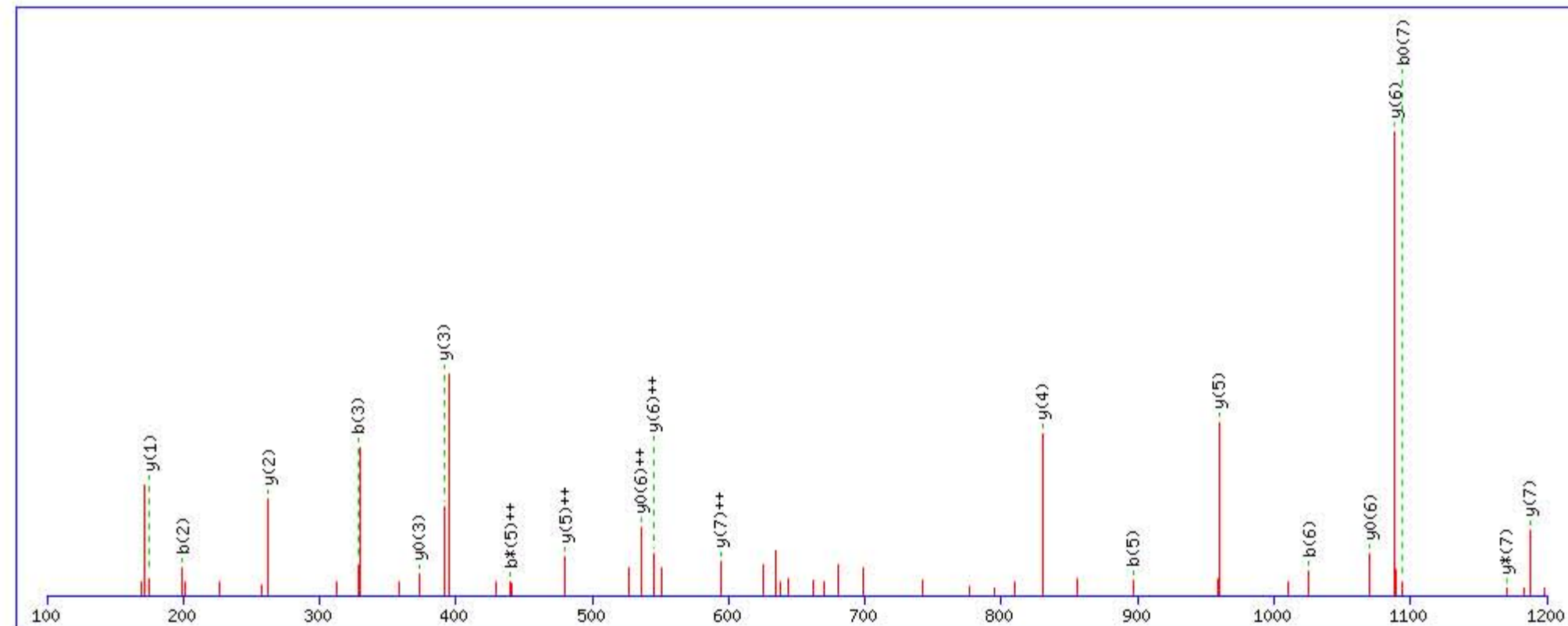
Title: Locus:1.1.1.1100.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1285.633621

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

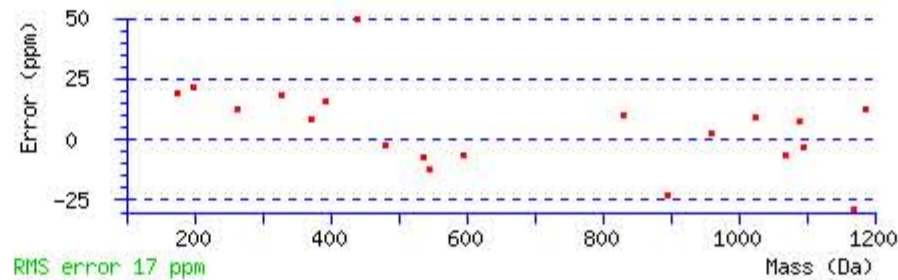
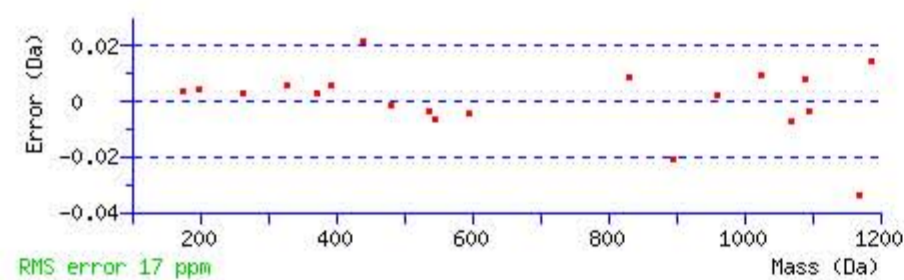
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 38 Expect: 0.00057

Matches : 20/70 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	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
37.8	1285.633621	0.000707	VVEEQESR
3.2	1285.644867	-0.010539	DTLHSAMAVVSR
2.3	1285.637451	-0.003123	TAPASGSAPRESR

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

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **CCQDGVTR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 26305: 1305.566628 from(653.790590,2+) rtinseconds(1405) index(48858)

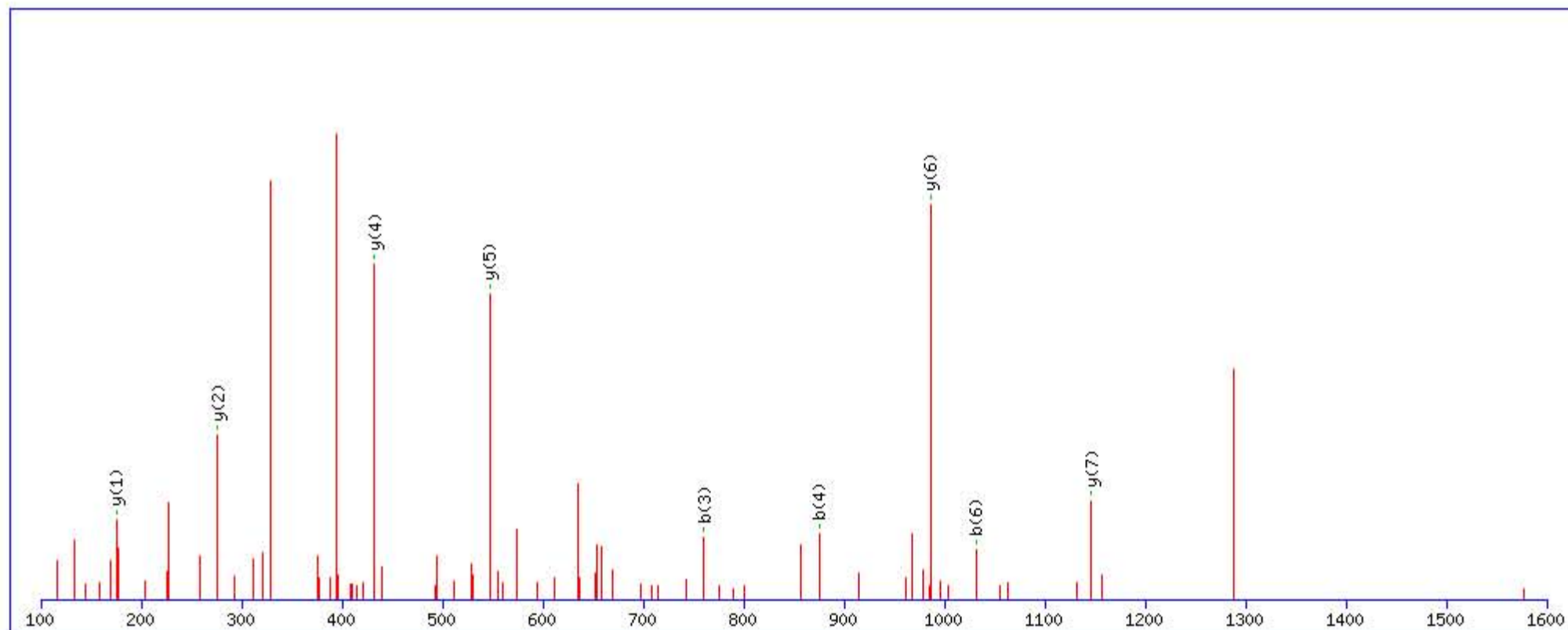
Title: Locus:1.1.1.1104.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1305.562820

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

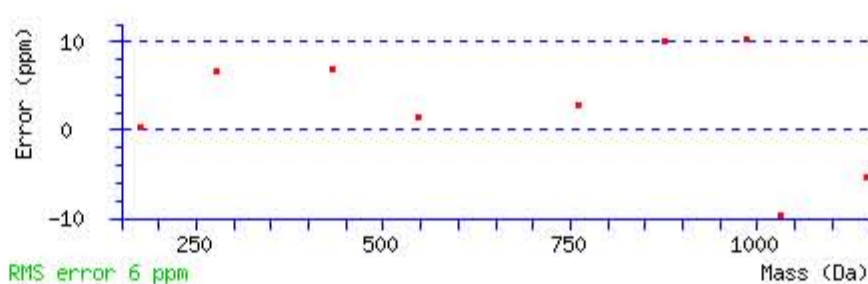
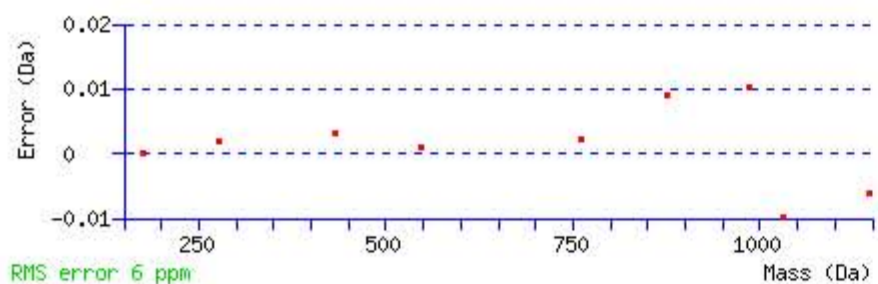
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 51 Expect: 7e-005

Matches : 9/72 fragment ions using 12 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	161.037925	81.022600					C							8
2	321.068574	161.037925					C	1146.539427	573.773352	1129.512878	565.260077	1128.528862	564.768069	7
3	760.293900	380.650588	743.267351	372.137314			Q	986.508778	493.758027	969.482229	485.244753	968.498213	484.752745	6
4	875.320843	438.164060	858.294294	429.650785	857.310278	429.158777	D	547.283452	274.145364	530.256903	265.632090	529.272887	265.140082	5
5	932.342307	466.674792	915.315758	458.161517	914.331742	457.669509	G	432.256509	216.631893	415.229960	208.118618	414.245944	207.626610	4
6	1031.410721	516.208999	1014.384172	507.695724	1013.400156	507.203716	V	375.235045	188.121161	358.208496	179.607886	357.224480	179.115878	3
7	1132.458400	566.732838	1115.431851	558.219564	1114.447835	557.727556	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
8							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [CCQDGVTR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.7	1305.562820	0.003808	CCQDGVTR
6.0	1305.577194	-0.010566	CDAGWLADGSVR
5.7	1305.562805	0.003823	CCTSPSQR
0.6	1305.583679	-0.017051	EQEPDFEEKR

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 27133: 1345.709368 from(673.861960,2+) rtinseconds(1630) index(50468)

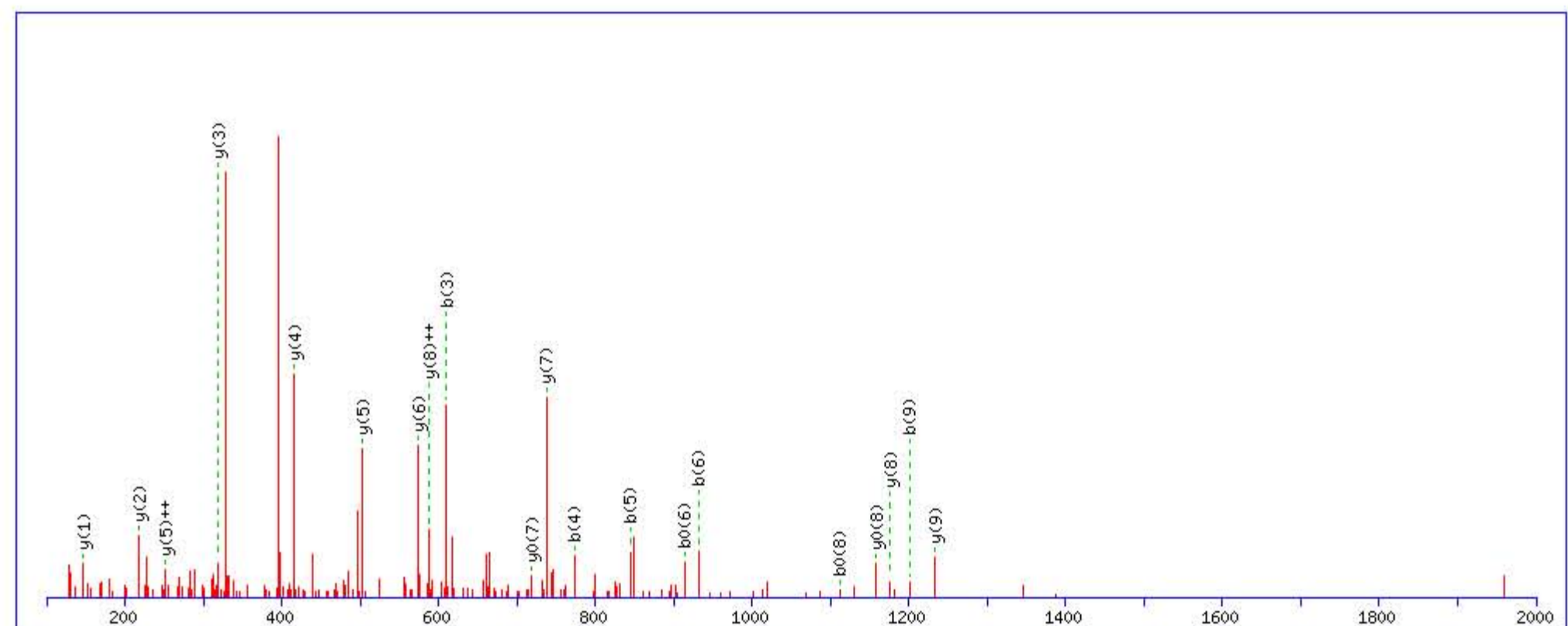
Title: Locus:1.1.1.1183.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1345.706390

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

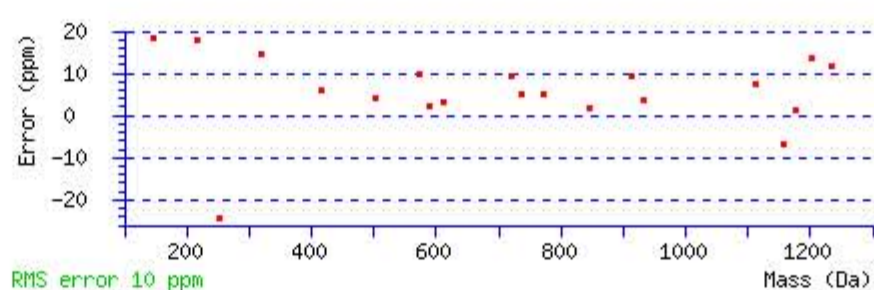
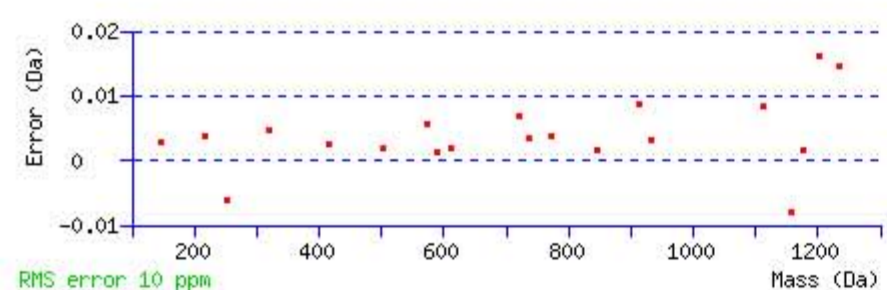
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 63 Expect: 1.4e-005

Matches : 20/90 fragment ions using 34 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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
63.1	1345.706390	0.002978	LGQYASPTAK
14.4	1345.706390	0.002978	LGQYDQALK
13.1	1345.724182	-0.014814	LGAVPATSGPTTFK
10.9	1345.706406	0.002962	QGLYTPQTK
7.0	1345.692474	0.016894	VASCRYPALGPR
6.7	1345.717636	-0.008268	QMPQPTFTLRK
5.8	1345.727509	-0.018141	LGLMDNEIKVAK
5.5	1345.727509	-0.018141	DKLKMEVDQLK
5.4	1345.720108	-0.010740	KQEEVSTLRK
3.0	1345.706390	0.002978	HEMTLKFPSIK

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLQDEDGYR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 28904: 1362.626348 from(682.320450,2+) rtinseconds(1742) index(51102)

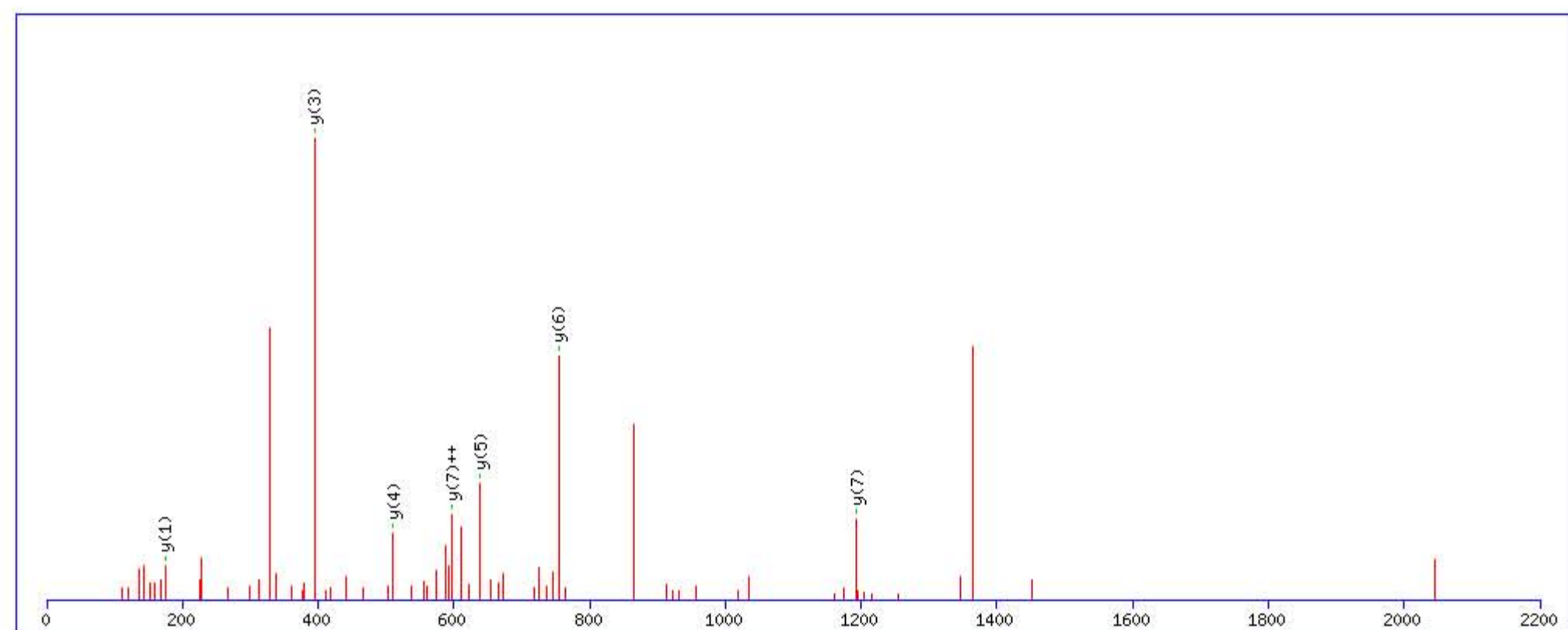
Title: Locus:1.1.1.1222.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1362.623795

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

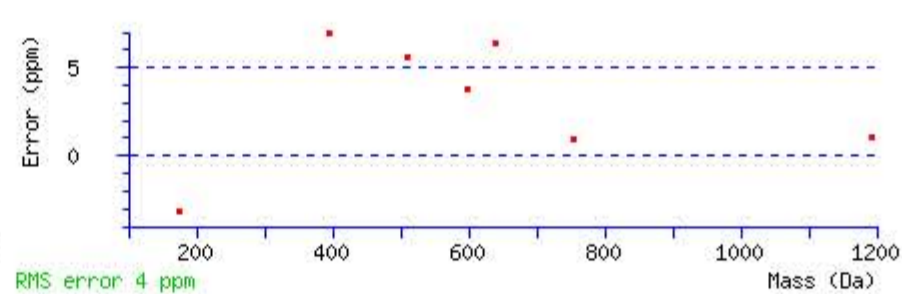
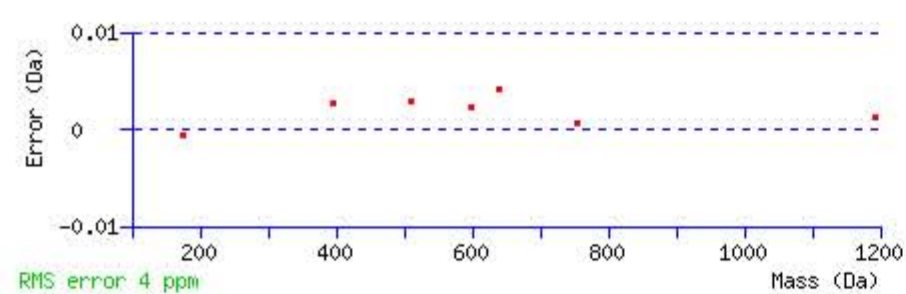
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.00027

Matches : 7/80 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	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
40.4	1362.623795	0.002553	GLQDEDGYR
2.4	1362.613251	0.013097	MGAGATGRAMDGPR
2.2	1362.623795	0.002553	TGFLEIDEHMR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **TEQWSTLPPETK**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 41020: 1726.871328 from(864.442940,2+) rtinseconds(2031) index(53160)

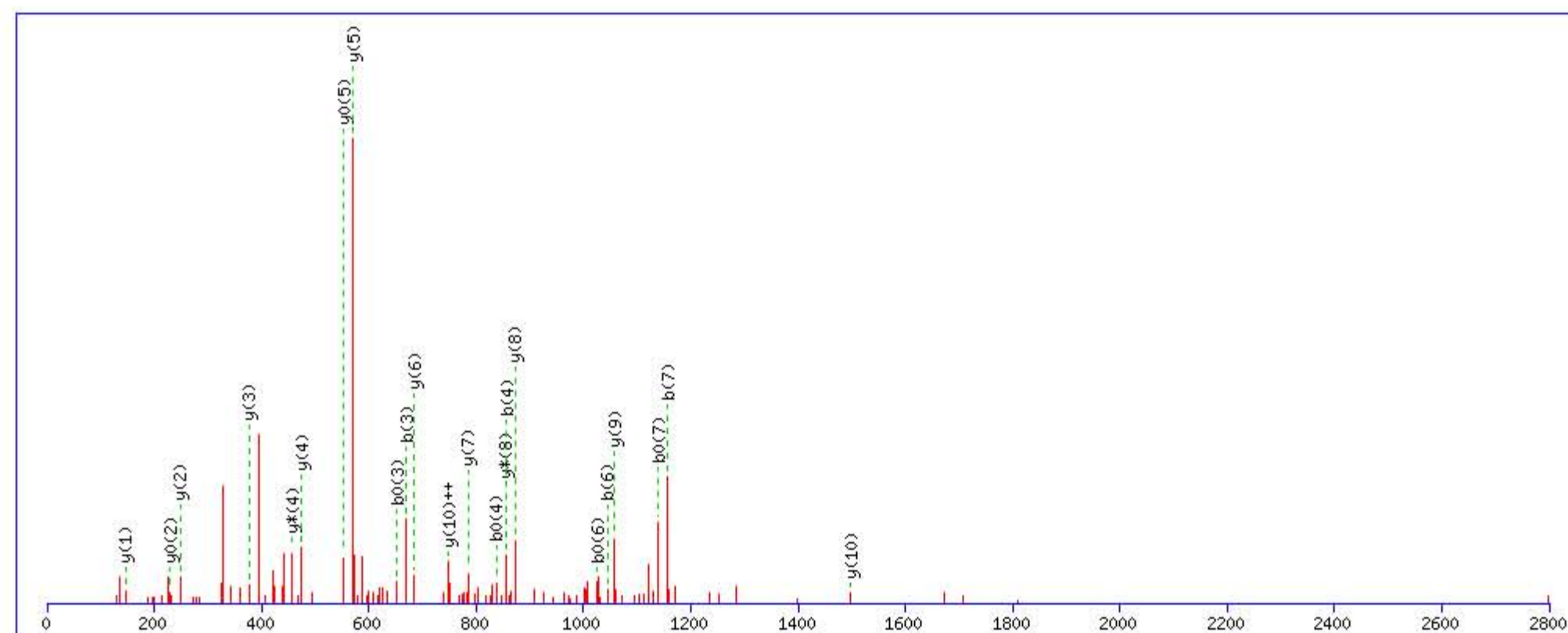
Title: Locus:1.1.1.1322.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1726.860001

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

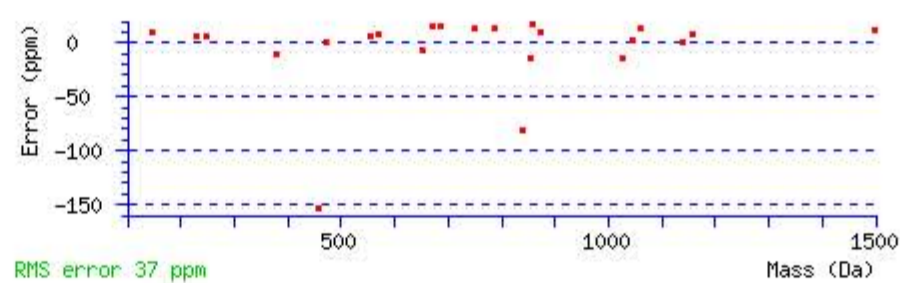
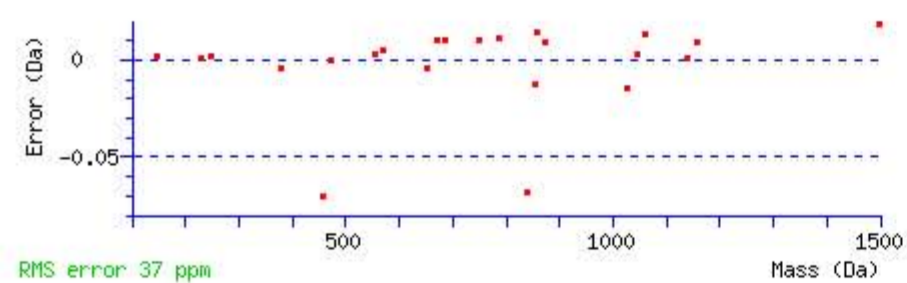
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 50 Expect: 0.00018

Matches : 23/126 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	102.054955	51.531116			84.044390	42.525833	T							12
2	231.097548	116.052412			213.086983	107.047130	E	1626.819607	813.913442	1609.793058	805.400167	1608.809042	804.908159	11
3	670.322874	335.665075	653.296325	327.151801	652.312309	326.659793	Q	1497.777014	749.392145	1480.750465	740.878871	1479.766449	740.386863	10
4	856.402187	428.704732	839.375638	420.191457	838.391622	419.699449	W	1058.551688	529.779482	1041.525139	521.266208	1040.541123	520.774200	9
5	943.434215	472.220746	926.407666	463.707471	925.423650	463.215463	S	872.472375	436.739826	855.445826	428.226551	854.461810	427.734543	8
6	1044.481894	522.744585	1027.455345	514.231311	1026.471329	513.739303	T	785.440347	393.223812	768.413798	384.710537	767.429782	384.218529	7
7	1157.565958	579.286617	1140.539409	570.773343	1139.555393	570.281334	L	684.392668	342.699972	667.366119	334.186698	666.382103	333.694690	6
8	1254.618722	627.812999	1237.592173	619.299725	1236.608157	618.807716	P	571.308604	286.157940	554.282055	277.644666	553.298039	277.152658	5
9	1351.671486	676.339381	1334.644937	667.826107	1333.660921	667.334098	P	474.255840	237.631558	457.229291	229.118284	456.245275	228.626276	4
10	1480.714079	740.860678	1463.687530	732.347403	1462.703514	731.855395	E	377.203076	189.105176	360.176527	180.591902	359.192511	180.099894	3
11	1581.761758	791.384517	1564.735209	782.871243	1563.751193	782.379235	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
12							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **TEQWSTLPPETK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.1	1726.860001	0.011327	TEQWSTLPPETK
9.6	1726.849960	0.021368	TERFGQGGAGPVGGQGPR
6.2	1726.867188	0.004140	KDHAEMQAVIDAKQK
3.5	1726.871216	0.000112	NLNTKLQMYFQSPK
1.9	1726.853485	0.017843	MASGHAFQPDLVK
1.1	1726.874573	-0.003245	VTKNQEMMSQIKYK

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 41586: 1746.900028 from(874.457290,2+) rtinseconds(2580) index(56406)

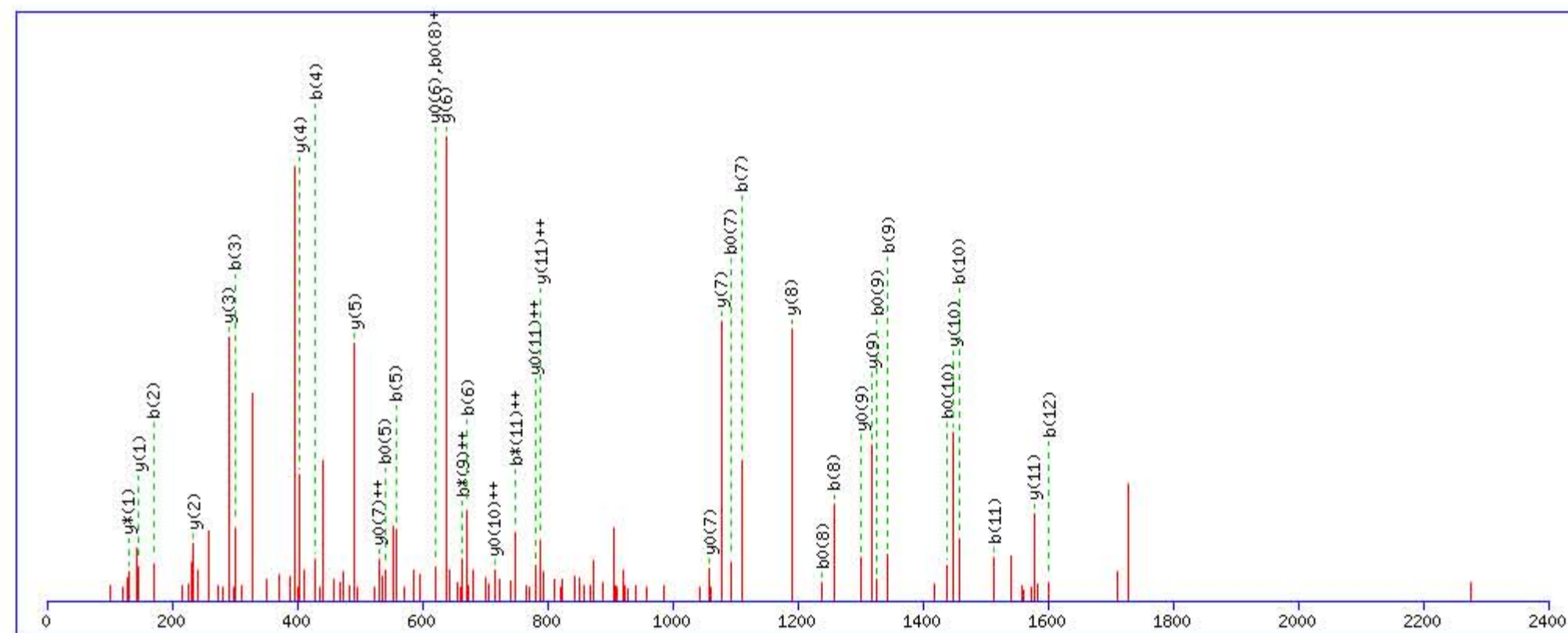
Title: Locus:1.1.1.1513.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1746.886200

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

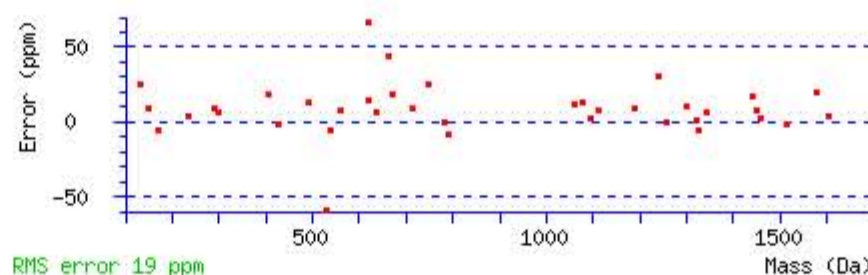
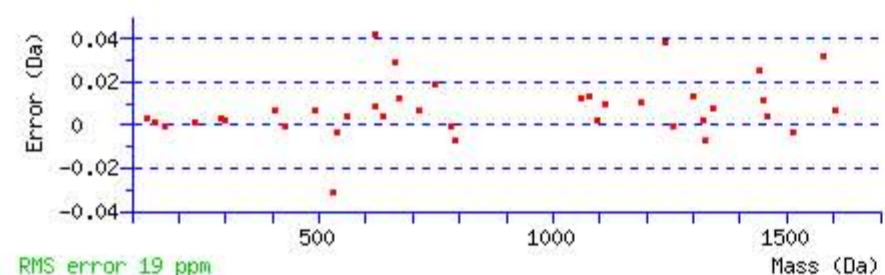
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 75 Expect: 1.9e-007

Matches : 38/126 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	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
74.7	1746.886200	0.013828	GLEEELQFSLGSK
2.9	1746.887558	0.012470	AVQSKAFCAGGLAPGWK
1.3	1746.918533	-0.018505	AKLQMTEAALALSEQK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VLSLAQEQVGGSP**EK

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 43649: 1851.979932 from(618.333920,3+) rtinseconds(2022) index(53085)

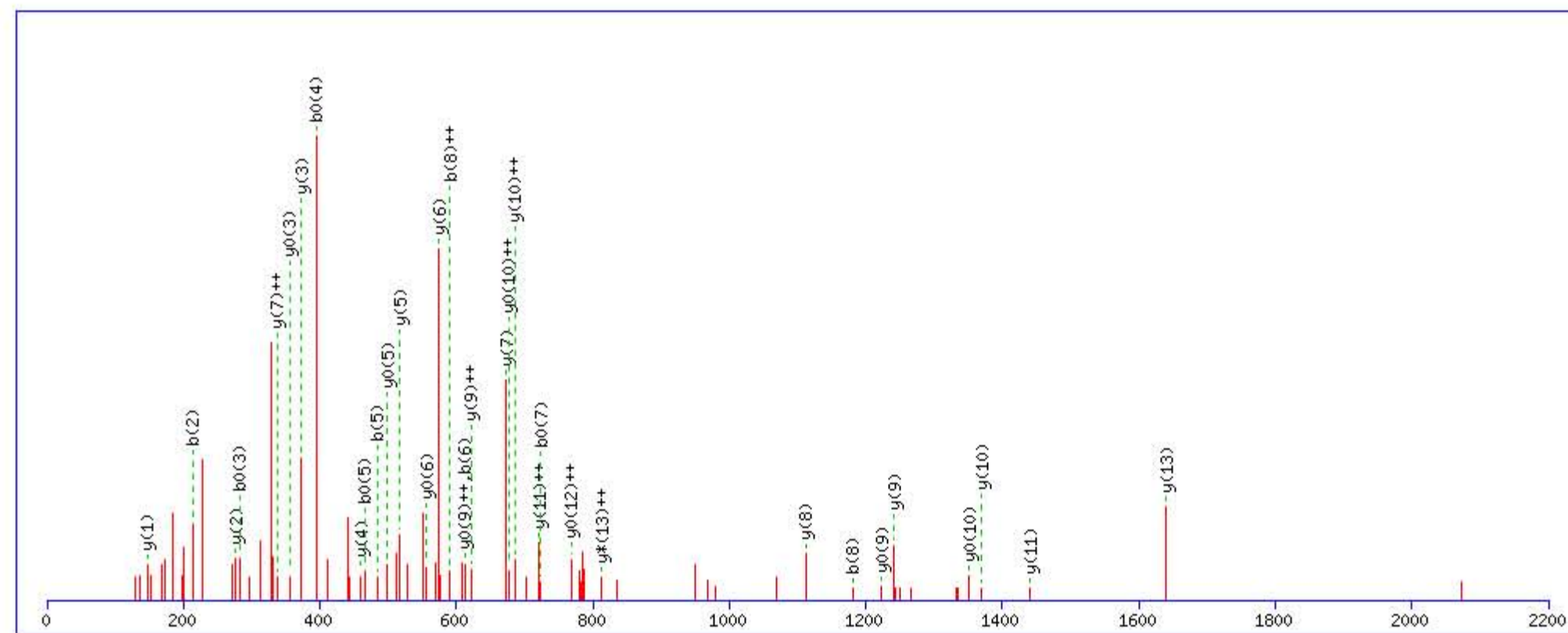
Title: Locus:1.1.1.1319.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1851.976425

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

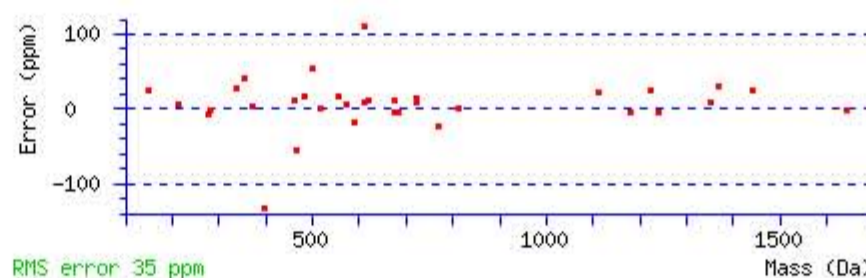
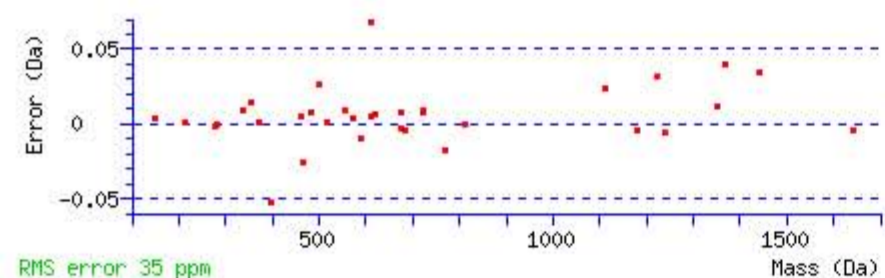
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 6.2e-006

Matches : 34/152 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	100.075690	50.541483					V							15
2	213.159754	107.083515					L	1753.915298	877.461287	1736.888749	868.948013	1735.904733	868.456004	14
3	300.191782	150.599529			282.181217	141.594247	S	1640.831234	820.919255	1623.804685	812.405981	1622.820669	811.913973	13
4	413.275846	207.141561			395.265281	198.136279	L	1553.799206	777.403241	1536.772657	768.889967	1535.788641	768.397958	12
5	484.312960	242.660118			466.302395	233.654836	A	1440.715142	720.861209	1423.688593	712.347935	1422.704577	711.855927	11
6	612.371538	306.689407	595.344989	298.176133	594.360973	297.684125	Q	1369.678028	685.342652	1352.651479	676.829378	1351.667463	676.337370	10
7	741.414131	371.210704	724.387582	362.697429	723.403566	362.205421	E	1241.619450	621.313363	1224.592901	612.800089	1223.608885	612.308080	9
8	1180.639457	590.823367	1163.612908	582.310092	1162.628892	581.818084	Q	1112.576857	556.792066	1095.550308	548.278792	1094.566292	547.786784	8
9	1279.707871	640.357574	1262.681322	631.844299	1261.697306	631.352291	V	673.351531	337.179404	656.324982	328.666129	655.340966	328.174121	7
10	1336.729335	668.868306	1319.702786	660.355031	1318.718770	659.863023	G	574.283117	287.645197	557.256568	279.131922	556.272552	278.639914	6
11	1393.750799	697.379037	1376.724250	688.865763	1375.740234	688.373755	G	517.261653	259.134465	500.235104	250.621190	499.251088	250.129182	5
12	1480.782827	740.895052	1463.756278	732.381777	1462.772262	731.889769	S	460.240189	230.623732	443.213640	222.110458	442.229624	221.618450	4
13	1577.835591	789.421434	1560.809042	780.908159	1559.825026	780.416151	P	373.208161	187.107718	356.181612	178.594444	355.197596	178.102436	3
14	1706.878184	853.942730	1689.851635	845.429456	1688.867619	844.937447	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
15							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **VLSLAQEQVGGSP**EK

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.0	1851.976425	0.003507	VLSLAQEQVGGSP EK
41.9	1851.976425	0.003507	VLSLAQEQVGGSP EK

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

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPEVQLVAHSPWLK**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 44158: 1871.022582 from(624.681470,3+) rtinseconds(2255) index(54583)

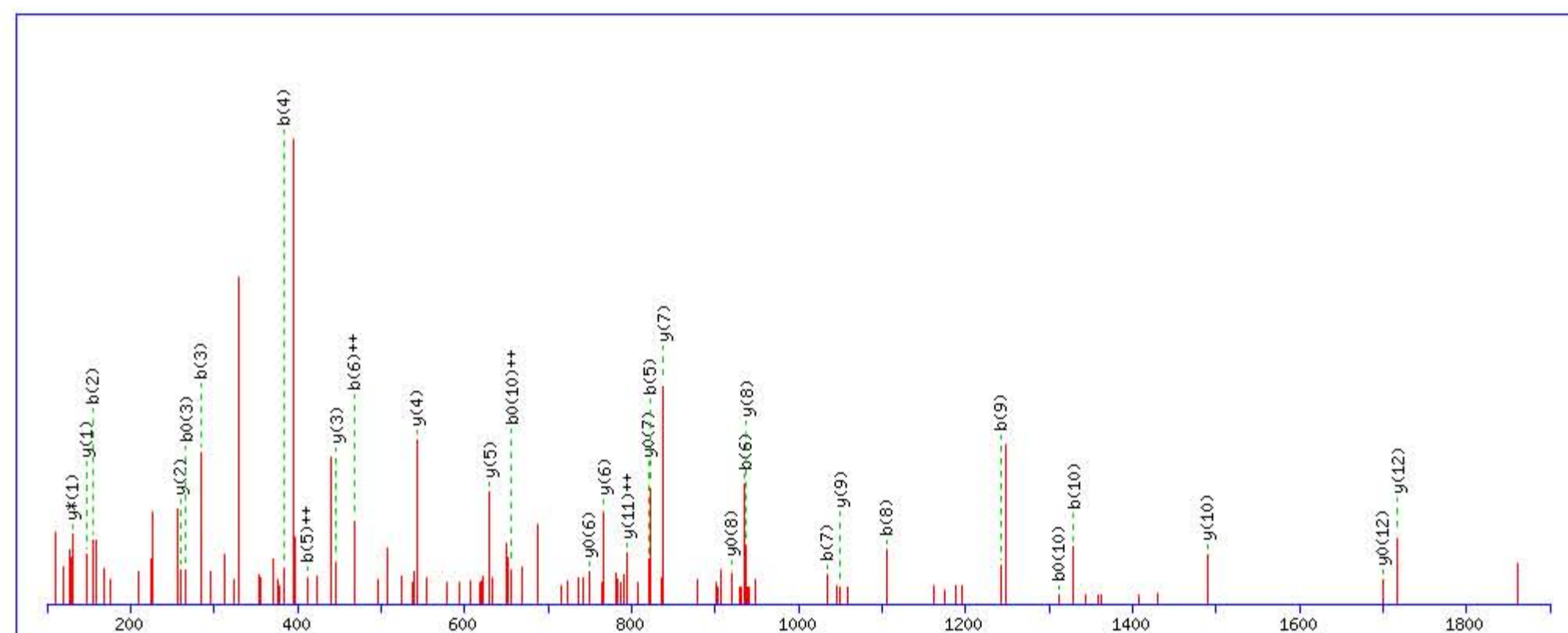
Title: Locus:1.1.1.1400.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1871.012756

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

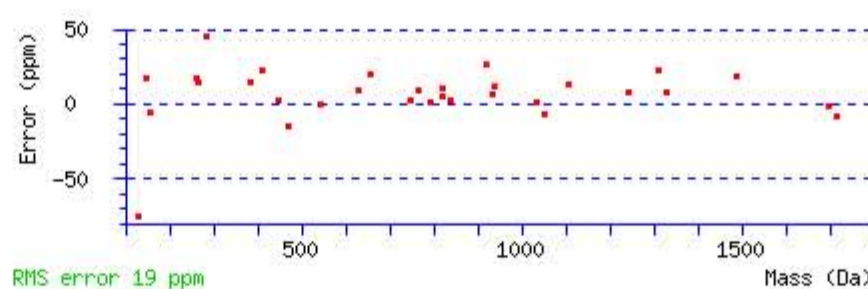
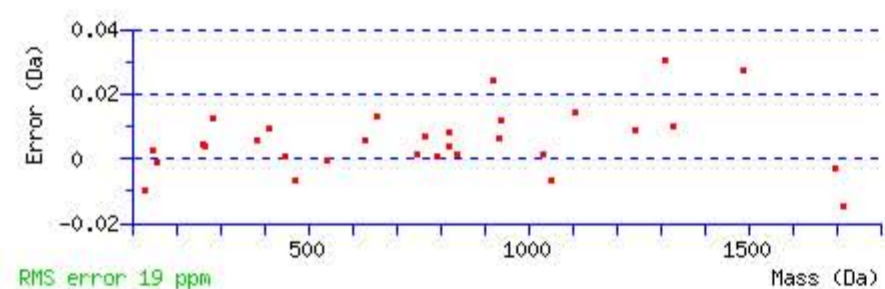
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 7.1e-005

Matches : 31/136 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	58.028740	29.518008					G							14
2	155.081504	78.044390					P	1814.998574	908.002925	1797.972025	899.489651	1796.988009	898.997643	13
3	284.124097	142.565687			266.113532	133.560404	E	1717.945810	859.476543	1700.919261	850.963269	1699.935245	850.471261	12
4	383.192511	192.099894			365.181946	183.094611	V	1588.903217	794.955247	1571.876668	786.441972	1570.892652	785.949964	11
5	822.417837	411.712557	805.391288	403.199282	804.407272	402.707274	Q	1489.834803	745.421040	1472.808254	736.907765	1471.824238	736.415757	10
6	935.501901	468.254589	918.475352	459.741314	917.491336	459.249306	L	1050.609477	525.808377	1033.582928	517.295102	1032.598912	516.803094	9
7	1034.570315	517.788796	1017.543766	509.275521	1016.559750	508.783513	V	937.525413	469.266345	920.498864	460.753070	919.514848	460.261062	8
8	1105.607429	553.307353	1088.580880	544.794078	1087.596864	544.302070	A	838.456999	419.732138	821.430450	411.218863	820.446434	410.726855	7
9	1242.666341	621.836809	1225.639792	613.323534	1224.655776	612.831526	H	767.419885	384.213581	750.393336	375.700306	749.409320	375.208298	6
10	1329.698369	665.352823	1312.671820	656.839548	1311.687804	656.347540	S	630.360973	315.684125	613.334424	307.170850	612.350408	306.678842	5
11	1426.751133	713.879205	1409.724584	705.365930	1408.740568	704.873922	P	543.328945	272.168111	526.302396	263.654836			4
12	1612.830446	806.918861	1595.803897	798.405587	1594.819881	797.913579	W	446.276181	223.641728	429.249632	215.128454			3
13	1725.914510	863.460893	1708.887961	854.947619	1707.903945	854.455611	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 **GPEVQLVAHSPWLK**

(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	1871.012756	0.009826	GPEVQLVAHSPWLK
1.8	1871.002686	0.019896	QRVLHWDLRGPGGGPAR
1.6	1870.994781	0.027801	NVNQAKLSEHRHK

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

MASCOT Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLVPGAPFLLQALVR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 45393: 1941.152712 from(648.058180,3+) rtinseconds(2868) index(58426)

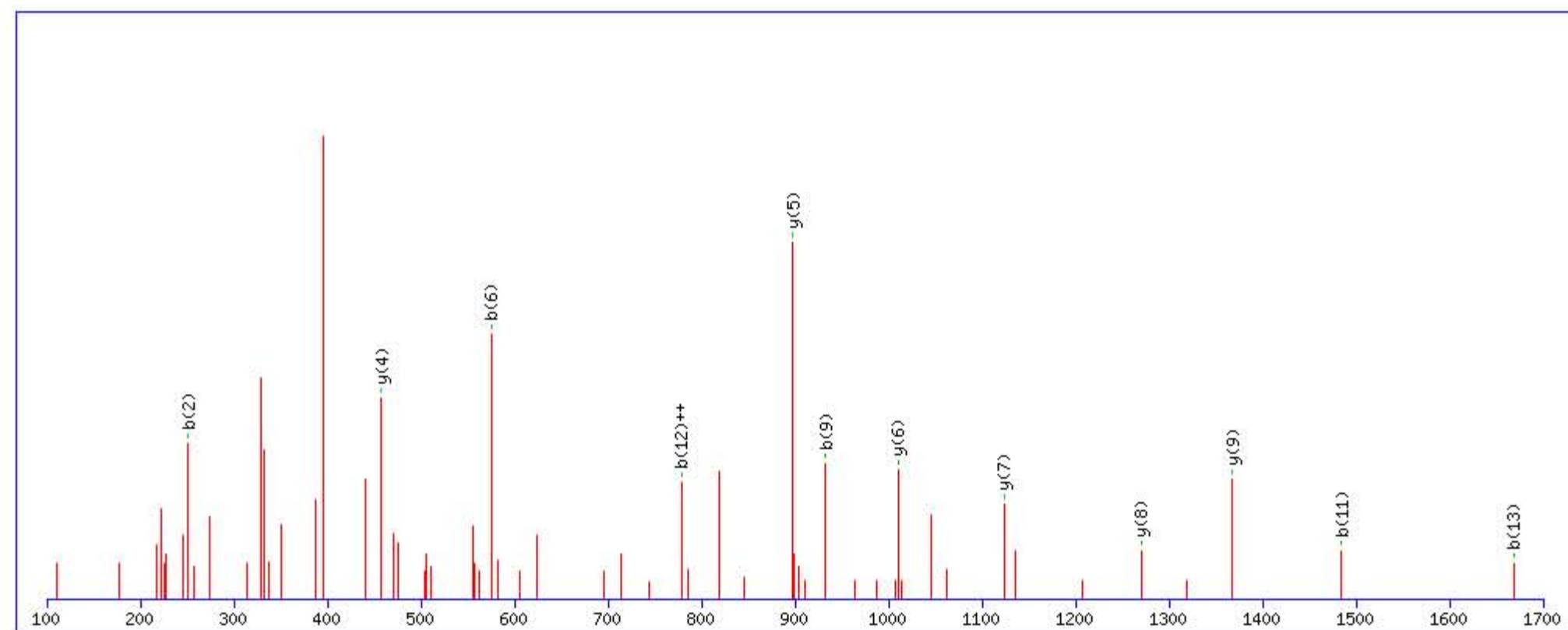
Title: Locus:1.1.1.1612.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1941.138626

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

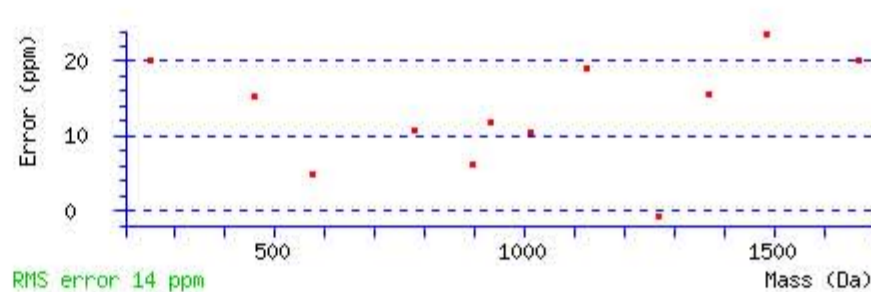
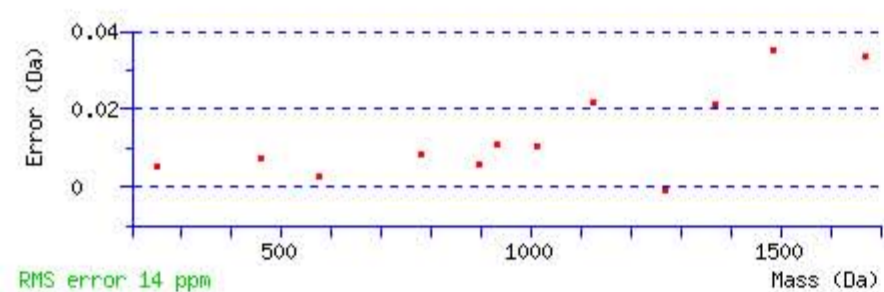
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 4.6e-005

Matches : 12/92 fragment ions using 15 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	138.066188	69.536732			H					15
2	251.150252	126.078764			L	1805.086996	903.047136	1788.060447	894.533862	14
3	350.218666	175.612971			V	1692.002932	846.505104	1674.976383	837.991830	13
4	447.271430	224.139353			P	1592.934518	796.970897	1575.907969	788.457623	12
5	504.292894	252.650085			G	1495.881754	748.444515	1478.855205	739.931241	11
6	575.330008	288.168642			A	1438.860290	719.933783	1421.833741	711.420509	10
7	672.382772	336.695024			P	1367.823176	684.415226	1350.796627	675.901952	9
8	819.451186	410.229231			F	1270.770412	635.888844	1253.743863	627.375570	8
9	932.535250	466.771263			L	1123.701998	562.354637	1106.675449	553.841363	7
10	1045.619314	523.313295			L	1010.617934	505.812605	993.591385	497.299331	6
11	1484.844640	742.925958	1467.818091	734.412684	Q	897.533870	449.270573	880.507321	440.757298	5
12	1555.881754	778.444515	1538.855205	769.931241	A	458.308544	229.657910	441.281995	221.144635	4
13	1668.965818	834.986547	1651.939269	826.473273	L	387.271430	194.139353	370.244881	185.626078	3
14	1768.034232	884.520754	1751.007683	876.007480	V	274.187366	137.597321	257.160817	129.084047	2
15					R	175.118952	88.063114	158.092403	79.549839	1



NCBI BLAST search of [HLVPGAPFLLQALVR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.9	1941.138626	0.014086	HLVPGAPFLLQALVR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **EPFLSCCQFAESLR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 48472: 2053.960542 from(685.660790,3+) rtinseconds(2519) index(56008)

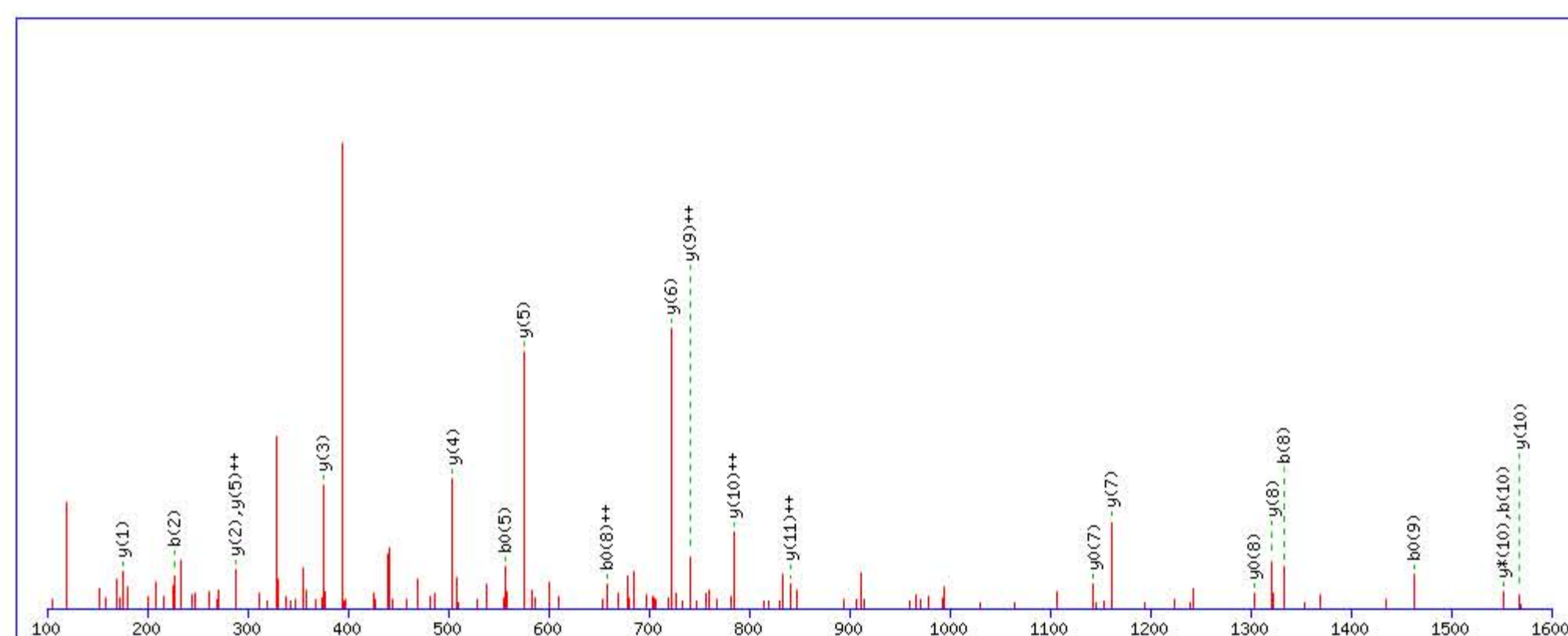
Title: Locus:1.1.1.1492.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2053.942368

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

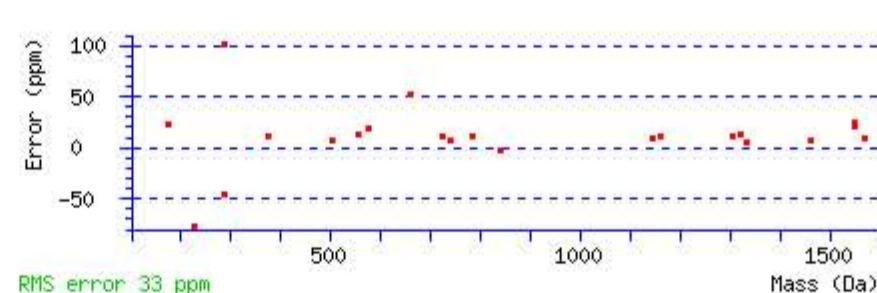
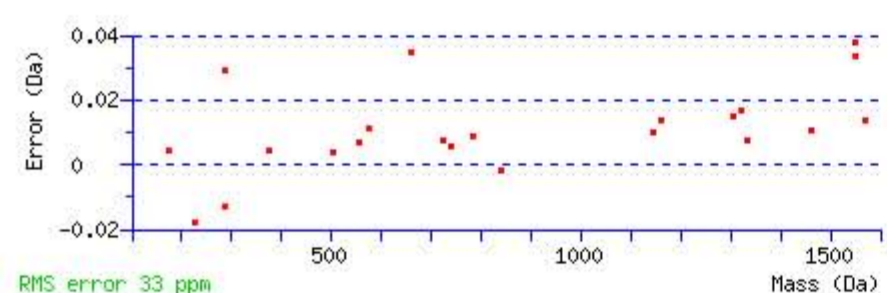
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.0012

Matches : 22/138 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							14
2	227.102633	114.054954			209.092068	105.049672	P	1925.907059	963.457168	1908.880510	954.943893	1907.896494	954.451885	13
3	374.171047	187.589161			356.160482	178.583879	F	1828.854295	914.930786	1811.827746	906.417511	1810.843730	905.925503	12
4	487.255111	244.131193			469.244546	235.125911	L	1681.785881	841.396579	1664.759332	832.883304	1663.775316	832.391296	11
5	574.287139	287.647208			556.276574	278.641925	S	1568.701817	784.854547	1551.675268	776.341272	1550.691252	775.849264	10
6	734.317788	367.662532			716.307223	358.657250	C	1481.669789	741.338533	1464.643240	732.825258	1463.659224	732.333250	9
7	894.348437	447.677857			876.337872	438.672574	C	1321.639140	661.323208	1304.612591	652.809934	1303.628575	652.317926	8
8	1333.573763	667.290520	1316.547214	658.777245	1315.563198	658.285237	Q	1161.608491	581.307884	1144.581942	572.794609	1143.597926	572.302601	7
9	1480.642177	740.824727	1463.615628	732.311452	1462.631612	731.819444	F	722.383165	361.695221	705.356616	353.181946	704.372600	352.689938	6
10	1551.679291	776.343284	1534.652742	767.830009	1533.668726	767.338001	A	575.314751	288.161014	558.288202	279.647739	557.304186	279.155731	5
11	1680.721884	840.864580	1663.695335	832.351306	1662.711319	831.859298	E	504.277637	252.642457	487.251088	244.129182	486.267072	243.637174	4
12	1767.753912	884.380594	1750.727363	875.867320	1749.743347	875.375312	S	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
13	1880.837976	940.922626	1863.811427	932.409352	1862.827411	931.917344	L	288.203016	144.605146	271.176467	136.091871			2
14							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **EPFLSCCQFAESLR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	2053.942368	0.018174	EPFLSCCQFAESLR

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 51483: 2220.042522 from(741.021450,3+) rtinseconds(2119) index(69497)

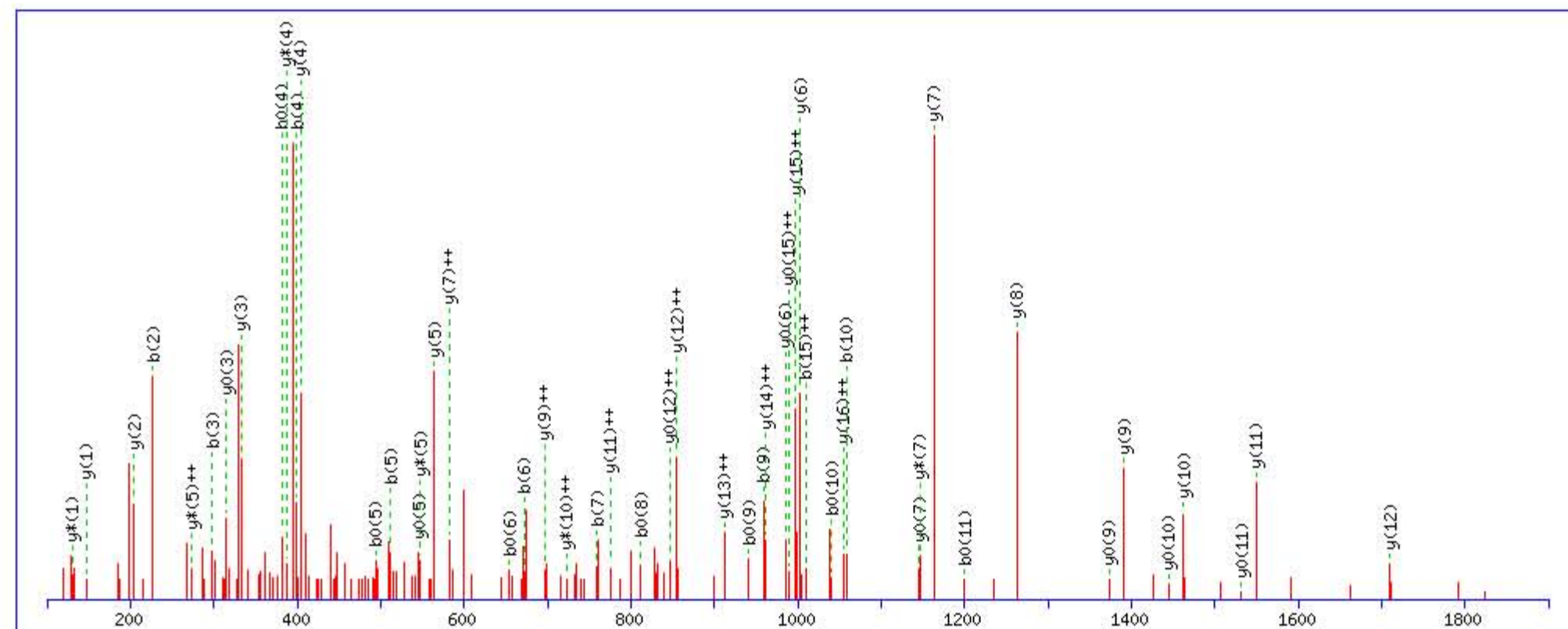
Title: Locus:1.1.1.1675.13 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2220.041092

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

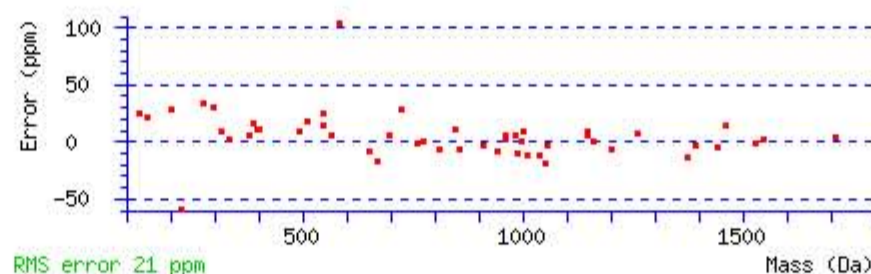
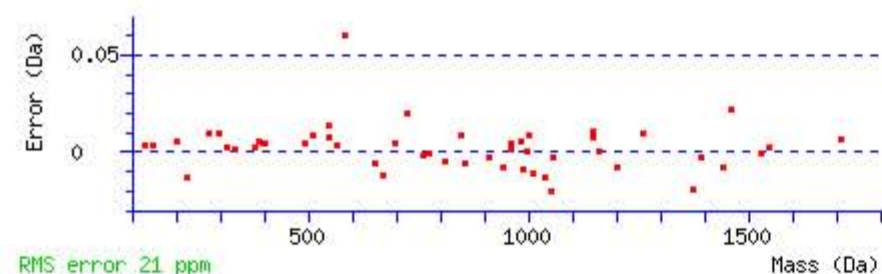
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 54 Expect: 1e-005

Matches : 51/160 fragment ions using 110 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
53.8	2220.041092	0.001430	LLATLCSAEVCQCAEGK
0.5	2220.048080	-0.005558	EPQEGAELPEATGTTSHR

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GCGEQTMIIYLAPTLAASR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 51975: 2249.122692 from(750.714840,3+) rtinseconds(2546) index(56228)

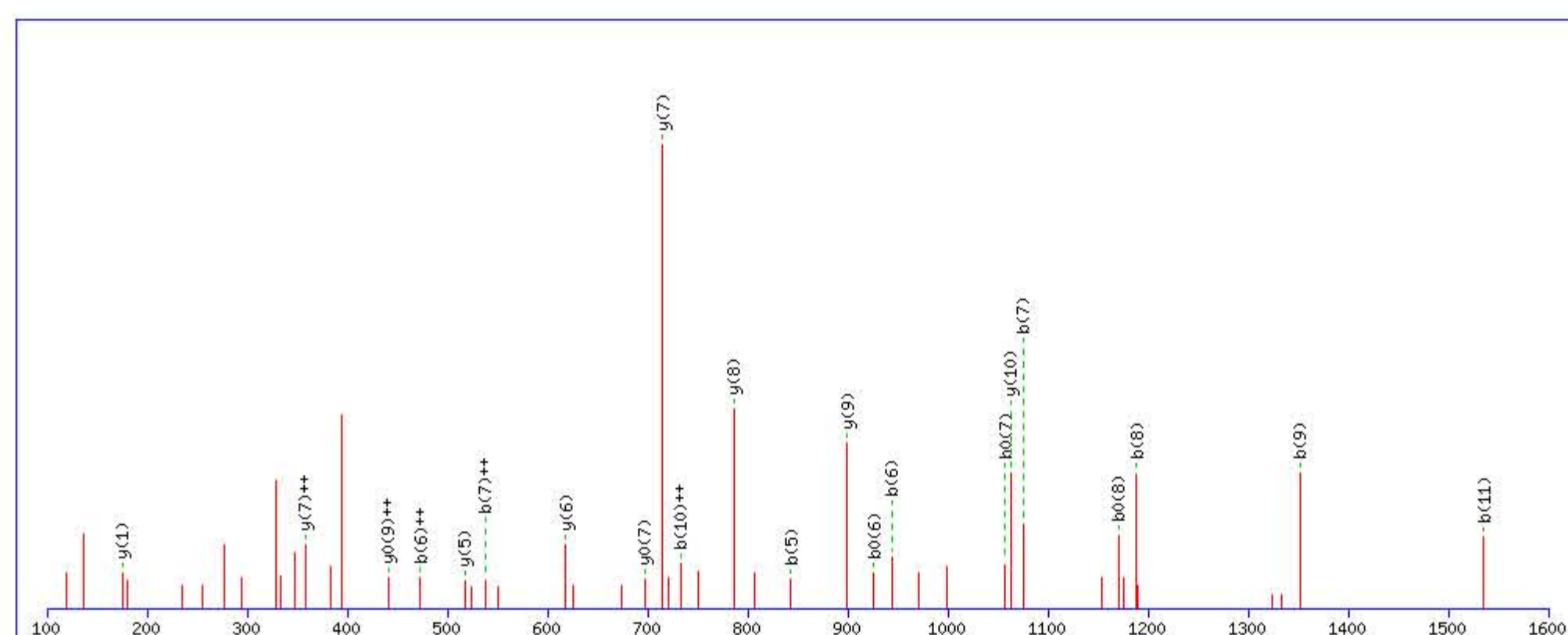
Title: Locus:1.1.1.1501.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2249.100647

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

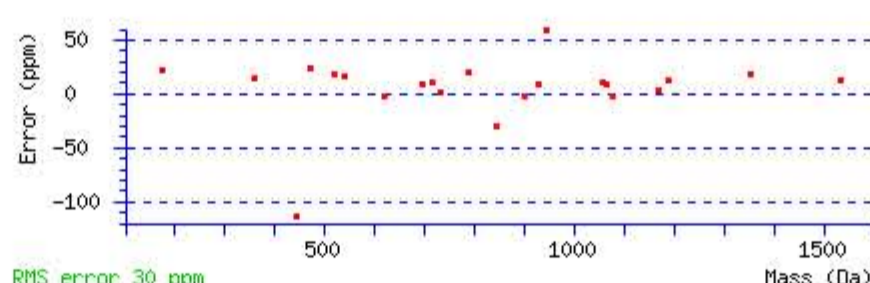
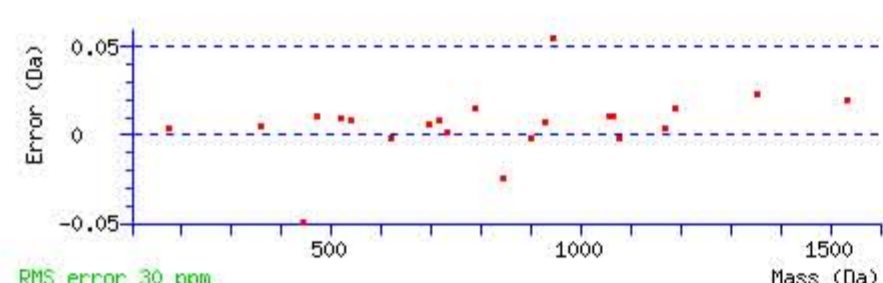
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 42 Expect: 0.00086

Matches : 22/188 fragment ions using 36 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							18
2	218.059389	109.533333					C	2193.086482	1097.046879	2176.059933	1088.533604	2175.075917	1088.041596	17
3	275.080853	138.044064					G	2033.055833	1017.031555	2016.029284	1008.518280	2015.045268	1008.026272	16
4	404.123446	202.565361			386.112881	193.560079	E	1976.034369	988.520822	1959.007820	980.007548	1958.023804	979.515540	15
5	843.348772	422.178024	826.322223	413.664750	825.338207	413.172742	Q	1846.991776	923.999526	1829.965227	915.486251	1828.981211	914.994243	14
6	944.396451	472.701864	927.369902	464.188589	926.385886	463.696581	T	1407.766450	704.386863	1390.739901	695.873588	1389.755885	695.381580	13
7	1075.436936	538.222106	1058.410387	529.708832	1057.426371	529.216824	M	1306.718771	653.863023	1289.692222	645.349749	1288.708206	644.857741	12
8	1188.521000	594.764138	1171.494451	586.250864	1170.510435	585.758855	I	1175.678286	588.342781	1158.651737	579.829506	1157.667721	579.337498	11
9	1351.584329	676.295803	1334.557780	667.782528	1333.573764	667.290520	Y	1062.594222	531.800749	1045.567673	523.287475	1044.583657	522.795466	10
10	1464.668393	732.837834	1447.641844	724.324560	1446.657828	723.832552	L	899.530893	450.269084	882.504344	441.755810	881.520328	441.263802	9
11	1535.705507	768.356391	1518.678958	759.843117	1517.694942	759.351109	A	786.446829	393.727053	769.420280	385.213778	768.436264	384.721770	8
12	1632.758271	816.882773	1615.731722	808.369499	1614.747706	807.877491	P	715.409715	358.208496	698.383166	349.695221	697.399150	349.203213	7
13	1733.805950	867.406613	1716.779401	858.893339	1715.795385	858.401330	T	618.356951	309.682114	601.330402	301.168839	600.346386	300.676831	6
14	1846.890014	923.948645	1829.863465	915.435370	1828.879449	914.943362	L	517.309272	259.158274	500.282723	250.644999	499.298707	250.152991	5
15	1917.927128	959.467202	1900.900579	950.953927	1899.916563	950.461919	A	404.225208	202.616242	387.198659	194.102967	386.214643	193.610959	4
16	1988.964242	994.985759	1971.937693	986.472484	1970.953677	985.980476	A	333.188094	167.097685	316.161545	158.584410	315.177529	158.092402	3
17	2075.996270	1038.501773	2058.969721	1029.988498	2057.985705	1029.496490	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
18							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **GCGEQTMIIYLAPTLAASR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.7	2249.100647	0.022045	GCGEQTMIIYLAPTLAASR
8.5	2249.115051	0.007641	YSTSLYASPSMVHEGVAVVPR
4.1	2249.104492	0.018200	AQLQQHNLEMVGEGRQ
1.0	2249.143570	-0.020878	TPPPQPPLISSMDSISQK
0.8	2249.089874	0.032818	EMIDIYSTREPQLAFHQ
0.6	2249.150742	-0.028050	LRSIMMSQDLENVTSKEIR
0.5	2249.137527	-0.014835	QKFERPICVSWSTDVKGGR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **DDPDAPLQPVTPLQLFEGR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 54809: 2418.243612 from(807.088480,3+) rtinseconds(3020) index(59691)

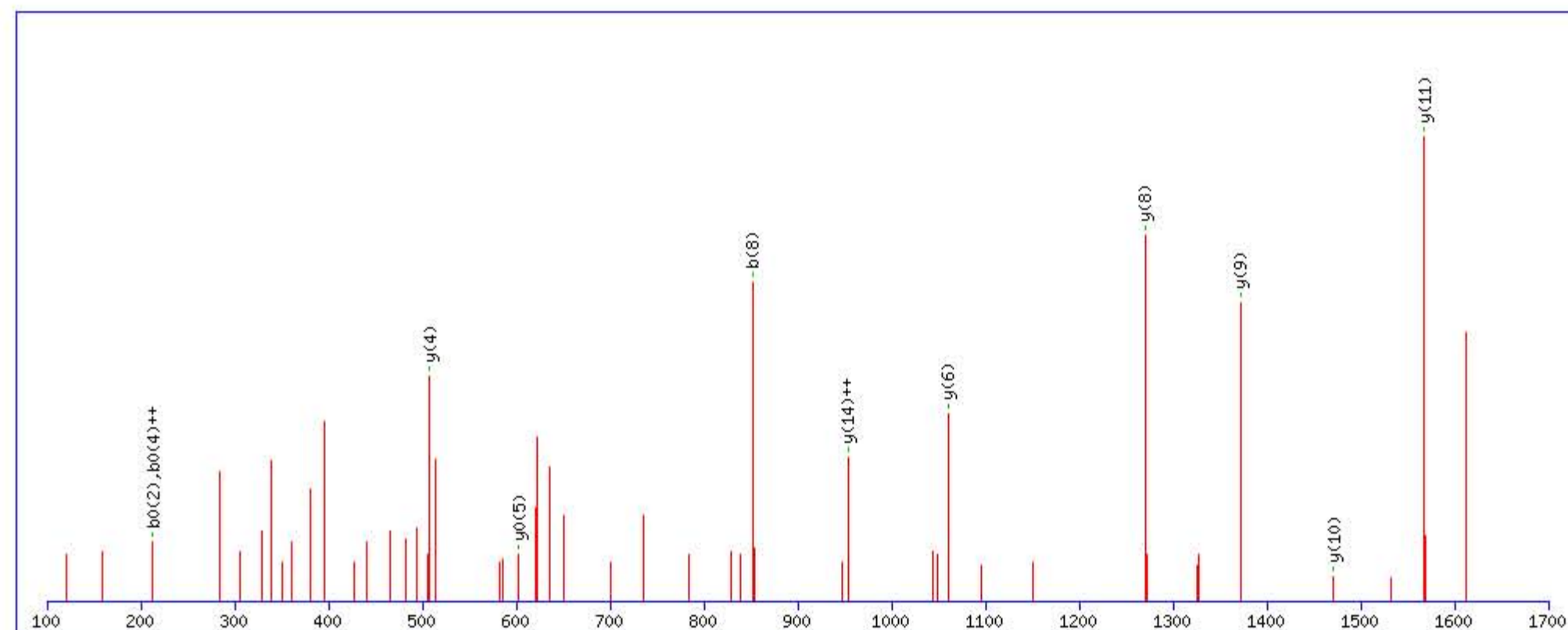
Title: Locus:1.1.1.1663.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2418.225342

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

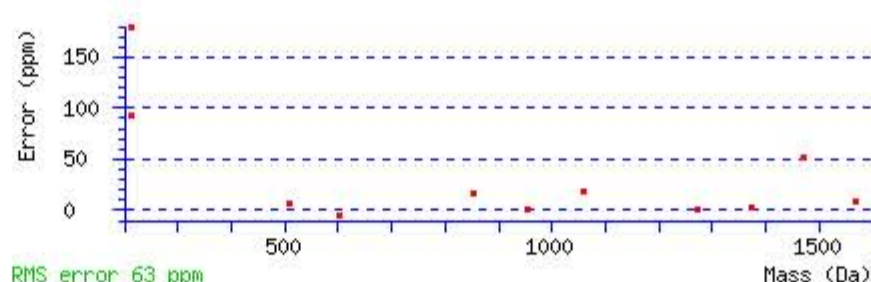
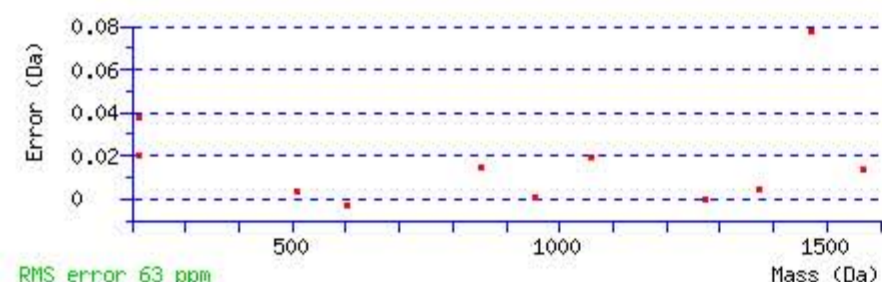
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.051

Matches : 11/198 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	116.034219	58.520748			98.023654	49.515465	D							19
2	231.061162	116.034219			213.050597	107.028936	D	2304.205668	1152.606472	2287.179119	1144.093197	2286.195103	1143.601189	18
3	328.113926	164.560601			310.103361	155.555319	P	2189.178725	1095.093000	2172.152176	1086.579726	2171.168160	1086.087718	17
4	443.140869	222.074073			425.130304	213.068790	D	2092.125961	1046.566618	2075.099412	1038.053344	2074.115396	1037.561336	16
5	514.177983	257.592630			496.167418	248.587347	A	1977.099018	989.053147	1960.072469	980.539873	1959.088453	980.047865	15
6	611.230747	306.119012			593.220182	297.113729	P	1906.061904	953.534590	1889.035355	945.021316	1888.051339	944.529308	14
7	724.314811	362.661044			706.304246	353.655761	L	1809.009140	905.008208	1791.982591	896.494934	1790.998575	896.002926	13
8	852.373389	426.690333	835.346840	418.177058	834.362824	417.685050	Q	1695.925076	848.466176	1678.898527	839.952902	1677.914511	839.460894	12
9	949.426153	475.216715	932.399604	466.703440	931.415588	466.211432	P	1567.866498	784.436887	1550.839949	775.923613	1549.855933	775.431605	11
10	1048.494567	524.750922	1031.468018	516.237647	1030.484002	515.745639	V	1470.813734	735.910505	1453.787185	727.397231	1452.803169	726.905223	10
11	1149.542246	575.274761	1132.515697	566.761487	1131.531681	566.269479	T	1371.745320	686.376298	1354.718771	677.863024	1353.734755	677.371016	9
12	1246.595010	623.801143	1229.568461	615.287869	1228.584445	614.795861	P	1270.697641	635.852459	1253.671092	627.339184	1252.687076	626.847176	8
13	1359.679074	680.343175	1342.652525	671.829901	1341.668509	671.337893	L	1173.644877	587.326077	1156.618328	578.812802	1155.634312	578.320794	7
14	1798.904400	899.955838	1781.877851	891.442564	1780.893835	890.950556	Q	1060.560813	530.784045	1043.534264	522.270770	1042.550248	521.778762	6
15	1911.988464	956.497870	1894.961915	947.984596	1893.977899	947.492588	L	621.335487	311.171382	604.308938	302.658107	603.324922	302.166099	5
16	2059.056878	1030.032077	2042.030329	1021.518803	2041.046313	1021.026794	F	508.251423	254.629350	491.224874	246.116075	490.240858	245.624067	4
17	2188.099471	1094.553373	2171.072922	1086.040099	2170.088906	1085.548091	E	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	3
18	2245.120935	1123.064105	2228.094386	1114.550831	2227.110370	1114.058823	G	232.140416	116.573846	215.113867	108.060571			2
19							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [DDPDAPLQPVTPLQLFEGR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.1	2418.225342	0.018270	DDPDAPLQPVTPLQLFEGR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AACAQLNDFLQEYGTQGCQV**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 57447: 2583.179442 from(862.067090,3+) rtinseconds(2758) index(57495)

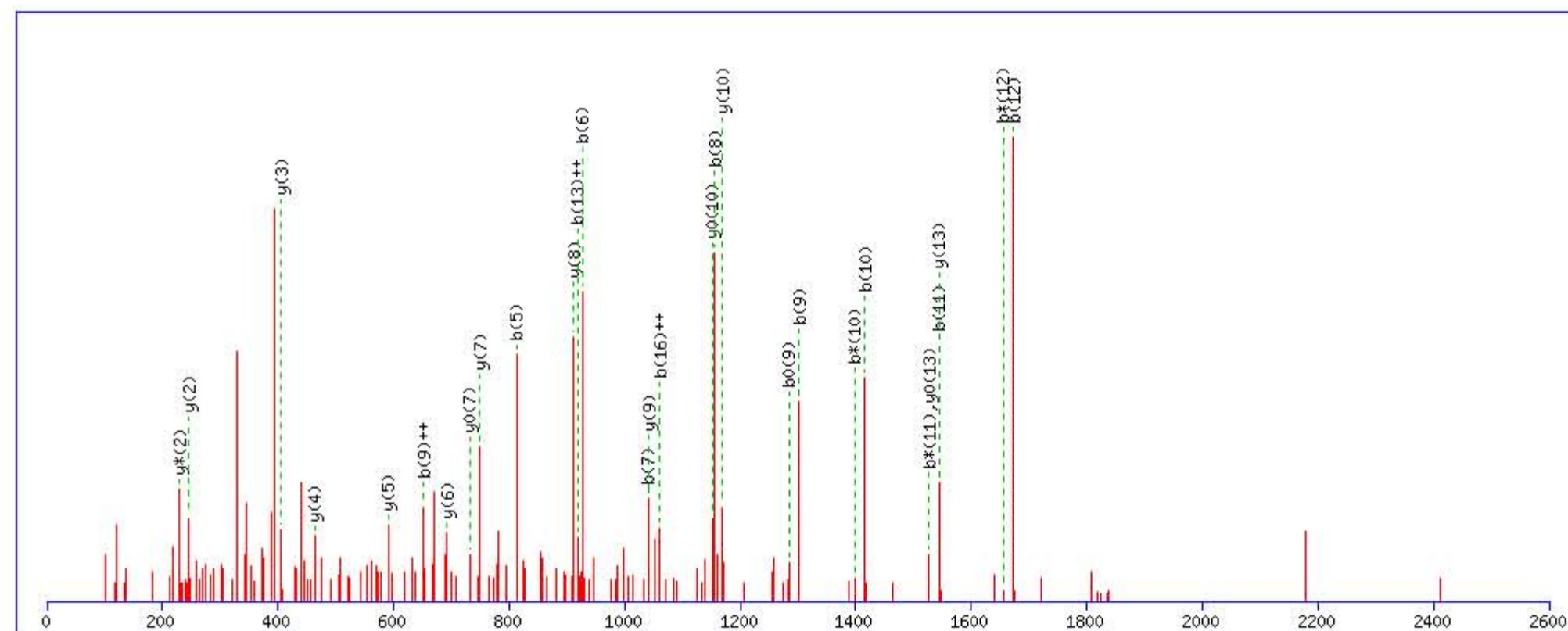
Title: Locus:1.1.1.1574.25 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2583.155624

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

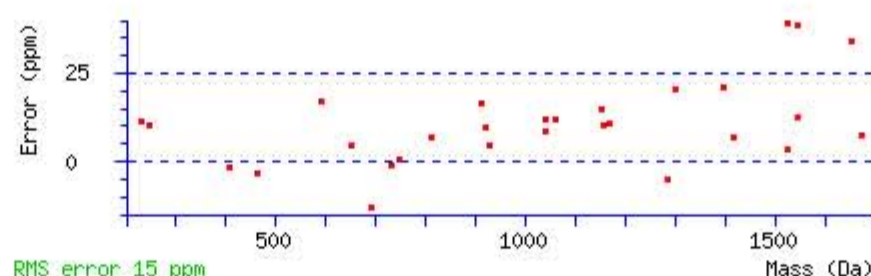
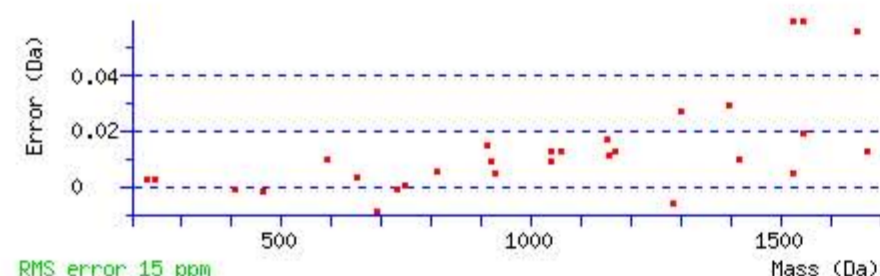
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 54 Expect: 4.4e-005

Matches : 29/194 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	72.044390	36.525833					A							20
2	143.081504	72.044390					A	2513.125782	1257.066529	2496.099233	1248.553254	2495.115217	1248.061246	19
3	303.112153	152.059714					C	2442.088668	1221.547972	2425.062119	1213.034697	2424.078103	1212.542689	18
4	374.149267	187.578271					A	2282.058019	1141.532647	2265.031470	1133.019373	2264.047454	1132.527365	17
5	813.374593	407.190935	796.348044	398.677660			Q	2211.020905	1106.014090	2193.994356	1097.500816	2193.010340	1097.008808	16
6	926.458657	463.732967	909.432108	455.219692			L	1771.795579	886.401428	1754.769030	877.888153	1753.785014	877.396145	15
7	1040.501584	520.754430	1023.475035	512.241155			N	1658.711515	829.859396	1641.684966	821.346121	1640.700950	820.854113	14
8	1155.528527	578.267902	1138.501978	569.754627	1137.517962	569.262619	D	1544.668588	772.837932	1527.642039	764.324658	1526.658023	763.832650	13
9	1302.596941	651.802109	1285.570392	643.288834	1284.586376	642.796826	F	1429.641645	715.324460	1412.615096	706.811186	1411.631080	706.319178	12
10	1415.681005	708.344141	1398.654456	699.830866	1397.670440	699.338858	L	1282.573231	641.790253	1265.546682	633.276979	1264.562666	632.784971	11
11	1543.739583	772.373430	1526.713034	763.860155	1525.729018	763.368147	Q	1169.489167	585.248222	1152.462618	576.734947	1151.478602	576.242939	10
12	1672.782176	836.894726	1655.755627	828.381452	1654.771611	827.889444	E	1041.430589	521.218932	1024.404040	512.705658	1023.420024	512.213650	9
13	1835.845505	918.426391	1818.818956	909.913116	1817.834940	909.421108	Y	912.387996	456.697636	895.361447	448.184361	894.377431	447.692353	8
14	1892.866969	946.937123	1875.840420	938.423848	1874.856404	937.931840	G	749.324667	375.165971	732.298118	366.652697	731.314102	366.160689	7
15	1993.914648	997.460962	1976.888099	988.947688	1975.904083	988.455680	T	692.303203	346.655239	675.276654	338.141965	674.292638	337.649957	6
16	2121.973226	1061.490251	2104.946677	1052.976976	2103.962661	1052.484968	Q	591.255524	296.131400	574.228975	287.618125			5
17	2178.994690	1090.000983	2161.968141	1081.487708	2160.984125	1080.995700	G	463.196946	232.102111	446.170397	223.588836			4
18	2339.025339	1170.016307	2321.998790	1161.503033	2321.014774	1161.011025	C	406.175482	203.591379	389.148933	195.078104			3
19	2467.083917	1234.045596	2450.057368	1225.532322	2449.073352	1225.040314	Q	246.144833	123.576054	229.118284	115.062780			2
20							V	118.086255	59.546765					1



NCBI BLAST search of [AACAQLNDFLQEYGTQGCQV](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.1	2583.155624	0.023818	AACAQLNDFLQEYGTQGCQV
16.9	2583.155624	0.023818	AACAQLNDFLQEYGTQGCQV

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQAGLQR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 17300: 1039.555588 from(520.785070,2+) rtinseconds(1467) index(49286)

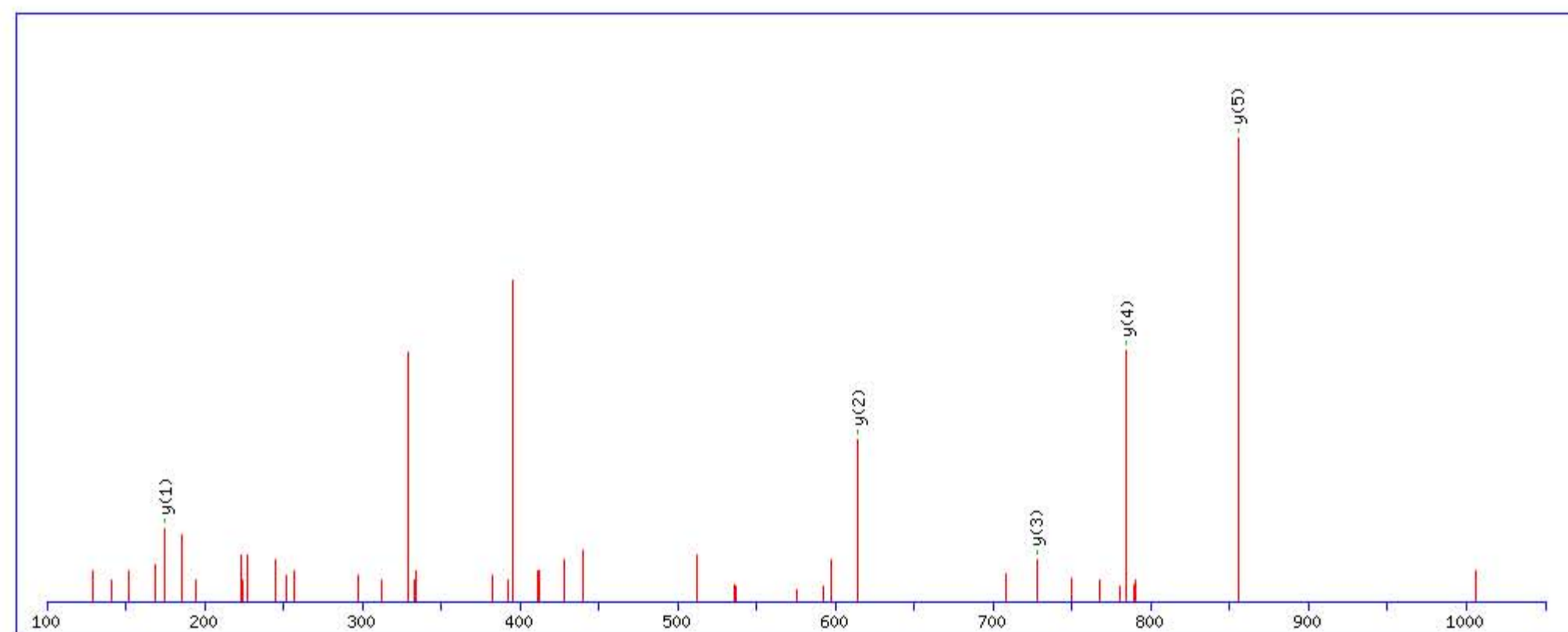
Title: Locus:1.1.1.1126.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1039.559677

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

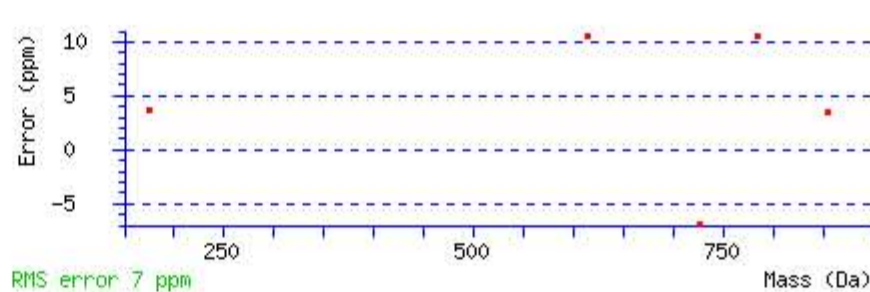
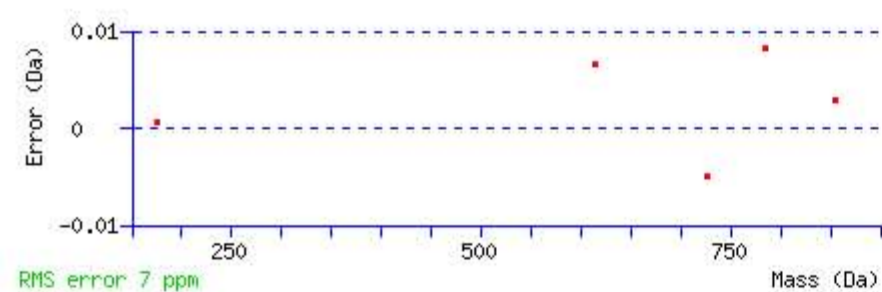
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 34 Expect: 0.0068

Matches : 5/46 fragment ions using 9 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	58.028740	29.518008			G					7
2	186.087318	93.547297	169.060769	85.034023	Q	983.545498	492.276387	966.518949	483.763113	6
3	257.124432	129.065854	240.097883	120.552580	A	855.486920	428.247098	838.460371	419.733824	5
4	314.145896	157.576586	297.119347	149.063312	G	784.449806	392.728541	767.423257	384.215267	4
5	427.229960	214.118618	410.203411	205.605344	L	727.428342	364.217809	710.401793	355.704535	3
6	866.455286	433.731281	849.428737	425.218007	Q	614.344278	307.675777	597.317729	299.162503	2
7					R	175.118952	88.063114	158.092403	79.549840	1



NCBI BLAST search of [GQAGLQR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.5	1039.559677	-0.004089	GQAGLQR
19.5	1039.559677	-0.004089	GQQIQR
9.5	1039.559677	-0.004089	KGGPSQR
7.8	1039.541061	0.014527	GQGDLLQPGR
5.5	1039.552277	0.003311	QRAALDGGPR
5.2	1039.548431	0.007157	SPEIQR
3.2	1039.541046	0.014542	NATTAPNPVR
1.8	1039.563522	-0.007934	ARRGGDGVPR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GLESQTK**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 18125: 1072.558368 from(537.286460,2+) rtinseconds(1491) index(49479)

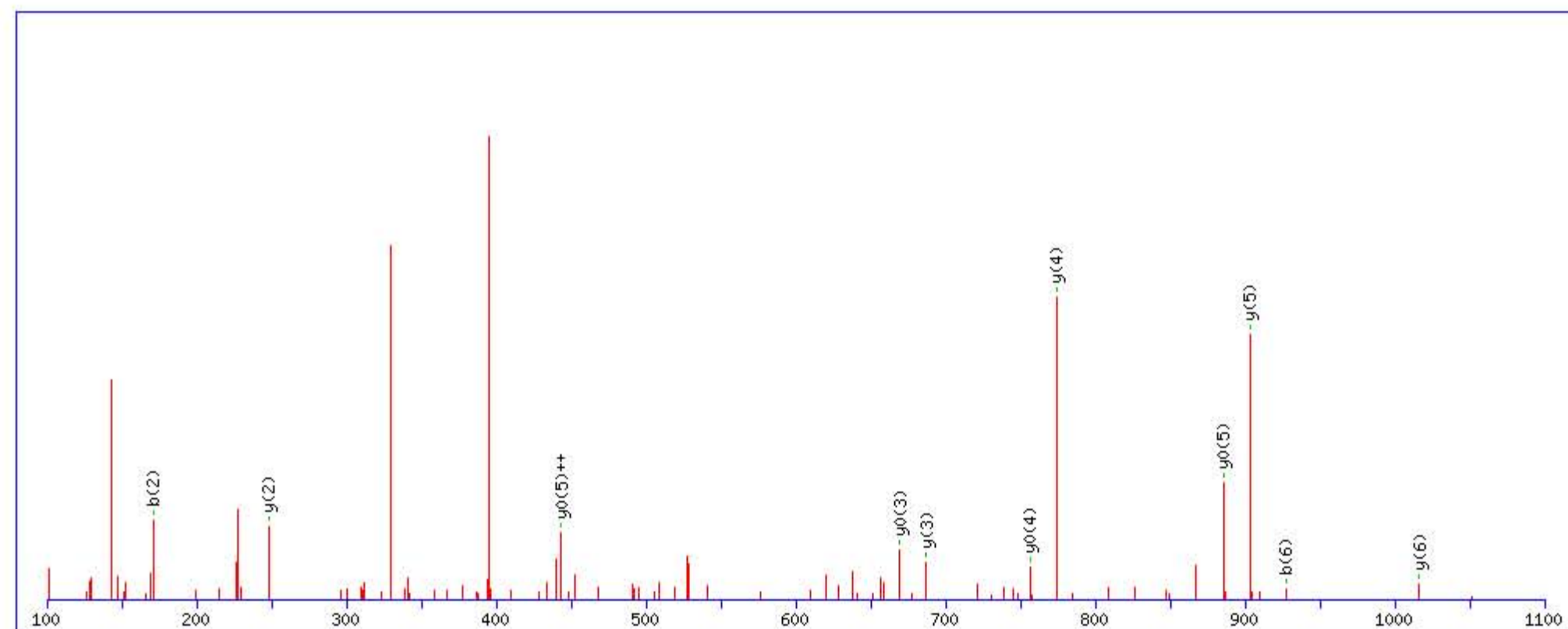
Title: Locus:1.1.1.1134.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1072.558670

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

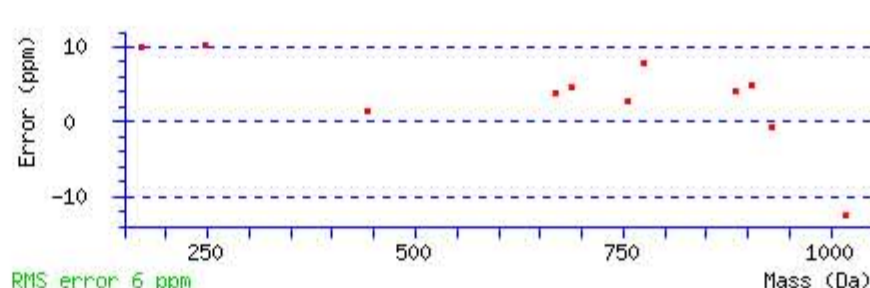
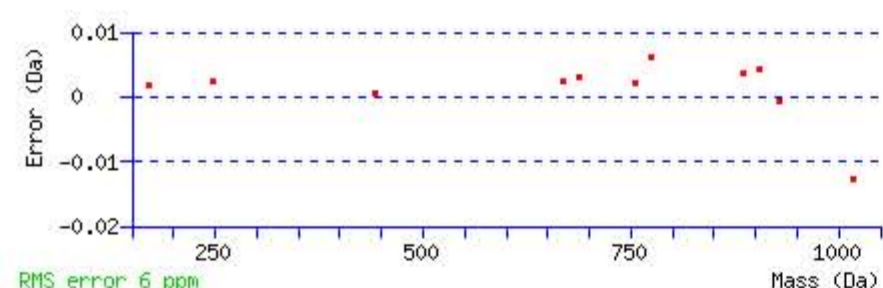
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 29 Expect: 0.011

Matches : 11/58 fragment ions using 20 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							7
2	171.112804	86.060040					L	1016.544494	508.775885	999.517945	500.262611	998.533929	499.770603	6
3	300.155397	150.581336			282.144832	141.576054	E	903.460430	452.233853	886.433881	443.720579	885.449865	443.228571	5
4	387.187425	194.097351			369.176860	185.092068	S	774.417837	387.712557	757.391288	379.199282	756.407272	378.707274	4
5	826.412751	413.710014	809.386202	405.196739	808.402186	404.704731	Q	687.385809	344.196543	670.359260	335.683268	669.375244	335.191260	3
6	927.460430	464.233853	910.433881	455.720579	909.449865	455.228571	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
7							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **GLESQTK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
29.2	1072.558670	-0.000302	GLESQTK
7.9	1072.558670	-0.000302	QSEGLTK
7.2	1072.558670	-0.000302	LGECPAVLSK
7.0	1072.551254	0.007114	KEAPRDETK
3.8	1072.551285	0.007083	GPRTTEPSTK
0.4	1072.566559	-0.008191	VQIHFGGSTK
0.3	1072.544739	0.013629	LGEPQARMR

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 23594: 1212.574068 from(607.294310,2+) rtinseconds(1319) index(48351)

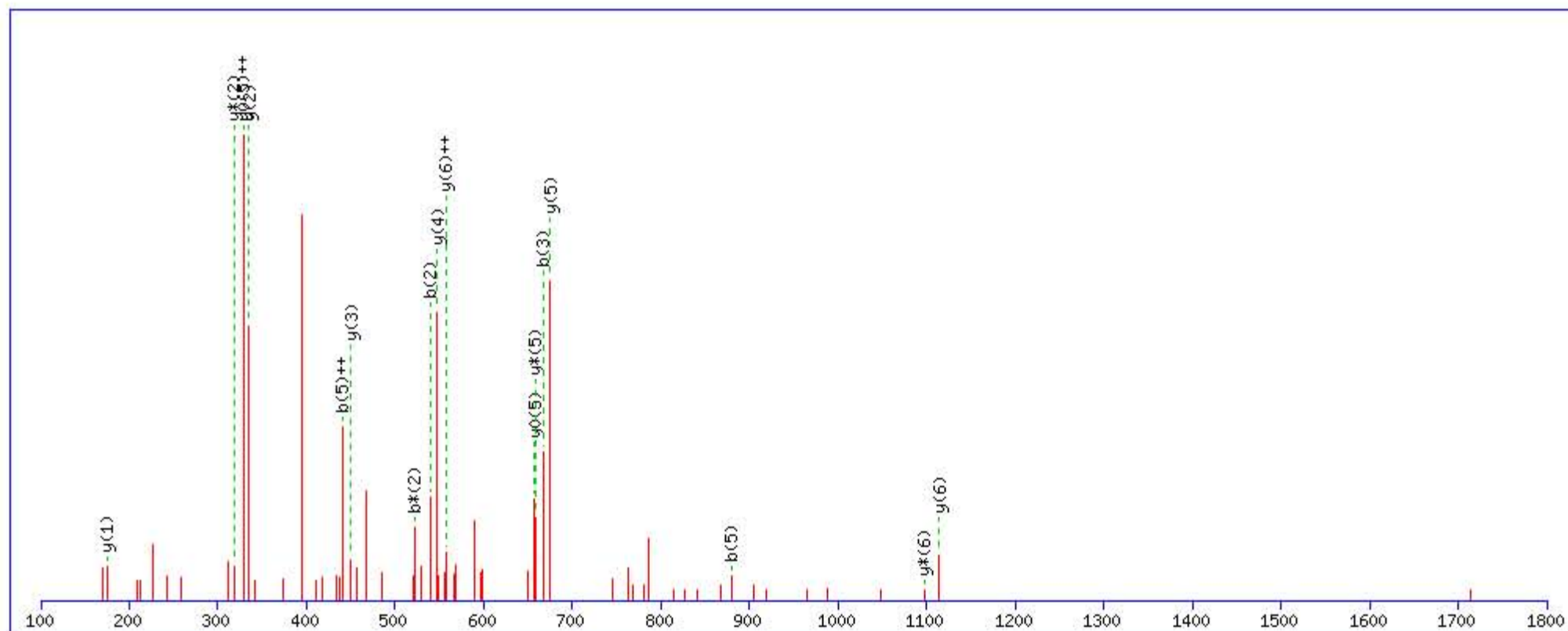
Title: Locus:1.1.1.1074.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1212.574356

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

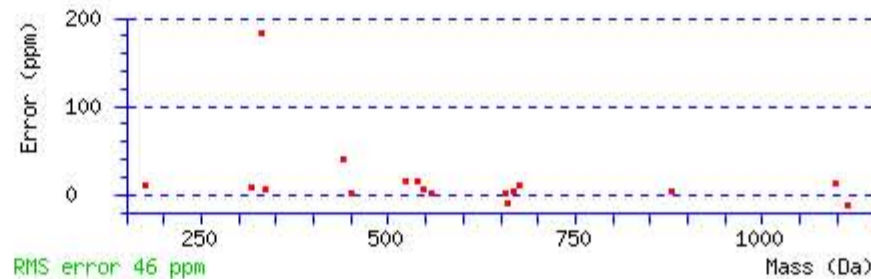
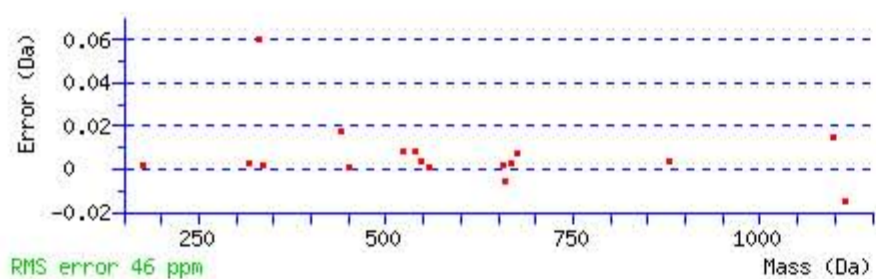
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.0052

Matches : 17/58 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	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
29.6	1212.574356	-0.000288	VQQPDCR
12.6	1212.574356	-0.000288	VQQPDCR
5.2	1212.592102	-0.018034	VQEDQQR

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 25584: 1279.667348 from(640.840950,2+) rtinseconds(2022) index(53086)

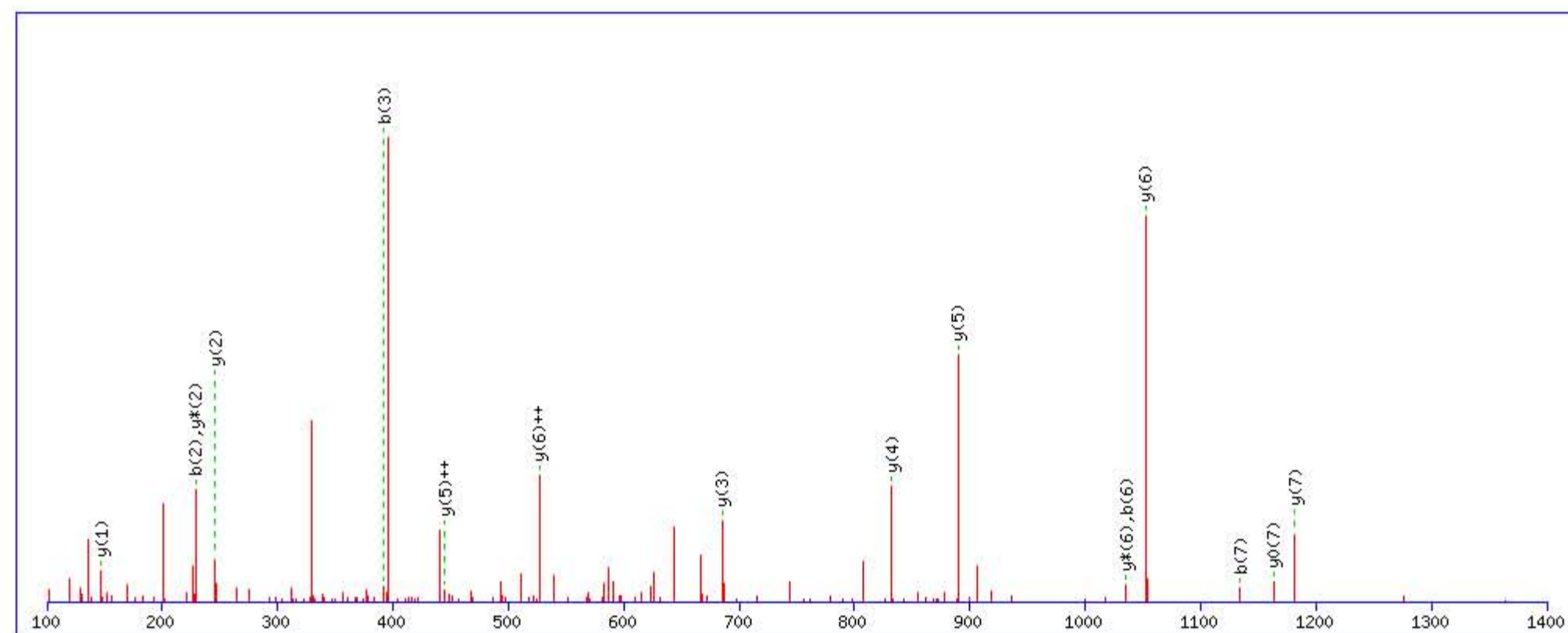
Title: Locus:1.1.1.1319.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1279.663483

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

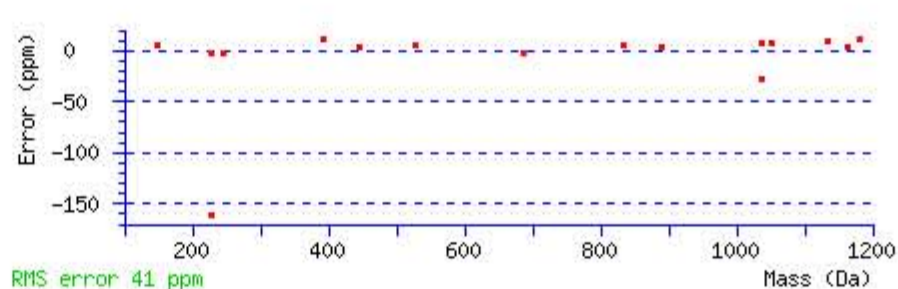
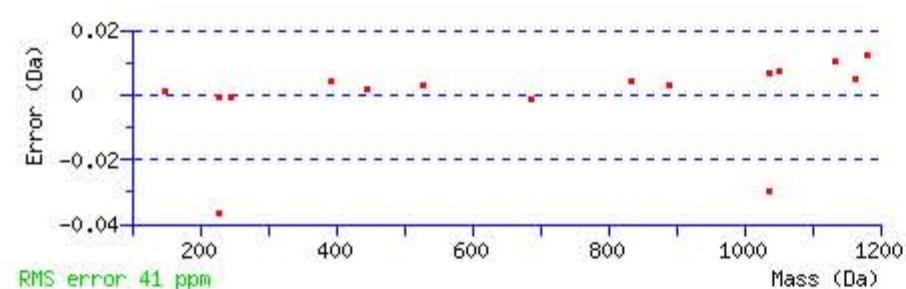
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.0029

Matches : 16/60 fragment ions using 34 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483					V							8
2	229.118283	115.062780			211.107718	106.057497	E	1181.602344	591.304810	1164.575795	582.791536	1163.591779	582.299528	7
3	392.181612	196.594444			374.171047	187.589162	Y	1052.559751	526.783514	1035.533202	518.270239			6
4	449.203076	225.105176			431.192511	216.099894	G	889.496422	445.251849	872.469873	436.738575			5
5	596.271490	298.639383			578.260925	289.634101	F	832.474958	416.741117	815.448409	408.227843			4
6	1035.496816	518.252046	1018.470267	509.738772	1017.486251	509.246764	Q	685.406544	343.206910	668.379995	334.693636			3
7	1134.565230	567.786253	1117.538681	559.272979	1116.554665	558.780971	V	246.181218	123.594247	229.154669	115.080973			2
8							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **VEYGFQVK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.1	1279.663483	0.003865	VEYGFQVK
5.9	1279.681229	-0.013881	EVTVKEWYVK
5.9	1279.663483	0.003865	QFVGYLDK
5.7	1279.659470	0.007878	VCSFGKQVVEK
4.0	1279.677216	-0.009868	VFKTEDTQGKK
3.8	1279.684601	-0.017253	MSASAVFILDVK
2.0	1279.666824	0.000524	VKEWSLMIMK

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVEEQESR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 25907: 1285.634328 from(643.824440,2+) rtinseconds(1393) index(48807)

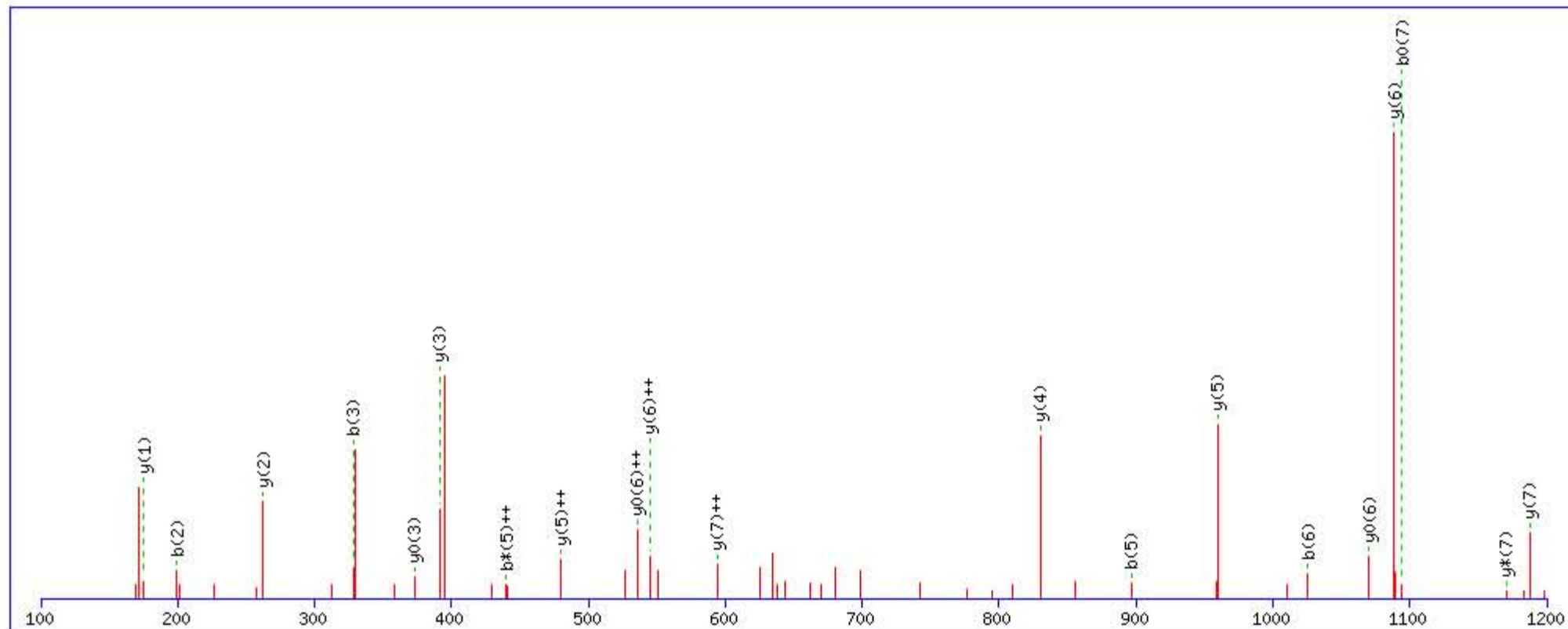
Title: Locus:1.1.1.1100.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1285.633621

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

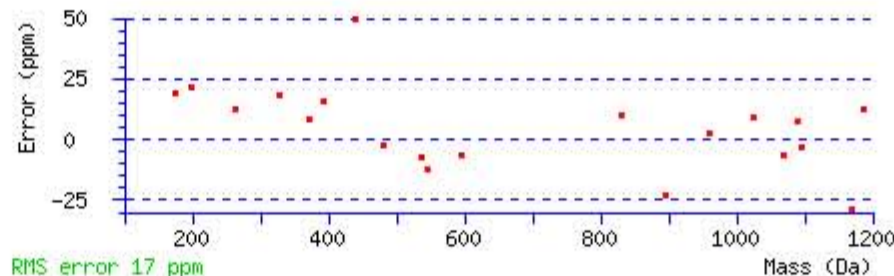
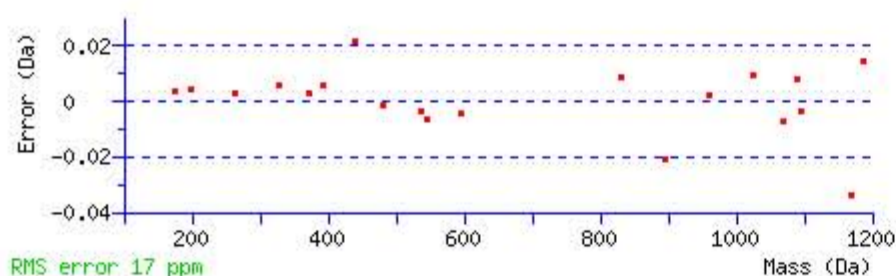
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 38 Expect: 0.00057

Matches : 20/70 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	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
37.8	1285.633621	0.000707	VVEEQESR
3.2	1285.644867	-0.010539	DTLHSAMAVVSR
2.3	1285.637451	-0.003123	TAPASGSAPRESR

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **CCQDGVTR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 26305: 1305.566628 from(653.790590,2+) rtinseconds(1405) index(48858)

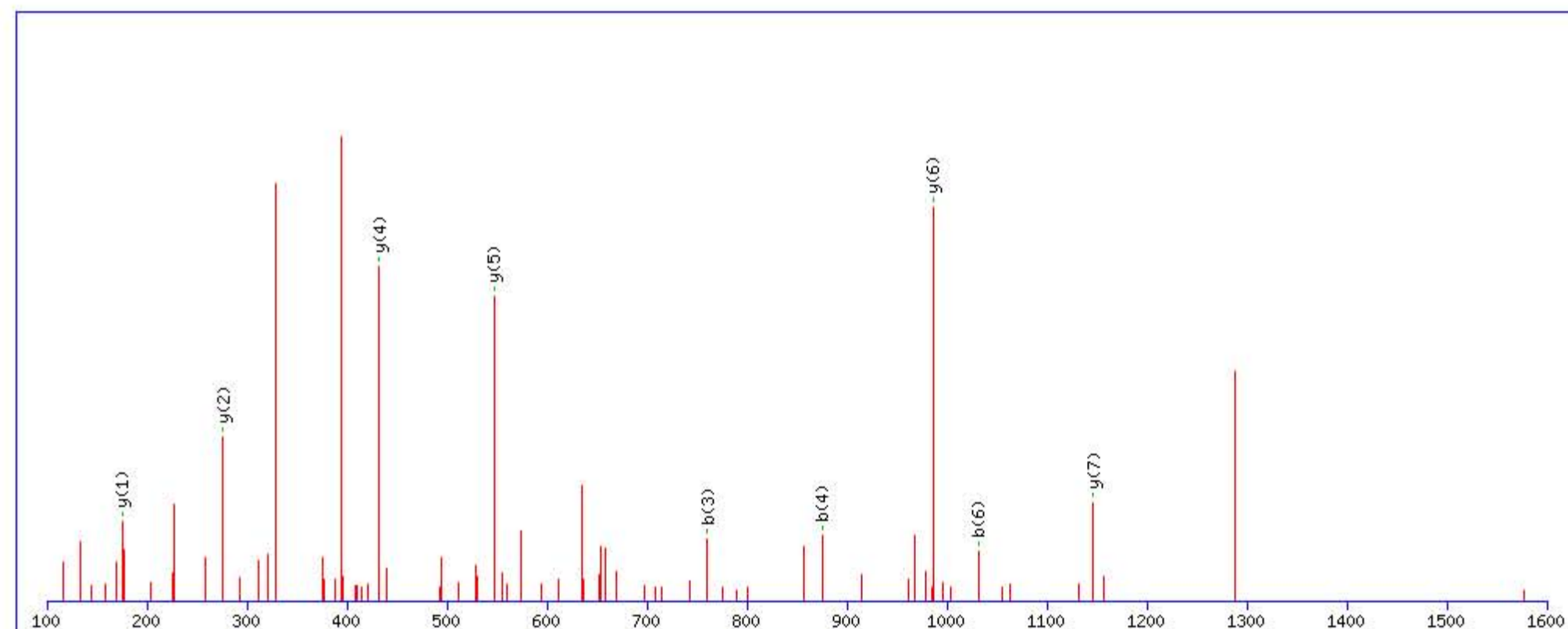
Title: Locus:1.1.1.1104.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1305.562820

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

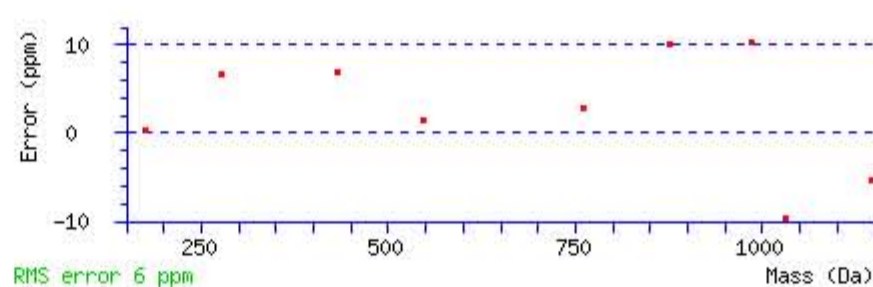
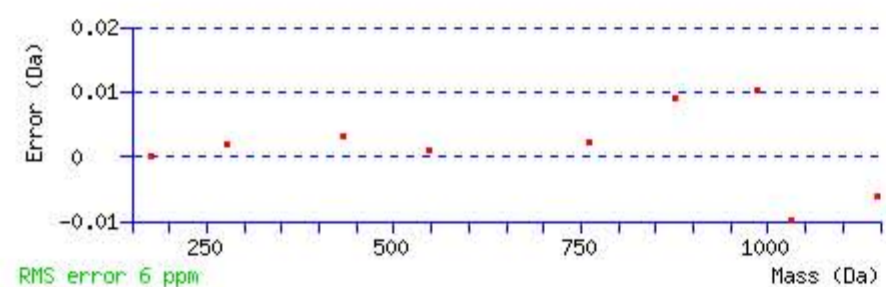
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 51 Expect: 7e-005

Matches : 9/72 fragment ions using 12 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	161.037925	81.022600					C							8
2	321.068574	161.037925					C	1146.539427	573.773352	1129.512878	565.260077	1128.528862	564.768069	7
3	760.293900	380.650588	743.267351	372.137314			Q	986.508778	493.758027	969.482229	485.244753	968.498213	484.752745	6
4	875.320843	438.164060	858.294294	429.650785	857.310278	429.158777	D	547.283452	274.145364	530.256903	265.632090	529.272887	265.140082	5
5	932.342307	466.674792	915.315758	458.161517	914.331742	457.669509	G	432.256509	216.631893	415.229960	208.118618	414.245944	207.626610	4
6	1031.410721	516.208999	1014.384172	507.695724	1013.400156	507.203716	V	375.235045	188.121161	358.208496	179.607886	357.224480	179.115878	3
7	1132.458400	566.732838	1115.431851	558.219564	1114.447835	557.727556	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
8							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **CCQDGVTR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.7	1305.562820	0.003808	CCQDGVTR
6.0	1305.577194	-0.010566	CDAGWLADGSVR
5.7	1305.562805	0.003823	CCTSPSQR
0.6	1305.583679	-0.017051	EQEPDFEEKR

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 27133: 1345.709368 from(673.861960,2+) rtinseconds(1630) index(50468)

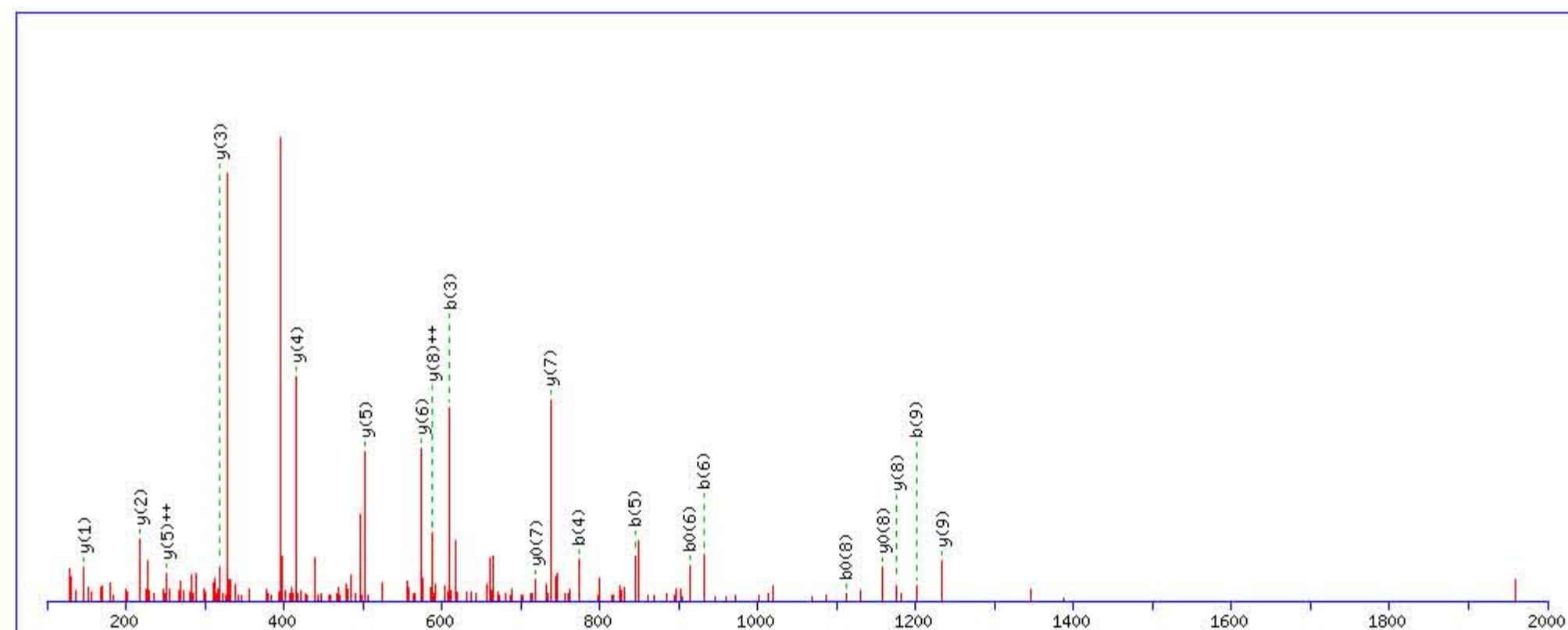
Title: Locus:1.1.1.1183.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1345.706390

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

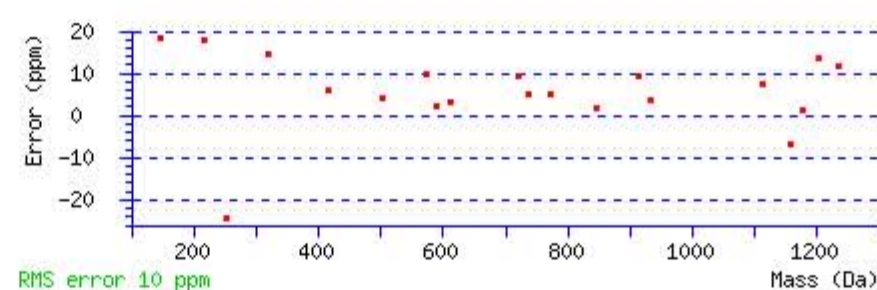
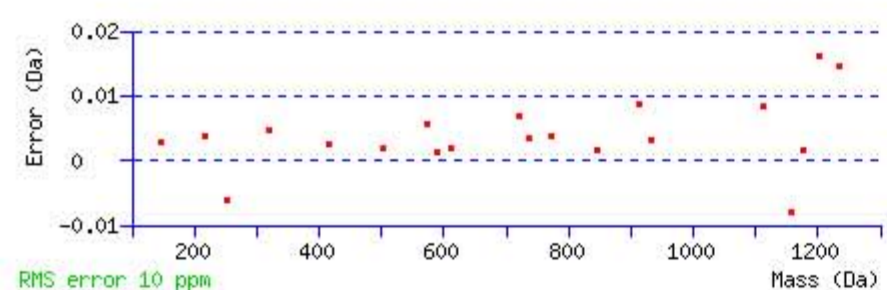
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 63 Expect: 1.4e-005

Matches : 20/90 fragment ions using 34 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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
63.1	1345.706390	0.002978	LGQYASPTAK
14.4	1345.706390	0.002978	LGQYDQALK
13.1	1345.724182	-0.014814	LGAVPATSGPTTFK
10.9	1345.706406	0.002962	QGLYTPQTK
7.0	1345.692474	0.016894	VASCRYPALGPR
6.7	1345.717636	-0.008268	QMPQPTFTRLK
5.8	1345.727509	-0.018141	LGLMDNEIKVAK
5.5	1345.727509	-0.018141	DKLKMEVDQLK
5.4	1345.720108	-0.010740	KQEEEVSTLRK
3.0	1345.706390	0.002978	HEMTLKFPSIK

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLQDEDGYR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 28904: 1362.626348 from(682.320450,2+) rtinseconds(1742) index(51102)

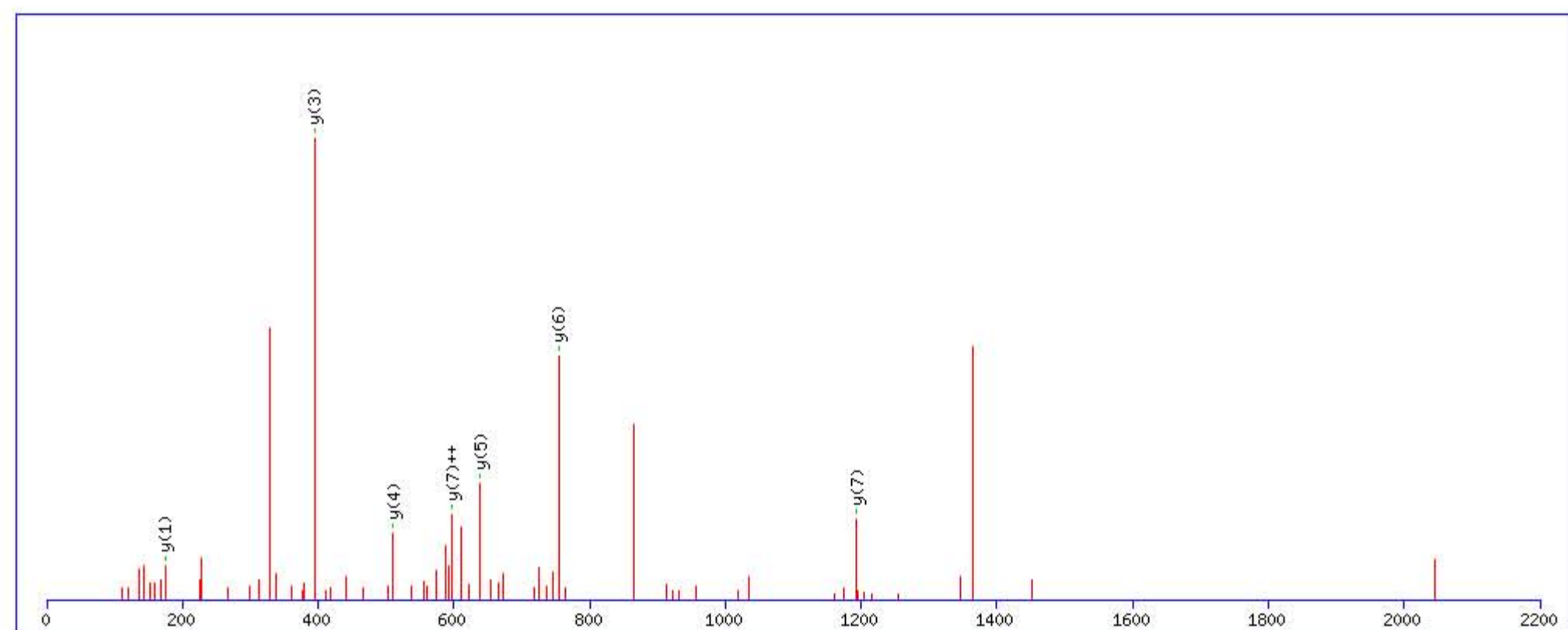
Title: Locus:1.1.1.1222.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1362.623795

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

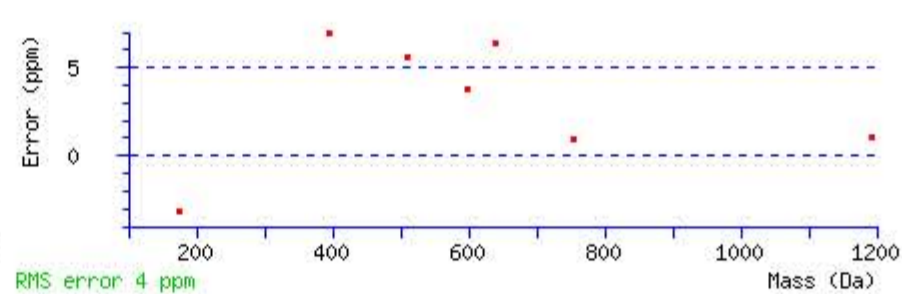
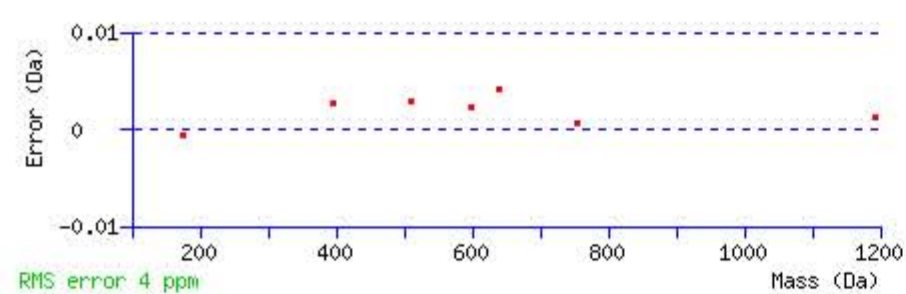
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.00027

Matches : 7/80 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	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
40.4	1362.623795	0.002553	GLQDEDGYR
2.4	1362.613251	0.013097	MGAGATGRAMDGPR
2.2	1362.623795	0.002553	TGFLEIDEHMR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **TEQWSTLPPETK**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 41020: 1726.871328 from(864.442940,2+) rtinseconds(2031) index(53160)

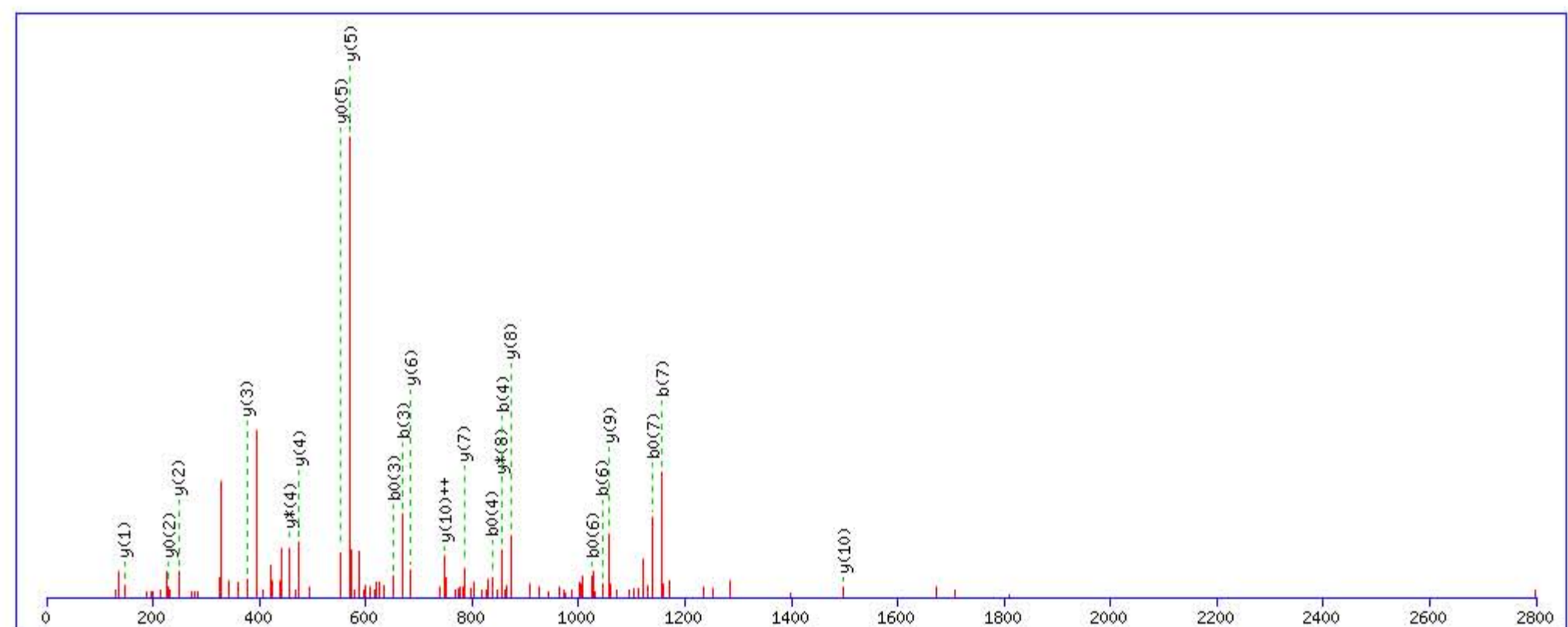
Title: Locus:1.1.1.1322.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1726.860001

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

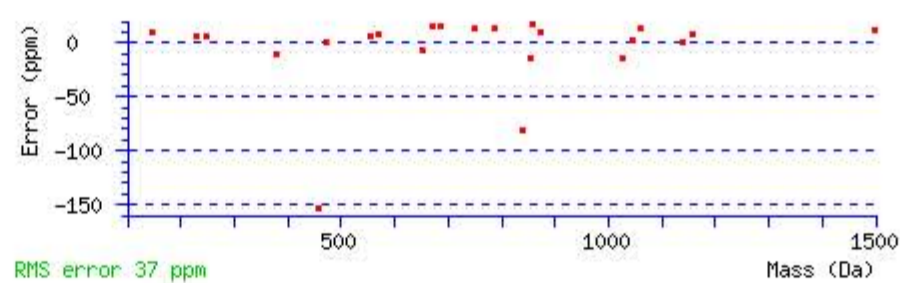
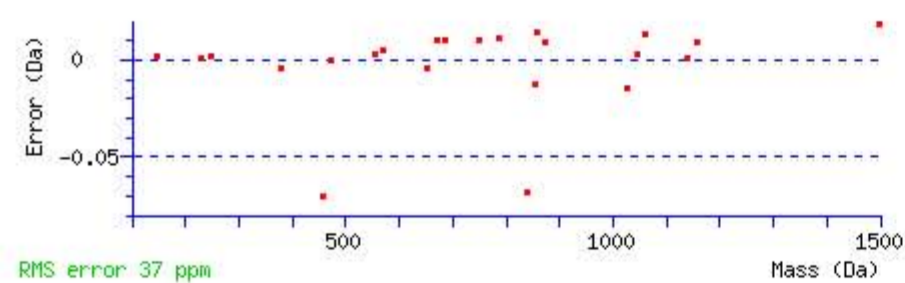
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 50 Expect: 0.00018

Matches : 23/126 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	102.054955	51.531116			84.044390	42.525833	T							12
2	231.097548	116.052412			213.086983	107.047130	E	1626.819607	813.913442	1609.793058	805.400167	1608.809042	804.908159	11
3	670.322874	335.665075	653.296325	327.151801	652.312309	326.659793	Q	1497.777014	749.392145	1480.750465	740.878871	1479.766449	740.386863	10
4	856.402187	428.704732	839.375638	420.191457	838.391622	419.699449	W	1058.551688	529.779482	1041.525139	521.266208	1040.541123	520.774200	9
5	943.434215	472.220746	926.407666	463.707471	925.423650	463.215463	S	872.472375	436.739826	855.445826	428.226551	854.461810	427.734543	8
6	1044.481894	522.744585	1027.455345	514.231311	1026.471329	513.739303	T	785.440347	393.223812	768.413798	384.710537	767.429782	384.218529	7
7	1157.565958	579.286617	1140.539409	570.773343	1139.555393	570.281334	L	684.392668	342.699972	667.366119	334.186698	666.382103	333.694690	6
8	1254.618722	627.812999	1237.592173	619.299725	1236.608157	618.807716	P	571.308604	286.157940	554.282055	277.644666	553.298039	277.152658	5
9	1351.671486	676.339381	1334.644937	667.826107	1333.660921	667.334098	P	474.255840	237.631558	457.229291	229.118284	456.245275	228.626276	4
10	1480.714079	740.860678	1463.687530	732.347403	1462.703514	731.855395	E	377.203076	189.105176	360.176527	180.591902	359.192511	180.099894	3
11	1581.761758	791.384517	1564.735209	782.871243	1563.751193	782.379235	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
12							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **TEQWSTLPPETK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.1	1726.860001	0.011327	TEQWSTLPPETK
9.6	1726.849960	0.021368	TERFGQGGAGPVGGQGPR
6.2	1726.867188	0.004140	KDHAEMQAVIDAKQK
3.5	1726.871216	0.000112	NLNTKLQMYFQSPK
1.9	1726.853485	0.017843	MASGHAFQPDLVK
1.1	1726.874573	-0.003245	VTKNQEMMSQIKYK

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 41586: 1746.900028 from(874.457290,2+) rtinseconds(2580) index(56406)

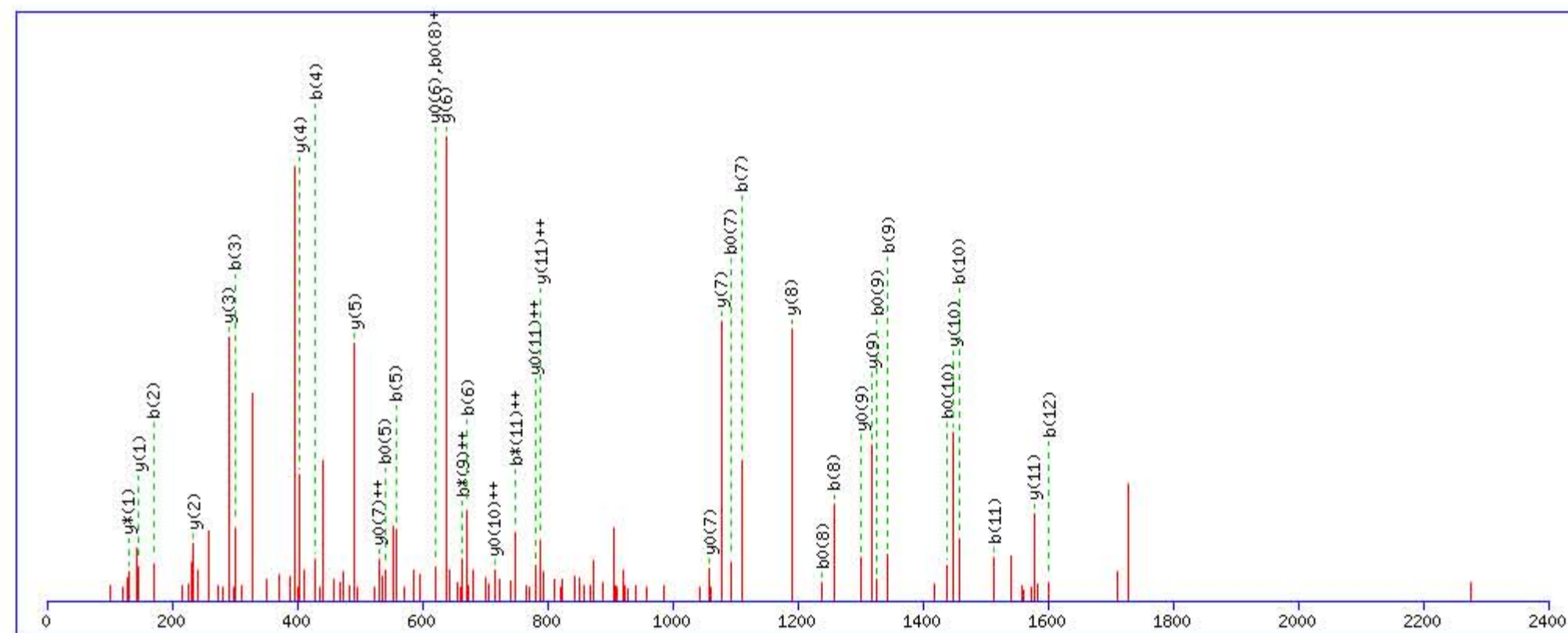
Title: Locus:1.1.1.1513.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1746.886200

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

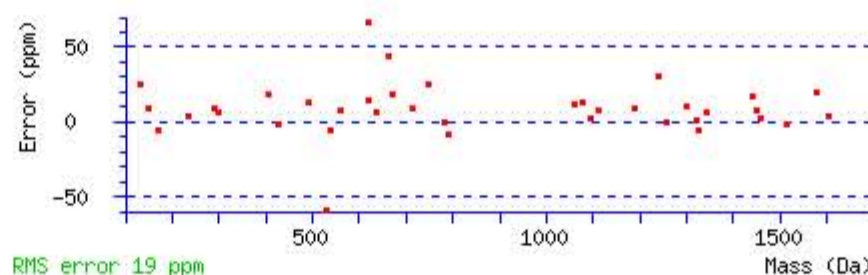
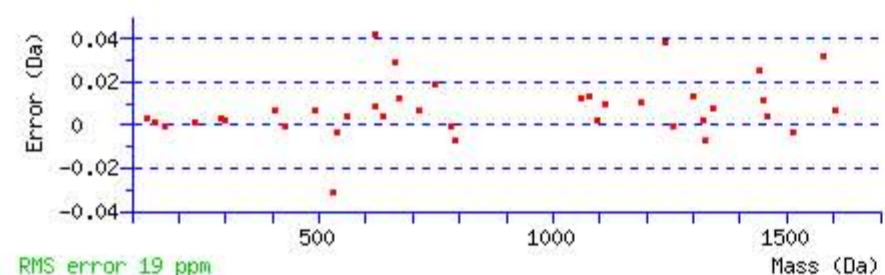
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 75 Expect: 1.9e-007

Matches : 38/126 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	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
74.7	1746.886200	0.013828	GLEEELQFSLGSK
2.9	1746.887558	0.012470	AVQSKAFCAGGLAPGWK
1.3	1746.918533	-0.018505	AKLQMTEAALALSEQK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VLSLAQEQVGGSP**EK

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 43649: 1851.979932 from(618.333920,3+) rtinseconds(2022) index(53085)

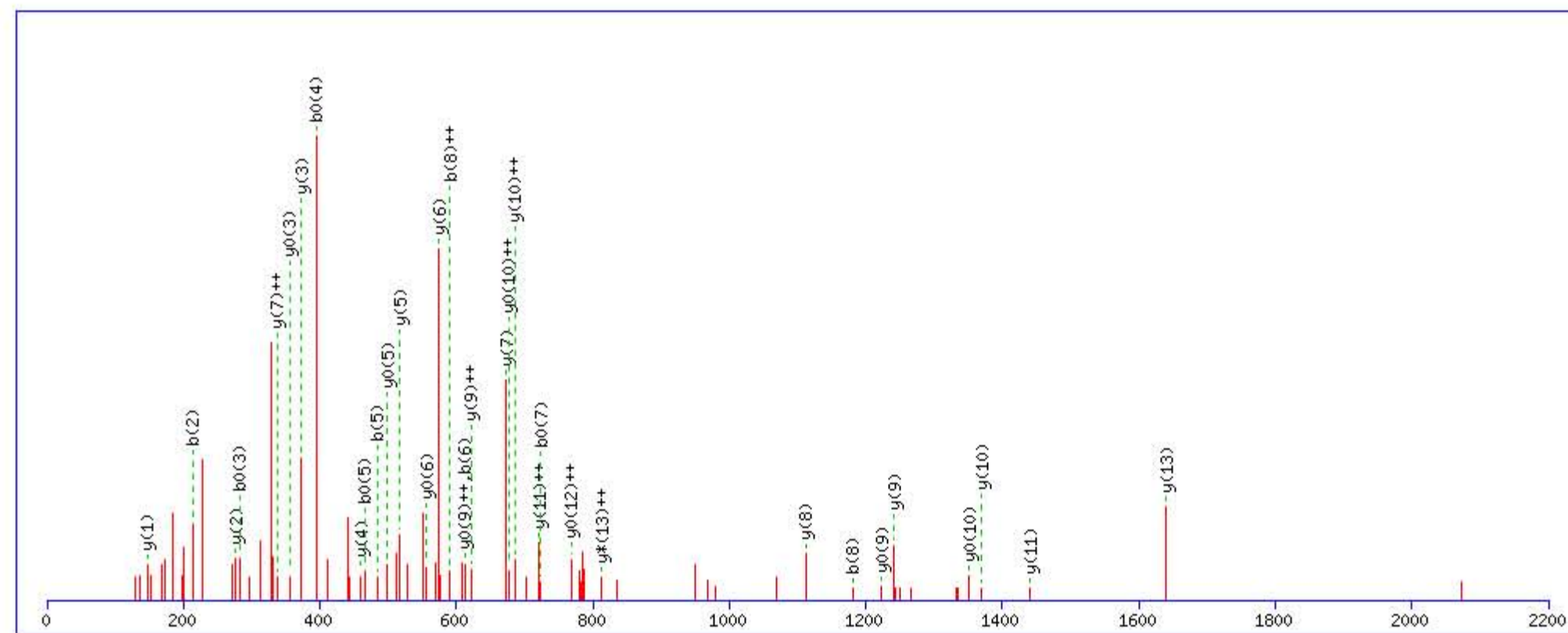
Title: Locus:1.1.1.1319.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1851.976425

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

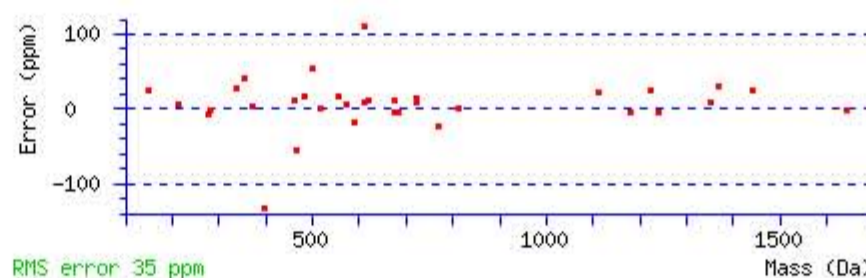
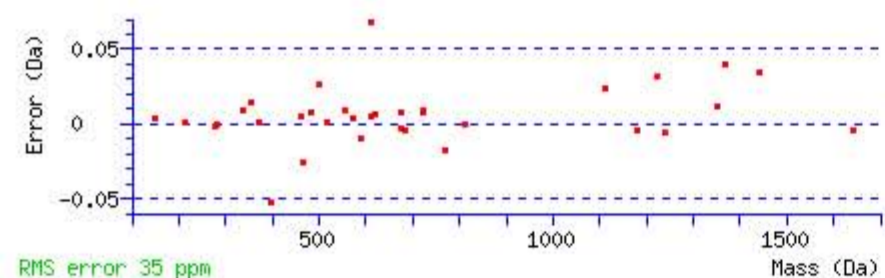
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 6.2e-006

Matches : 34/152 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	100.075690	50.541483					V							15
2	213.159754	107.083515					L	1753.915298	877.461287	1736.888749	868.948013	1735.904733	868.456004	14
3	300.191782	150.599529			282.181217	141.594247	S	1640.831234	820.919255	1623.804685	812.405981	1622.820669	811.913973	13
4	413.275846	207.141561			395.265281	198.136279	L	1553.799206	777.403241	1536.772657	768.889967	1535.788641	768.397958	12
5	484.312960	242.660118			466.302395	233.654836	A	1440.715142	720.861209	1423.688593	712.347935	1422.704577	711.855927	11
6	612.371538	306.689407	595.344989	298.176133	594.360973	297.684125	Q	1369.678028	685.342652	1352.651479	676.829378	1351.667463	676.337370	10
7	741.414131	371.210704	724.387582	362.697429	723.403566	362.205421	E	1241.619450	621.313363	1224.592901	612.800089	1223.608885	612.308080	9
8	1180.639457	590.823367	1163.612908	582.310092	1162.628892	581.818084	Q	1112.576857	556.792066	1095.550308	548.278792	1094.566292	547.786784	8
9	1279.707871	640.357574	1262.681322	631.844299	1261.697306	631.352291	V	673.351531	337.179404	656.324982	328.666129	655.340966	328.174121	7
10	1336.729335	668.868306	1319.702786	660.355031	1318.718770	659.863023	G	574.283117	287.645197	557.256568	279.131922	556.272552	278.639914	6
11	1393.750799	697.379037	1376.724250	688.865763	1375.740234	688.373755	G	517.261653	259.134465	500.235104	250.621190	499.251088	250.129182	5
12	1480.782827	740.895052	1463.756278	732.381777	1462.772262	731.889769	S	460.240189	230.623732	443.213640	222.110458	442.229624	221.618450	4
13	1577.835591	789.421434	1560.809042	780.908159	1559.825026	780.416151	P	373.208161	187.107718	356.181612	178.594444	355.197596	178.102436	3
14	1706.878184	853.942730	1689.851635	845.429456	1688.867619	844.937447	E	276.155397	138.581336	259.128848	130.068062	258.144832	129.576054	2
15							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **VLSLAQEQVGGSP**EK

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.0	1851.976425	0.003507	VLSLAQEQVGGSP EK
41.9	1851.976425	0.003507	VLSLAQEQVGGSP EK

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

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPEVQLVAHSPWLK**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 44158: 1871.022582 from(624.681470,3+) rtinseconds(2255) index(54583)

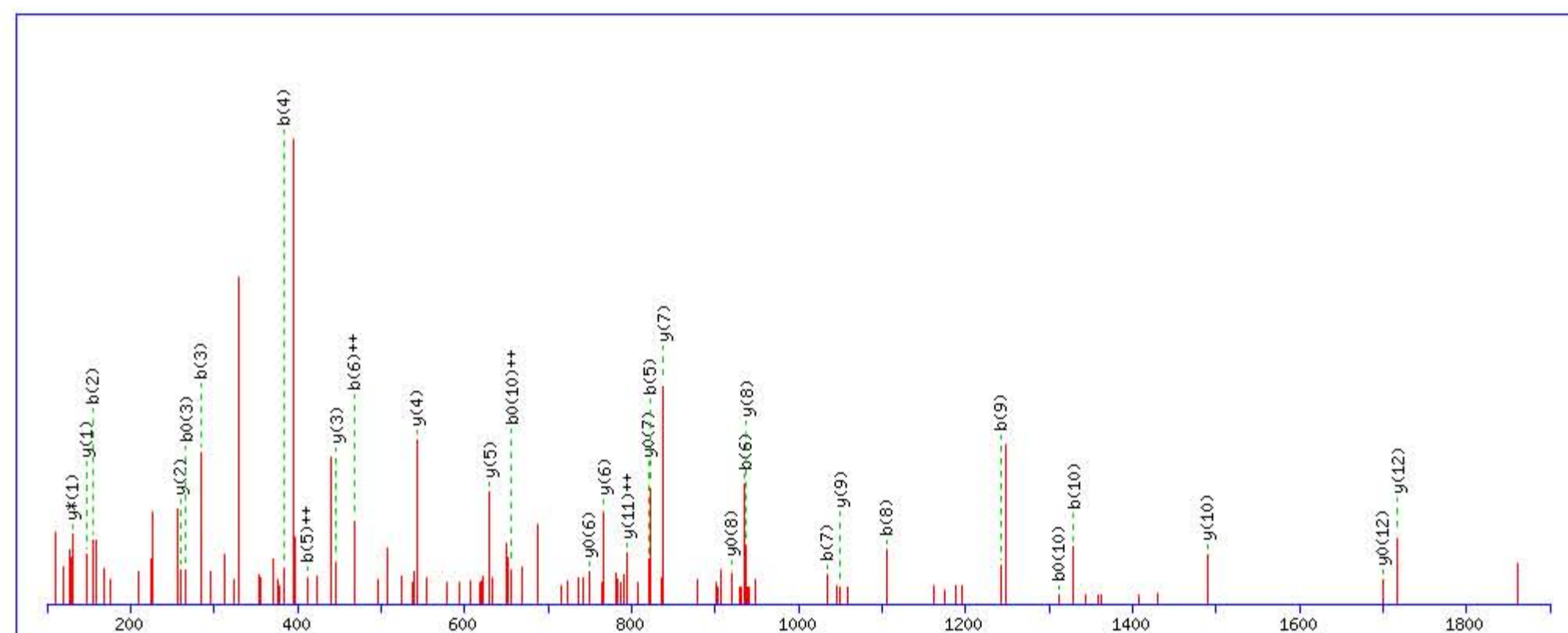
Title: Locus:1.1.1.1400.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1871.012756

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

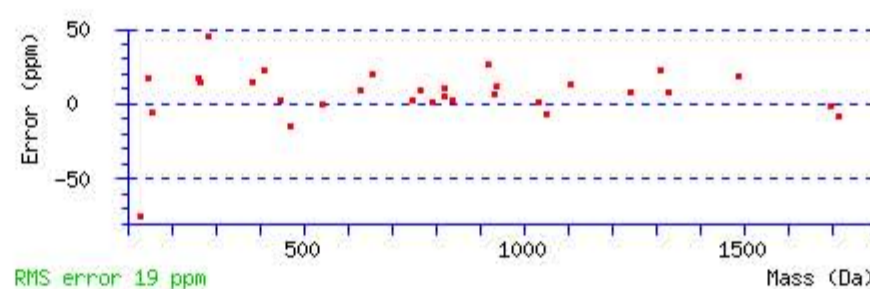
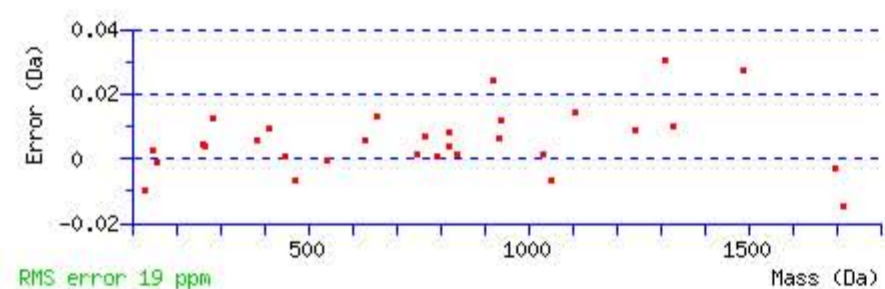
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 7.1e-005

Matches : 31/136 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	58.028740	29.518008					G							14
2	155.081504	78.044390					P	1814.998574	908.002925	1797.972025	899.489651	1796.988009	898.997643	13
3	284.124097	142.565687			266.113532	133.560404	E	1717.945810	859.476543	1700.919261	850.963269	1699.935245	850.471261	12
4	383.192511	192.099894			365.181946	183.094611	V	1588.903217	794.955247	1571.876668	786.441972	1570.892652	785.949964	11
5	822.417837	411.712557	805.391288	403.199282	804.407272	402.707274	Q	1489.834803	745.421040	1472.808254	736.907765	1471.824238	736.415757	10
6	935.501901	468.254589	918.475352	459.741314	917.491336	459.249306	L	1050.609477	525.808377	1033.582928	517.295102	1032.598912	516.803094	9
7	1034.570315	517.788796	1017.543766	509.275521	1016.559750	508.783513	V	937.525413	469.266345	920.498864	460.753070	919.514848	460.261062	8
8	1105.607429	553.307353	1088.580880	544.794078	1087.596864	544.302070	A	838.456999	419.732138	821.430450	411.218863	820.446434	410.726855	7
9	1242.666341	621.836809	1225.639792	613.323534	1224.655776	612.831526	H	767.419885	384.213581	750.393336	375.700306	749.409320	375.208298	6
10	1329.698369	665.352823	1312.671820	656.839548	1311.687804	656.347540	S	630.360973	315.684125	613.334424	307.170850	612.350408	306.678842	5
11	1426.751133	713.879205	1409.724584	705.365930	1408.740568	704.873922	P	543.328945	272.168111	526.302396	263.654836			4
12	1612.830446	806.918861	1595.803897	798.405587	1594.819881	797.913579	W	446.276181	223.641728	429.249632	215.128454			3
13	1725.914510	863.460893	1708.887961	854.947619	1707.903945	854.455611	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 **GPEVQLVAHSPWLK**

(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	1871.012756	0.009826	GPEVQLVAHSPWLK
1.8	1871.002686	0.019896	QRVLHWDLRGPGGGPAR
1.6	1870.994781	0.027801	NVNQAKLSEHRHK

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

MASCOT Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLVPGAPFLLQALVR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 45393: 1941.152712 from(648.058180,3+) rtinseconds(2868) index(58426)

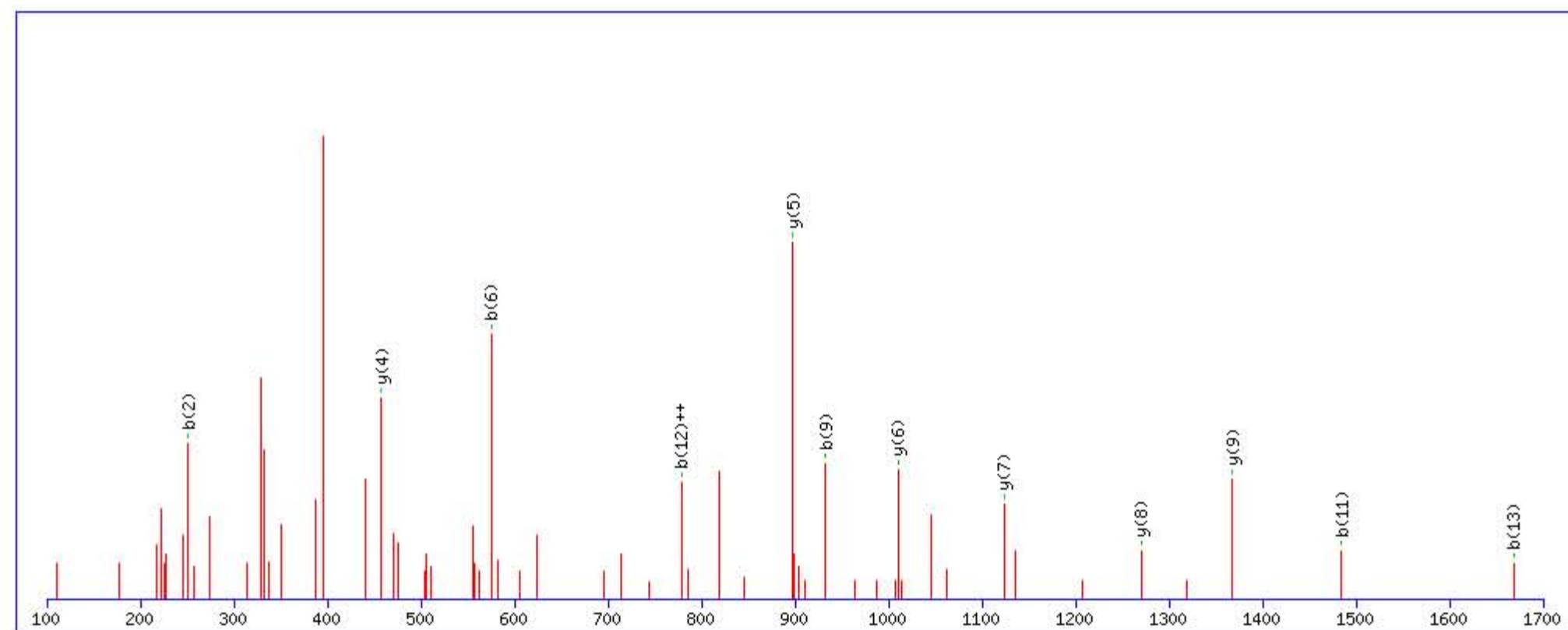
Title: Locus:1.1.1.1612.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1941.138626

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

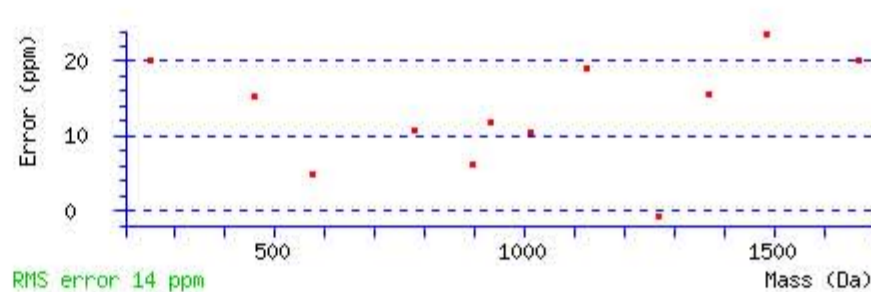
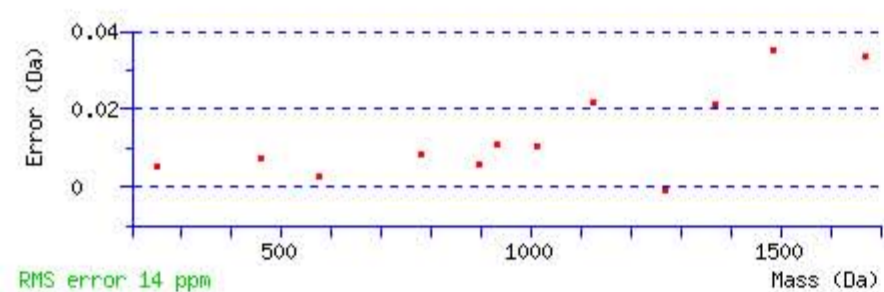
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 4.6e-005

Matches : 12/92 fragment ions using 15 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	138.066188	69.536732			H					15
2	251.150252	126.078764			L	1805.086996	903.047136	1788.060447	894.533862	14
3	350.218666	175.612971			V	1692.002932	846.505104	1674.976383	837.991830	13
4	447.271430	224.139353			P	1592.934518	796.970897	1575.907969	788.457623	12
5	504.292894	252.650085			G	1495.881754	748.444515	1478.855205	739.931241	11
6	575.330008	288.168642			A	1438.860290	719.933783	1421.833741	711.420509	10
7	672.382772	336.695024			P	1367.823176	684.415226	1350.796627	675.901952	9
8	819.451186	410.229231			F	1270.770412	635.888844	1253.743863	627.375570	8
9	932.535250	466.771263			L	1123.701998	562.354637	1106.675449	553.841363	7
10	1045.619314	523.313295			L	1010.617934	505.812605	993.591385	497.299331	6
11	1484.844640	742.925958	1467.818091	734.412684	Q	897.533870	449.270573	880.507321	440.757298	5
12	1555.881754	778.444515	1538.855205	769.931241	A	458.308544	229.657910	441.281995	221.144635	4
13	1668.965818	834.986547	1651.939269	826.473273	L	387.271430	194.139353	370.244881	185.626078	3
14	1768.034232	884.520754	1751.007683	876.007480	V	274.187366	137.597321	257.160817	129.084047	2
15					R	175.118952	88.063114	158.092403	79.549839	1



NCBI BLAST search of [HLVPGAPFLLQALVR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.9	1941.138626	0.014086	HLVPGAPFLLQALVR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **EPFLSCCQFAESLR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 48472: 2053.960542 from(685.660790,3+) rtinseconds(2519) index(56008)

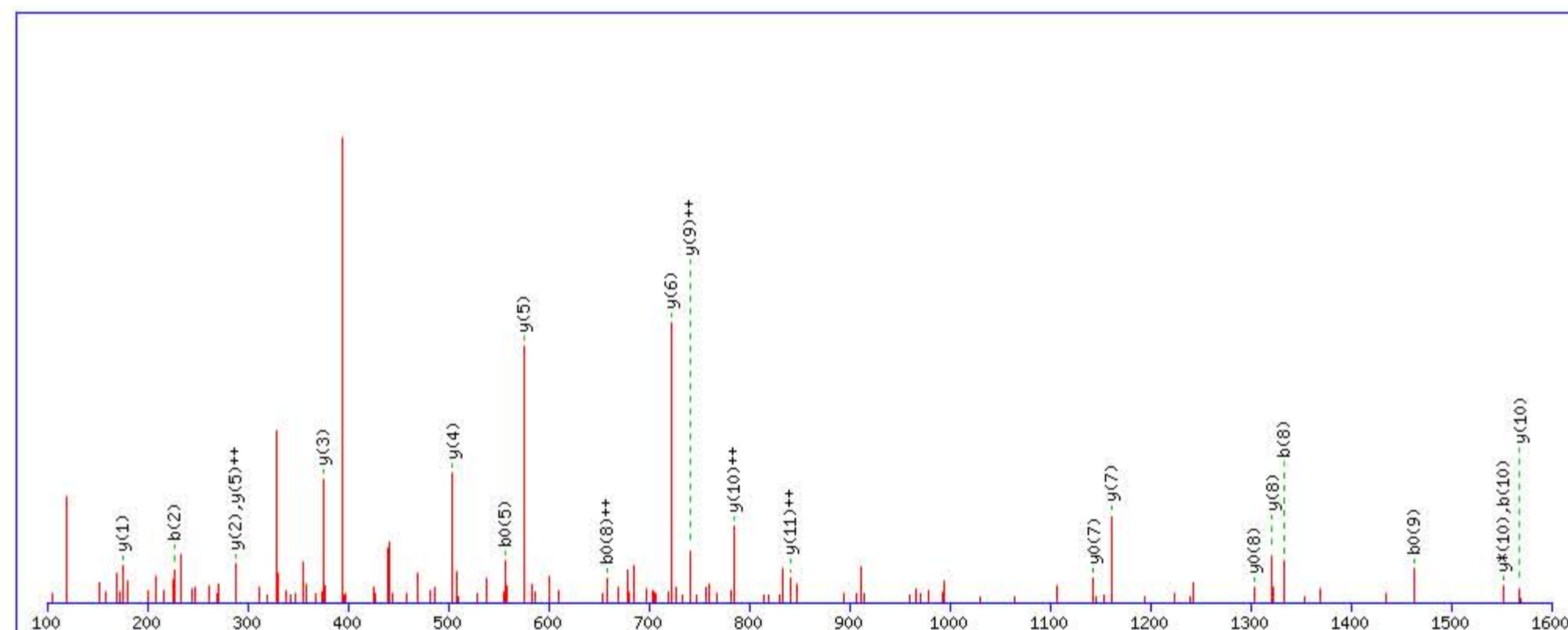
Title: Locus:1.1.1.1492.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2053.942368

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

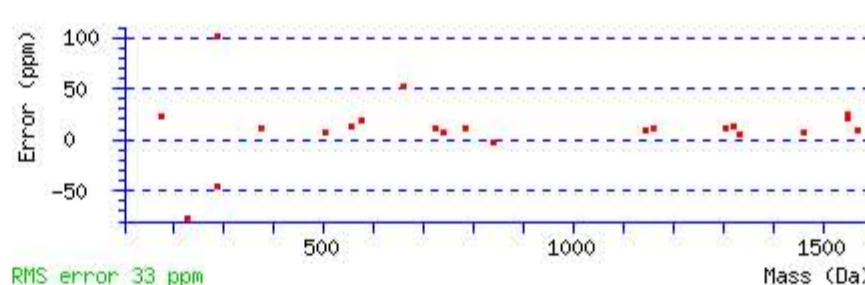
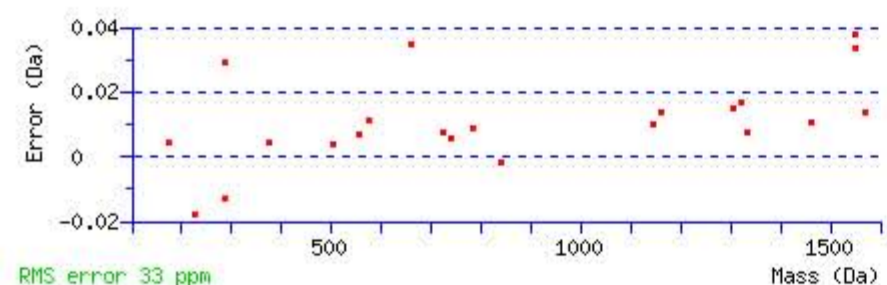
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.0012

Matches : 22/138 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							14
2	227.102633	114.054954			209.092068	105.049672	P	1925.907059	963.457168	1908.880510	954.943893	1907.896494	954.451885	13
3	374.171047	187.589161			356.160482	178.583879	F	1828.854295	914.930786	1811.827746	906.417511	1810.843730	905.925503	12
4	487.255111	244.131193			469.244546	235.125911	L	1681.785881	841.396579	1664.759332	832.883304	1663.775316	832.391296	11
5	574.287139	287.647208			556.276574	278.641925	S	1568.701817	784.854547	1551.675268	776.341272	1550.691252	775.849264	10
6	734.317788	367.662532			716.307223	358.657250	C	1481.669789	741.338533	1464.643240	732.825258	1463.659224	732.333250	9
7	894.348437	447.677857			876.337872	438.672574	C	1321.639140	661.323208	1304.612591	652.809934	1303.628575	652.317926	8
8	1333.573763	667.290520	1316.547214	658.777245	1315.563198	658.285237	Q	1161.608491	581.307884	1144.581942	572.794609	1143.597926	572.302601	7
9	1480.642177	740.824727	1463.615628	732.311452	1462.631612	731.819444	F	722.383165	361.695221	705.356616	353.181946	704.372600	352.689938	6
10	1551.679291	776.343284	1534.652742	767.830009	1533.668726	767.338001	A	575.314751	288.161014	558.288202	279.647739	557.304186	279.155731	5
11	1680.721884	840.864580	1663.695335	832.351306	1662.711319	831.859298	E	504.277637	252.642457	487.251088	244.129182	486.267072	243.637174	4
12	1767.753912	884.380594	1750.727363	875.867320	1749.743347	875.375312	S	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
13	1880.837976	940.922626	1863.811427	932.409352	1862.827411	931.917344	L	288.203016	144.605146	271.176467	136.091871			2
14							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **EPFLSCCQFAESLR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	2053.942368	0.018174	EPFLSCCQFAESLR

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 51483: 2220.042522 from(741.021450,3+) rtinseconds(2119) index(69497)

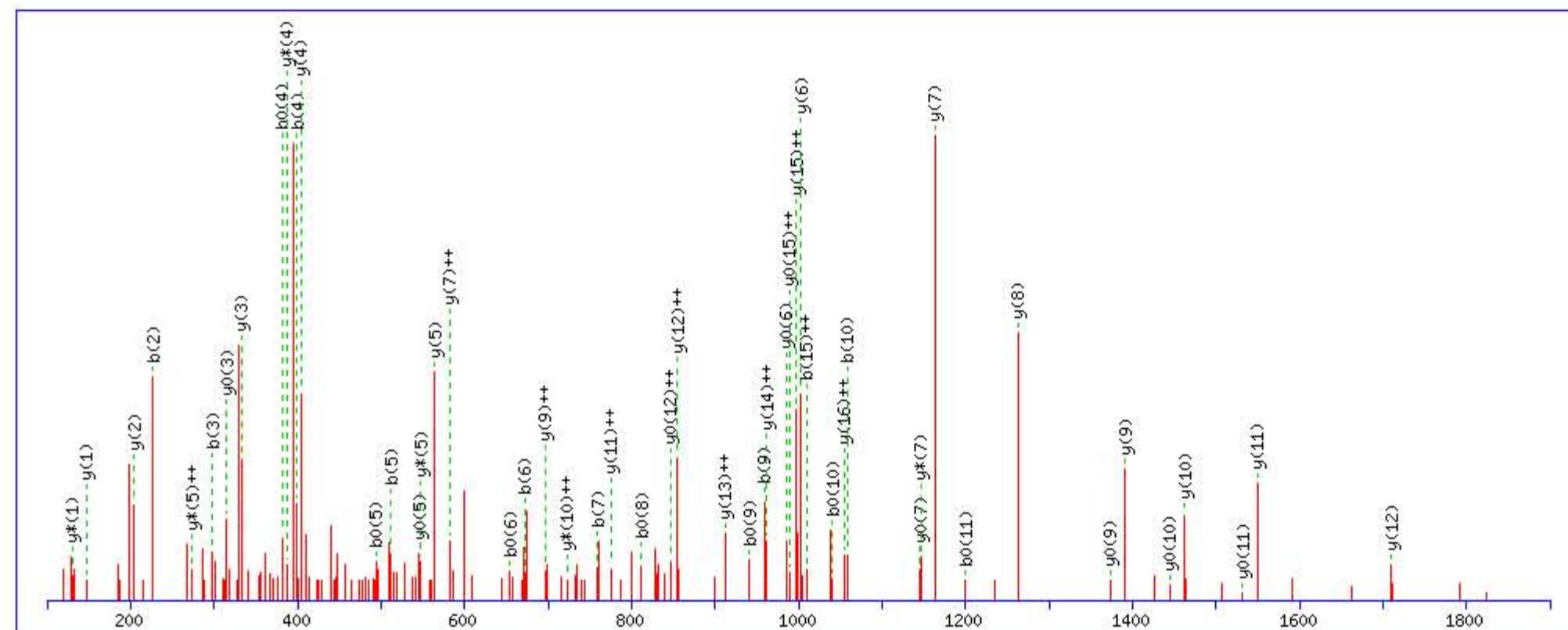
Title: Locus:1.1.1.1675.13 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2220.041092

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

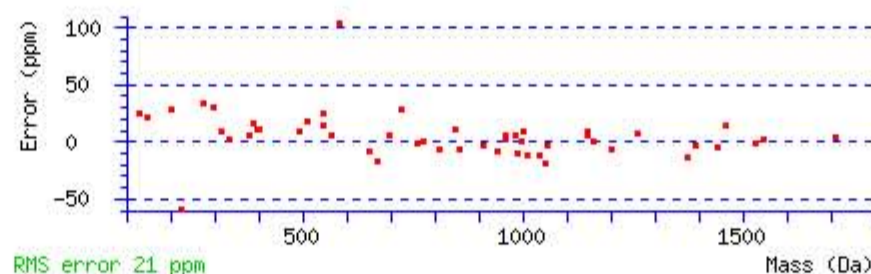
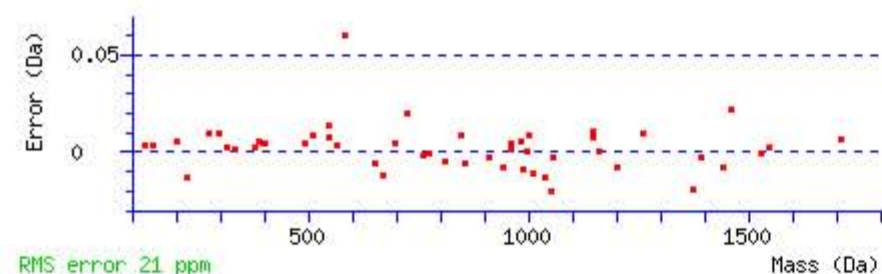
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 54 Expect: 1e-005

Matches : 51/160 fragment ions using 110 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
53.8	2220.041092	0.001430	LLATLCSAEVCQCAEGK
0.5	2220.048080	-0.005558	EPQEGAELPEATGTTSHR

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GCGEQTMIIYLAPTLAASR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 51975: 2249.122692 from(750.714840,3+) rtinseconds(2546) index(56228)

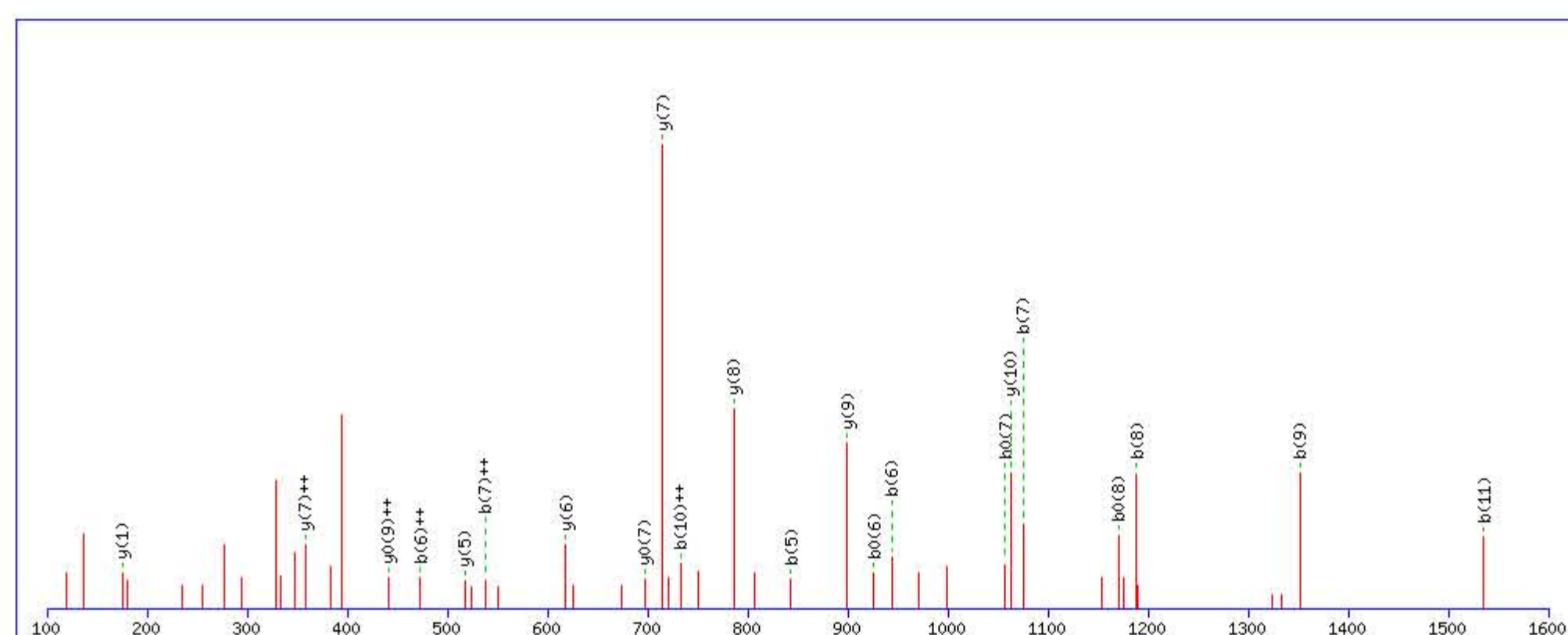
Title: Locus:1.1.1.1501.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2249.100647

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

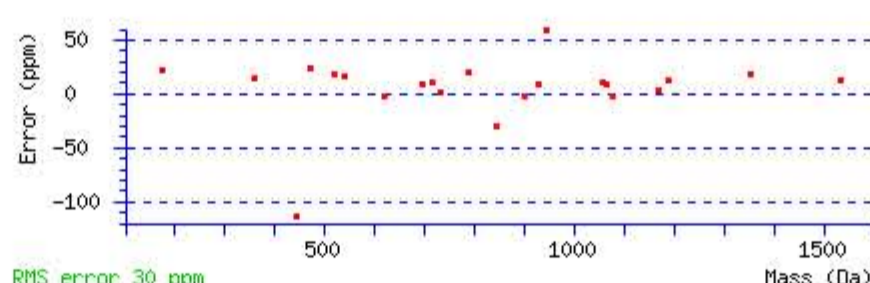
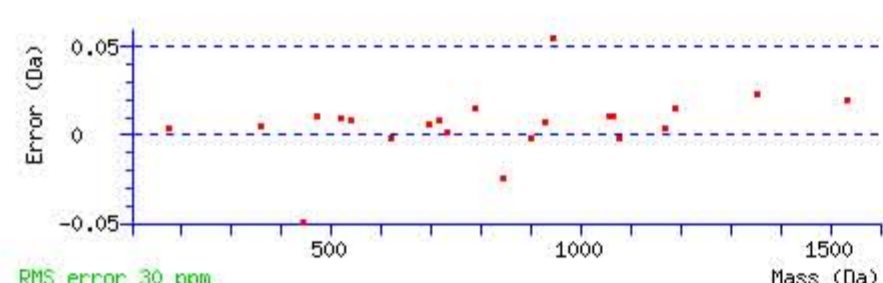
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 42 Expect: 0.00086

Matches : 22/188 fragment ions using 36 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							18
2	218.059389	109.533333					C	2193.086482	1097.046879	2176.059933	1088.533604	2175.075917	1088.041596	17
3	275.080853	138.044064					G	2033.055833	1017.031555	2016.029284	1008.518280	2015.045268	1008.026272	16
4	404.123446	202.565361			386.112881	193.560079	E	1976.034369	988.520822	1959.007820	980.007548	1958.023804	979.515540	15
5	843.348772	422.178024	826.322223	413.664750	825.338207	413.172742	Q	1846.991776	923.999526	1829.965227	915.486251	1828.981211	914.994243	14
6	944.396451	472.701864	927.369902	464.188589	926.385886	463.696581	T	1407.766450	704.386863	1390.739901	695.873588	1389.755885	695.381580	13
7	1075.436936	538.222106	1058.410387	529.708832	1057.426371	529.216824	M	1306.718771	653.863023	1289.692222	645.349749	1288.708206	644.857741	12
8	1188.521000	594.764138	1171.494451	586.250864	1170.510435	585.758855	I	1175.678286	588.342781	1158.651737	579.829506	1157.667721	579.337498	11
9	1351.584329	676.295803	1334.557780	667.782528	1333.573764	667.290520	Y	1062.594222	531.800749	1045.567673	523.287475	1044.583657	522.795466	10
10	1464.668393	732.837834	1447.641844	724.324560	1446.657828	723.832552	L	899.530893	450.269084	882.504344	441.755810	881.520328	441.263802	9
11	1535.705507	768.356391	1518.678958	759.843117	1517.694942	759.351109	A	786.446829	393.727053	769.420280	385.213778	768.436264	384.721770	8
12	1632.758271	816.882773	1615.731722	808.369499	1614.747706	807.877491	P	715.409715	358.208496	698.383166	349.695221	697.399150	349.203213	7
13	1733.805950	867.406613	1716.779401	858.893339	1715.795385	858.401330	T	618.356951	309.682114	601.330402	301.168839	600.346386	300.676831	6
14	1846.890014	923.948645	1829.863465	915.435370	1828.879449	914.943362	L	517.309272	259.158274	500.282723	250.644999	499.298707	250.152991	5
15	1917.927128	959.467202	1900.900579	950.953927	1899.916563	950.461919	A	404.225208	202.616242	387.198659	194.102967	386.214643	193.610959	4
16	1988.964242	994.985759	1971.937693	986.472484	1970.953677	985.980476	A	333.188094	167.097685	316.161545	158.584410	315.177529	158.092402	3
17	2075.996270	1038.501773	2058.969721	1029.988498	2057.985705	1029.496490	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
18							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **GCGEQTMIIYLAPTLAASR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.7	2249.100647	0.022045	GCGEQTMIIYLAPTLAASR
8.5	2249.115051	0.007641	YSTSLYASPSMVHEGVAVVPR
4.1	2249.104492	0.018200	AQLQQHNLEMVGEGRQ
1.0	2249.143570	-0.020878	TPPPQPPLISSMDSISQK
0.8	2249.089874	0.032818	EMIDIYSTREPQLAFHQ
0.6	2249.150742	-0.028050	LRSIMMSQDLENVTSKEIR
0.5	2249.137527	-0.014835	QKFERPICVSWSTDVKGGR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **DDPDAPLQPVTPLQLFEGR**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 54809: 2418.243612 from(807.088480,3+) rtinseconds(3020) index(59691)

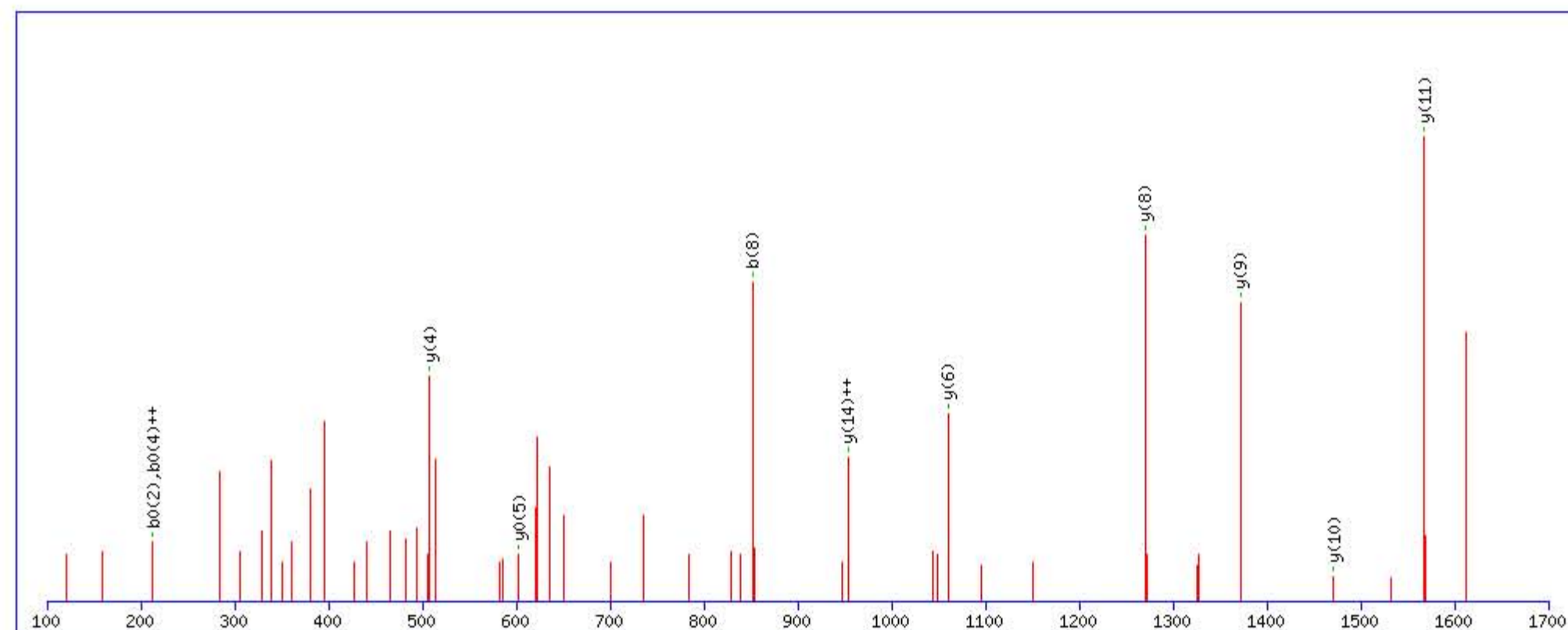
Title: Locus:1.1.1.1663.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2418.225342

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

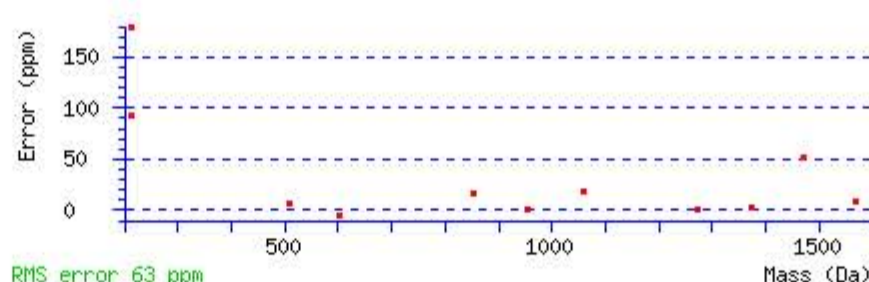
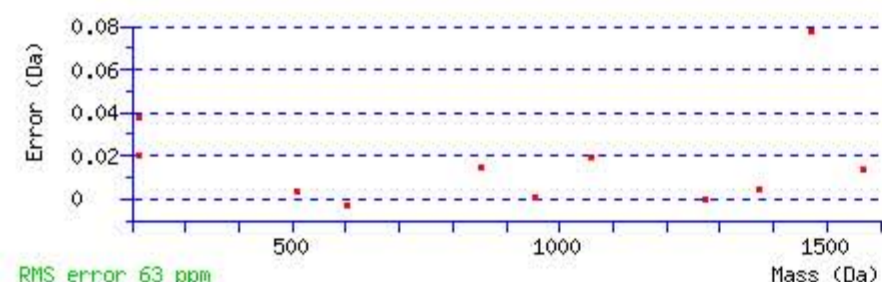
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.051

Matches : 11/198 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	116.034219	58.520748			98.023654	49.515465	D							19
2	231.061162	116.034219			213.050597	107.028936	D	2304.205668	1152.606472	2287.179119	1144.093197	2286.195103	1143.601189	18
3	328.113926	164.560601			310.103361	155.555319	P	2189.178725	1095.093000	2172.152176	1086.579726	2171.168160	1086.087718	17
4	443.140869	222.074073			425.130304	213.068790	D	2092.125961	1046.566618	2075.099412	1038.053344	2074.115396	1037.561336	16
5	514.177983	257.592630			496.167418	248.587347	A	1977.099018	989.053147	1960.072469	980.539873	1959.088453	980.047865	15
6	611.230747	306.119012			593.220182	297.113729	P	1906.061904	953.534590	1889.035355	945.021316	1888.051339	944.529308	14
7	724.314811	362.661044			706.304246	353.655761	L	1809.009140	905.008208	1791.982591	896.494934	1790.998575	896.002926	13
8	852.373389	426.690333	835.346840	418.177058	834.362824	417.685050	Q	1695.925076	848.466176	1678.898527	839.952902	1677.914511	839.460894	12
9	949.426153	475.216715	932.399604	466.703440	931.415588	466.211432	P	1567.866498	784.436887	1550.839949	775.923613	1549.855933	775.431605	11
10	1048.494567	524.750922	1031.468018	516.237647	1030.484002	515.745639	V	1470.813734	735.910505	1453.787185	727.397231	1452.803169	726.905223	10
11	1149.542246	575.274761	1132.515697	566.761487	1131.531681	566.269479	T	1371.745320	686.376298	1354.718771	677.863024	1353.734755	677.371016	9
12	1246.595010	623.801143	1229.568461	615.287869	1228.584445	614.795861	P	1270.697641	635.852459	1253.671092	627.339184	1252.687076	626.847176	8
13	1359.679074	680.343175	1342.652525	671.829901	1341.668509	671.337893	L	1173.644877	587.326077	1156.618328	578.812802	1155.634312	578.320794	7
14	1798.904400	899.955838	1781.877851	891.442564	1780.893835	890.950556	Q	1060.560813	530.784045	1043.534264	522.270770	1042.550248	521.778762	6
15	1911.988464	956.497870	1894.961915	947.984596	1893.977899	947.492588	L	621.335487	311.171382	604.308938	302.658107	603.324922	302.166099	5
16	2059.056878	1030.032077	2042.030329	1021.518803	2041.046313	1021.026794	F	508.251423	254.629350	491.224874	246.116075	490.240858	245.624067	4
17	2188.099471	1094.553373	2171.072922	1086.040099	2170.088906	1085.548091	E	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	3
18	2245.120935	1123.064105	2228.094386	1114.550831	2227.110370	1114.058823	G	232.140416	116.573846	215.113867	108.060571			2
19							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **DDPDAPLQPVTPLQLFEGR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.1	2418.225342	0.018270	DDPDAPLQPVTPLQLFEGR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AACAQLNDFLQEYGTQGCQV**

Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 57447: 2583.179442 from(862.067090,3+) rtinseconds(2758) index(57495)

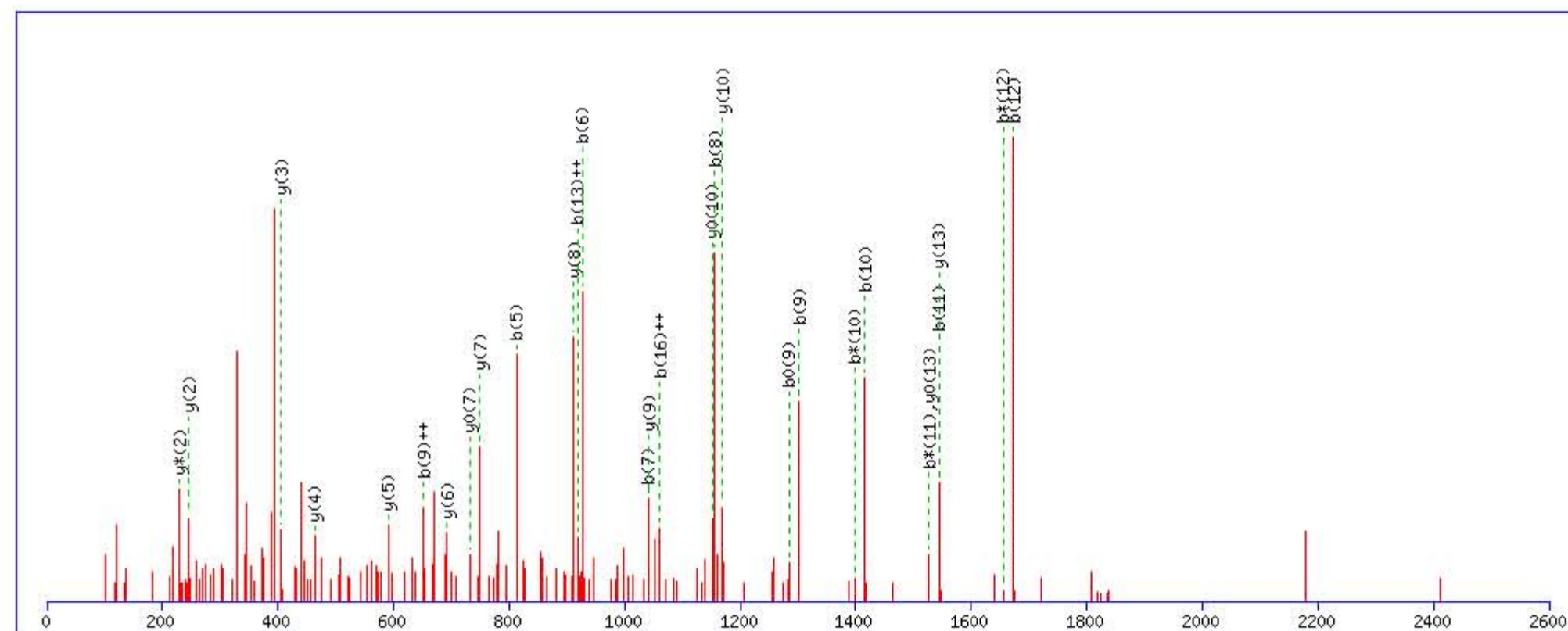
Title: Locus:1.1.1.1574.25 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2583.155624

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

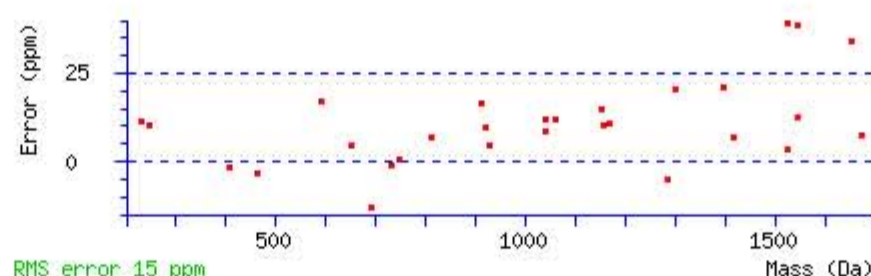
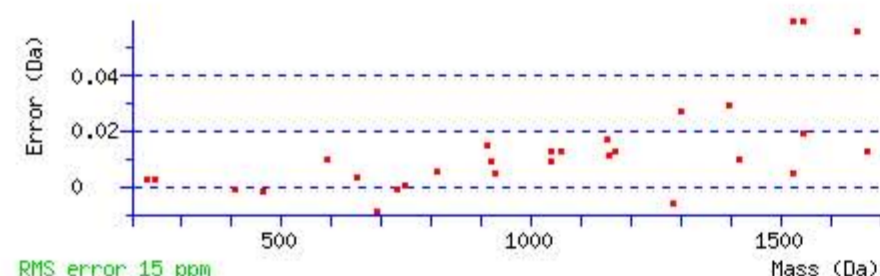
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 54 Expect: 4.4e-005

Matches : 29/194 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	72.044390	36.525833					A							20
2	143.081504	72.044390					A	2513.125782	1257.066529	2496.099233	1248.553254	2495.115217	1248.061246	19
3	303.112153	152.059714					C	2442.088668	1221.547972	2425.062119	1213.034697	2424.078103	1212.542689	18
4	374.149267	187.578271					A	2282.058019	1141.532647	2265.031470	1133.019373	2264.047454	1132.527365	17
5	813.374593	407.190935	796.348044	398.677660			Q	2211.020905	1106.014090	2193.994356	1097.500816	2193.010340	1097.008808	16
6	926.458657	463.732967	909.432108	455.219692			L	1771.795579	886.401428	1754.769030	877.888153	1753.785014	877.396145	15
7	1040.501584	520.754430	1023.475035	512.241155			N	1658.711515	829.859396	1641.684966	821.346121	1640.700950	820.854113	14
8	1155.528527	578.267902	1138.501978	569.754627	1137.517962	569.262619	D	1544.668588	772.837932	1527.642039	764.324658	1526.658023	763.832650	13
9	1302.596941	651.802109	1285.570392	643.288834	1284.586376	642.796826	F	1429.641645	715.324460	1412.615096	706.811186	1411.631080	706.319178	12
10	1415.681005	708.344141	1398.654456	699.830866	1397.670440	699.338858	L	1282.573231	641.790253	1265.546682	633.276979	1264.562666	632.784971	11
11	1543.739583	772.373430	1526.713034	763.860155	1525.729018	763.368147	Q	1169.489167	585.248222	1152.462618	576.734947	1151.478602	576.242939	10
12	1672.782176	836.894726	1655.755627	828.381452	1654.771611	827.889444	E	1041.430589	521.218932	1024.404040	512.705658	1023.420024	512.213650	9
13	1835.845505	918.426391	1818.818956	909.913116	1817.834940	909.421108	Y	912.387996	456.697636	895.361447	448.184361	894.377431	447.692353	8
14	1892.866969	946.937123	1875.840420	938.423848	1874.856404	937.931840	G	749.324667	375.165971	732.298118	366.652697	731.314102	366.160689	7
15	1993.914648	997.460962	1976.888099	988.947688	1975.904083	988.455680	T	692.303203	346.655239	675.276654	338.141965	674.292638	337.649957	6
16	2121.973226	1061.490251	2104.946677	1052.976976	2103.962661	1052.484968	Q	591.255524	296.131400	574.228975	287.618125			5
17	2178.994690	1090.000983	2161.968141	1081.487708	2160.984125	1080.995700	G	463.196946	232.102111	446.170397	223.588836			4
18	2339.025339	1170.016307	2321.998790	1161.503033	2321.014774	1161.011025	C	406.175482	203.591379	389.148933	195.078104			3
19	2467.083917	1234.045596	2450.057368	1225.532322	2449.073352	1225.040314	Q	246.144833	123.576054	229.118284	115.062780			2
20							V	118.086255	59.546765					1



NCBI BLAST search of [AACAQLNDFLQEYGTQGCQV](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.1	2583.155624	0.023818	AACAQLNDFLQEYGTQGCQV
16.9	2583.155624	0.023818	AACAQLNDFLQEYGTQGCQV

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEQIQLK**

Found in **COS_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

Match to Query 20103: 1125.617288 from(563.815920,2+) rtinseconds(1728) index(34604)

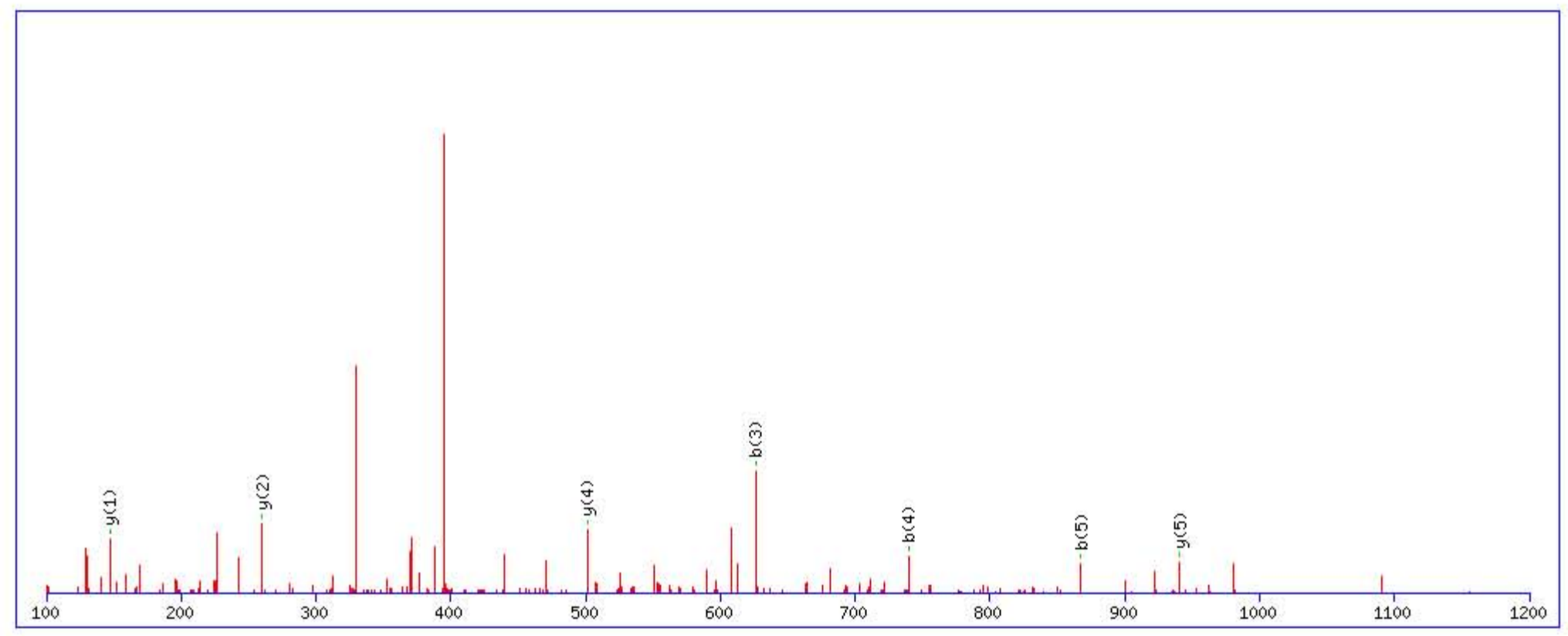
Title: Locus:1.1.1.3021.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1125.621597

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

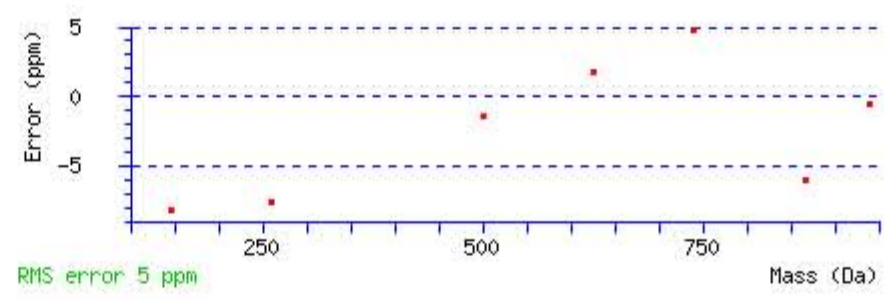
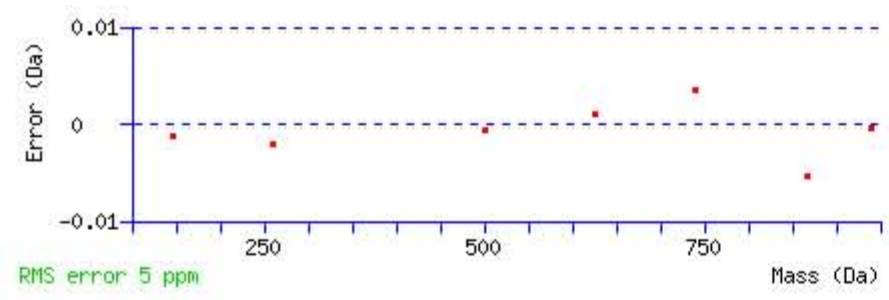
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.036

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
27.9	1125.621597	-0.004309	GEQIQLK
16.1	1125.607666	0.009622	QMDRHAKIK
12.5	1125.632828	-0.015540	KLCLSHLQK
7.6	1125.621597	-0.004309	EQVAQLK
6.6	1125.606979	0.010309	LKEAFDYIK
6.5	1125.621597	-0.004309	GEQIQLK
6.5	1125.633499	-0.016211	VSHFLPWIK
6.3	1125.629486	-0.012198	RVDGWVGLK
4.6	1125.602966	0.014322	VSISKSTYK
4.5	1125.632813	-0.015525	EQAARK

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TSGMQFCVK**

Found in **CO5_HUMAN**, Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

Match to Query 29128: 1367.639588 from(684.827070,2+) rtinseconds(1921) index(35844)

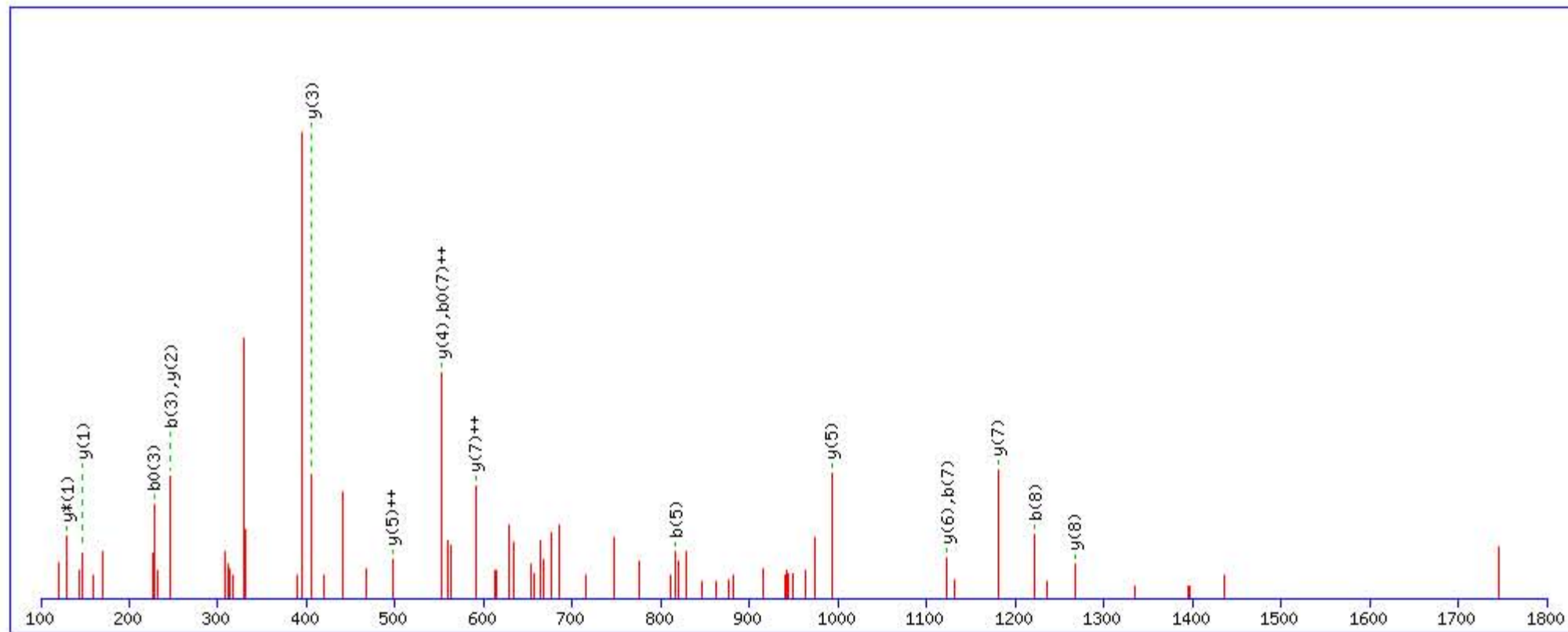
Title: Locus:1.1.1.3088.21 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1367.639999

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

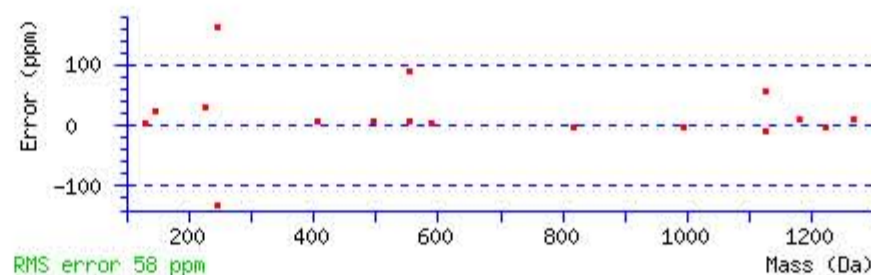
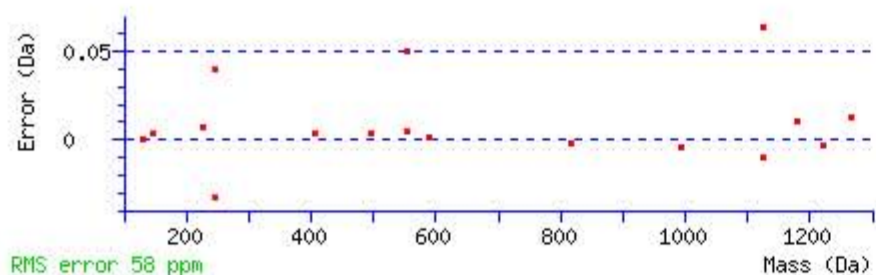
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 41 Expect: 0.00023

Matches : 17/74 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							9
2	189.086983	95.047129			171.076418	86.041847	S	1267.599584	634.303430	1250.573035	625.790156	1249.589019	625.298148	8
3	246.108447	123.557861			228.097882	114.552579	G	1180.567556	590.787416	1163.541007	582.274142			7
4	377.148932	189.078104			359.138367	180.072822	M	1123.546092	562.276684	1106.519543	553.763410			6
5	816.374258	408.690767	799.347709	400.177493	798.363693	399.685485	Q	992.505607	496.756442	975.479058	488.243167			5
6	963.442672	482.224974	946.416123	473.711700	945.432107	473.219692	F	553.280281	277.143779	536.253732	268.630504			4
7	1123.473321	562.240298	1106.446772	553.727024	1105.462756	553.235016	C	406.211867	203.609571	389.185318	195.096297			3
8	1222.541735	611.774506	1205.515186	603.261231	1204.531170	602.769223	V	246.181218	123.594247	229.154669	115.080973			2
9							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [TSGMQFCVK](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.4	1367.639999	-0.000411	TSGMQFCVK
2.6	1367.650314	-0.010726	TLQGERMENYK

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 57242: 2556.205902 from(853.075910,3+) rtinseconds(1939) index(35998)

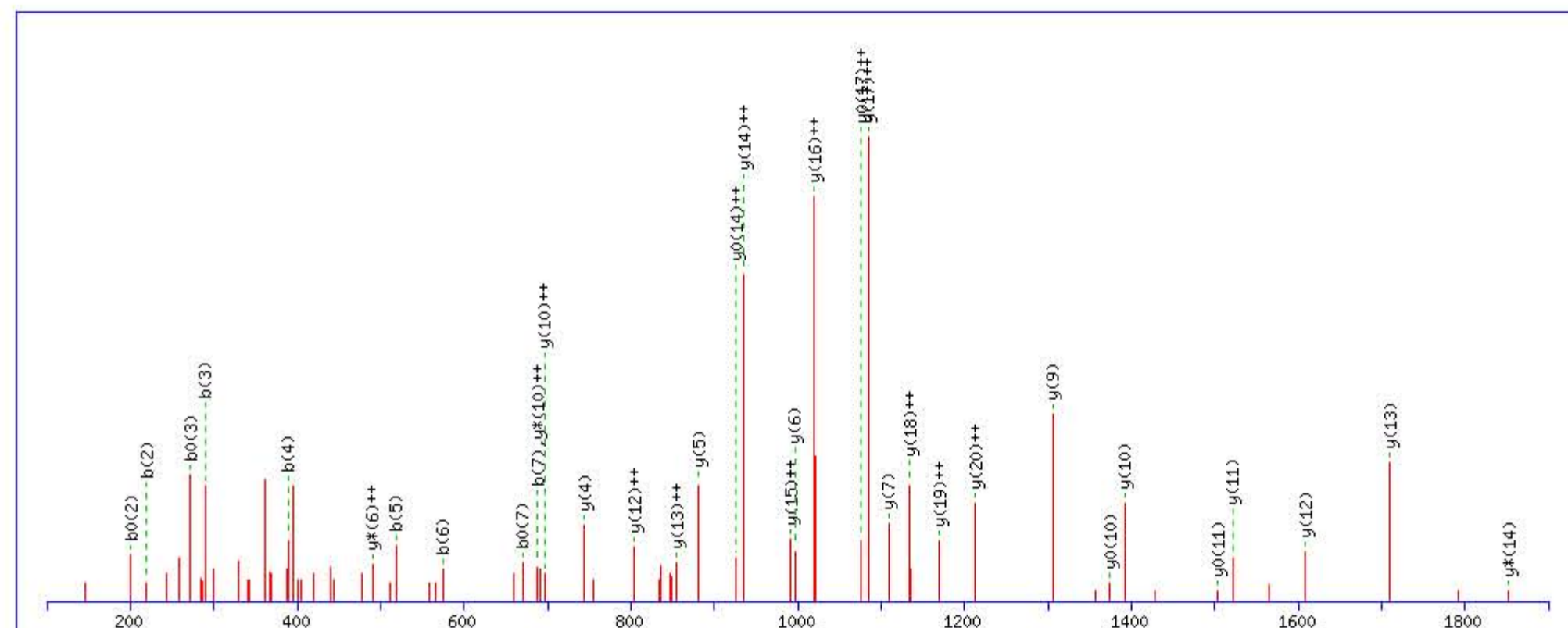
Title: Locus:1.1.1.3094.25 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2556.202240

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

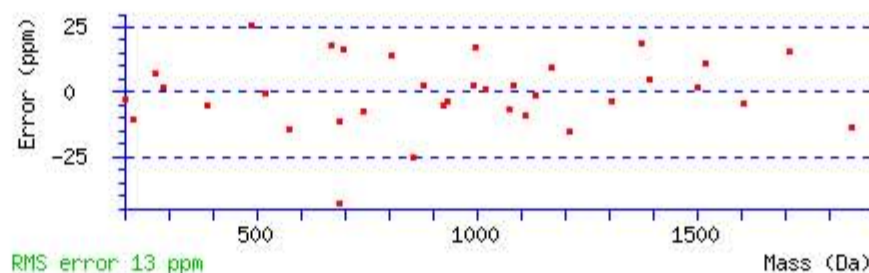
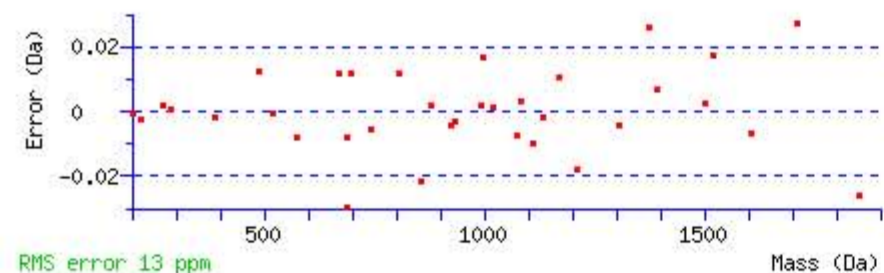
Variable modifications:

Q18 : Biotin:Thermo-21345 (Q)

Ions Score: 68 Expect: 3.1e-006

Matches : 35/202 fragment ions using 60 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	132.047761	66.527518					M							21
2	219.079789	110.043532			201.069224	101.038250	S	2426.169024	1213.588150	2409.142475	1205.074875	2408.158459	1204.582867	20
3	290.116903	145.562089			272.106338	136.556807	A	2339.136996	1170.072136	2322.110447	1161.558861	2321.126431	1161.066853	19
4	389.185317	195.096296			371.174752	186.091014	V	2268.099882	1134.553579	2251.073333	1126.040304	2250.089317	1125.548296	18
5	518.227910	259.617593			500.217345	250.612311	E	2169.031468	1085.019372	2152.004919	1076.506097	2151.020903	1076.014089	17
6	575.249374	288.128325			557.238809	279.123043	G	2039.988875	1020.498076	2022.962326	1011.984801	2021.978310	1011.492793	16
7	688.333438	344.670357			670.322873	335.665075	I	1982.967411	991.987343	1965.940862	983.474069	1964.956846	982.982061	15
8	848.364087	424.685682			830.353522	415.680399	C	1869.883347	935.445312	1852.856798	926.932037	1851.872782	926.440029	14
9	949.411766	475.209521			931.401201	466.204239	T	1709.852698	855.429987	1692.826149	846.916713	1691.842133	846.424704	13
10	1036.443794	518.725535			1018.433229	509.720253	S	1608.805019	804.906147	1591.778470	796.392873	1590.794454	795.900865	12
11	1165.486387	583.246832			1147.475822	574.241549	E	1521.772991	761.390133	1504.746442	752.876859	1503.762426	752.384851	11
12	1252.518415	626.762846			1234.507850	617.757563	S	1392.730398	696.868837	1375.703849	688.355563	1374.719833	687.863554	10
13	1349.571179	675.289228			1331.560614	666.283945	P	1305.698370	653.352823	1288.671821	644.839548	1287.687805	644.347540	9
14	1448.639593	724.823435			1430.629028	715.818152	V	1208.645606	604.826441	1191.619057	596.313166	1190.635041	595.821158	8
15	1561.723657	781.365467			1543.713092	772.360184	I	1109.577192	555.292234	1092.550643	546.778959	1091.566627	546.286951	7
16	1676.750600	838.878938			1658.740035	829.873656	D	996.493128	498.750202	979.466579	490.236927	978.482563	489.744919	6
17	1813.809512	907.408394			1795.798947	898.403112	H	881.466185	441.236730	864.439636	432.723456	863.455620	432.231448	5
18	2253.034838	1127.021057	2236.008289	1118.507782	2235.024273	1118.015774	Q	744.407273	372.707274	727.380724	364.194000	726.396708	363.701992	4
19	2310.056302	1155.531789	2293.029753	1147.018514	2292.045737	1146.526506	G	305.181947	153.094611	288.155398	144.581337	287.171382	144.089329	3
20	2411.103981	1206.055628	2394.077432	1197.542354	2393.093416	1197.050346	T	248.160483	124.583879	231.133934	116.070605	230.149918	115.578597	2
21							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **MSAVEGICTSESPVIDHQGTK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.0	2556.202240	0.003662	MSAVEGICTSESPVIDHQGTK

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

MASCOT 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 26249: 1301.584428 from(651.799490,2+) rtinseconds(1341) index(17305)

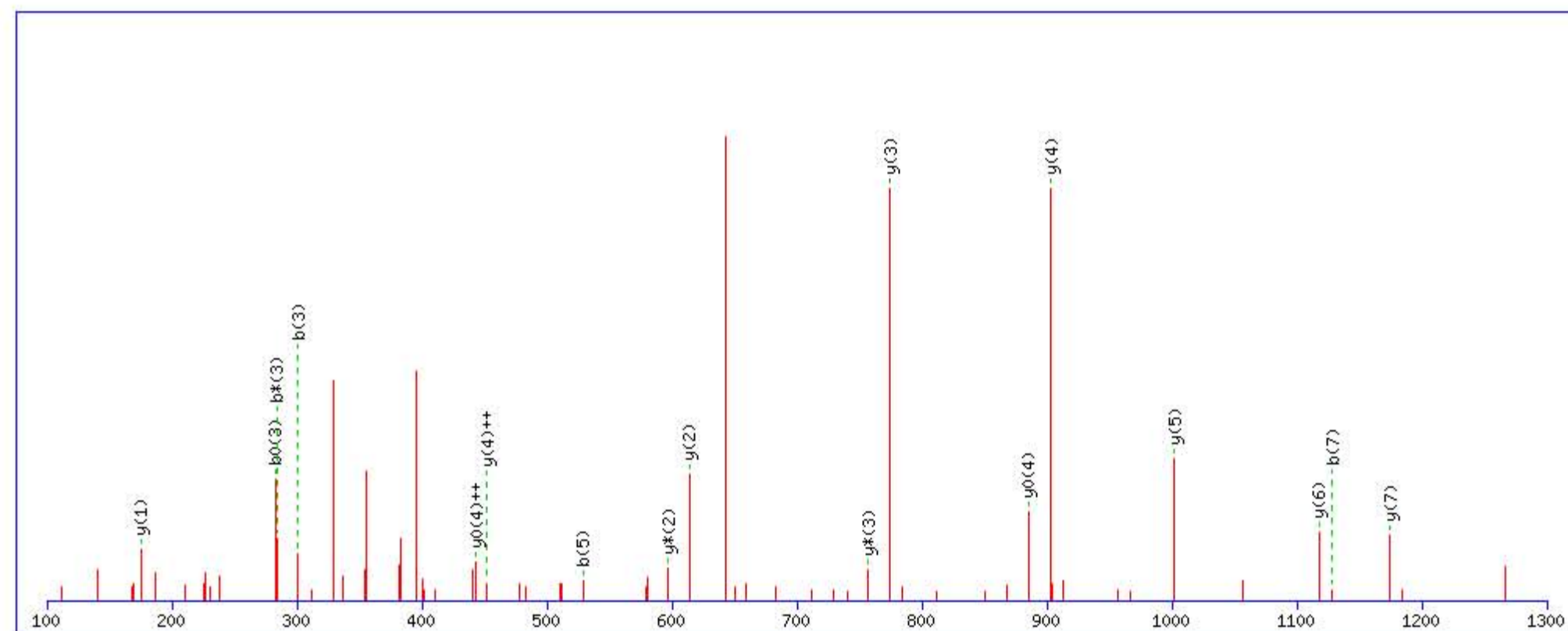
Title: Locus:1.1.1.469.21 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1301.585648

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

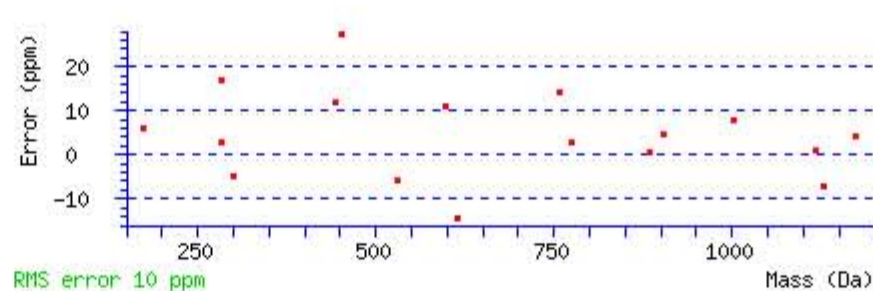
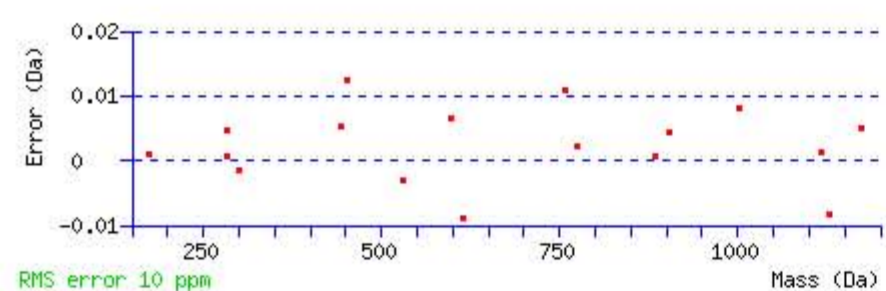
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 45 Expect: 0.00017

Matches : 17/74 fragment ions using 32 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.065854	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
44.6	1301.585648	-0.001220	QGDVECQR
10.6	1301.584763	-0.000335	KATEDAEGGDGPR
3.6	1301.584747	-0.000319	ESENLASGDQPR
2.2	1301.584747	-0.000319	QESPSQENIDR

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **YYQENFCEQICK**

Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

Match to Query 48853: 2078.896032 from(693.972620,3+) rtinseconds(2021) index(21814)

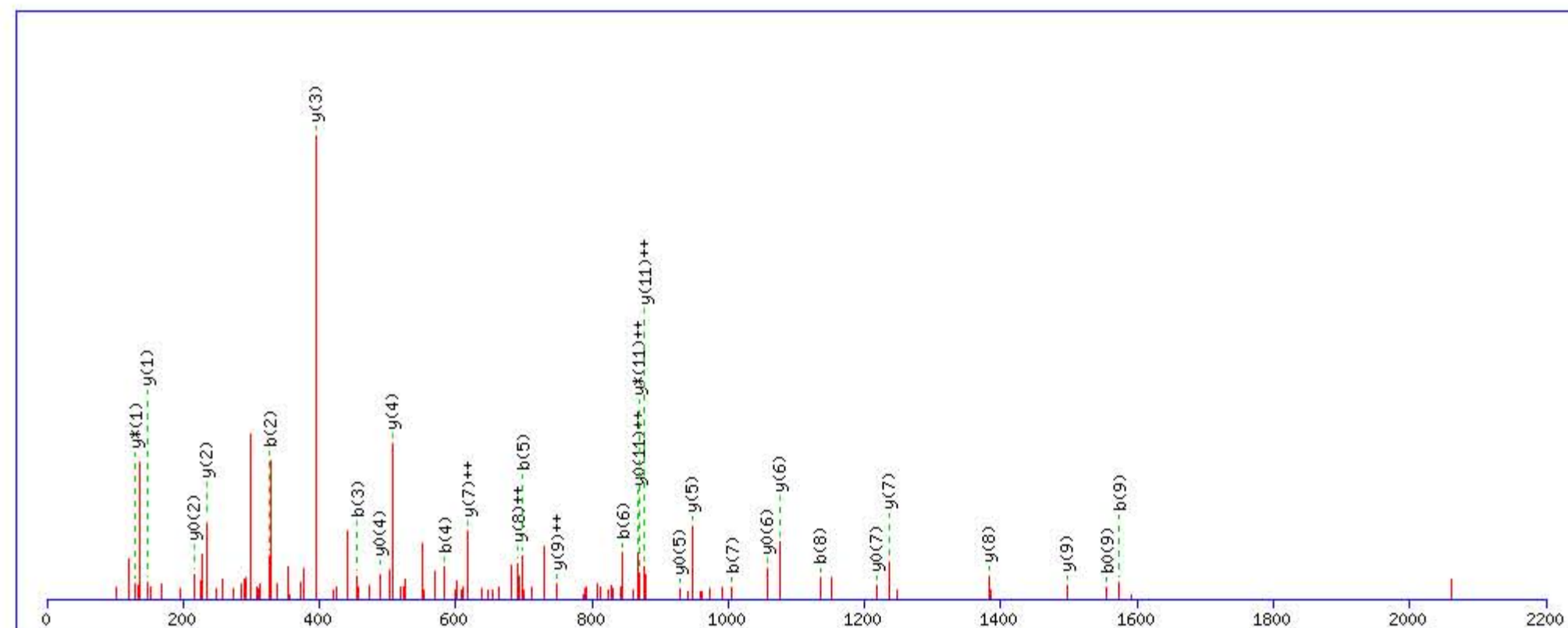
Title: Locus:1.1.1.706.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2078.889984

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

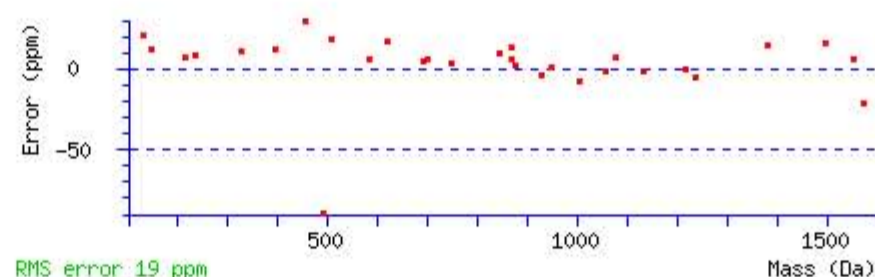
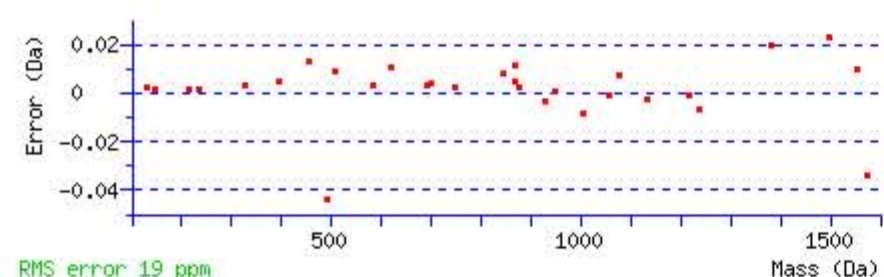
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 51 Expect: 3.1e-005

Matches : 30/132 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							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 **YYQENFCEQICK**

(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	2078.889984	0.006048	YYQENFCEQICK

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

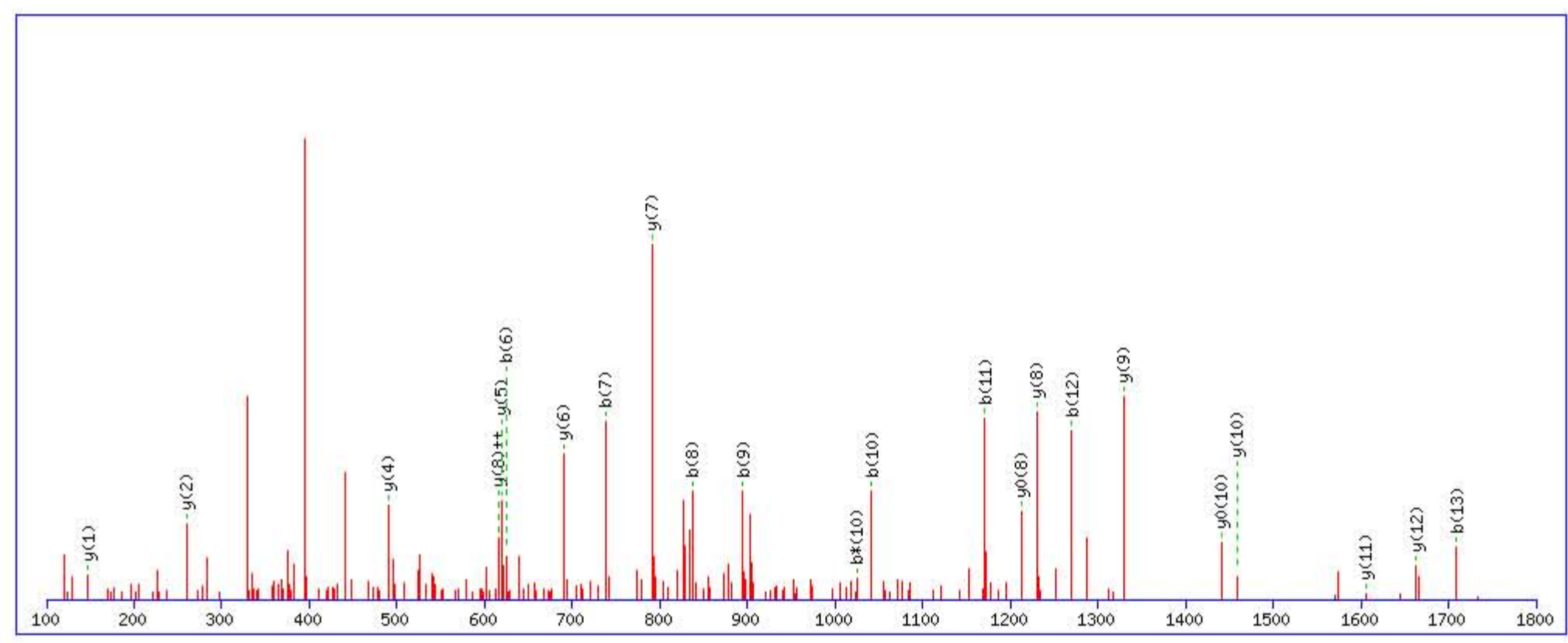
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VPANLENVGFVQTAEDDLK**
 Found in **CO6_HUMAN**, Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

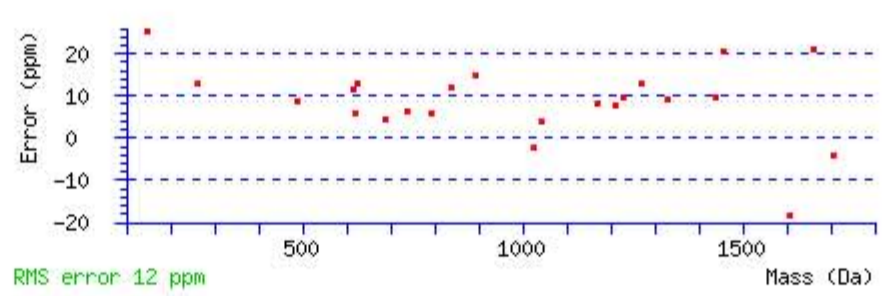
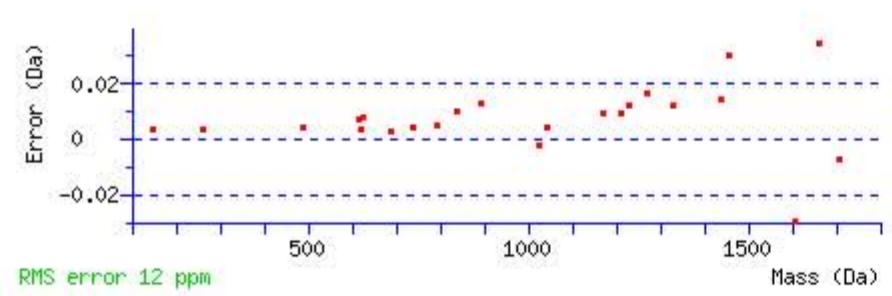
Match to Query 56675: 2498.245212 from(833.755680,3+) rtinseconds(2635) index(25329)
 Title: Locus:1.1.1.919.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2498.236282
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q13 : Biotin:Thermo-21345 (Q)
 Ions Score: 76 Expect: 6.7e-007
 Matches : 23/208 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							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 [VPANLENVGFVQTAEDDLK](#)
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
76.5	2498.236282	0.008930	VPANLENVGFVQTAEDDLK

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFGGQCR**

Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

Match to Query 20008: 1121.506508 from(561.760530,2+) rtinseconds(1531) index(3100)

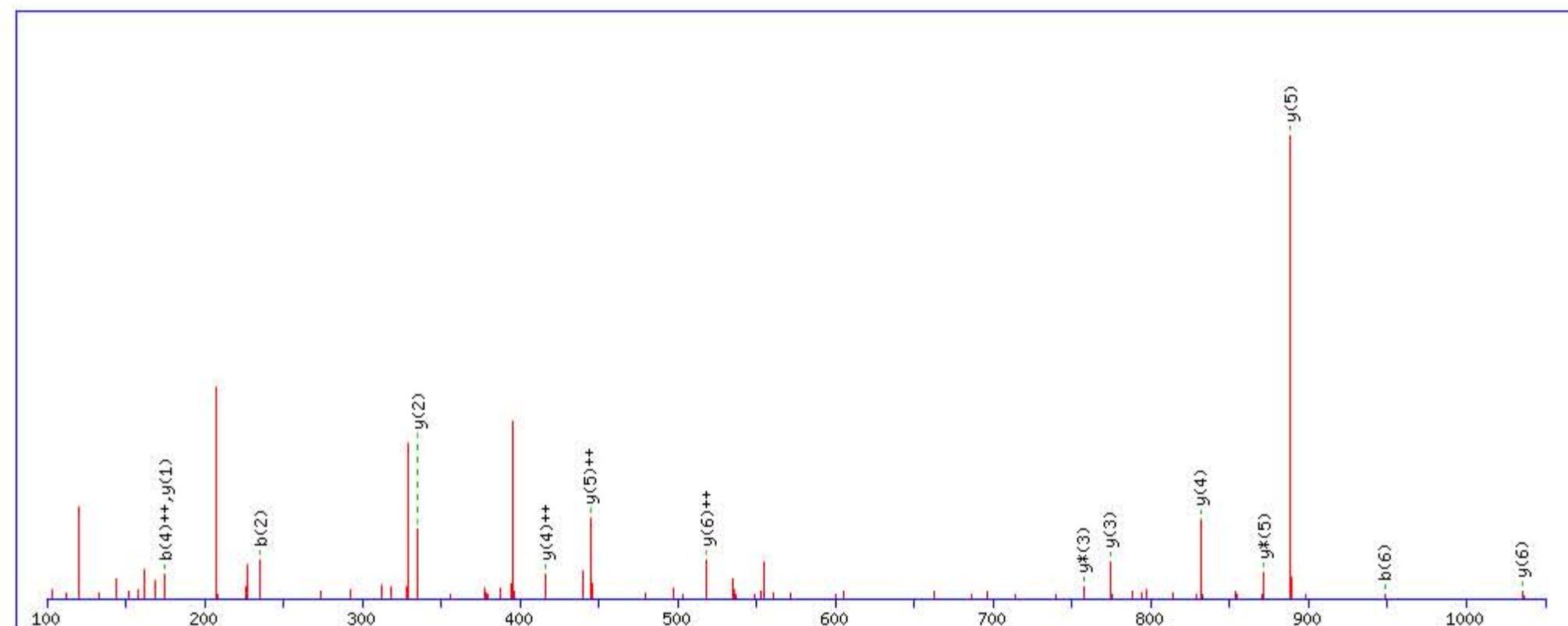
Title: Locus:1.1.1.1342.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1121.511032

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

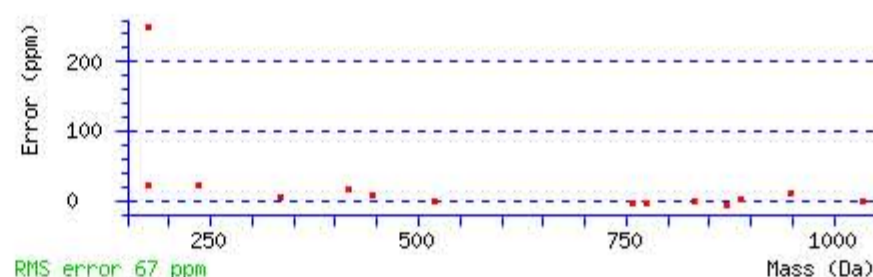
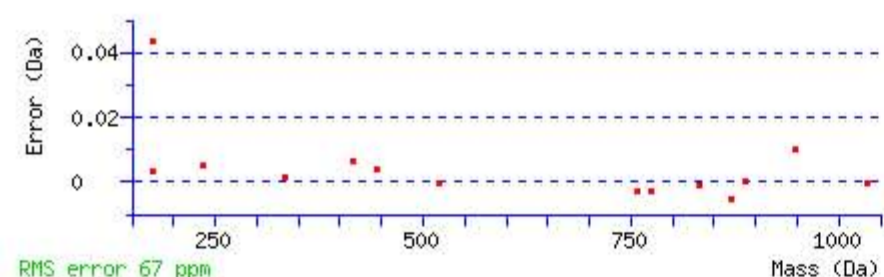
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 31 Expect: 0.0035

Matches : 14/52 fragment ions using 27 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	88.039304	44.523290			70.028739	35.518008	S					7
2	235.107718	118.057497			217.097153	109.052214	F	1035.486269	518.246773	1018.459720	509.733498	6
3	292.129182	146.568229			274.118617	137.562946	G	888.417855	444.712566	871.391306	436.199291	5
4	349.150646	175.078961			331.140081	166.073678	G	831.396391	416.201834	814.369842	407.688559	4
5	788.375972	394.691624	771.349423	386.178350	770.365407	385.686342	Q	774.374927	387.691102	757.348378	379.177827	3
6	948.406621	474.706949	931.380072	466.193674	930.396056	465.701666	C	335.149601	168.078438	318.123052	159.565164	2
7							R	175.118952	88.063114	158.092403	79.549839	1



NCBI BLAST search of **SFGGQCR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.4	1121.511032	-0.004524	SFGGQCR
5.0	1121.500259	0.006249	HPGFHQEDR
1.9	1121.502274	0.004234	MSVEEQIDR
1.9	1121.494873	0.011635	SANTSPSSSR
0.9	1121.513535	-0.007027	MGSGGDSLLGGR

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

MASCOT 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 30058: 1396.624348 from(699.319450,2+) rtinseconds(1635) index(3725)

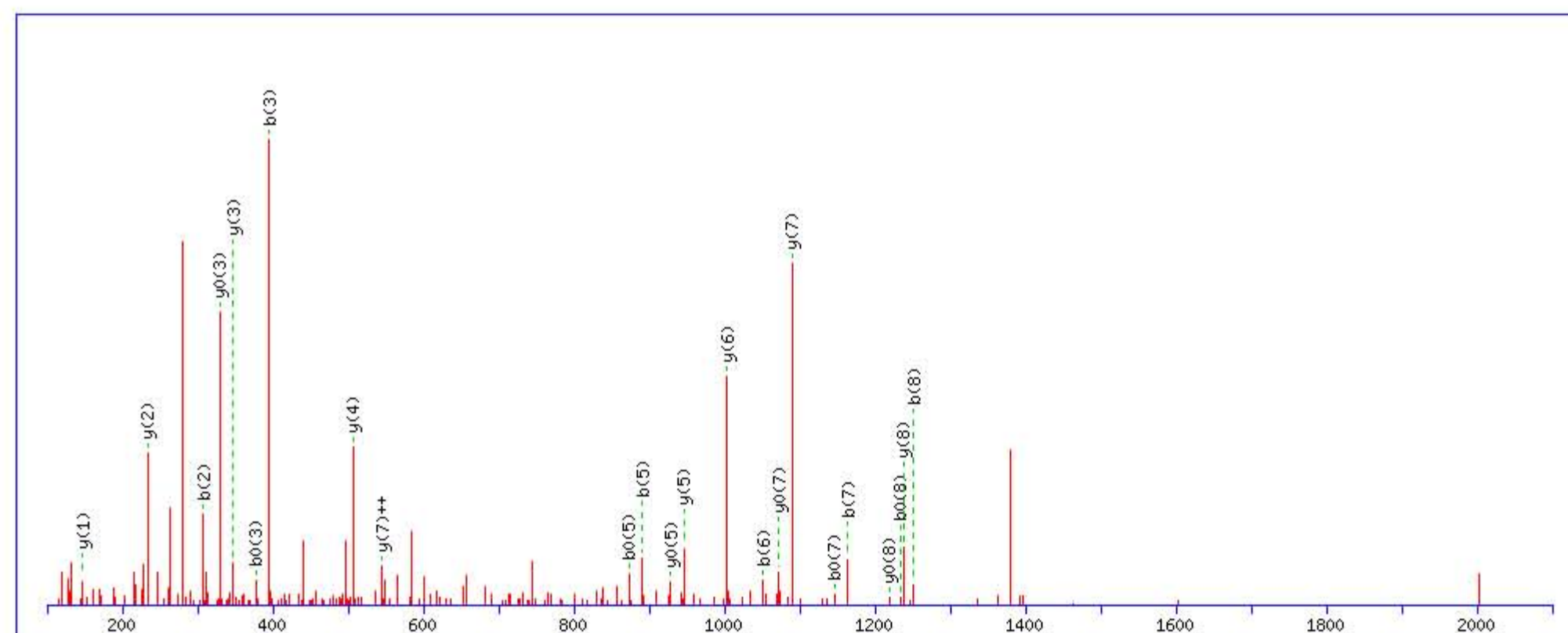
Title: Locus:1.1.1.1378.5 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1396.630157

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

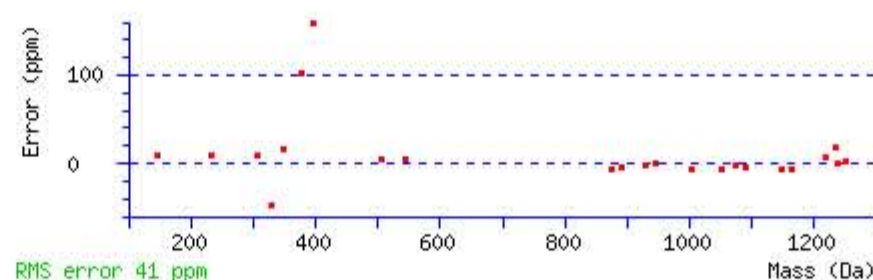
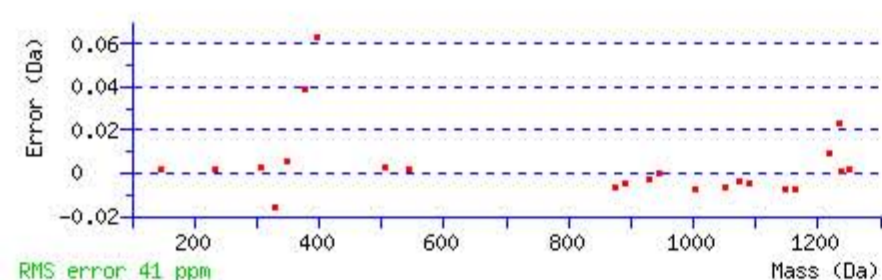
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 42 Expect: 0.0016

Matches : 23/82 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	161.037925	81.022600					C							9
2	308.106339	154.556807					F	1237.606777	619.307027	1220.580228	610.793752	1219.596212	610.301744	8
3	395.138367	198.072821			377.127802	189.067539	S	1090.538363	545.772819	1073.511814	537.259545	1072.527798	536.767537	7
4	452.159831	226.583553			434.149266	217.578271	G	1003.506335	502.256806	986.479786	493.743531	985.495770	493.251523	6
5	891.385157	446.196217	874.358608	437.682942	873.374592	437.190934	Q	946.484871	473.746074	929.458322	465.232799	928.474306	464.740791	5
6	1051.415806	526.211541	1034.389257	517.698267	1033.405241	517.206258	C	507.259545	254.133410	490.232996	245.620136	489.248980	245.128128	4
7	1164.499870	582.753573	1147.473321	574.240298	1146.489305	573.748290	I	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	3
8	1251.531898	626.269587	1234.505349	617.756313	1233.521333	617.264304	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
9							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **CFSGQCISK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.7	1396.630157	-0.005809	CFSGQCISK
11.2	1396.629272	-0.004924	QLSQAETDFCK
1.2	1396.629257	-0.004909	FDNLMNQKEDK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AASGTQNNVLR**

Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

Match to Query 32220: 1440.747668 from(721.381110,2+) rtinseconds(1571) index(3347)

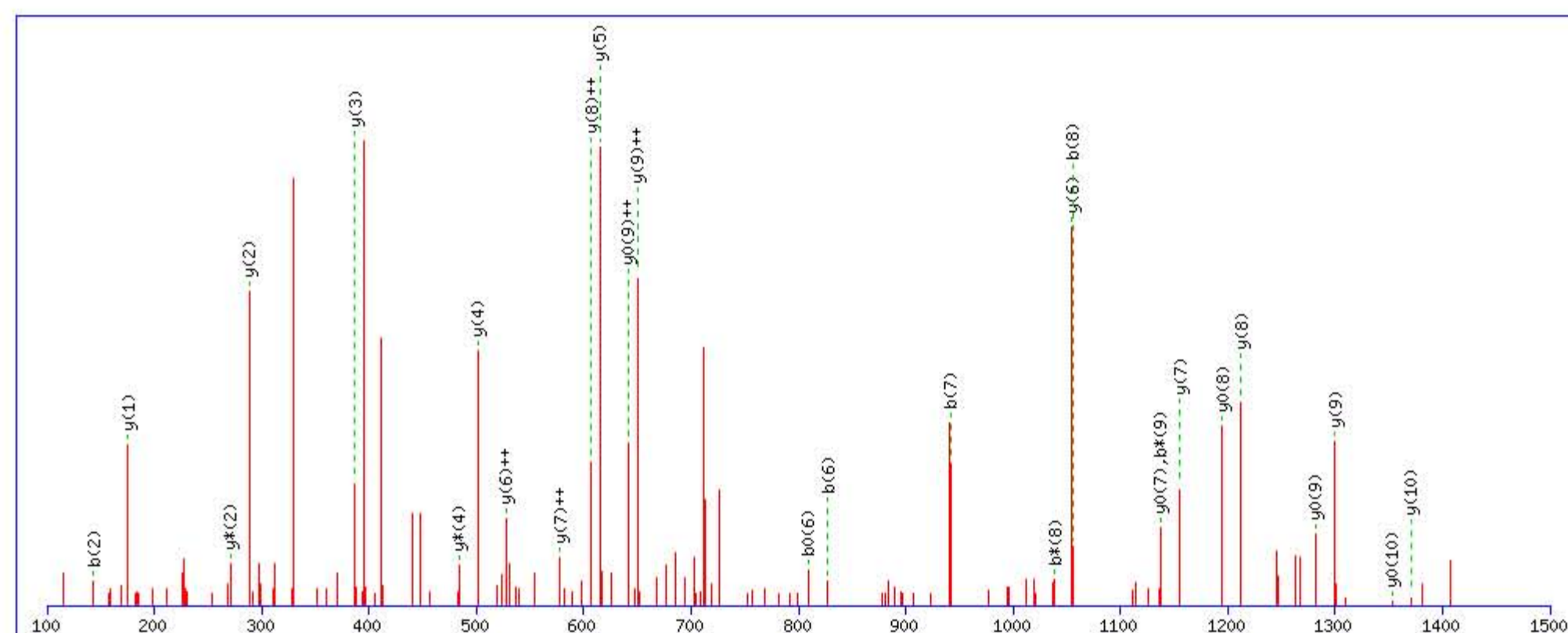
Title: Locus:1.1.1.1356.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1440.750717

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

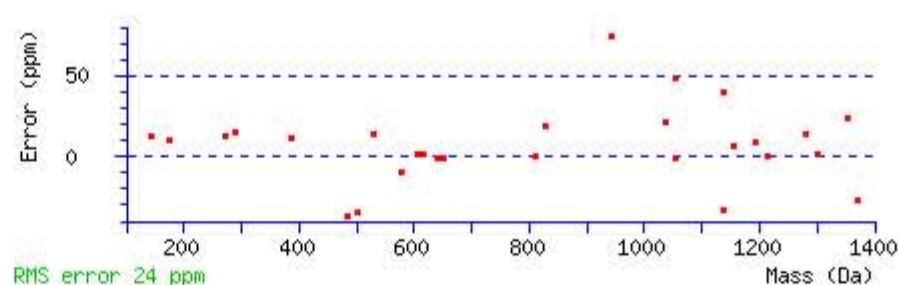
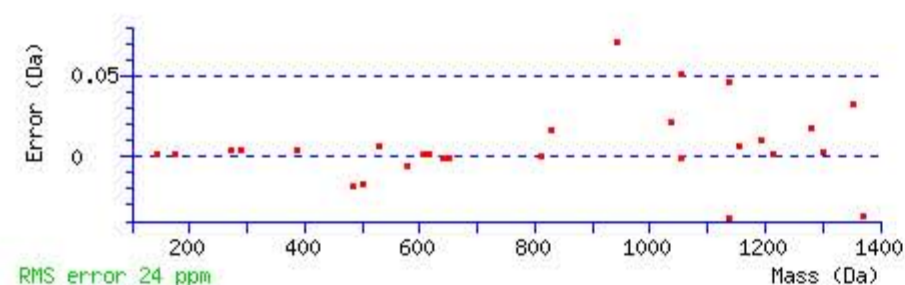
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 1.9e-006

Matches : 28/94 fragment ions using 52 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.044390	36.525833					A							11
2	143.081504	72.044390					A	1370.720895	685.864086	1353.694346	677.350811	1352.710330	676.858803	10
3	230.113532	115.560404			212.102967	106.555121	S	1299.683781	650.345529	1282.657232	641.832254	1281.673216	641.340246	9
4	287.134996	144.071136			269.124431	135.065854	G	1212.651753	606.829515	1195.625204	598.316240	1194.641188	597.824232	8
5	388.182675	194.594976			370.172110	185.589693	T	1155.630289	578.318783	1138.603740	569.805508	1137.619724	569.313500	7
6	827.408001	414.207639	810.381452	405.694364	809.397436	405.202356	Q	1054.582610	527.794943	1037.556061	519.281669			6
7	941.450928	471.229102	924.424379	462.715828	923.440363	462.223820	N	615.357284	308.182280	598.330735	299.669006			5
8	1055.493855	528.250566	1038.467306	519.737291	1037.483290	519.245283	N	501.314357	251.160816	484.287808	242.647542			4
9	1154.562269	577.784773	1137.535720	569.271498	1136.551704	568.779490	V	387.271430	194.139353	370.244881	185.626078			3
10	1267.646333	634.326805	1250.619784	625.813530	1249.635768	625.321522	L	288.203016	144.605146	271.176467	136.091871			2
11							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **AASGTQNNVLR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.7	1440.750717	-0.003049	AASGTQNNVLR
4.5	1440.743515	0.004153	FIQLLTEFQMR
3.0	1440.736099	0.011569	AAGSLAAAEFSPPR
2.8	1440.739487	0.008181	AAVTGQDEAIR
2.6	1440.732086	0.015582	GEENDVPSLRGLR
2.3	1440.736115	0.011553	ETFEGPKHEVLR
2.2	1440.756073	-0.008405	WKHYLRVHMR
1.6	1440.732071	0.015597	ASEASKVHNEITR
1.4	1440.750748	-0.003080	MDVLP TGGGRPGLR
1.3	1440.739471	0.008197	EEKCPLGTAPALR

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 41989: 1765.952862 from(589.658230,3+) rtinseconds(2466) index(8422)

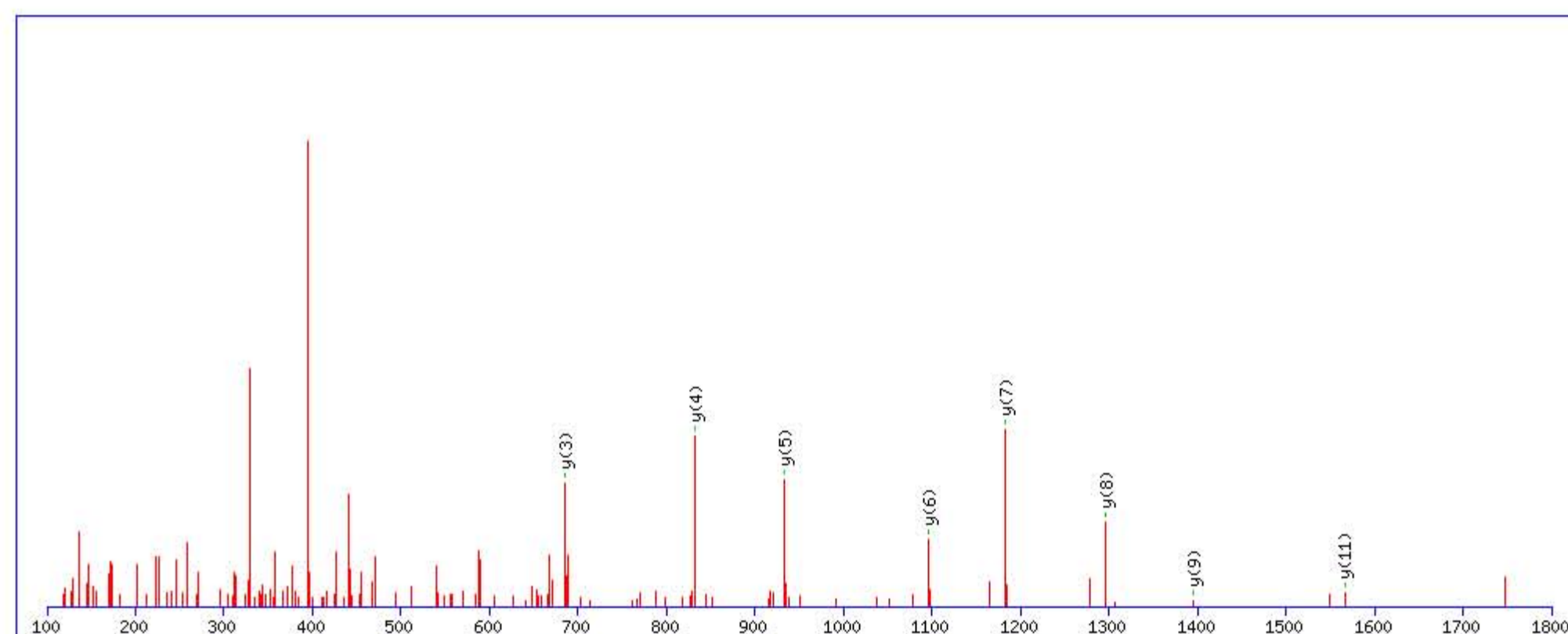
Title: Locus:1.1.1.1668.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1765.943680

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

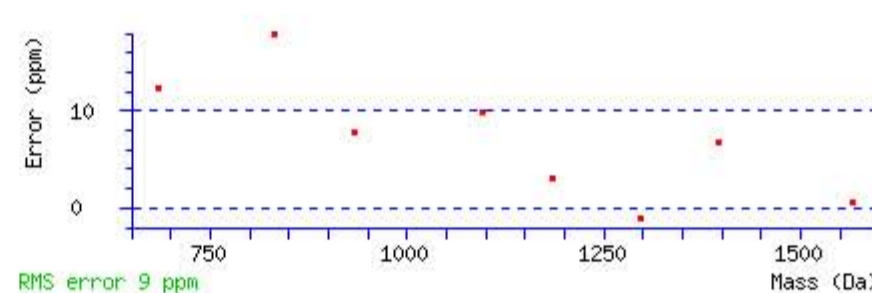
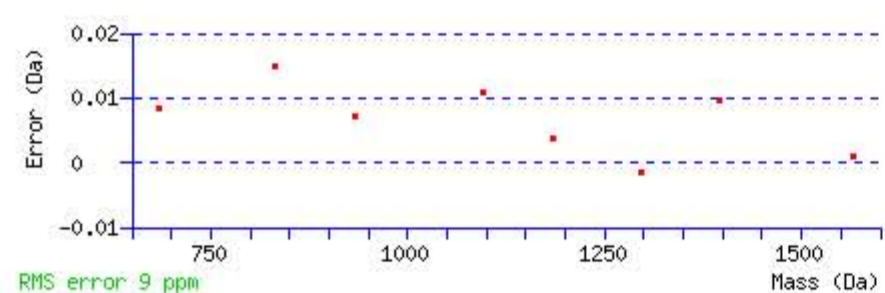
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 49 Expect: 4.3e-005

Matches : 8/128 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							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
49.2	1765.943680	0.009182	LSGNVLSYTFQVK
2.7	1765.950882	0.001980	VTGNVSKKINYLVMGR

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 42575: 1791.808588 from(896.911570,2+) rtinseconds(1744) index(4356)

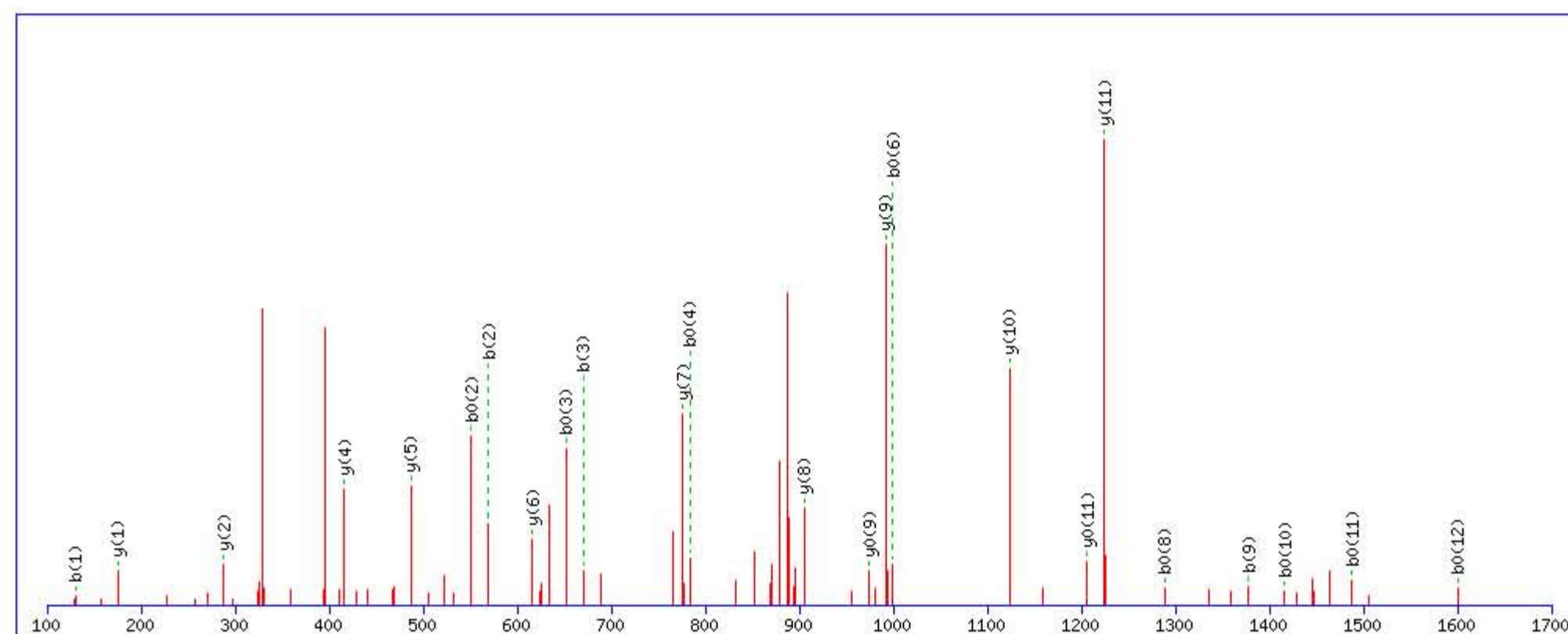
Title: Locus:1.1.1.1416.23 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1791.795349

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

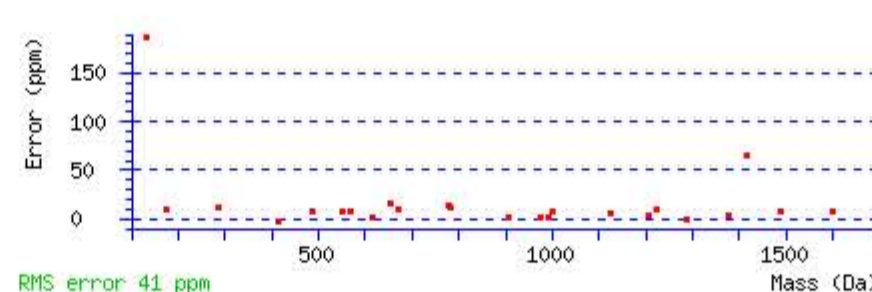
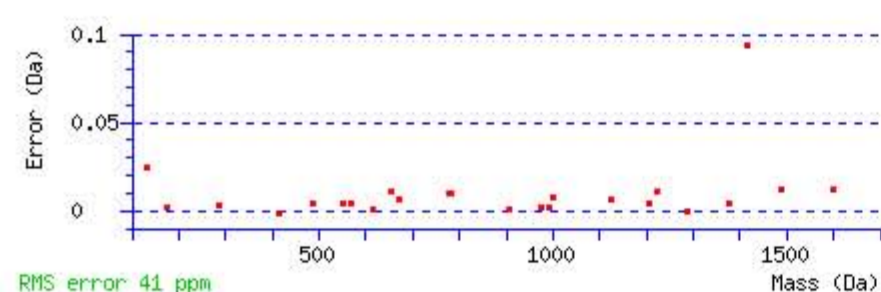
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 70 Expect: 9.9e-007

Matches : 24/132 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	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
70.1	1791.795349	0.013239	EQTMSECEAGALR

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

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 53638: 2336.992182 from(780.004670,3+) rtinseconds(2109) index(6493)

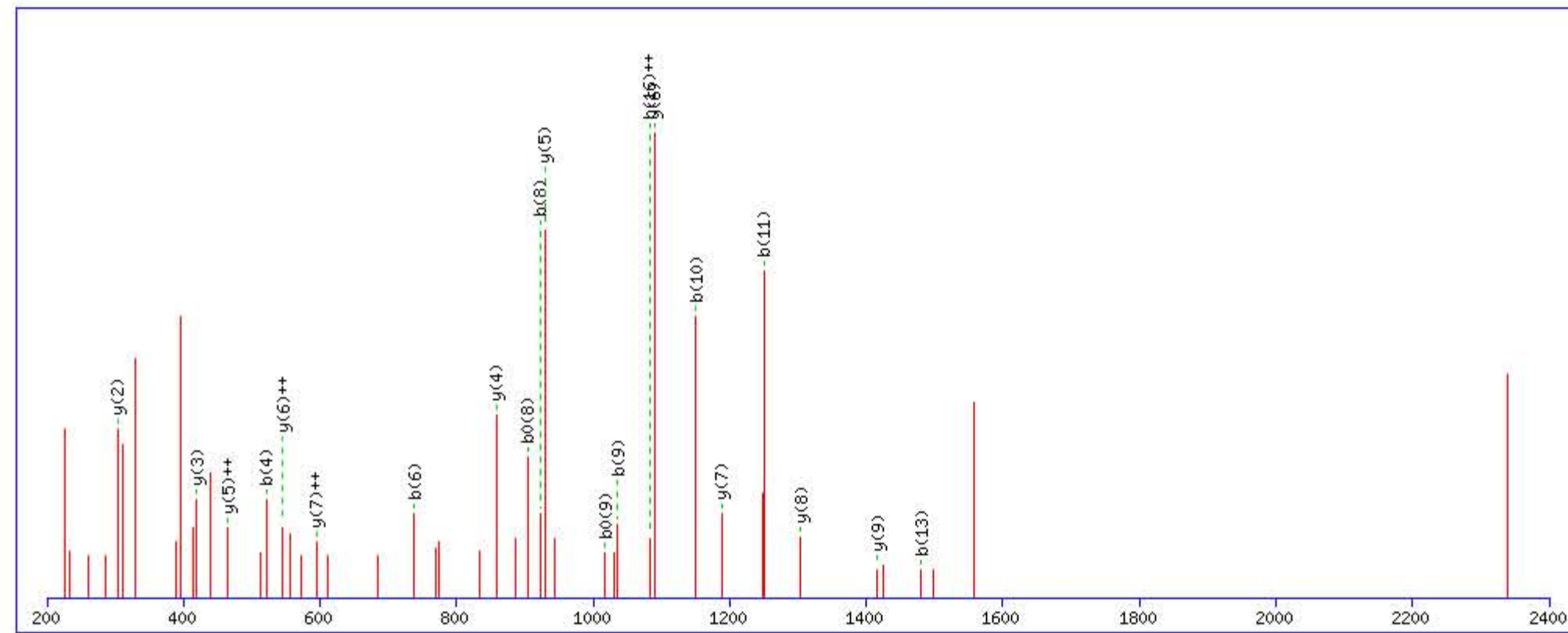
Title: Locus:1.1.1.1543.24 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2336.989792

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

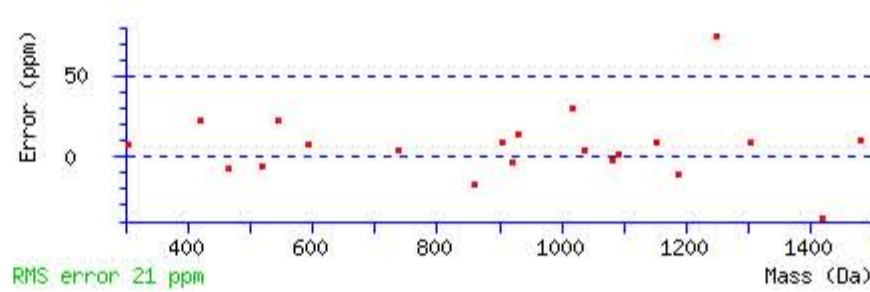
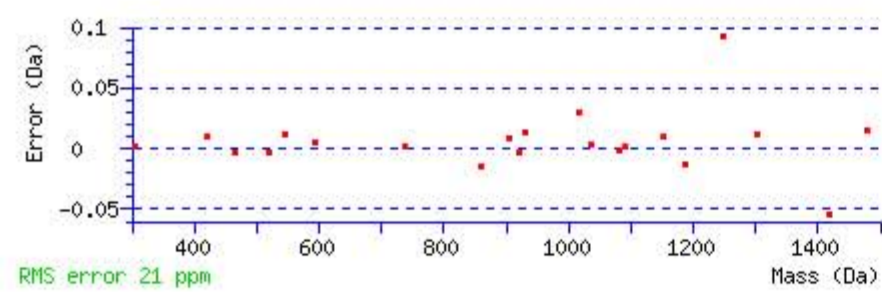
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 7.5e-005

Matches : 21/158 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	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
45.6	2336.989792	0.002390	MPYECGPSLDVCAQDER

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **IACVLPVLM DGIQSH P QKPFYTVGEK**

Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

Match to Query 64467: 3237.697020 from(648.546680,5+) rtinseconds(2566) index(8899)

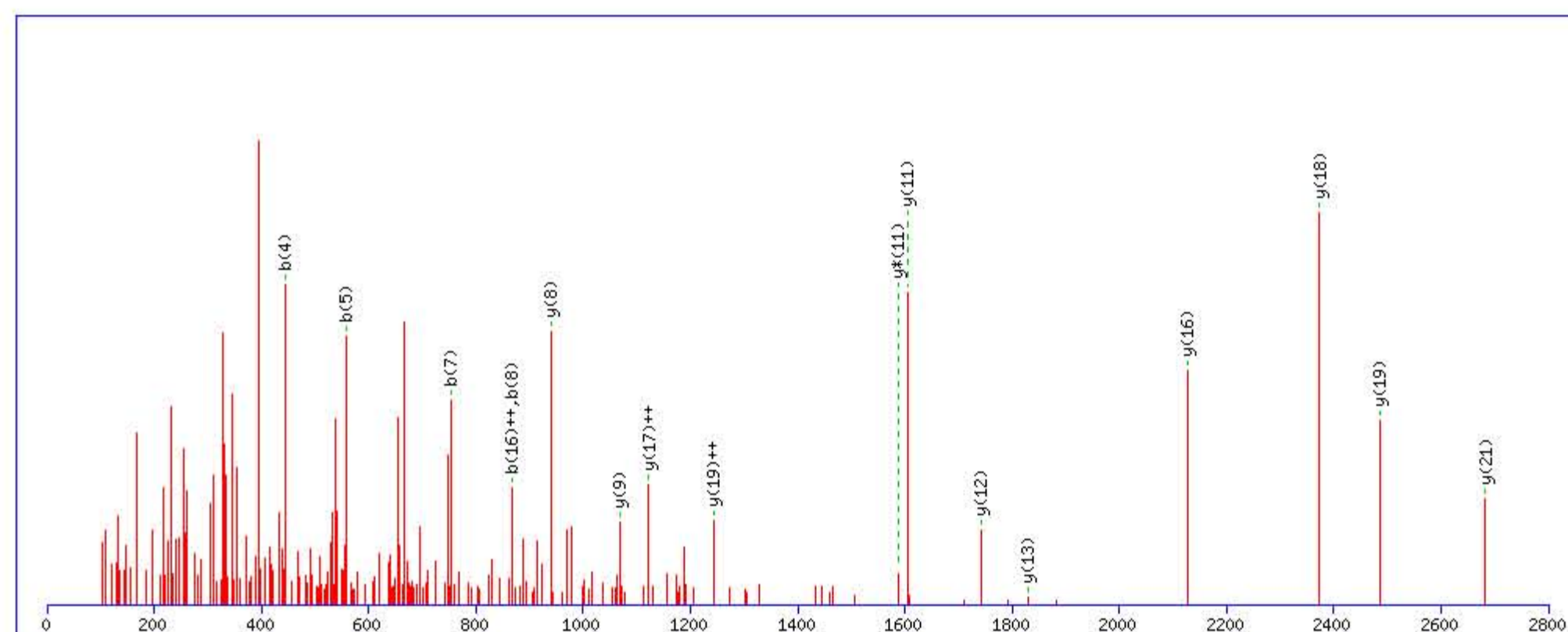
Title: Locus:1.1.1.1703.5 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3237.675262

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

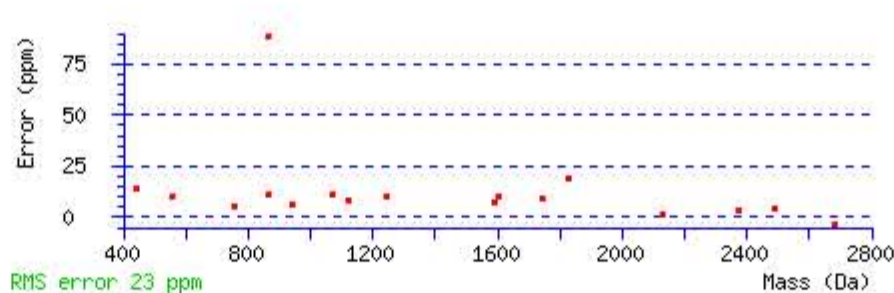
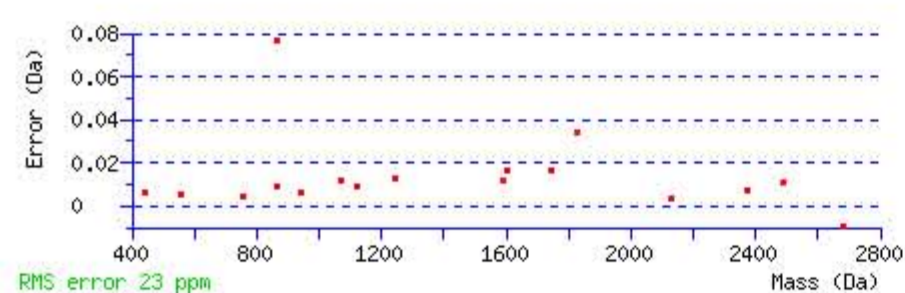
Variable modifications:

Q17 : Biotin:Thermo-21345 (Q)

Ions Score: 55 Expect: 7.3e-005

Matches : 17/256 fragment ions using 22 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					I							26
2	185.128454	93.067865					A	3125.598471	1563.302873	3108.571922	1554.789599	3107.587906	1554.297591	25
3	345.159103	173.083190					C	3054.561357	1527.784316	3037.534808	1519.271042	3036.550792	1518.779034	24
4	444.227517	222.617397					V	2894.530708	1447.768992	2877.504159	1439.255717	2876.520143	1438.763709	23
5	557.311581	279.159429					L	2795.462294	1398.234785	2778.435745	1389.721510	2777.451729	1389.229502	22
6	654.364345	327.685811					P	2682.378230	1341.692753	2665.351681	1333.179478	2664.367665	1332.687470	21
7	753.432759	377.220018					V	2585.325466	1293.166371	2568.298917	1284.653096	2567.314901	1284.161088	20
8	866.516823	433.762050					L	2486.257052	1243.632164	2469.230503	1235.118889	2468.246487	1234.626881	19
9	997.557308	499.282292					M	2373.172988	1187.090132	2356.146439	1178.576857	2355.162423	1178.084849	18
10	1112.584251	556.795764			1094.573686	547.790481	D	2242.132503	1121.569889	2225.105954	1113.056615	2224.121938	1112.564607	17
11	1169.605715	585.306495			1151.595150	576.301213	G	2127.105560	1064.056418	2110.079011	1055.543143	2109.094995	1055.051135	16
12	1282.689779	641.848527			1264.679214	632.843245	I	2070.084096	1035.545686	2053.057547	1027.032411	2052.073531	1026.540403	15
13	1410.748357	705.877816	1393.721808	697.364542	1392.737792	696.872534	Q	1957.000032	979.003654	1939.973483	970.490380	1938.989467	969.998371	14
14	1497.780385	749.393830	1480.753836	740.880556	1479.769820	740.388548	S	1828.941454	914.974365	1811.914905	906.461091	1810.930889	905.969083	13
15	1634.839297	817.923286	1617.812748	809.410012	1616.828732	808.918004	H	1741.909426	871.458351	1724.882877	862.945077	1723.898861	862.453068	12
16	1731.892061	866.449668	1714.865512	857.936394	1713.881496	857.444386	P	1604.850514	802.928895	1587.823965	794.415621	1586.839949	793.923612	11
17	2171.117387	1086.062331	2154.090838	1077.549057	2153.106822	1077.057049	Q	1507.797750	754.402513	1490.771201	745.889239	1489.787185	745.397230	10
18	2299.212350	1150.109813	2282.185801	1141.596538	2281.201785	1141.104530	K	1068.572424	534.789850	1051.545875	526.276575	1050.561859	525.784567	9
19	2396.265114	1198.636195	2379.238565	1190.122920	2378.254549	1189.630912	P	940.477461	470.742368	923.450912	462.229094	922.466896	461.737086	8
20	2543.333528	1272.170402	2526.306979	1263.657127	2525.322963	1263.165119	F	843.424697	422.215986	826.398148	413.702712	825.414132	413.210704	7
21	2706.396857	1353.702066	2689.370308	1345.188792	2688.386292	1344.696784	Y	696.356283	348.681779	679.329734	340.168505	678.345718	339.676497	6
22	2807.444536	1404.225906	2790.417987	1395.712631	2789.433971	1395.220623	T	533.292954	267.150115	516.266405	258.636840	515.282389	258.144832	5
23	2906.512950	1453.760113	2889.486401	1445.246838	2888.502385	1444.754830	V	432.245275	216.626275	415.218726	208.113001	414.234710	207.620993	4
24	2963.534414	1482.270845	2946.507865	1473.757570	2945.523849	1473.265562	G	333.176861	167.092069	316.150312	158.578794	315.166296	158.086786	3
25	3092.577007	1546.792141	3075.550458	1538.278867	3074.566442	1537.786859	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
26							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **IACVLPVLM DGIQSH P QKPFYTVGEK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.8	3237.675262	0.021758	IACVLPVLM DGIQSH P QKPFYTVGEK
23.1	3237.675262	0.021758	IACVLPVLM DGIQSH P QKPFYTVGEK

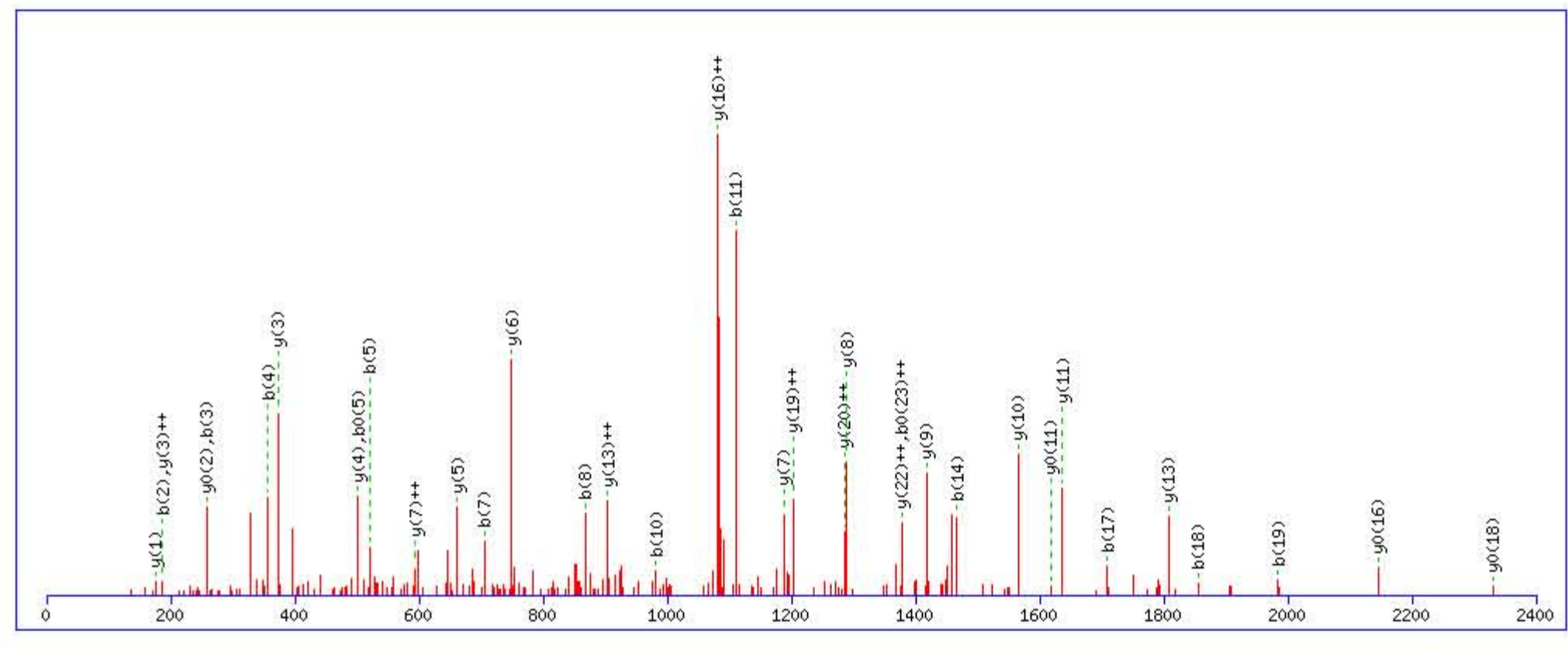
MASCOT Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVAVYGQYGGQPCVGNAFETQSCEPTR**
 Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

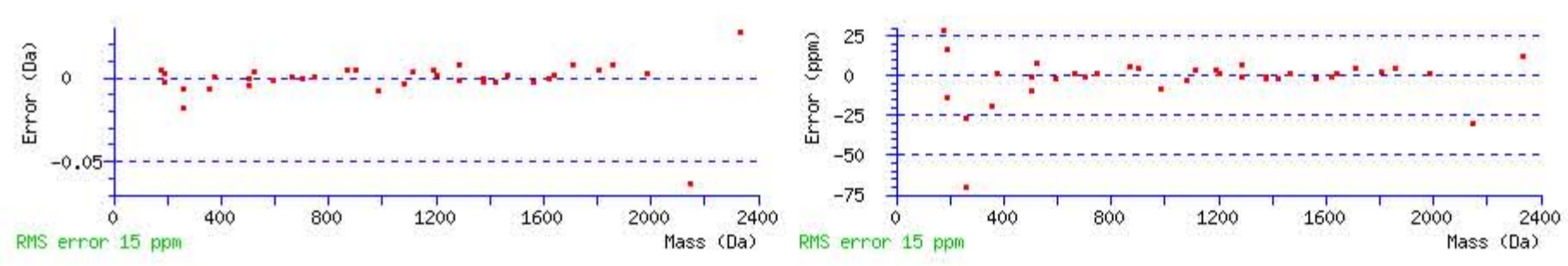
Match to Query 65401: 3272.482782 from(1091.834870,3+) rtinseconds(2163) index(6833)
 Title: Locus:1.1.1.1562.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 3272.468933
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q21 : Biotin:Thermo-21345 (Q)
 Ions Score: 116 Expect: 2.1e-011
 Matches : 36/298 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							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
116.4	3272.468933	0.013849	SVAVYGQYGGQPCVGNAFETQSCEPTR
23.9	3272.468933	0.013849	SVAVYGQYGGQPCVGNAFETQSCEPTR
7.5	3272.468933	0.013849	SVAVYGQYGGQPCVGNAFETQSCEPTR

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 15468: 983.519868 from(492.767210,2+) rtinseconds(1404) index(17786)

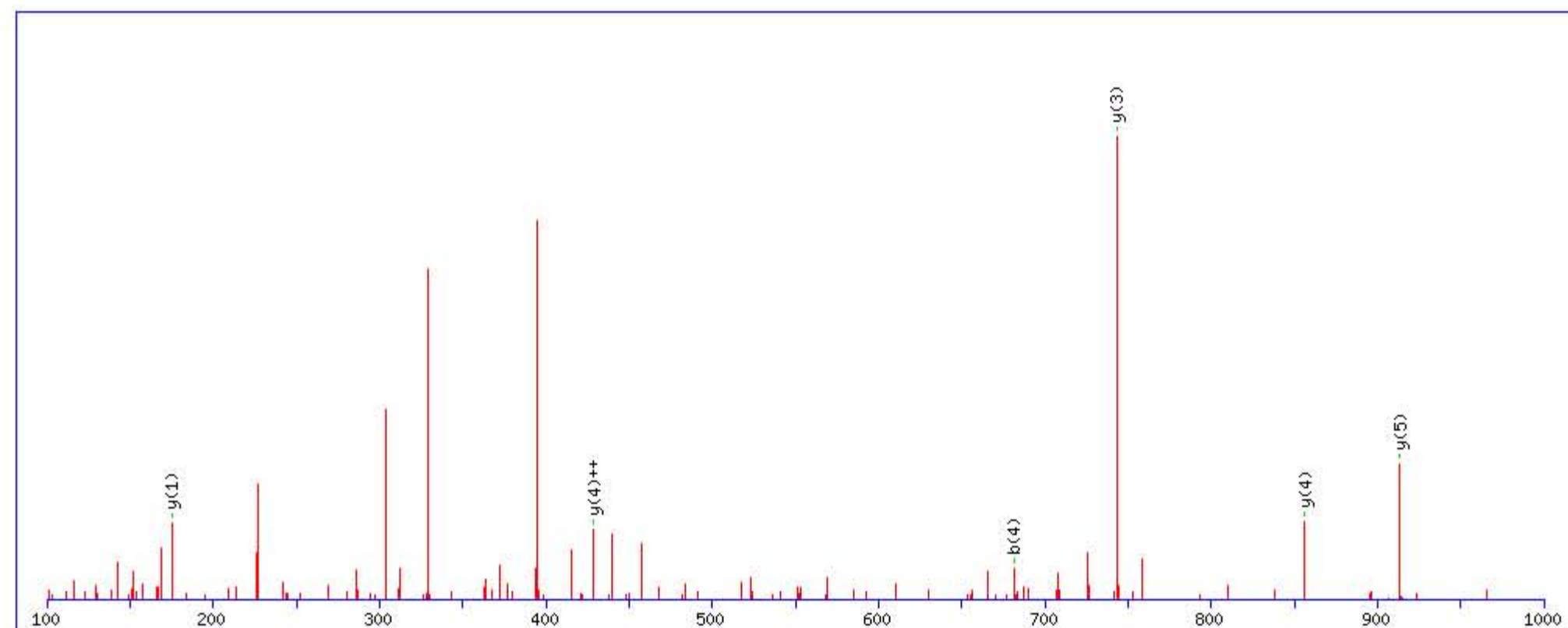
Title: Locus:1.1.1.491.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 983.522217

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

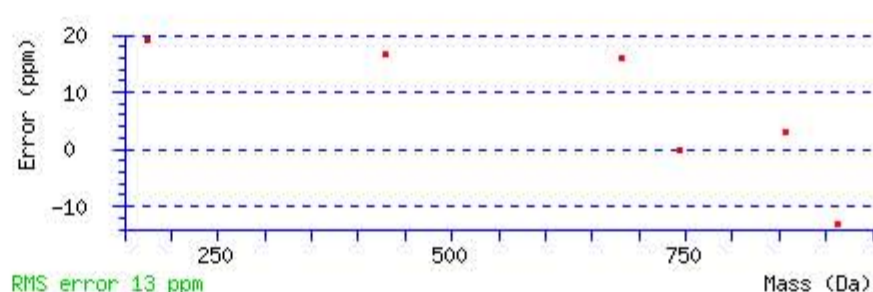
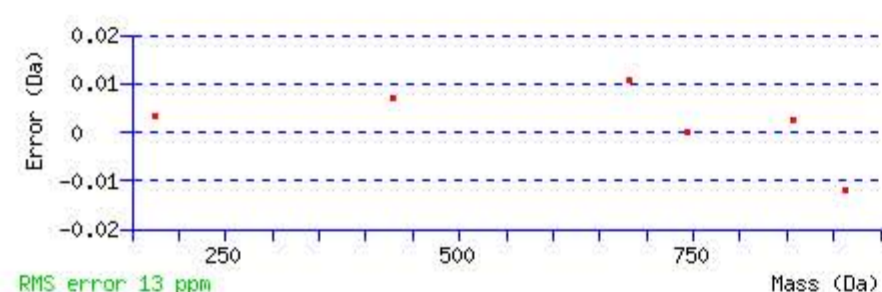
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.051

Matches : 6/44 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
26.0	983.522217	-0.002349	AGIQER
23.0	983.522217	-0.002349	AGLEQR
13.3	983.522217	-0.002349	QIQER
13.3	983.522217	-0.002349	QLQER
11.1	983.522202	-0.002334	KLMENPPR
11.1	983.522217	-0.002349	QLEQR
11.1	983.530090	-0.010222	QLLNHFGR
10.0	983.514816	0.005052	QPVREAER
8.2	983.522217	-0.002349	AGQELR
4.1	983.522217	-0.002349	AAQVER

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 40040: 1679.723448 from(840.869000,2+) rtinseconds(1510) index(18554)

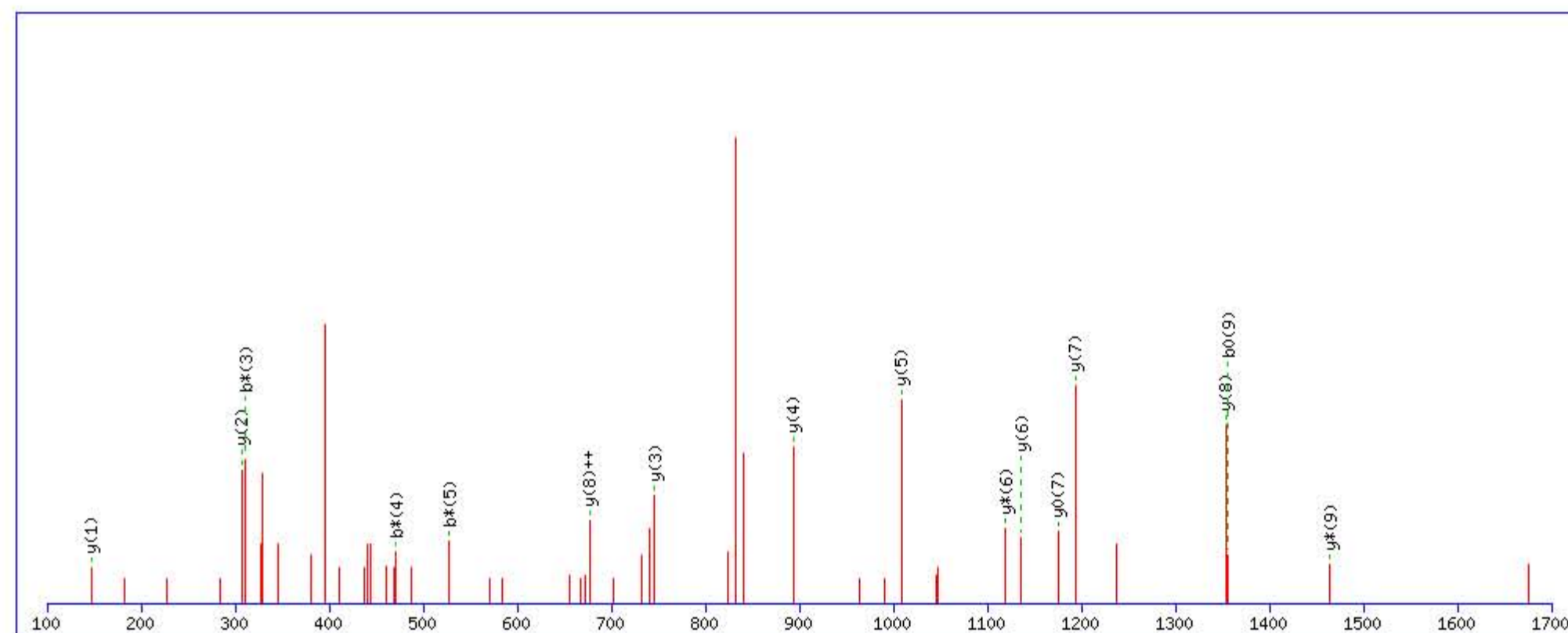
Title: Locus:1.1.1.528.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1679.721832

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

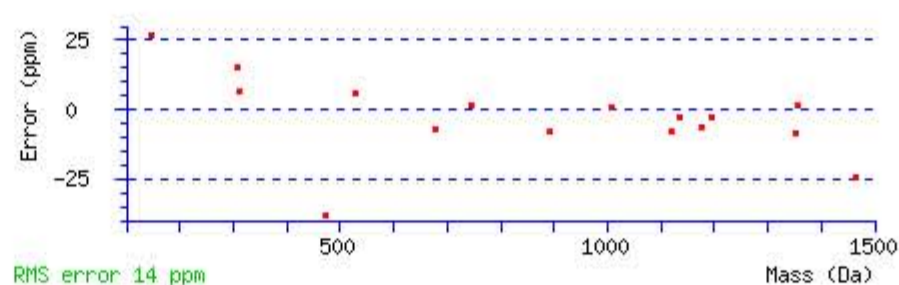
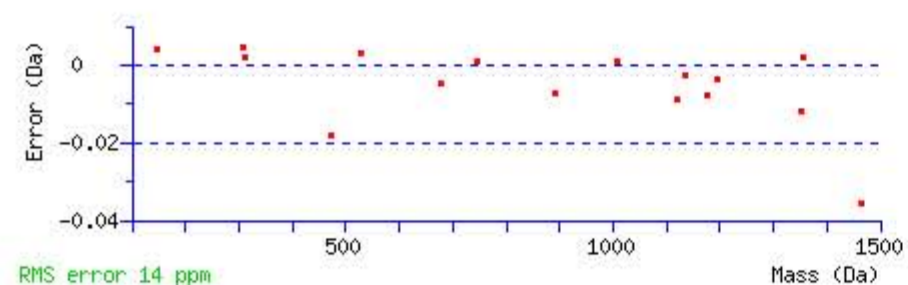
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 47 Expect: 8e-005

Matches : 16/100 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	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	$M_r(\text{calc})$:	Delta	Sequence
47.2	1679.721832	0.001616	QAQCGQDFQCK
17.3	1679.721832	0.001616	QAQCGQDFQCK

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

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **ALDQYLMEFNACR**

Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

Match to Query 45377: 1940.896808 from(971.455680,2+) rtinseconds(2560) index(39843)

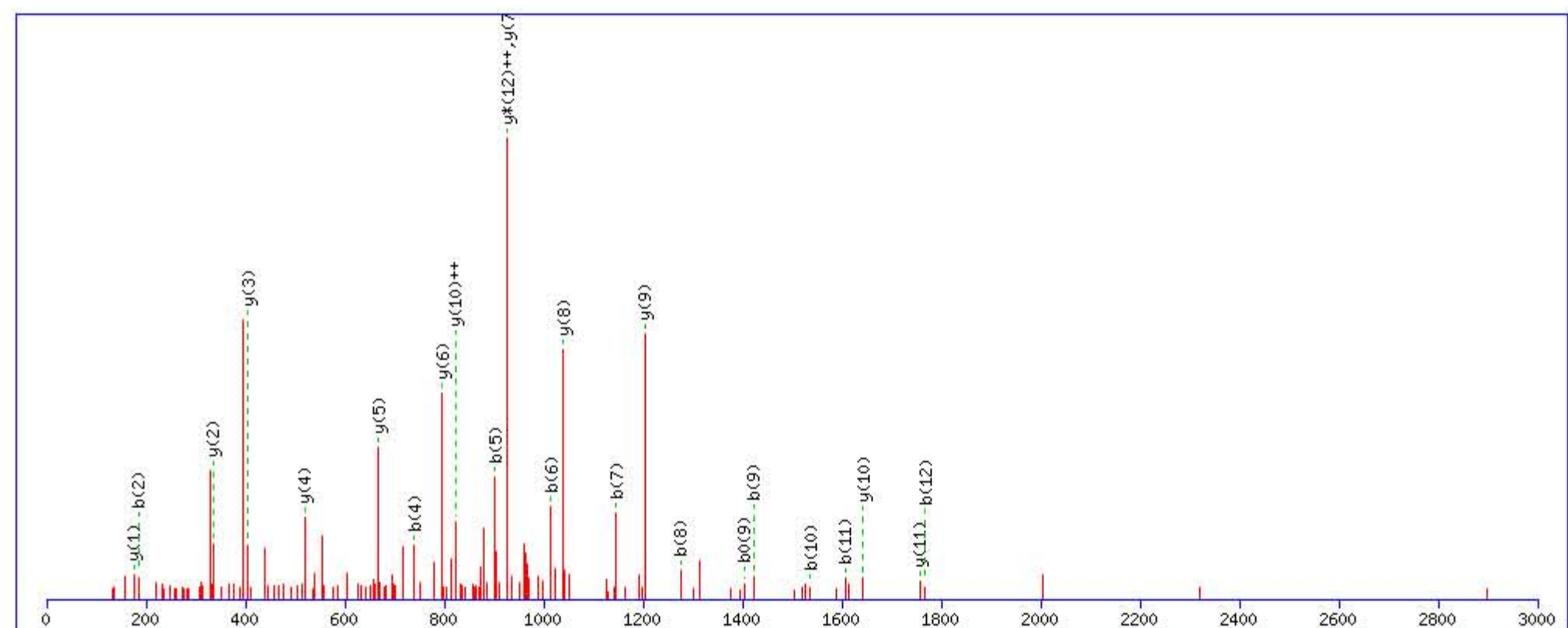
Title: Locus:1.1.1.3310.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1940.894669

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

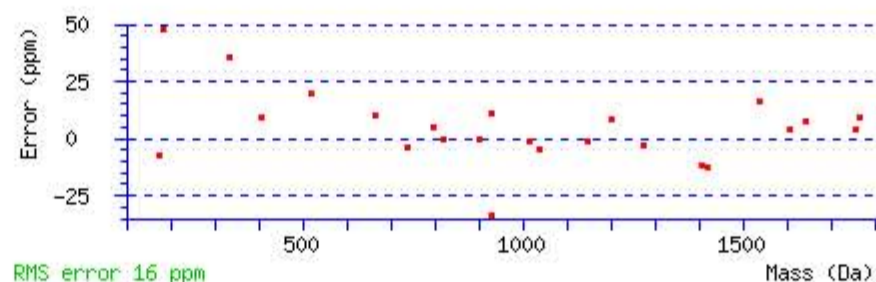
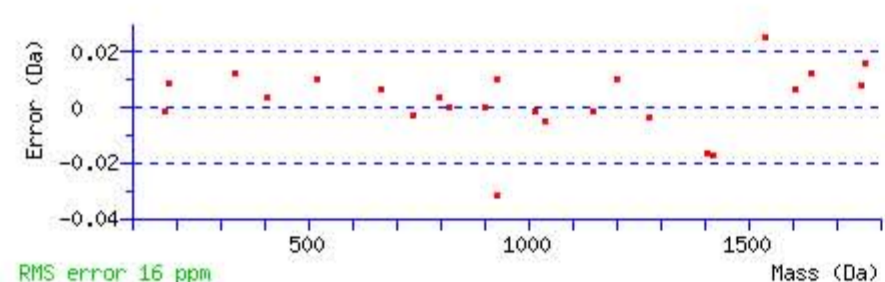
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 61 Expect: 8.3e-006

Matches : 24/124 fragment ions using 48 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.044390	36.525833					A							13
2	185.128454	93.067865					L	1870.864860	935.936068	1853.838311	927.422794	1852.854295	926.930786	12
3	300.155397	150.581336			282.144832	141.576054	D	1757.780796	879.394036	1740.754247	870.880762	1739.770231	870.388754	11
4	739.380723	370.194000	722.354174	361.680725	721.370158	361.188717	Q	1642.753853	821.880565	1625.727304	813.367290	1624.743288	812.875282	10
5	902.444052	451.725664	885.417503	443.212390	884.433487	442.720382	Y	1203.528527	602.267902	1186.501978	593.754627	1185.517962	593.262619	9
6	1015.528116	508.267696	998.501567	499.754422	997.517551	499.262414	L	1040.465198	520.736237	1023.438649	512.222963	1022.454633	511.730955	8
7	1146.568601	573.787939	1129.542052	565.274664	1128.558036	564.782656	M	927.381134	464.194205	910.354585	455.680931	909.370569	455.188923	7
8	1275.611194	638.309235	1258.584645	629.795961	1257.600629	629.303953	E	796.340649	398.673963	779.314100	390.160688	778.330084	389.668680	6
9	1422.679608	711.843442	1405.653059	703.330168	1404.669043	702.838160	F	667.298056	334.152666	650.271507	325.639392			5
10	1536.722535	768.864906	1519.695986	760.351631	1518.711970	759.859623	N	520.229642	260.618459	503.203093	252.105185			4
11	1607.759649	804.383463	1590.733100	795.870188	1589.749084	795.378180	A	406.186715	203.596995	389.160166	195.083721			3
12	1767.790298	884.398787	1750.763749	875.885513	1749.779733	875.393505	C	335.149601	168.078438	318.123052	159.565164			2
13							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [ALDQYLMEFNACR](#)

(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	1940.894669	0.002139	ALDQYLMEFNACR

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

MASCOT SCIENCE 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 46251: 1990.900122 from(664.640650,3+) rtinseconds(1837) index(35232)

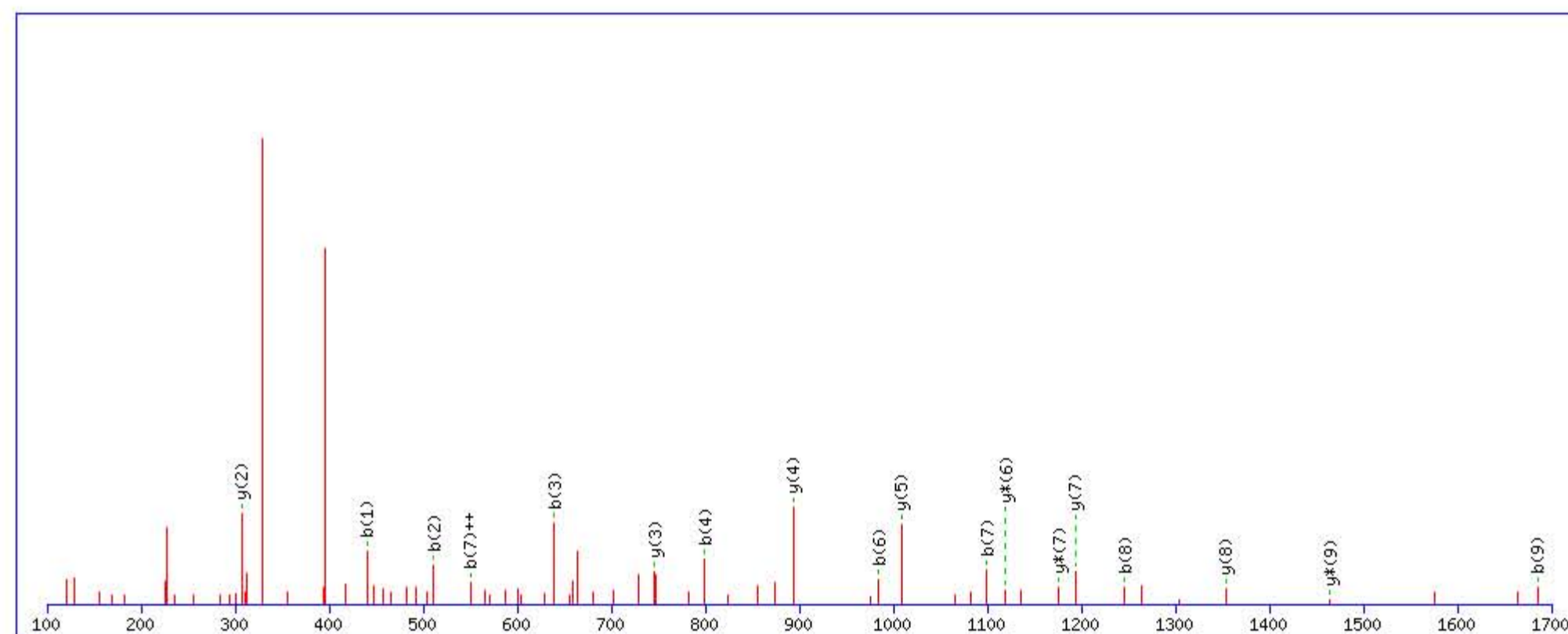
Title: Locus:1.1.1.3059.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1990.888580

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

Variable modifications:

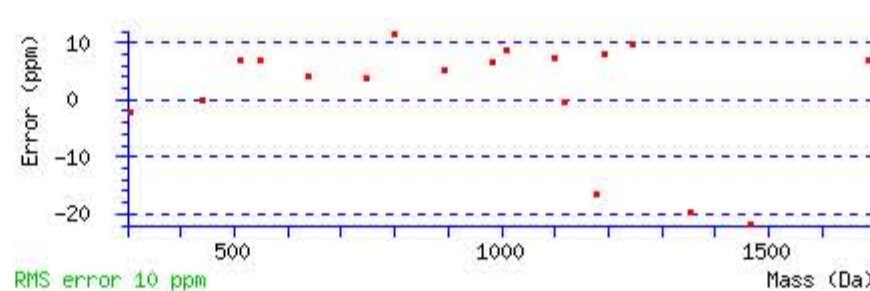
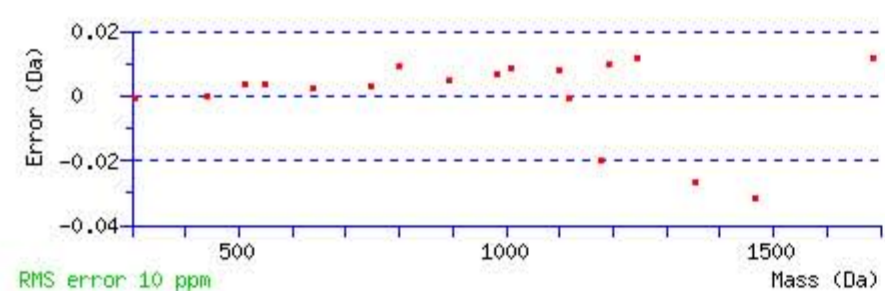
Q1 : Biotin:Thermo-21345 (Q)

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.00048

Matches : 18/100 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	440.232602	220.619939	423.206053	212.106664			Q							11
2	511.269716	256.138496	494.243167	247.625221			A	1552.670519	776.838898	1535.643970	768.325623	1534.659954	767.833615	10
3	639.328294	320.167785	622.301745	311.654511			Q	1481.633405	741.320341	1464.606856	732.807066	1463.622840	732.315058	9
4	799.358943	400.183110	782.332394	391.669835			C	1353.574827	677.291052	1336.548278	668.777777	1335.564262	668.285769	8
5	856.380407	428.693842	839.353858	420.180567			G	1193.544178	597.275727	1176.517629	588.762453	1175.533613	588.270445	7
6	984.438985	492.723131	967.412436	484.209856			Q	1136.522714	568.764995	1119.496165	560.251721	1118.512149	559.759713	6
7	1099.465928	550.236602	1082.439379	541.723328	1081.455363	541.231320	D	1008.464136	504.735706	991.437587	496.222432	990.453571	495.730424	5
8	1246.534342	623.770809	1229.507793	615.257535	1228.523777	614.765527	F	893.437193	447.222235	876.410644	438.708960			4
9	1685.759668	843.383472	1668.733119	834.870198	1667.749103	834.378190	Q	746.368779	373.688028	729.342230	365.174753			3
10	1845.790317	923.398797	1828.763768	914.885522	1827.779752	914.393514	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
42.6	1990.888580	0.011542	QAQCGQDFQCK
31.0	1990.888580	0.011542	QAQCGQDFQCK
12.9	1990.888580	0.011542	QAQCGQDFQCK
8.3	1990.888580	0.011542	QAQCGQDFQCK
7.4	1990.888580	0.011542	QAQCGQDFQCK

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 47909: 2030.973372 from(677.998400,3+) rtinseconds(1704) index(34443)

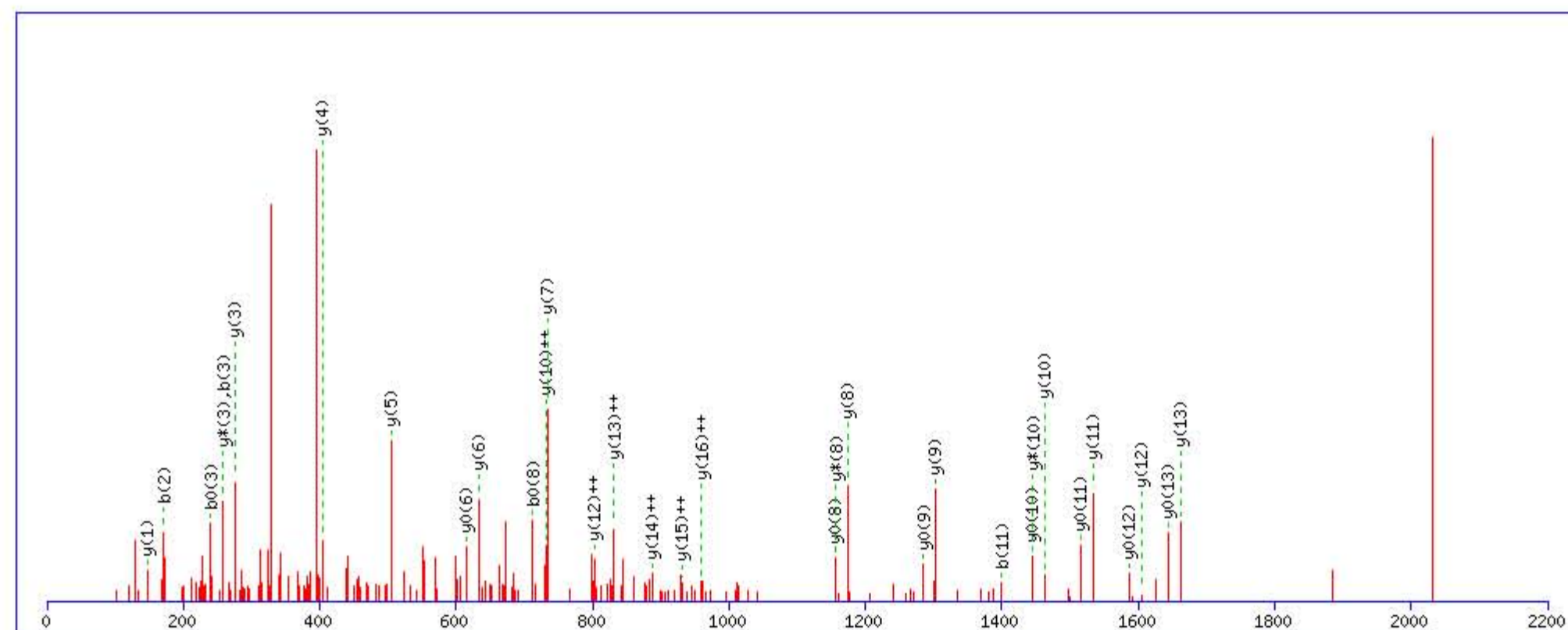
Title: Locus:1.1.1.3013.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2030.976501

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

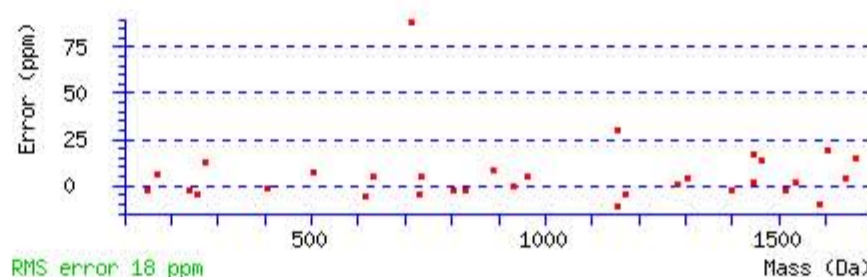
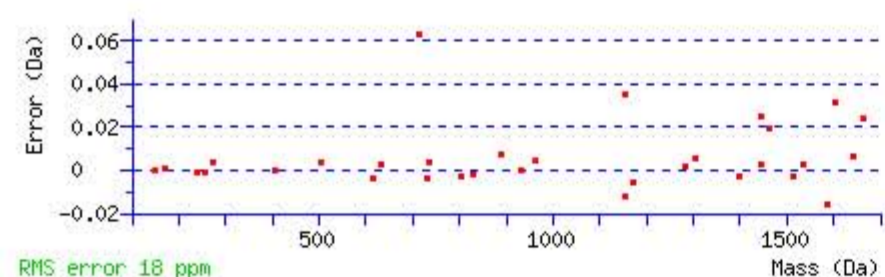
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 63 Expect: 1.6e-006

Matches : 33/164 fragment ions using 65 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							17
2	171.112804	86.060040					G	1918.899727	959.953502	1901.873178	951.440227	1900.889162	950.948219	16
3	258.144832	129.576054			240.134267	120.570772	S	1861.878263	931.442770	1844.851714	922.929495	1843.867698	922.437487	15
4	371.228896	186.118086			353.218331	177.112804	L	1774.846235	887.926756	1757.819686	879.413481	1756.835670	878.921473	14
5	428.250360	214.628818			410.239795	205.623536	G	1661.762171	831.384724	1644.735622	822.871449	1643.751606	822.379441	13
6	499.287474	250.147375			481.276909	241.142093	A	1604.740707	802.873992	1587.714158	794.360717	1586.730142	793.868709	12
7	570.324588	285.665932			552.314023	276.660650	A	1533.703593	767.355435	1516.677044	758.842160	1515.693028	758.350152	11
8	730.355237	365.681257			712.344672	356.675974	C	1462.666479	731.836878	1445.639930	723.323603	1444.655914	722.831595	10
9	859.397830	430.202553			841.387265	421.197271	E	1302.635830	651.821553	1285.609281	643.308279	1284.625265	642.816270	9
10	1298.623156	649.815216	1281.596607	641.301942	1280.612591	640.809934	Q	1173.593237	587.300257	1156.566688	578.786982	1155.582672	578.294974	8
11	1399.670835	700.339056	1382.644286	691.825781	1381.660270	691.333773	T	734.367911	367.687594	717.341362	359.174319	716.357346	358.682311	7
12	1527.729413	764.368345	1510.702864	755.855070	1509.718848	755.363062	Q	633.320232	317.163754	616.293683	308.650480	615.309667	308.158472	6
13	1628.777092	814.892184	1611.750543	806.378910	1610.766527	805.886902	T	505.261654	253.134465	488.235105	244.621190	487.251089	244.129182	5
14	1757.819685	879.413481	1740.793136	870.900206	1739.809120	870.408198	E	404.213975	202.610625	387.187426	194.097351	386.203410	193.605343	4
15	1814.841149	907.924213	1797.814600	899.410938	1796.830584	898.918930	G	275.171382	138.089329	258.144833	129.576054			3
16	1885.878263	943.442770	1868.851714	934.929495	1867.867698	934.437487	A	218.149918	109.578597	201.123369	101.065322			2
17							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **LGSLGAACEQTQTEGAK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.1	2030.976501	-0.003129	LGSLGAACEQTQTEGAK
47.2	2030.976501	-0.003129	LGSLGAACEQTQTEGAK
1.4	2031.000748	-0.027376	LEQQVEDLESSLEQEKK

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

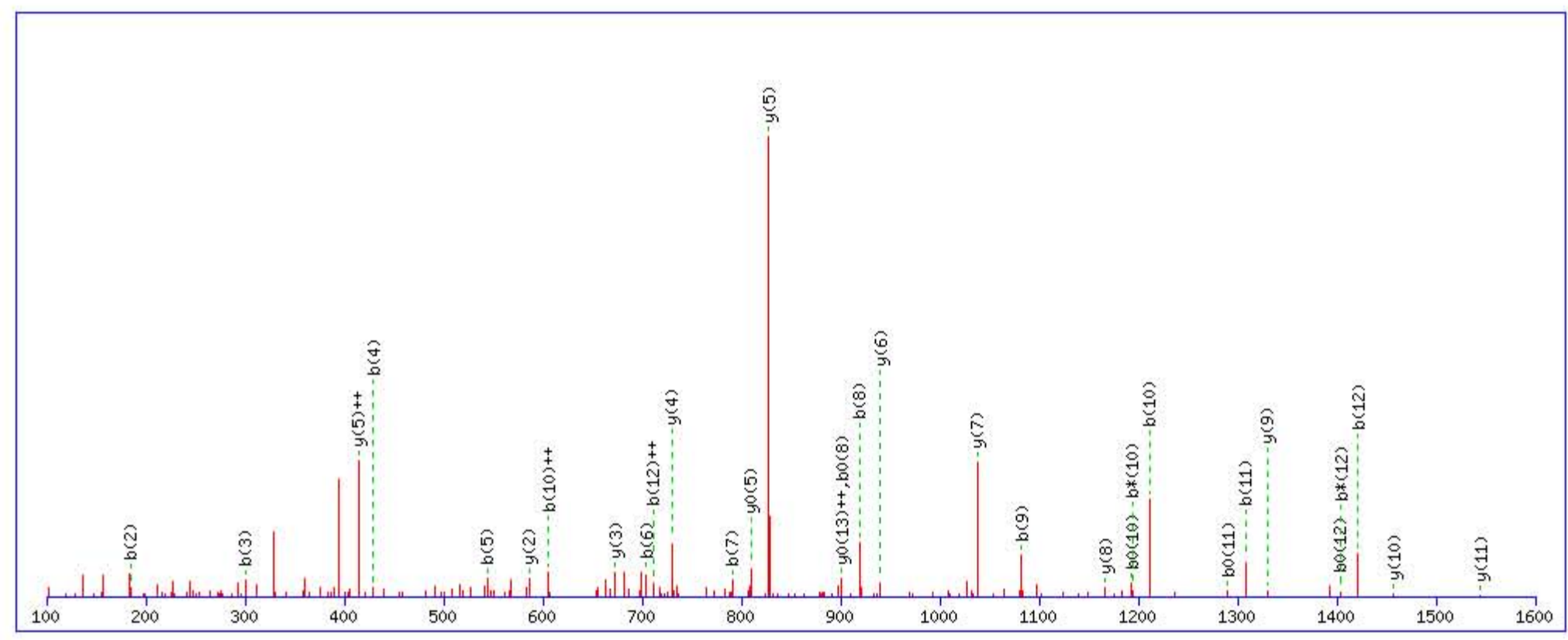
MASCOT Search Results

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

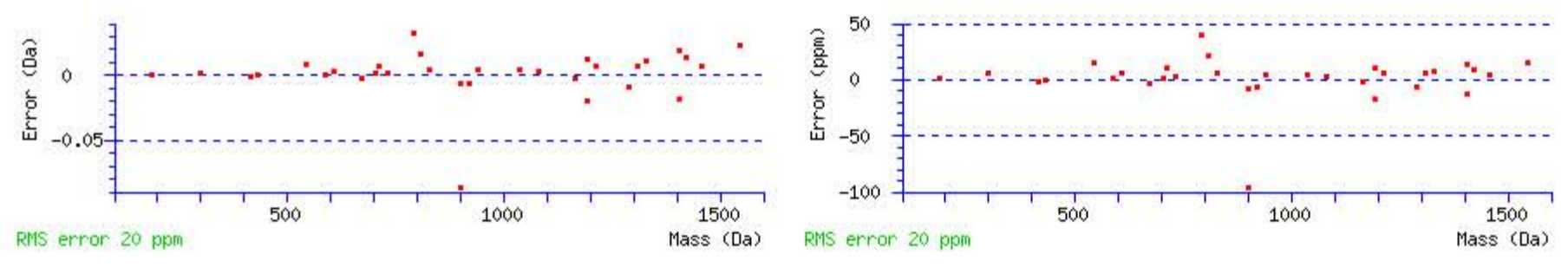
Match to Query 51945: 2247.023082 from(750.014970,3+) rtinseconds(1892) index(35596)
 Title: Locus:1.1.1.3078.23 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2247.018753
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q16 : Biotin:Thermo-21345 (Q)
 Ions Score: 66 Expect: 3.2e-006
 Matches : 32/170 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	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
65.7	2247.018753	0.004329	AIDEDCSQYEPIPGSQK
2.8	2247.018753	0.004329	AIDEDCSQYEPIPGSQK

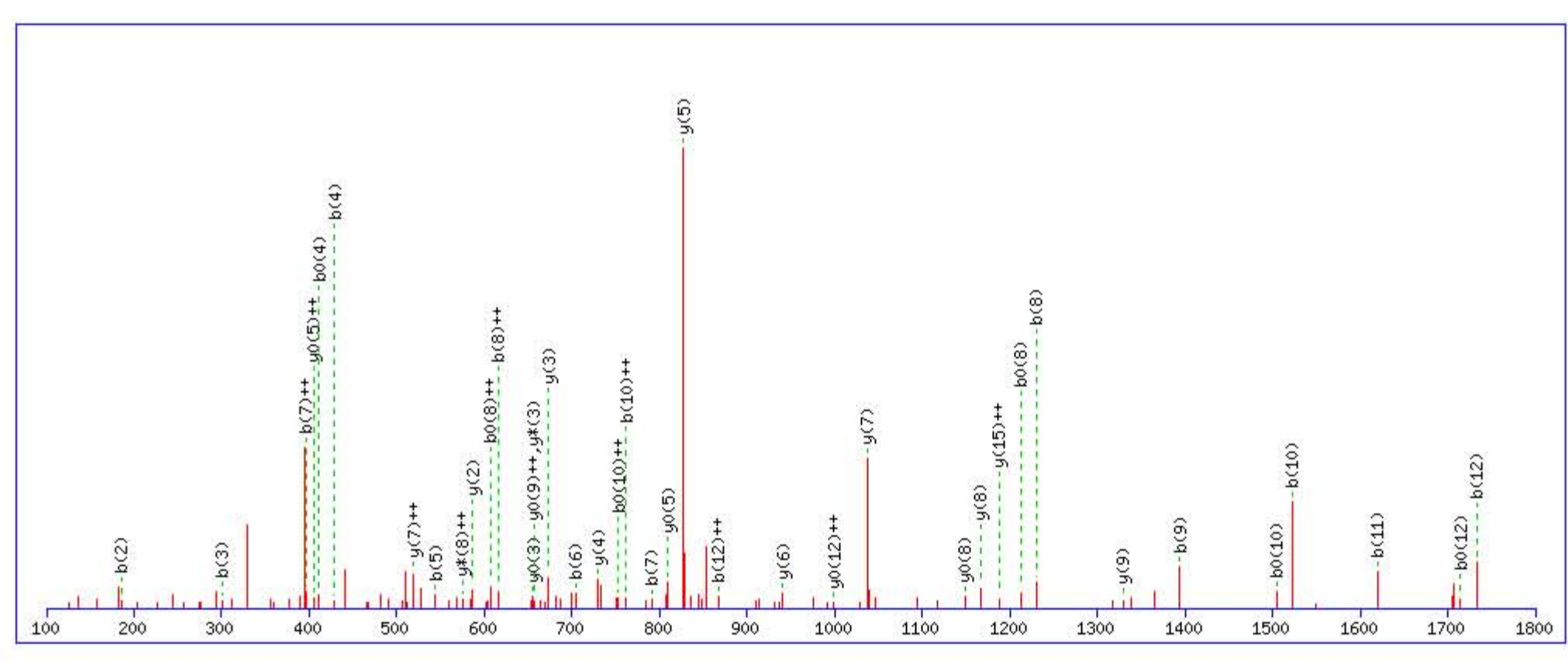
MASCOT Search Results

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

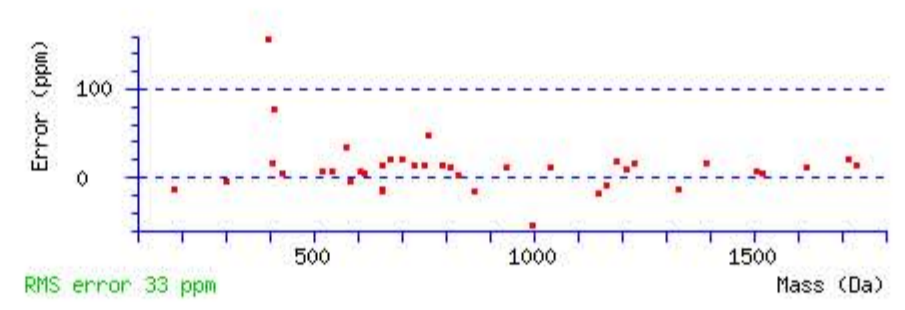
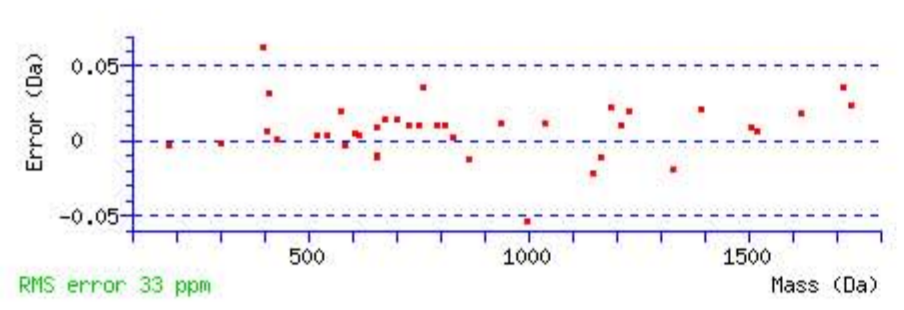
Match to Query 57259: 2558.212182 from(853.744670,3+) rtinseconds(2148) index(37306)
 Title: Locus:1.1.1.3167.23 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2558.185501
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q8 : Biotin:Thermo-21345 (Q)
 Q16 : Biotin:Thermo-21345 (Q)
 Ions Score: 38 Expect: 0.00086
 Matches : 39/170 fragment ions using 95 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.044390	36.525833					A							17
2	185.128454	93.067865					I	2488.155682	1244.581479	2471.129133	1236.068204	2470.145117	1235.576196	16
3	300.155397	150.581336			282.144832	141.576054	D	2375.071618	1188.039447	2358.045069	1179.526172	2357.061053	1179.034164	15
4	429.197990	215.102633			411.187425	206.097351	E	2260.044675	1130.525975	2243.018126	1122.012701	2242.034110	1121.520693	14
5	544.224933	272.616105			526.214368	263.610822	D	2131.002082	1066.004679	2113.975533	1057.491404	2112.991517	1056.999396	13
6	704.255582	352.631429			686.245017	343.626147	C	2015.975139	1008.491208	1998.948590	999.977933	1997.964574	999.485925	12
7	791.287610	396.147443			773.277045	387.142161	S	1855.944490	928.475883	1838.917941	919.962609	1837.933925	919.470601	11
8	1230.512936	615.760106	1213.486387	607.246832	1212.502371	606.754824	Q	1768.912462	884.959869	1751.885913	876.446595	1750.901897	875.954587	10
9	1393.576265	697.291771	1376.549716	688.778496	1375.565700	688.286488	Y	1329.687136	665.347206	1312.660587	656.833932	1311.676571	656.341924	9
10	1522.618858	761.813067	1505.592309	753.299793	1504.608293	752.807785	E	1166.623807	583.815541	1149.597258	575.302267	1148.613242	574.810259	8
11	1619.671622	810.339449	1602.645073	801.826175	1601.661057	801.334167	P	1037.581214	519.294245	1020.554665	510.780971	1019.570649	510.288963	7
12	1732.755686	866.881481	1715.729137	858.368207	1714.745121	857.876198	I	940.528450	470.767863	923.501901	462.254589	922.517885	461.762581	6
13	1829.808450	915.407863	1812.781901	906.894589	1811.797885	906.402581	P	827.444386	414.225831	810.417837	405.712557	809.433821	405.220549	5
14	1886.829914	943.918595	1869.803365	935.405321	1868.819349	934.913312	G	730.391622	365.699449	713.365073	357.186175	712.381057	356.694167	4
15	1973.861942	987.434609	1956.835393	978.921335	1955.851377	978.429327	S	673.370158	337.188717	656.343609	328.675443	655.359593	328.183435	3
16	2413.087268	1207.047272	2396.060719	1198.533997	2395.076703	1198.041989	Q	586.338130	293.672703	569.311581	285.159429			2
17							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.4	2558.185501	0.026681	AIDEDCSQYEPIPGSQK
5.7	2558.214981	-0.002799	TSPQSAPPSSPLSPNWVSPSDHQR

Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGGTICSGDIWDQASCSSTTCVR**

Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

Match to Query 61435: 2962.301742 from(988.441190,3+) rtinseconds(2367) index(23815)

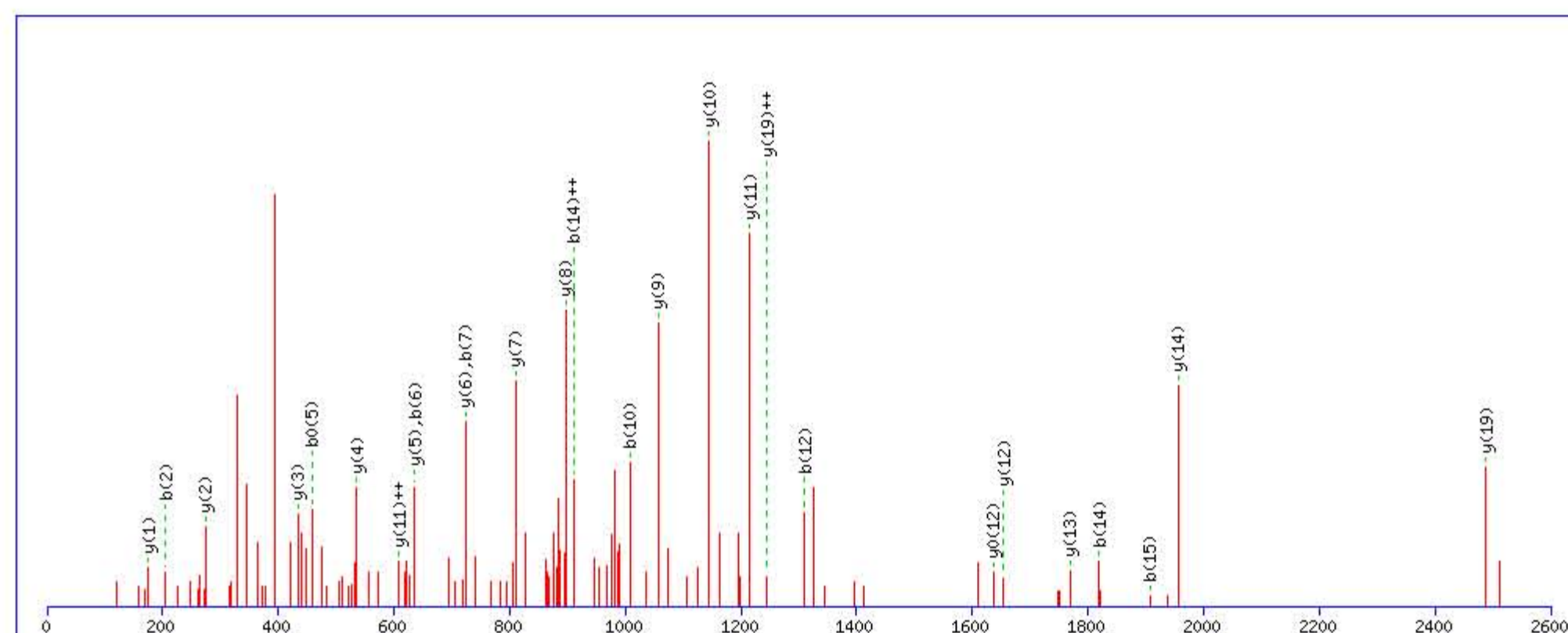
Title: Locus:1.1.1.826.25 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2962.271835

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

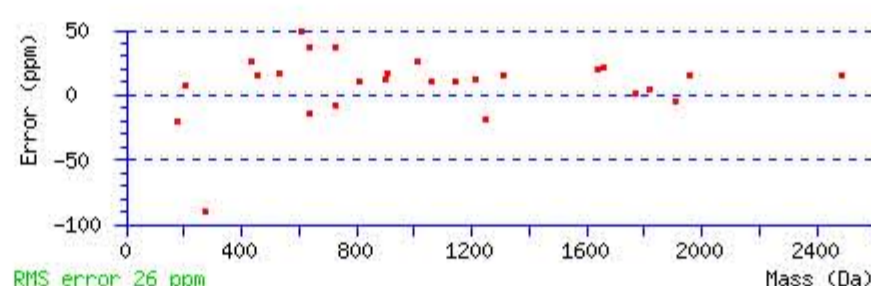
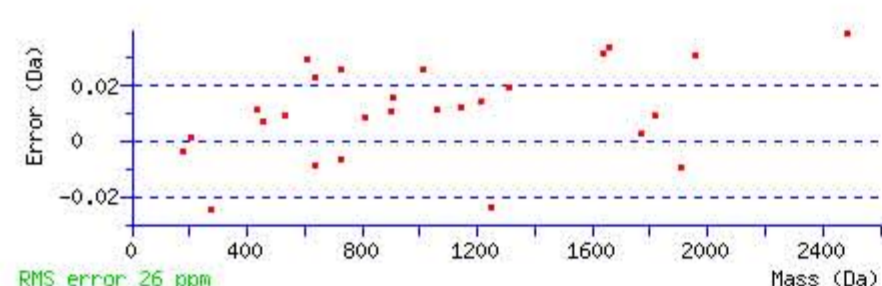
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 107 Expect: 1.3e-010

Matches : 27/240 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	148.075690	74.541483					F							24
2	205.097154	103.052215					G	2816.210649	1408.608962	2799.184100	1400.095688	2798.200084	1399.603680	23
3	262.118618	131.562947					G	2759.189185	1380.098230	2742.162636	1371.584956	2741.178620	1371.092948	22
4	363.166297	182.086786			345.155732	173.081504	T	2702.167721	1351.587498	2685.141172	1343.074224	2684.157156	1342.582216	21
5	476.250361	238.628818			458.239796	229.623536	I	2601.120042	1301.063659	2584.093493	1292.550384	2583.109477	1292.058376	20
6	636.281010	318.644143			618.270445	309.638861	C	2488.035978	1244.521627	2471.009429	1236.008352	2470.025413	1235.516344	19
7	723.313038	362.160157			705.302473	353.154875	S	2328.005329	1164.506302	2310.978780	1155.993028	2309.994764	1155.501020	18
8	780.334502	390.670889			762.323937	381.665607	G	2240.973301	1120.990288	2223.946752	1112.477014	2222.962736	1111.985006	17
9	895.361445	448.184361			877.350880	439.179078	D	2183.951837	1092.479556	2166.925288	1083.966282	2165.941272	1083.474274	16
10	1008.445509	504.726393			990.434944	495.721110	I	2068.924894	1034.966085	2051.898345	1026.452810	2050.914329	1025.968082	15
11	1194.524822	597.766049			1176.514257	588.760767	W	1955.840830	978.424053	1938.814281	969.910778	1937.830265	969.418770	14
12	1309.551765	655.279521			1291.541200	646.274238	D	1769.761517	885.384396	1752.734968	876.871122	1751.750952	876.379114	13
13	1748.777091	874.892184	1731.750542	866.378909	1730.766526	865.886901	Q	1654.734574	827.870925	1637.708025	819.357650	1636.724009	818.865642	12
14	1819.814205	910.410741	1802.787656	901.897466	1801.803640	901.405458	A	1215.509248	608.258262	1198.482699	599.744987	1197.498683	599.252979	11
15	1906.846233	953.926755	1889.819684	945.413480	1888.835668	944.921472	S	1144.472134	572.739705	1127.445585	564.226430	1126.461569	563.734422	10
16	2066.876882	1033.942079	2049.850333	1025.428804	2048.866317	1024.936796	C	1057.440106	529.223691	1040.413557	520.710416	1039.429541	520.218408	9
17	2153.908910	1077.458093	2136.882361	1068.944818	2135.898345	1068.452810	S	897.409457	449.208366	880.382908	440.695092	879.398892	440.203084	8
18	2240.940938	1120.974107	2223.914389	1112.460832	2222.930373	1111.968825	S	810.377429	405.692352	793.350880	397.179078	792.366864	396.687070	7
19	2327.972966	1164.490121	2310.946417	1155.976847	2309.962401	1155.484839	S	723.345401	362.176338	706.318852	353.663064	705.334836	353.171056	6
20	2429.020645	1215.013960	2411.994096	1206.500686	2411.010080	1206.008678	T	636.313373	318.660324	619.286824	310.147050	618.302808	309.655042	5
21	2530.068324	1265.537800	2513.041775	1257.024525	2512.057759	1256.532517	T	535.265694	268.136485	518.239145	259.623210	517.255129	259.131202	4
22	2690.098973	1345.553124	2673.072424	1337.039850	2672.088408	1336.547842	C	434.218015	217.612645	417.191466	209.099371			3
23	2789.167387	1395.087331	2772.140838	1386.574057	2771.156822	1386.082049	V	274.187366	137.597321	257.160817	129.084046			2
24							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [FGGTICSGDIWDQASCSSTTCVR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
106.9	2962.271835	0.029907	FGGTICSGDIWDQASCSSTTCVR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **CEGFVCAQTGR**

Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

Match to Query 36888: 1594.703388 from(798.358970,2+) rtinseconds(1772) index(20168)

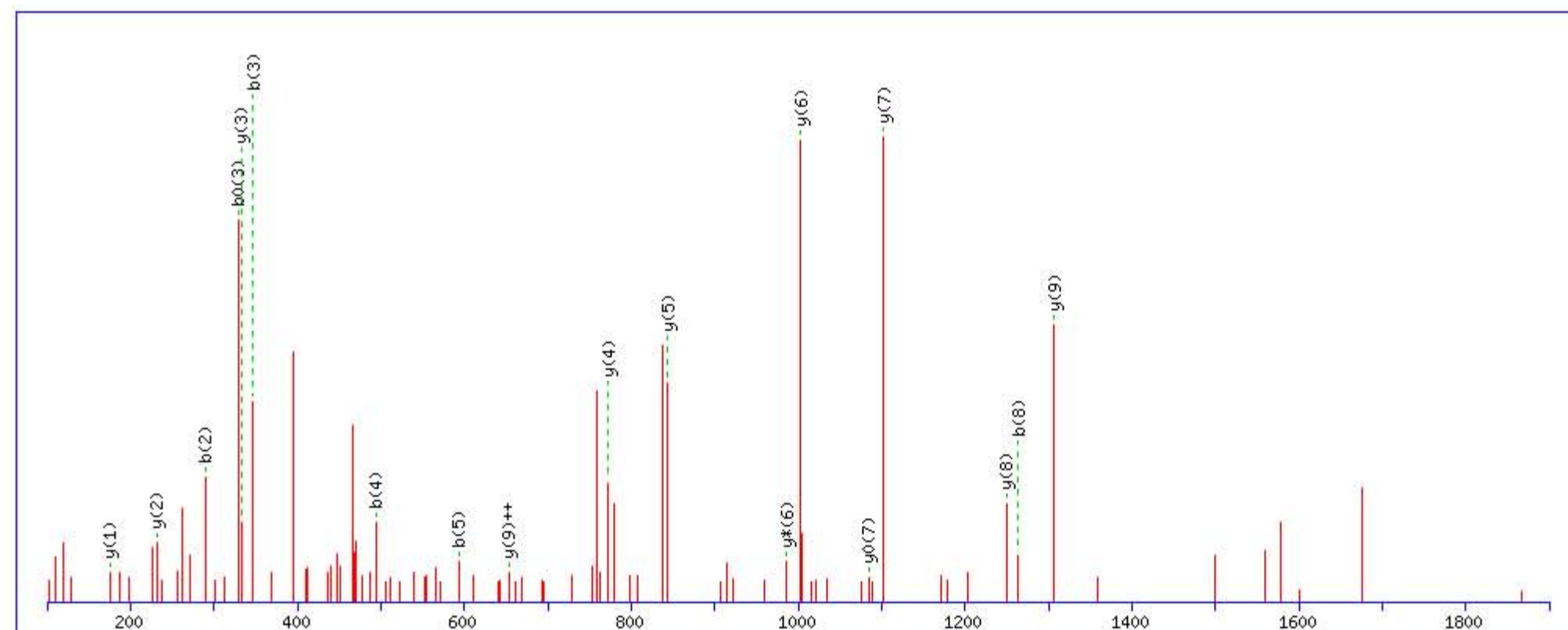
Title: Locus:1.1.1.619.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1594.705460

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

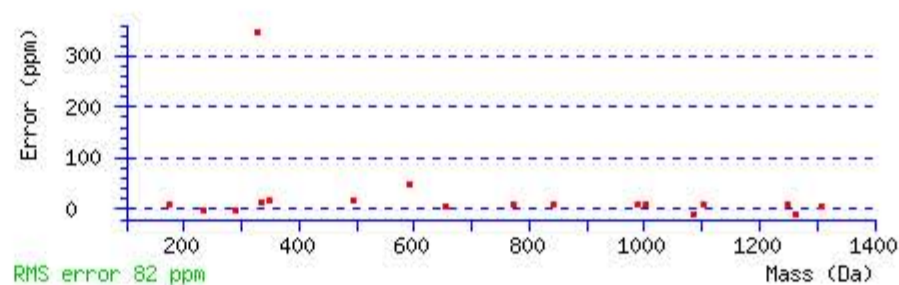
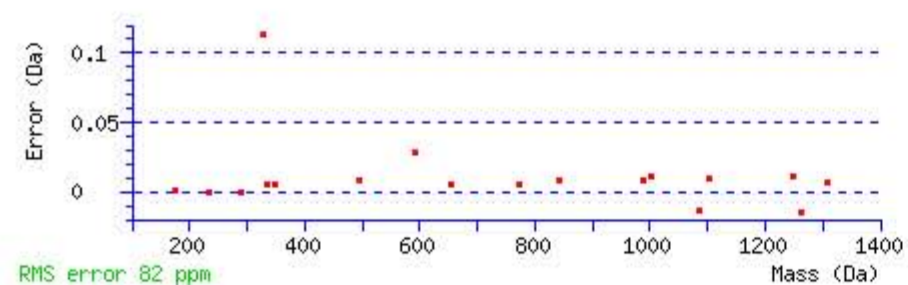
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.00056

Matches : 18/100 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	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	$M_r(\text{calc})$:	Delta	Sequence
40.4	1594.705460	-0.002072	CEGFVCAQTGR

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

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **KPYNVESYTPQTQ GK**

Found in **CO8B_HUMAN**, Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3

Match to Query 48400: 2050.012212 from(684.344680,3+) rtinseconds(1582) index(19018)

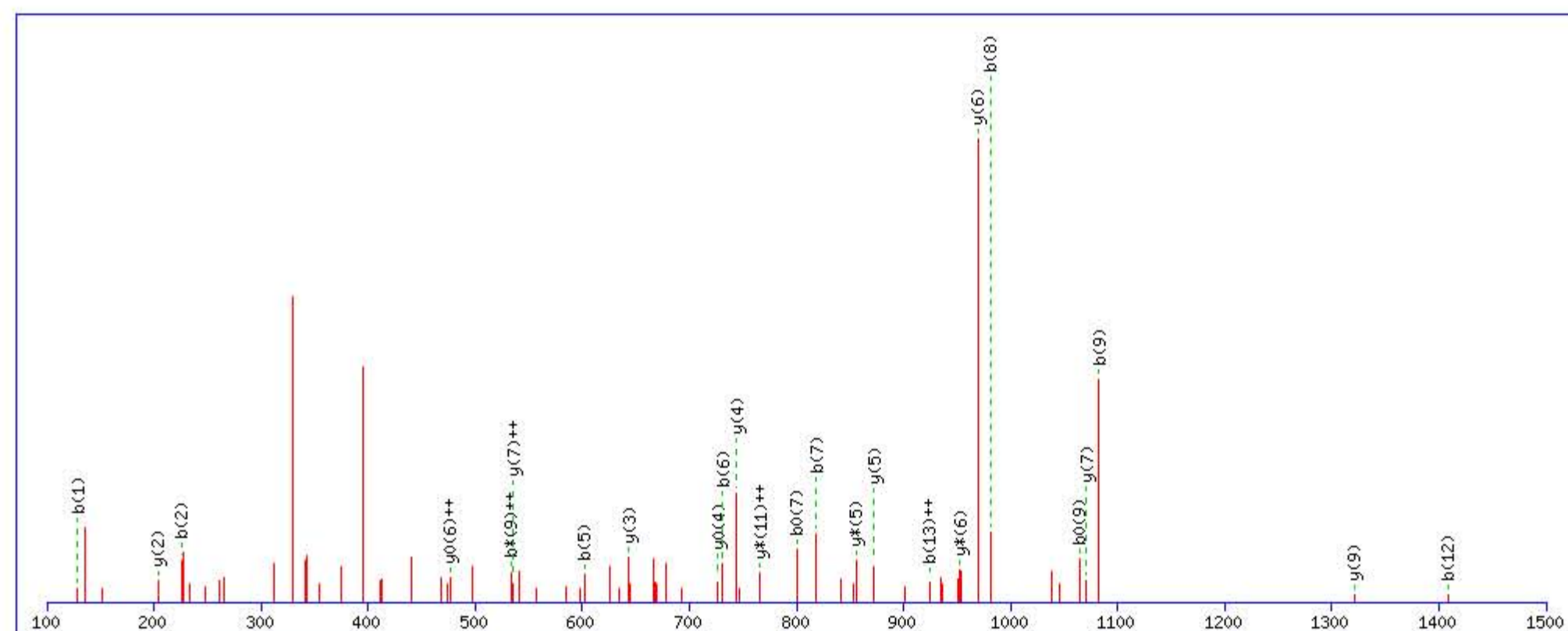
Title: Locus:1.1.1.553.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2050.019348

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

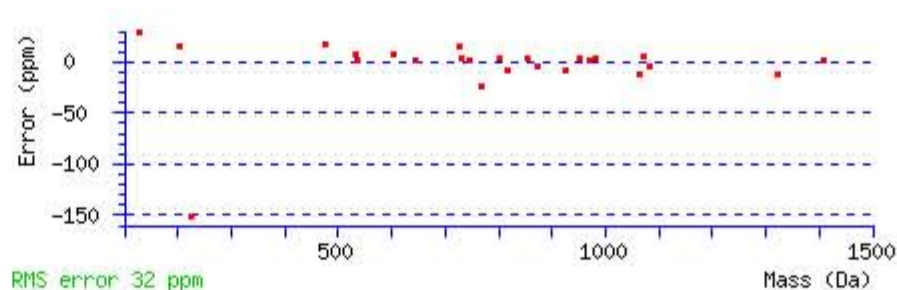
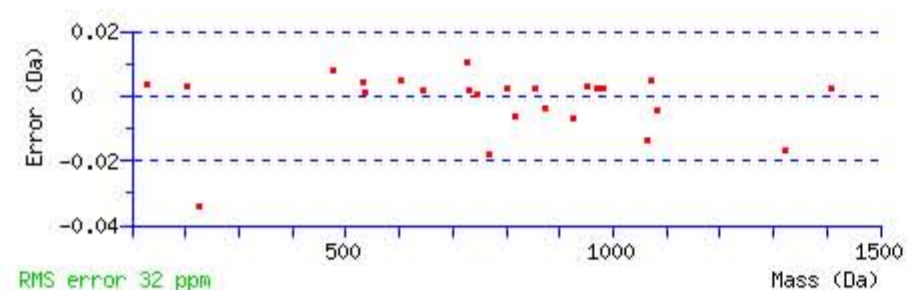
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.0045

Matches : 25/152 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	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 **KPYNVESYTPQTQ GK**

(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	2050.019348	-0.007136	KPYNVESYTPQTQ GK
21.3	2050.019348	-0.007136	KPYNVESYTPQTQ GK

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

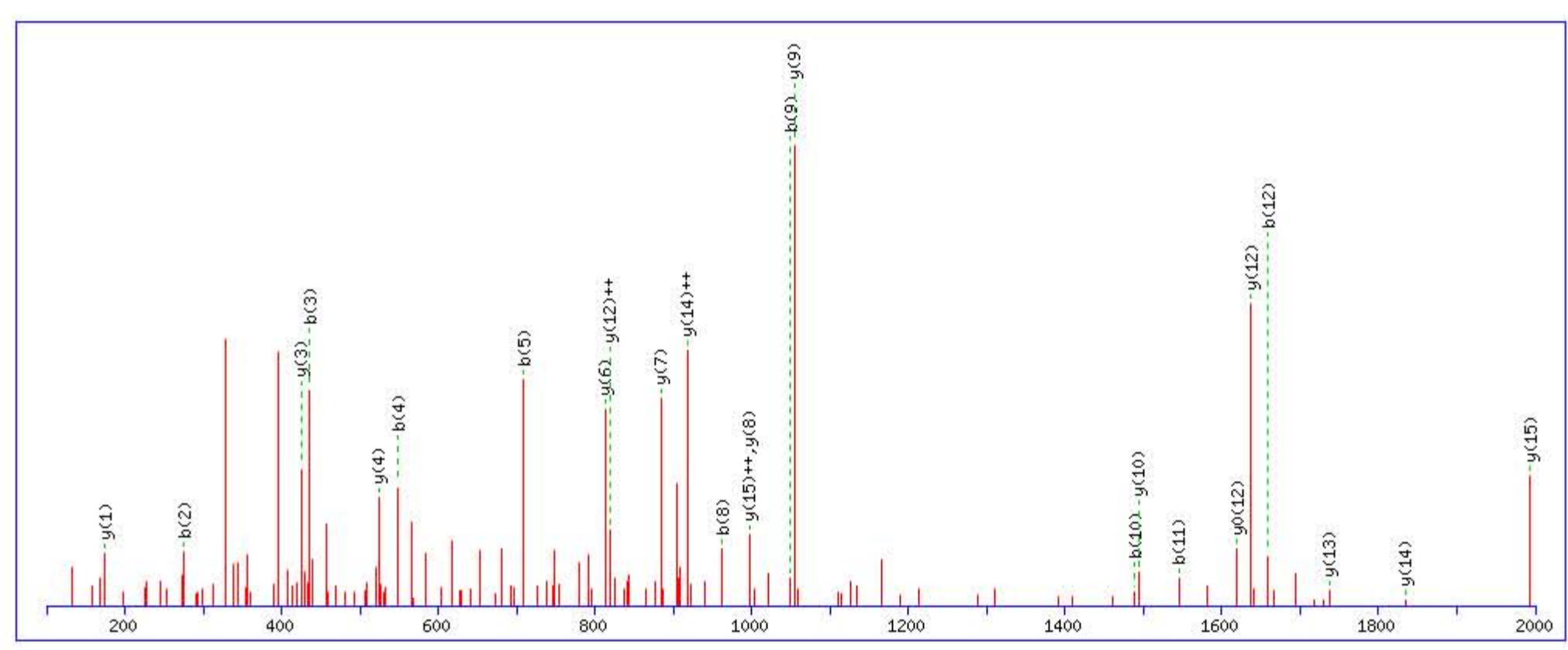
MASCOT SCIENCE Mascot Search Results

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

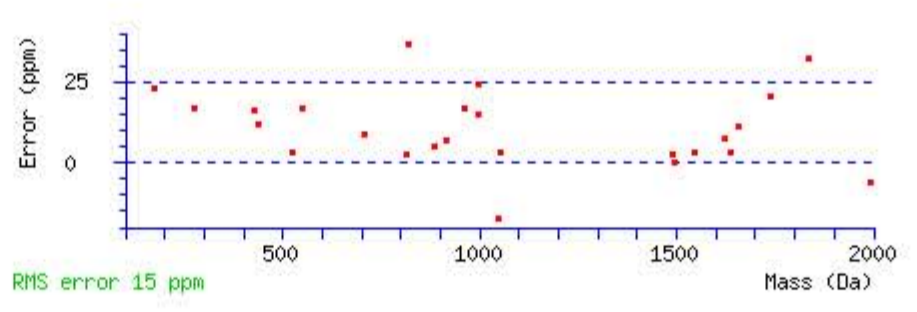
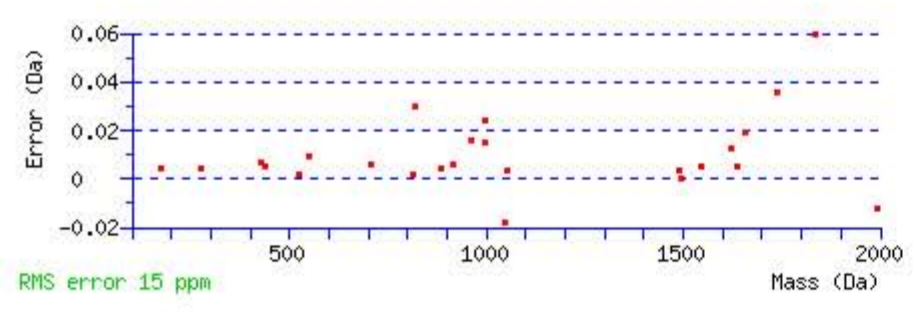
Match to Query 57167: 2541.100812 from(848.040880,3+) rtinseconds(2149) index(22589)
 Title: Locus:1.1.1.750.24 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2541.094299
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q10 : Biotin:Thermo-21345 (Q)
 Ions Score: 90 Expect: 3.9e-009
 Matches : 25/192 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	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
90.5	2541.094299	0.006513	CDCICPVGSQGLACEVSYR

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGQLSVK**

Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

Match to Query 16066: 1012.569648 from(507.292100,2+) rtinseconds(1562) index(18906)

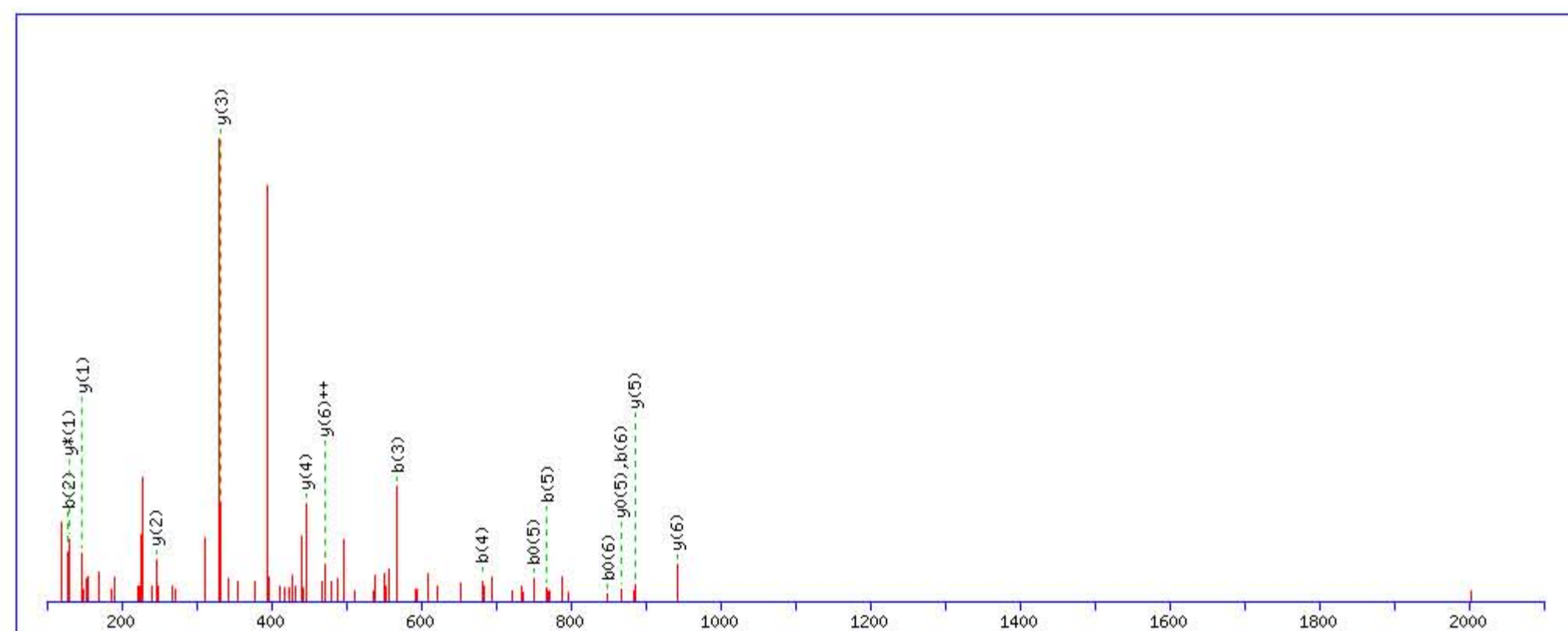
Title: Locus:1.1.1.546.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1012.573929

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

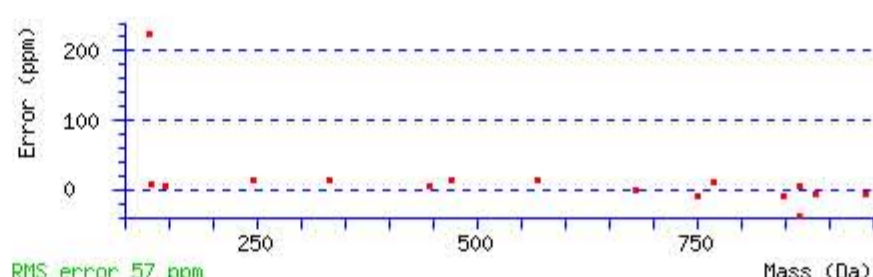
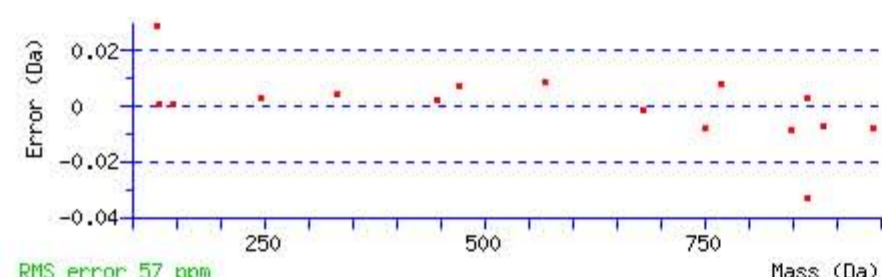
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.037

Matches : 16/56 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							7
2	129.065854	65.036565					G	942.544100	471.775688	925.517551	463.262414	924.533535	462.770406	6
3	568.291180	284.649228	551.264631	276.135954			Q	885.522636	443.264956	868.496087	434.751682	867.512071	434.259674	5
4	681.375244	341.191260	664.348695	332.677986			L	446.297310	223.652293	429.270761	215.139018	428.286745	214.647010	4
5	768.407272	384.707274	751.380723	376.194000	750.396707	375.701992	S	333.213246	167.110261	316.186697	158.596986	315.202681	158.104978	3
6	867.475686	434.241481	850.449137	425.728207	849.465121	425.236199	V	246.181218	123.594247	229.154669	115.080972			2
7							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **AGQLSVK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.0	1012.573929	-0.004281	AGQLSVK
10.1	1012.573914	-0.004266	KEAQVK
8.2	1012.573929	-0.004281	QAGLVSK
8.2	1012.573914	-0.004266	QKLEGK
7.4	1012.555267	0.014381	EPSKPAEKK
6.2	1012.570557	-0.000909	IIDFGLAHK
6.2	1012.570557	-0.000909	LIDFGIAHK
5.8	1012.555267	0.014381	EPSKPKAEK
4.2	1012.555313	0.014335	GGEIQPVSVK
3.4	1012.573929	-0.004281	QNLTVK

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

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **KLDGICWQVR**

Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

Match to Query 36473: 1584.828072 from(529.283300,3+) rtinseconds(2075) index(36864)

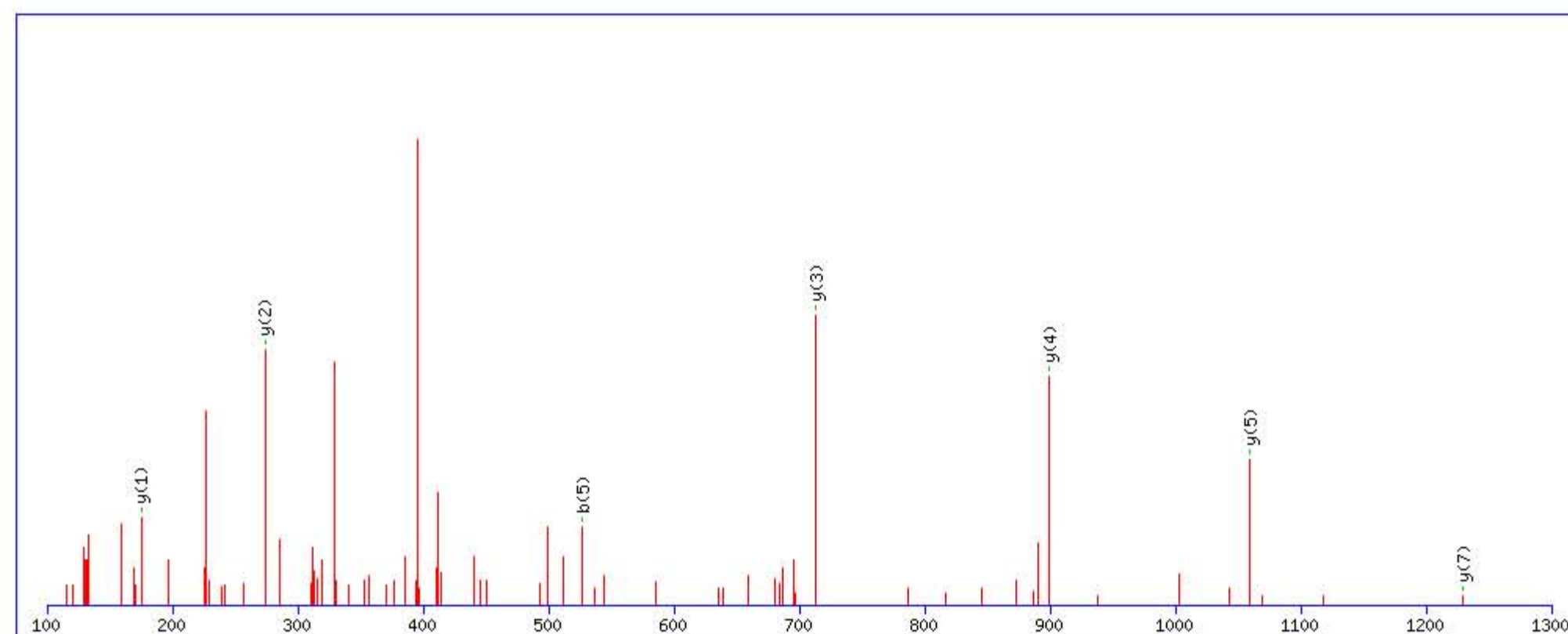
Title: Locus:1.1.1.3142.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1584.826874

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

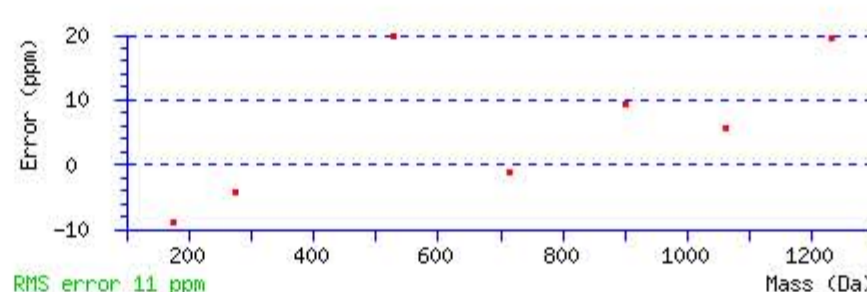
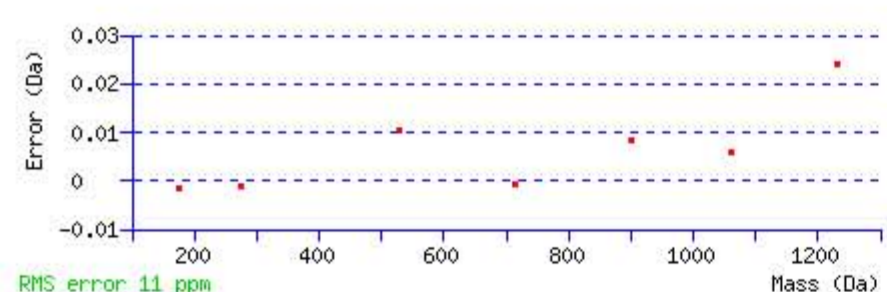
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.0017

Matches : 7/90 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	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
36.0	1584.826874	0.001198	KLDGICWQVR
6.1	1584.805099	0.022973	SQCVPICRR
4.5	1584.829346	-0.001274	QAESQINKQTK
1.0	1584.822845	0.005227	SQMSPQGLRVR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SLPVSDSVLSGFQQR**

Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

Match to Query 45137: 1930.989312 from(644.670380,3+) rtinseconds(2510) index(39574)

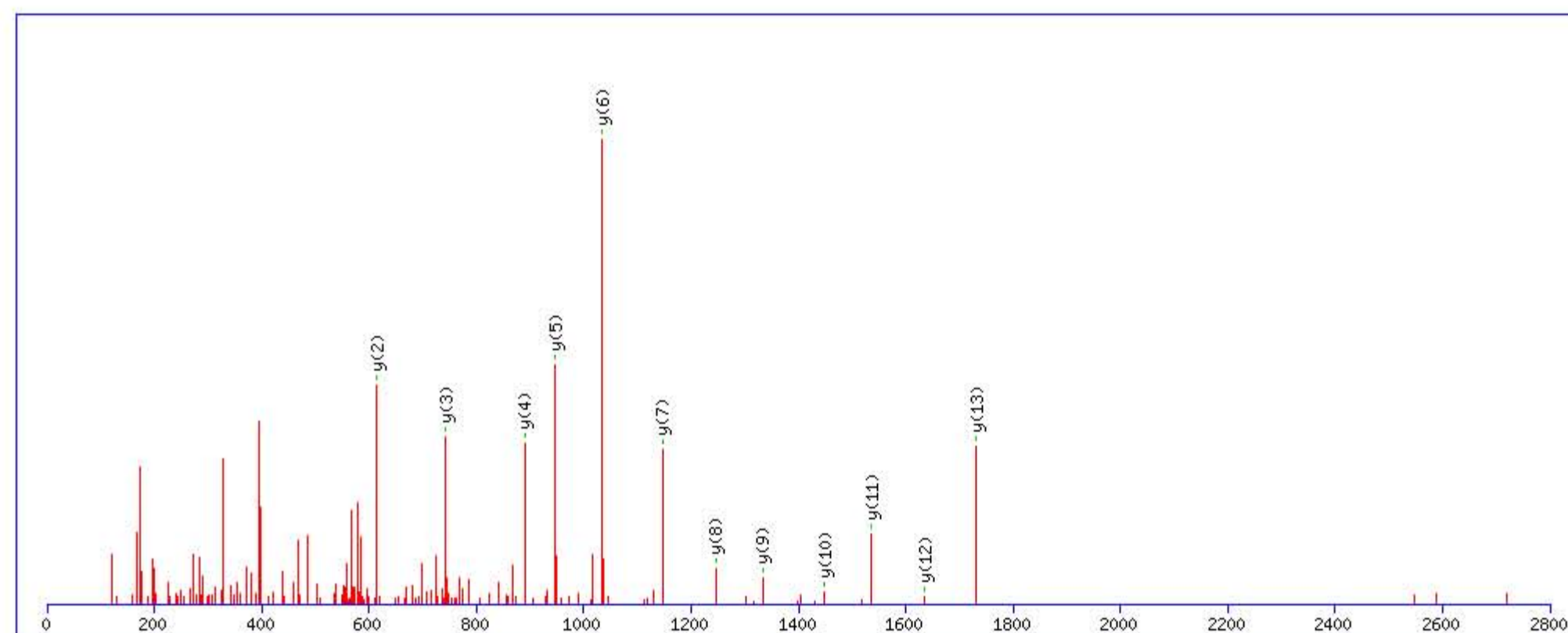
Title: Locus:1.1.1.3293.14 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1930.982254

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

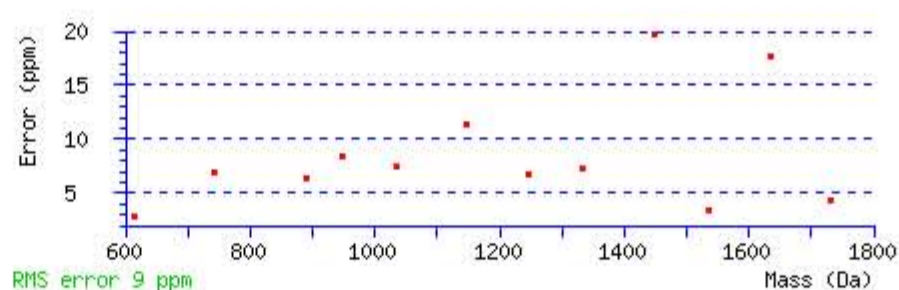
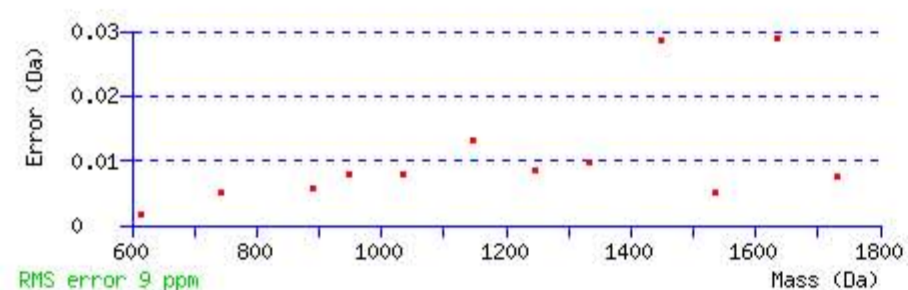
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 104 Expect: 2.1e-010

Matches : 12/138 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 [SLPVSDSVLSGFQQR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
104.2	1930.982254	0.007058	SLPVSDSVLSGFQQR
1.0	1931.000885	-0.011573	LSPVTACAGQTLQFK

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 52614: 2275.148982 from(759.390270,3+) rtinseconds(2364) index(23784)

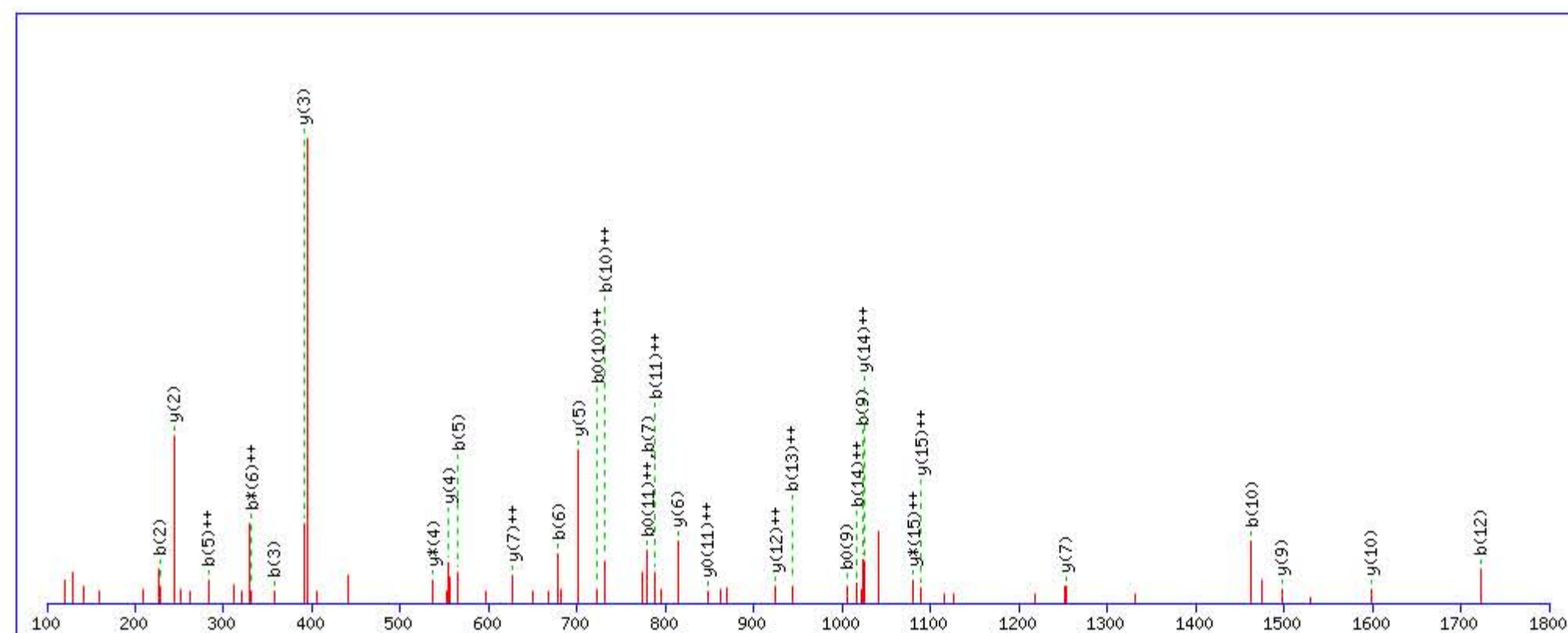
Title: Locus:1.1.1.825.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2275.134720

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

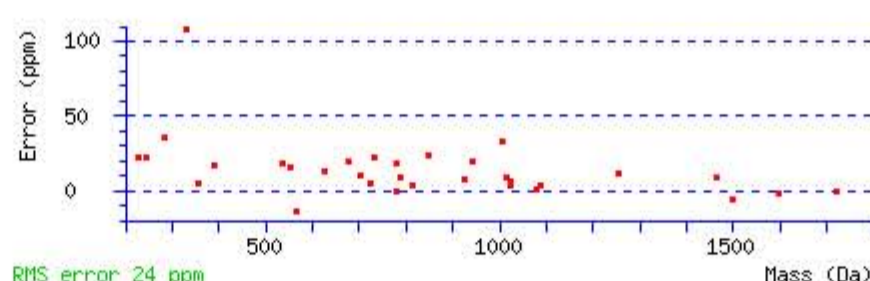
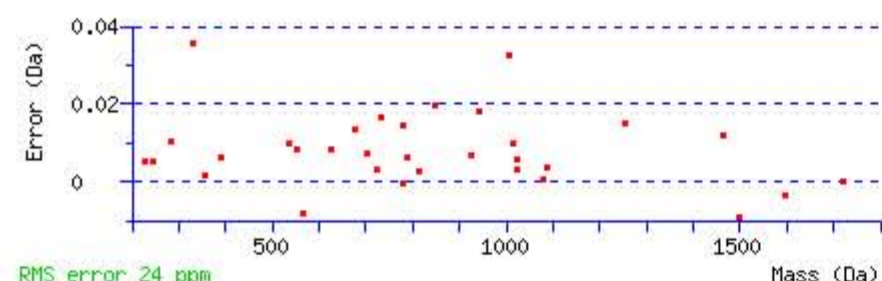
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 39 Expect: 0.0036

Matches : 32/160 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	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	$M_r(\text{calc})$	Delta	Sequence
39.5	2275.134720	0.014262	VQEAHLTEDQIFYFPK
12.4	2275.134720	0.014262	VQEAHLTEDQIFYFPK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **YGFCEAADQFHVLDEVR**

Found in **CO8G_HUMAN**, Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3

Match to Query 53929: 2366.094732 from(789.705520,3+) rtinseconds(2567) index(39873)

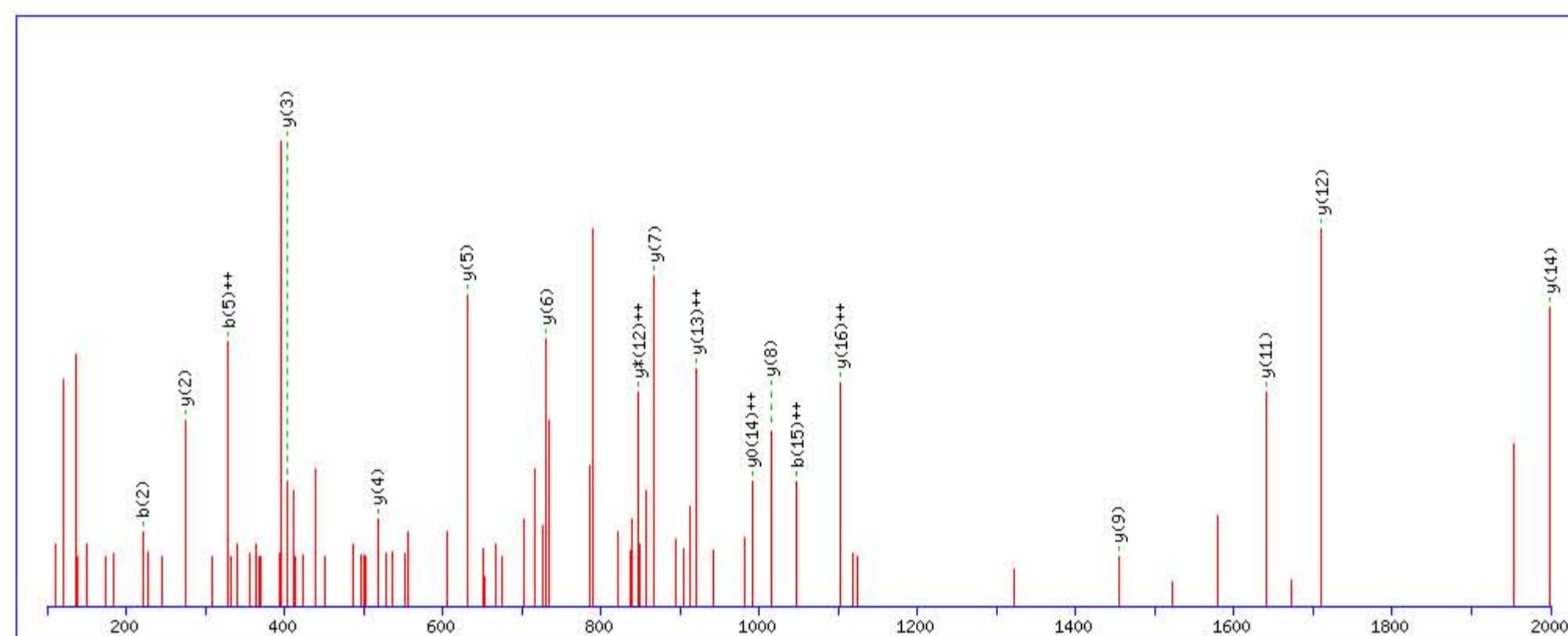
Title: Locus:1.1.1.3313.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2366.082382

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

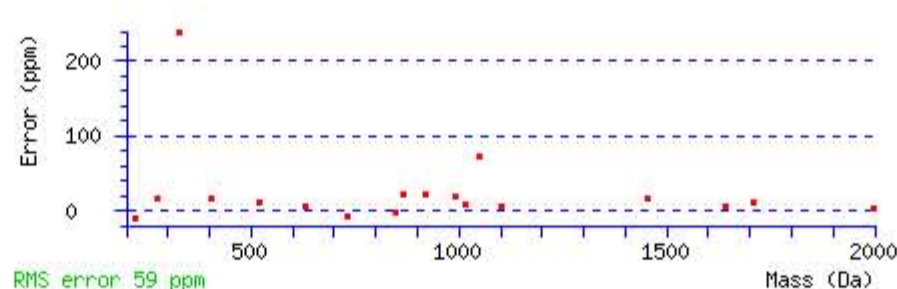
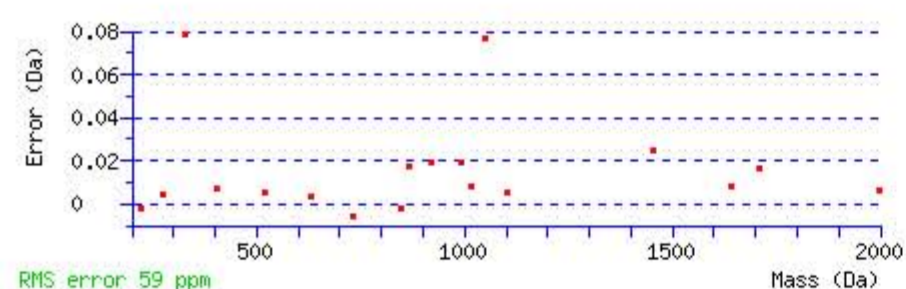
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 51 Expect: 0.00011

Matches : 18/164 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	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
51.3	2366.082382	0.012350	YGFCEAADQFHVLDEVR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **TEHYEEQIEAFK**

Found in **CO9_HUMAN**, Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

Match to Query 43357: 1833.861522 from(612.294450,3+) rtinseconds(1972) index(36258)

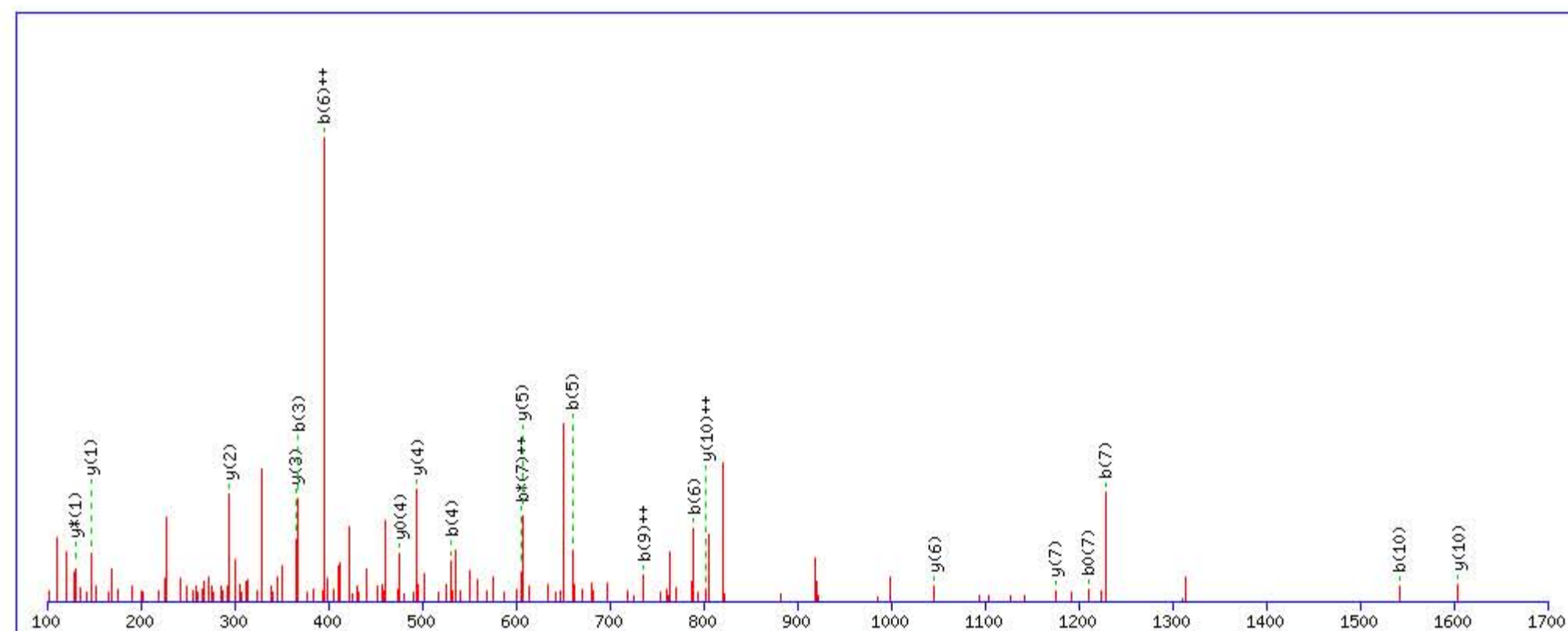
Title: Locus:1.1.1.3106.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1833.860703

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

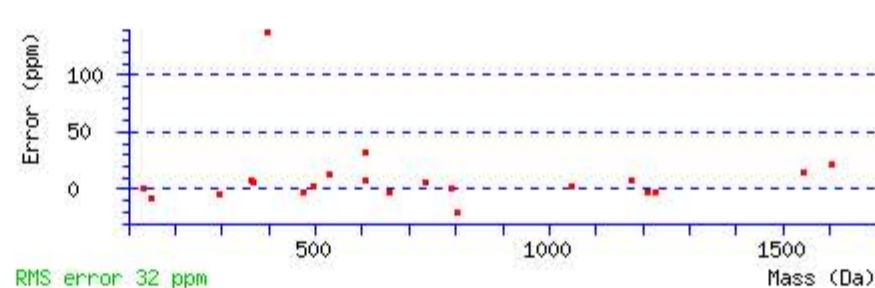
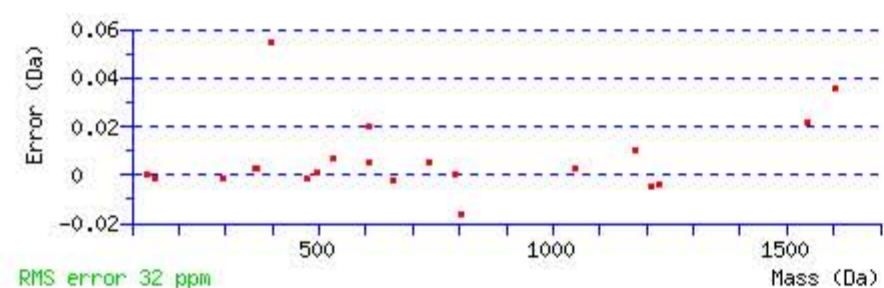
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.011

Matches : 21/114 fragment ions using 49 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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
32.5	1833.860703	0.000819	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 51399: 2216.981232 from(740.001020,3+) rtinseconds(1542) index(33562)

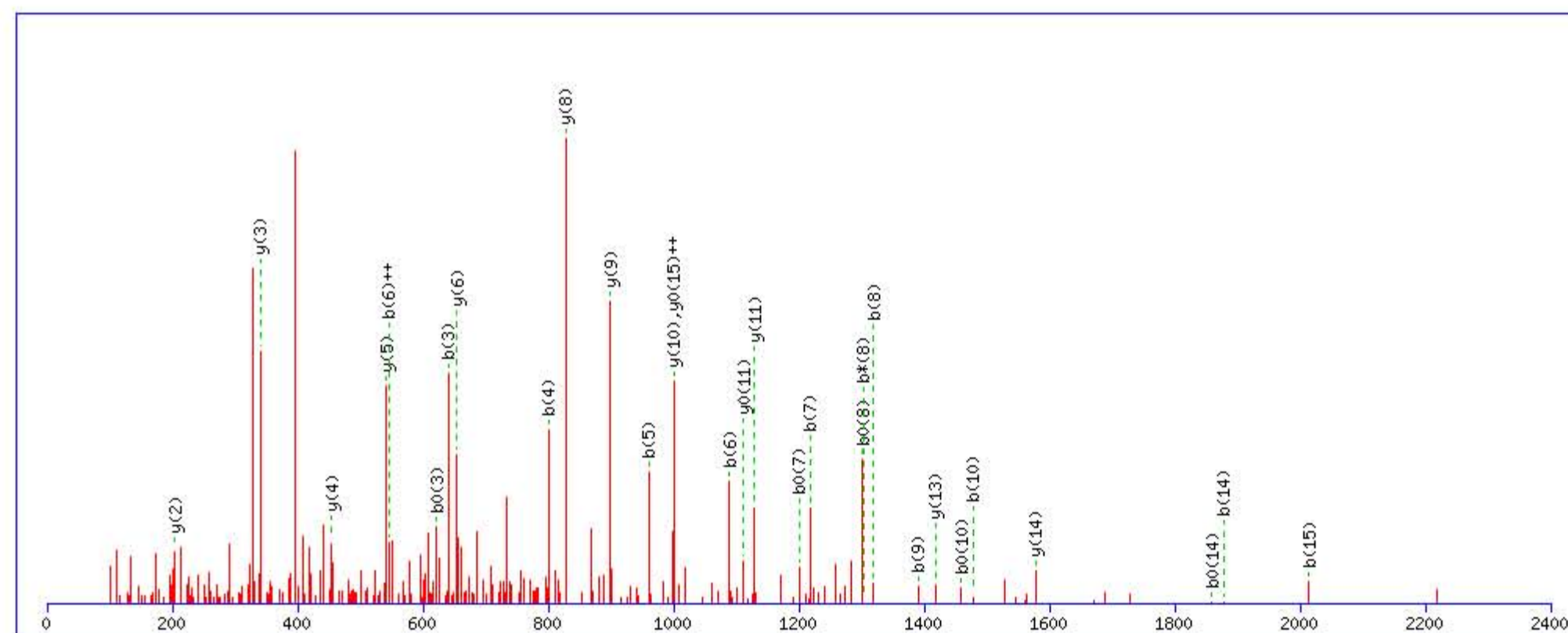
Title: Locus:1.1.1.2956.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2216.986404

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

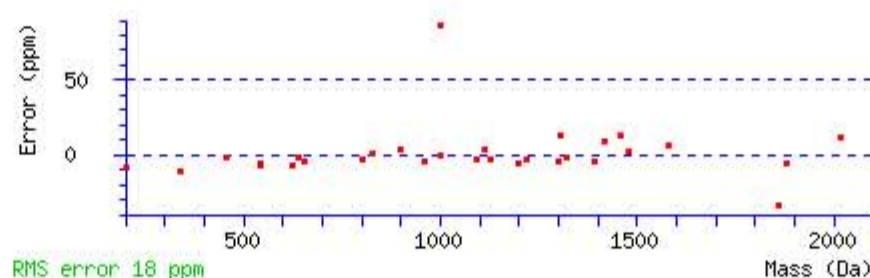
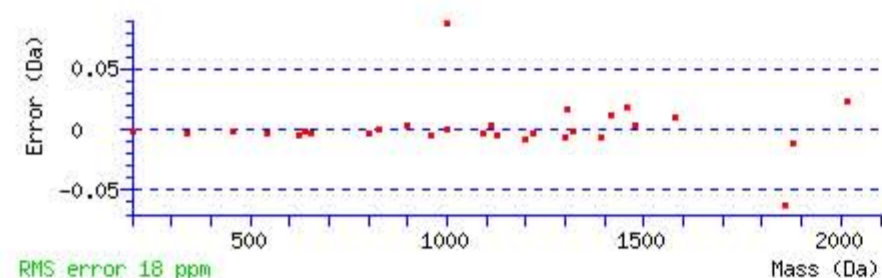
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 1.9e-006

Matches : 30/178 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	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
65.9	2216.986404	-0.005172	AEQCCEETASSISLHGK

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

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGSQYR**

Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

Match to Query 16615: 1019.519788 from(510.767170,2+) rtinseconds(1399) index(65104)

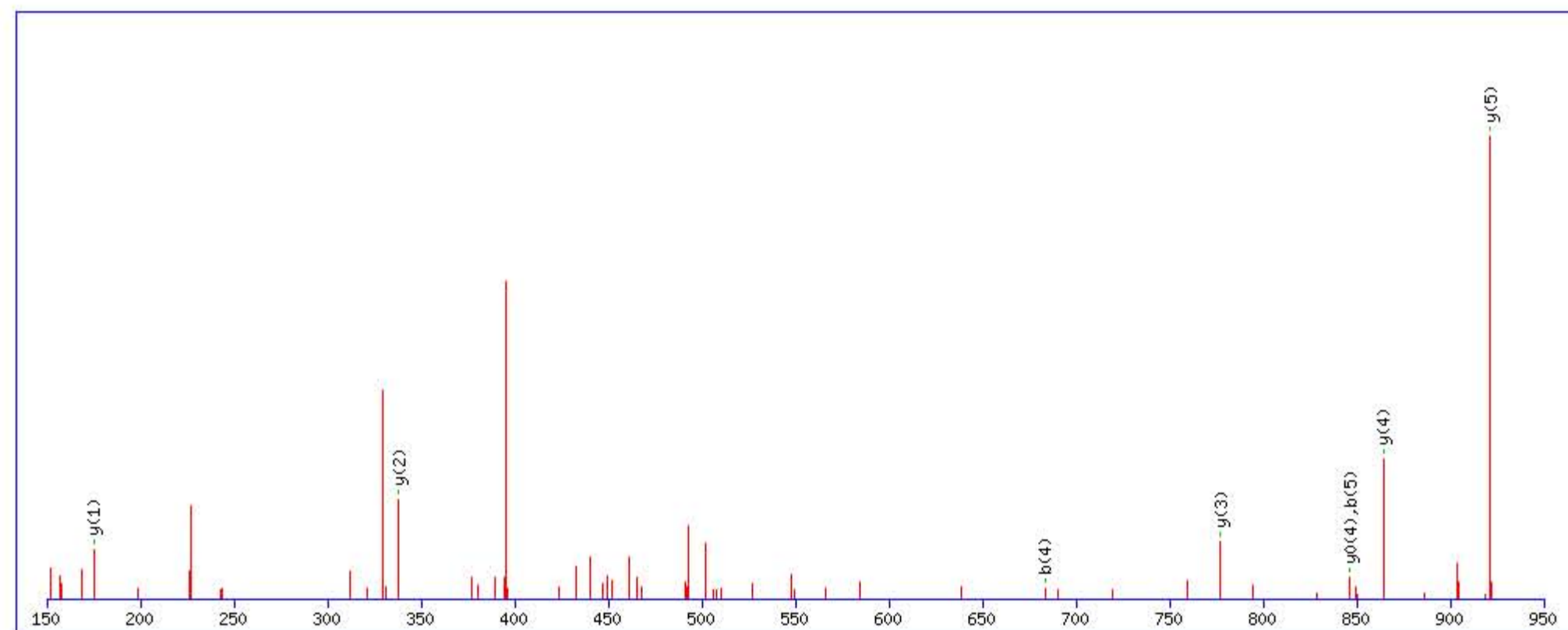
Title: Locus:1.1.1.1424.15 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1019.522232

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

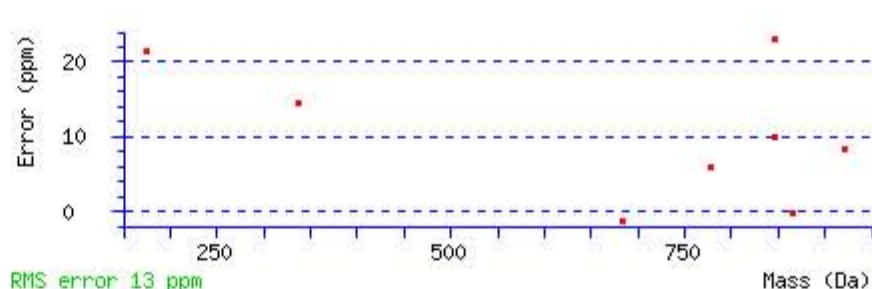
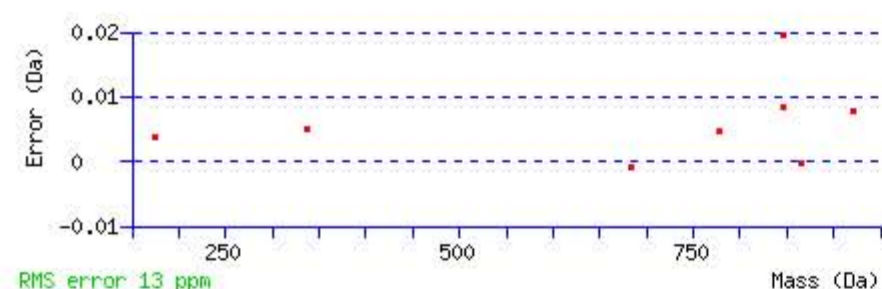
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.021

Matches : 8/44 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							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
30.2	1019.522232	-0.002444	VGSQYR
18.9	1019.533447	-0.013659	RSQYR
15.1	1019.510818	0.008970	RSSVSSGGAGR
8.4	1019.526047	-0.006259	SRERGPYR
7.2	1019.533447	-0.013659	RQSYR
7.1	1019.522217	-0.002429	QKDYR
6.1	1019.533447	-0.013659	QSRYR
6.1	1019.504944	0.014844	SHLWGHQR
5.7	1019.512146	0.007642	RSRGHHDR
4.6	1019.530090	-0.010302	SPLPWQHR

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 37672: 1611.800922 from(538.274250,3+) rtinseconds(1425) index(2386)

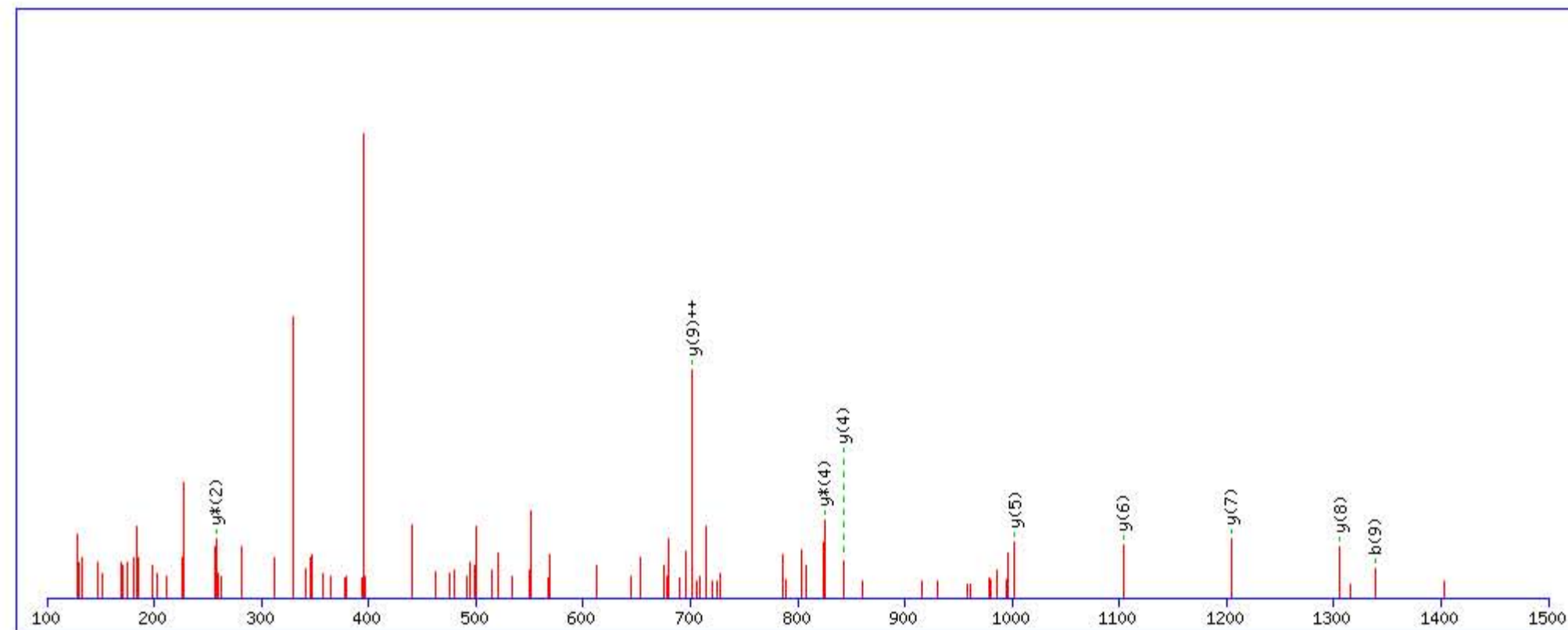
Title: Locus:1.1.1.1305.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1611.811295

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

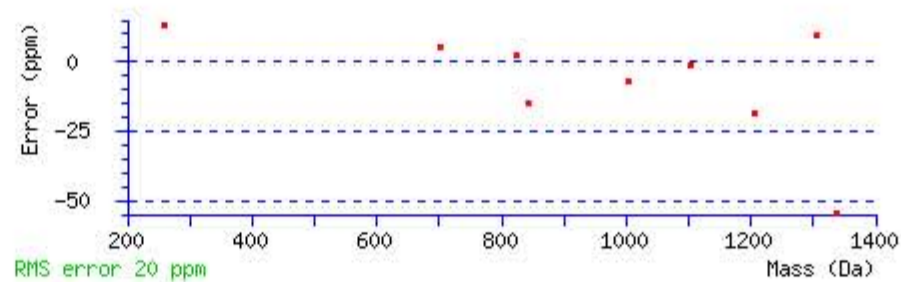
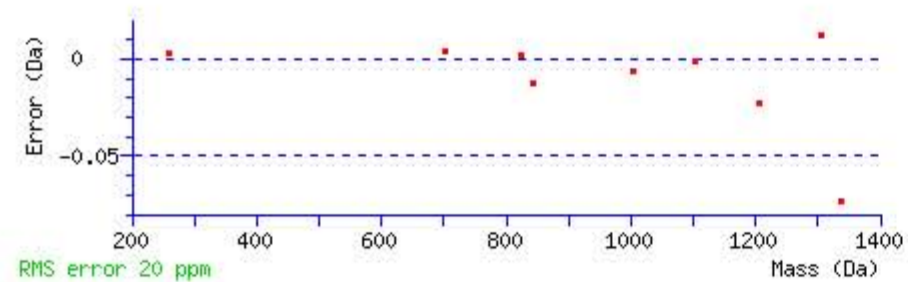
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.0049

Matches : 9/90 fragment ions using 13 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							11
2	211.144104	106.075690					P	1499.734500	750.370888	1482.707951	741.857614	1481.723935	741.365606	10
3	308.196868	154.602072					P	1402.681736	701.844506	1385.655187	693.331232	1384.671171	692.839224	9
4	409.244547	205.125911			391.233982	196.120629	T	1305.628972	653.318124	1288.602423	644.804850	1287.618407	644.312842	8
5	510.292226	255.649751			492.281661	246.644468	T	1204.581293	602.794285	1187.554744	594.281010	1186.570728	593.789002	7
6	611.339905	306.173591			593.329340	297.168308	T	1103.533614	552.270445	1086.507065	543.757171	1085.523049	543.265163	6
7	771.370554	386.188915			753.359989	377.183633	C	1002.485935	501.746606	985.459386	493.233331			5
8	899.429132	450.218204	882.402583	441.704930	881.418567	441.212922	Q	842.455286	421.731281	825.428737	413.218007			4
9	1338.654458	669.830867	1321.627909	661.317593	1320.643893	660.825585	Q	714.396708	357.701992	697.370159	349.188718			3
10	1466.713036	733.860156	1449.686487	725.346882	1448.702471	724.854874	Q	275.171382	138.089329	258.144833	129.576055			2
11							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **LPPTTTCQQQK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.6	1611.811295	-0.010373	LPPTTTCQQQK
27.6	1611.811295	-0.010373	LPPTTTCQQQK
22.2	1611.811295	-0.010373	LPPTTTCQQQK
3.0	1611.803879	-0.002957	RVQMEQPDAVPAQK
2.3	1611.803406	-0.002484	TPIKMGISASTMTMK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **YGQTIKIPICLPCTEGTTR**

Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

Match to Query 55089: 2433.196872 from(812.072900,3+) rtinseconds(2065) index(6244)

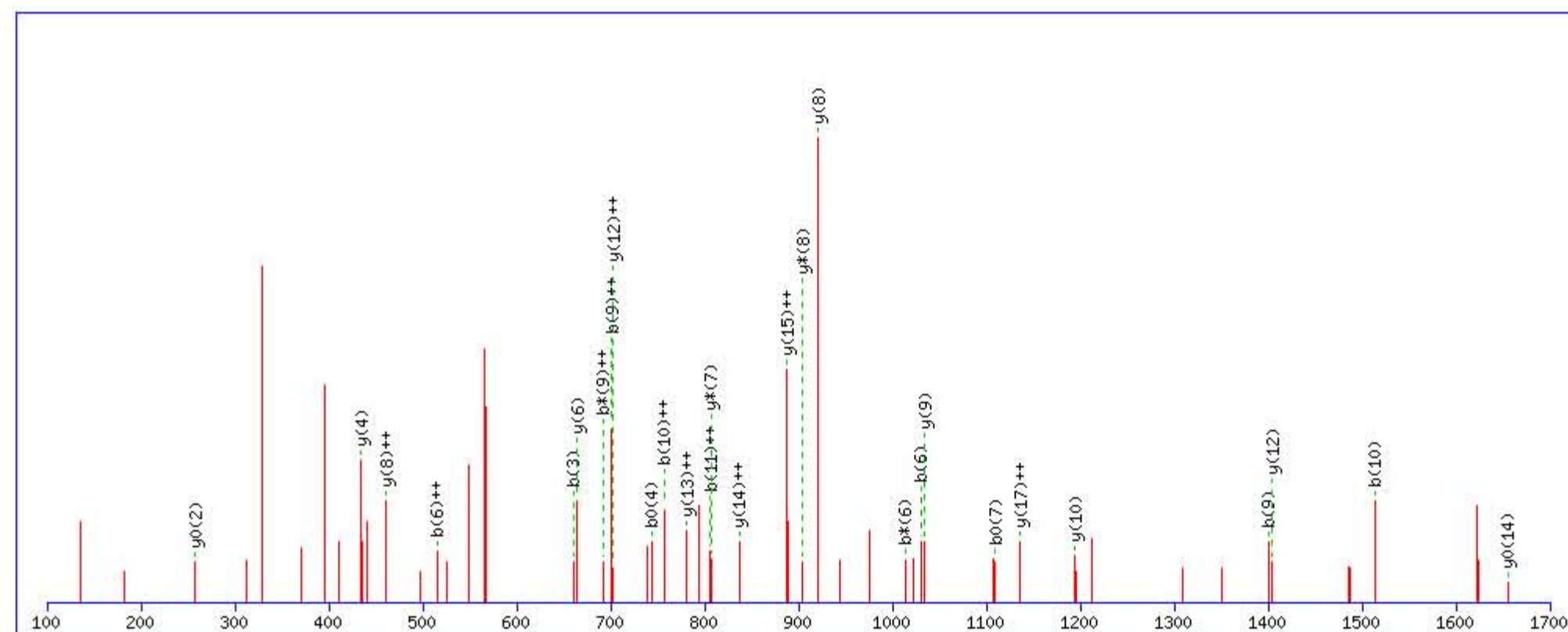
Title: Locus:1.1.1.1528.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2433.196701

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

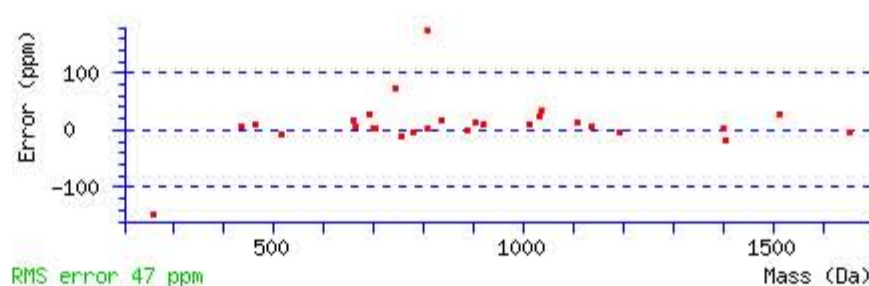
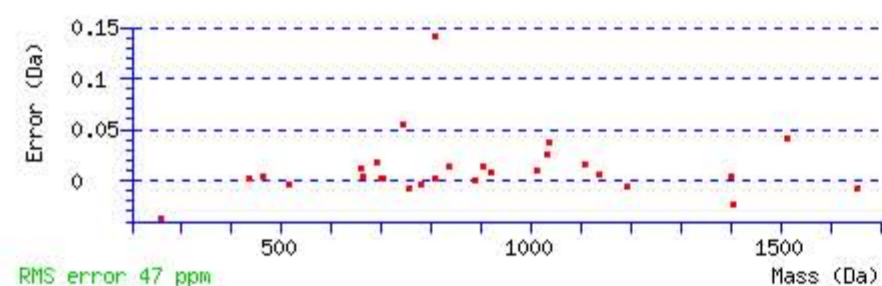
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.054

Matches : 28/192 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	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 **YGQTIKIPICLPCTEGTTR**

(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	2433.196701	0.000171	YGQTIKIPICLPCTEGTTR

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 43906: 1855.843512 from(619.621780,3+) rtinseconds(1898) index(21034)

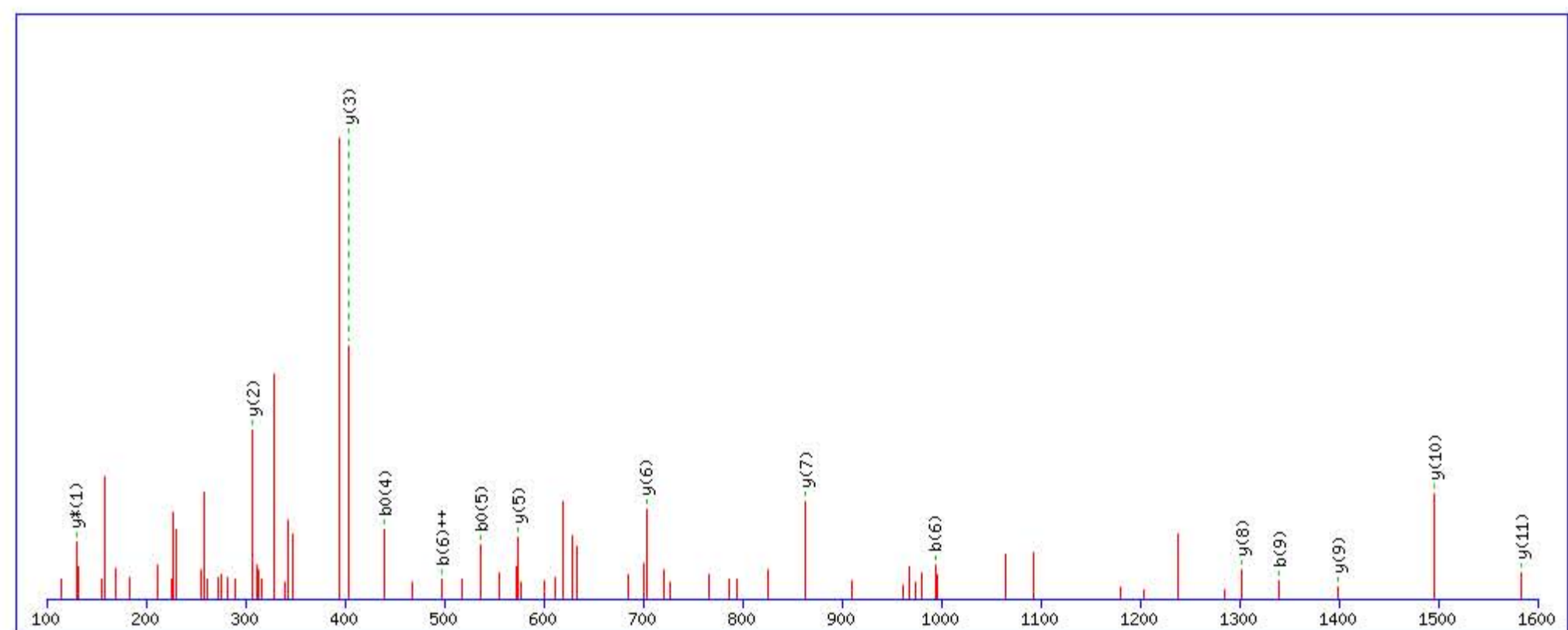
Title: Locus:1.1.1.663.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1855.841934

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

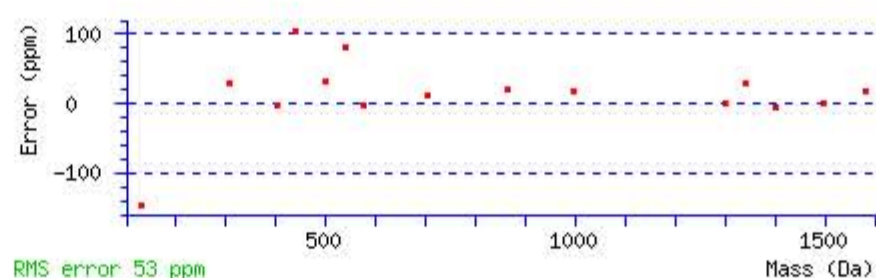
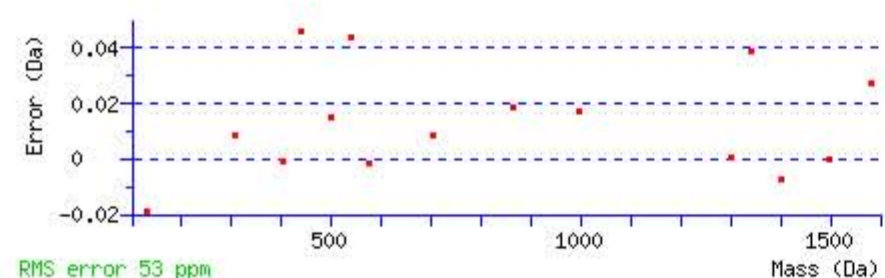
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 50 Expect: 9.5e-005

Matches : 15/122 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	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	423.185849	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
50.2	1855.841934	0.001578	WSSPPQCEGLPCK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AGEQVITYTCATYYK**

Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

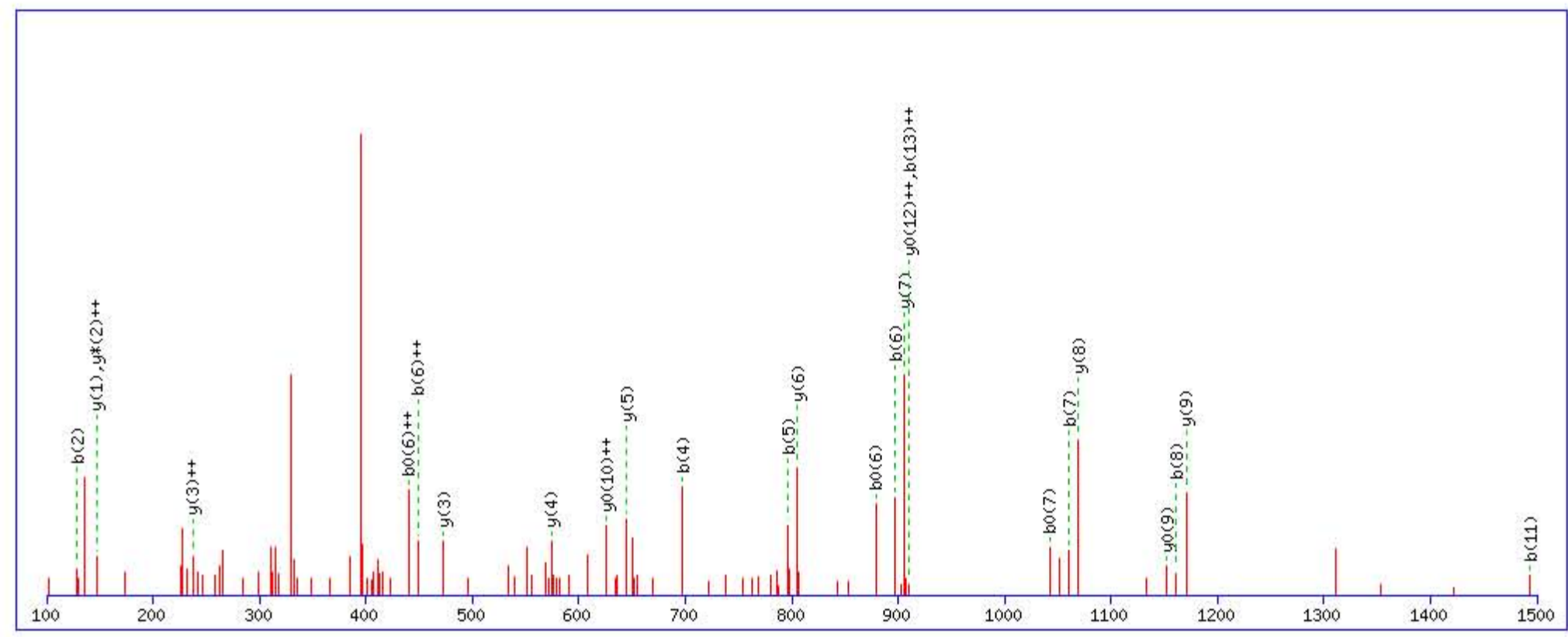
Match to Query 45865: 1964.900352 from(655.974060,3+) rtinseconds(1868) index(35393)
 Title: Locus:1.1.1.3070.8 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1964.901215

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

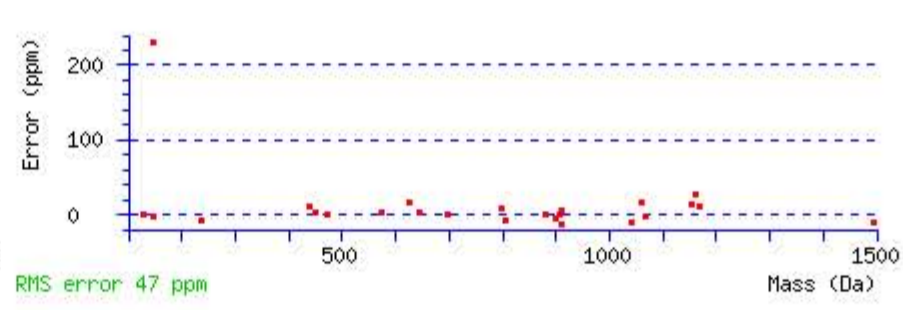
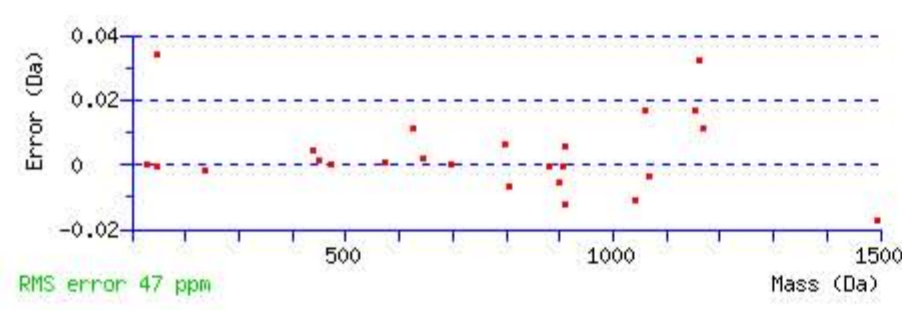
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 48 Expect: 0.00017

Matches : 25/140 fragment ions using 37 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	72.044390	36.525833					A							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 **AGEQVITYTCATYYK**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.3	1964.901215	-0.000863	AGEQVITYTCATYYK

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 55930: 2473.192812 from(825.404880,3+) rtinseconds(2519) index(24667)

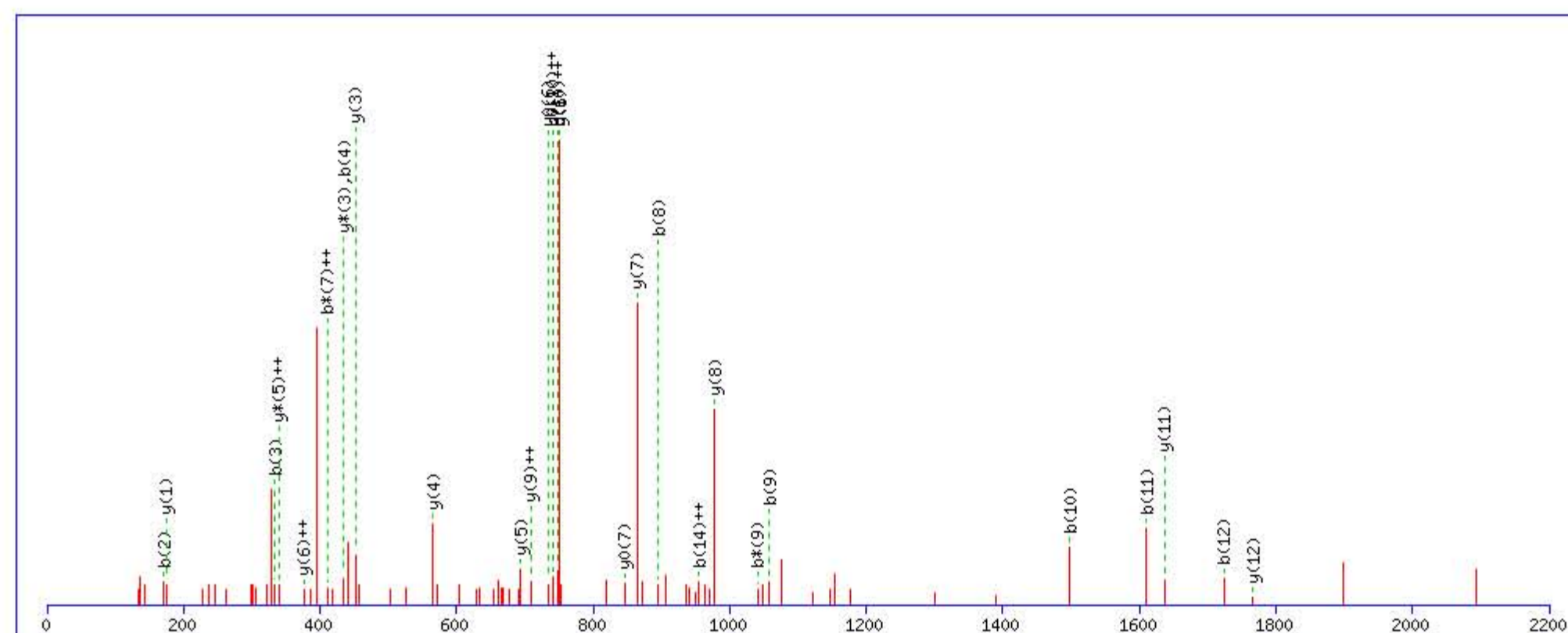
Title: Locus:1.1.1.879.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2473.176971

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

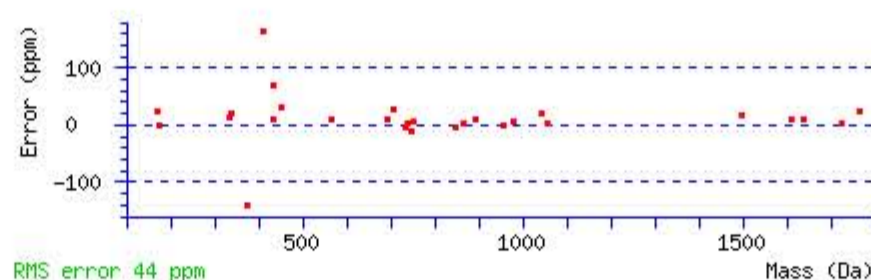
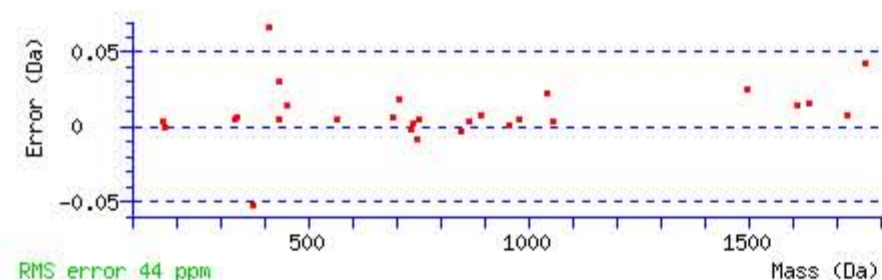
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 45 Expect: 0.00057

Matches : 28/180 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							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
45.2	2473.176971	0.015841	AVYTCNEGYQLLGEINYR
10.2	2473.192047	0.000765	ECDKAFIYGSQSEHQRHR
4.5	2473.188065	0.004747	GEAGAQQPMGSPGAPARGIQGPQGR

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 56705: 2502.216456 from(626.561390,4+) rtinseconds(1837) index(20560)

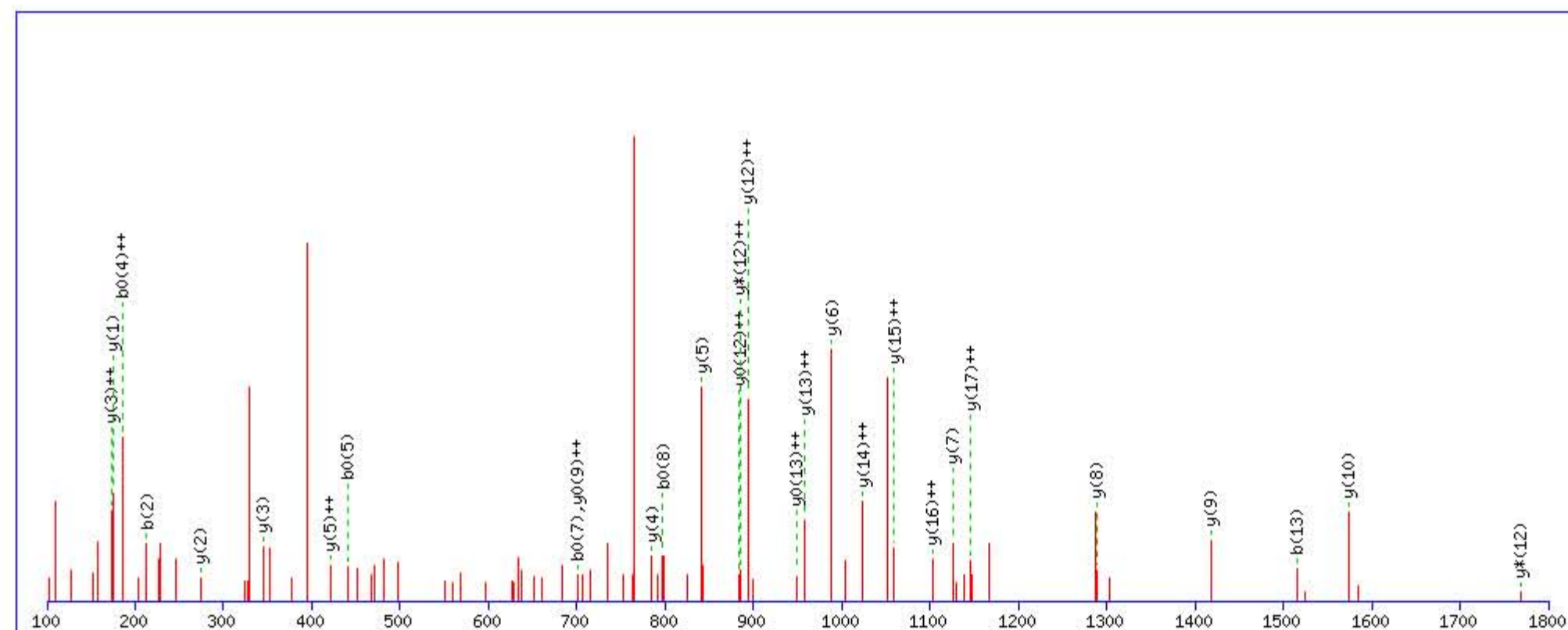
Title: Locus:1.1.1.642.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2502.214767

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

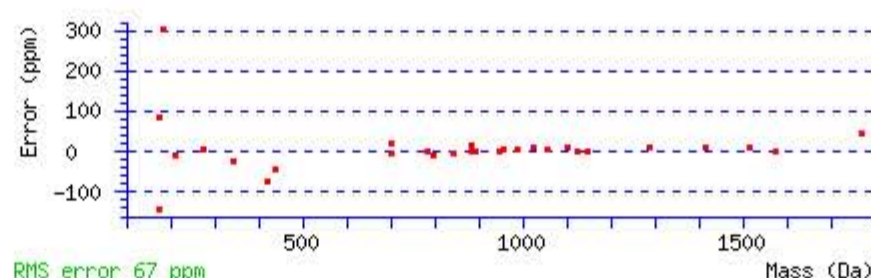
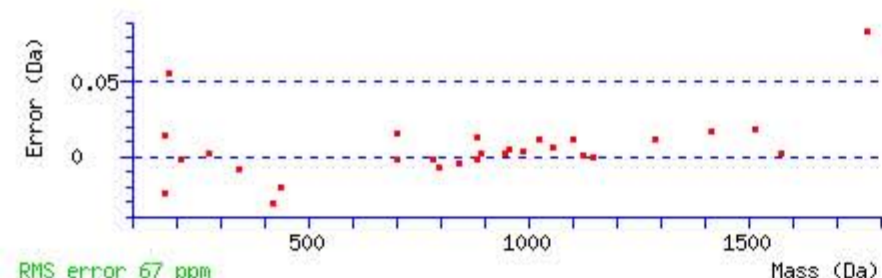
Variable modifications:

Q16 : Biotin:Thermo-21345 (Q)

Ions Score: 48 Expect: 0.00039

Matches : 29/178 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	114.091340	57.549308					I							19
2	213.159754	107.083515					V	2390.137998	1195.572637	2373.111449	1187.059362	2372.127433	1186.567354	18
3	300.191782	150.599529			282.181217	141.594247	S	2291.069584	1146.038430	2274.043035	1137.525155	2273.059019	1137.033147	17
4	387.223810	194.115543			369.213245	185.110261	S	2204.037556	1102.522416	2187.011007	1094.009141	2186.026991	1093.517133	16
5	458.260924	229.634100			440.250359	220.628818	A	2117.005528	1059.006402	2099.978979	1050.493127	2098.994963	1050.001119	15
6	589.301409	295.154343			571.290844	286.149060	M	2045.968414	1023.487845	2028.941865	1014.974571	2027.957849	1014.482563	14
7	718.344002	359.675639			700.333437	350.670357	E	1914.927929	957.967603	1897.901380	949.454328	1896.917364	948.962320	13
8	815.396766	408.202021			797.386201	399.196739	P	1785.885336	893.446306	1768.858787	884.933032	1767.874771	884.441024	12
9	930.423709	465.715493			912.413144	456.710210	D	1688.832572	844.919924	1671.806023	836.406650	1670.822007	835.914642	11
10	1086.524820	543.766048	1069.498271	535.252774	1068.514255	534.760766	R	1573.805629	787.406453	1556.779080	778.893178	1555.795064	778.401170	10
11	1215.567413	608.287345	1198.540864	599.774070	1197.556848	599.282062	E	1417.704518	709.355897	1400.677969	700.842623	1399.693953	700.350615	9
12	1378.630742	689.819009	1361.604193	681.305735	1360.620177	680.813727	Y	1288.661925	644.834601	1271.635376	636.321326			8
13	1515.689654	758.348465	1498.663105	749.835191	1497.679089	749.343183	H	1125.598596	563.302936	1108.572047	554.789662			7
14	1662.758068	831.882672	1645.731519	823.369398	1644.747503	822.877390	F	988.539684	494.773480	971.513135	486.260206			6
15	1719.779532	860.393404	1702.752983	851.880130	1701.768967	851.388122	G	841.471270	421.239273	824.444721	412.725999			5
16	2159.004858	1080.006067	2141.978309	1071.492792	2140.994293	1071.000784	Q	784.449806	392.728541	767.423257	384.215267			4
17	2230.041972	1115.524624	2213.015423	1107.011349	2212.031407	1106.519341	A	345.224480	173.115878	328.197931	164.602603			3
18	2329.110386	1165.058831	2312.083837	1156.545556	2311.099821	1156.053548	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
47.7	2502.214767	0.001689	IVSSAMEPDREYHFGQAVR

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 57881: 2636.345712 from(879.789180,3+) rtinseconds(2379) index(23862)

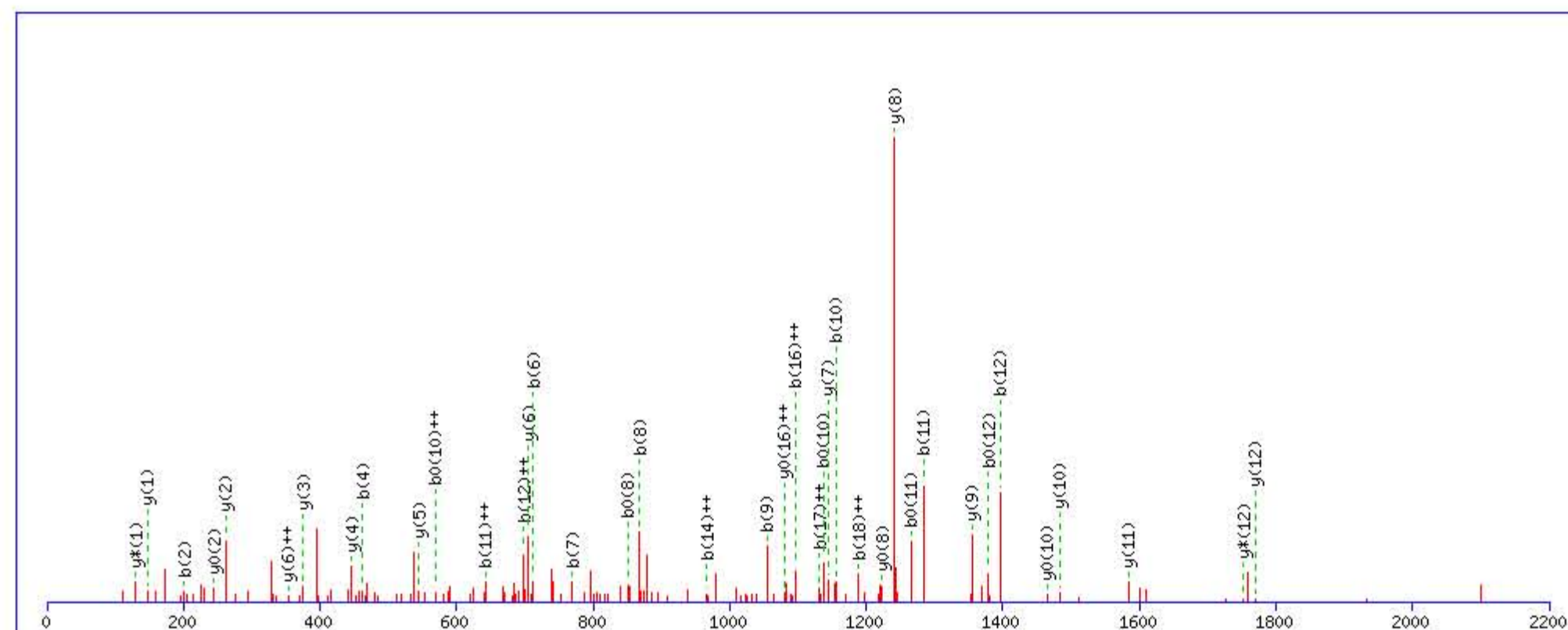
Title: Locus:1.1.1.830.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2636.327728

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

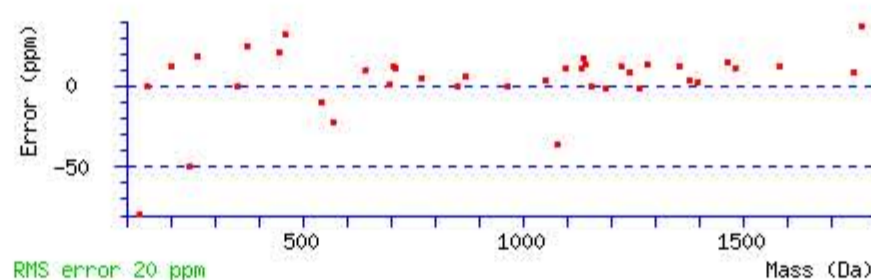
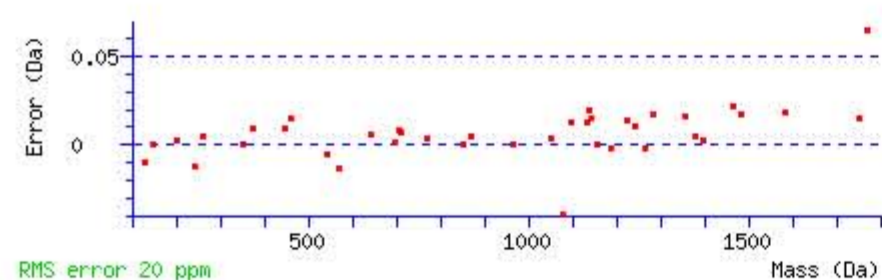
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 51 Expect: 1.7e-005

Matches : 39/206 fragment ions using 91 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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
51.0	2636.327728	0.017984	SITCIHGVWTQLPQCVAIDK
22.7	2636.327728	0.017984	SITCIHGVWTQLPQCVAIDK
0.1	2636.366592	-0.020880	ASKTTDLRIPASVCTMFNVLDK

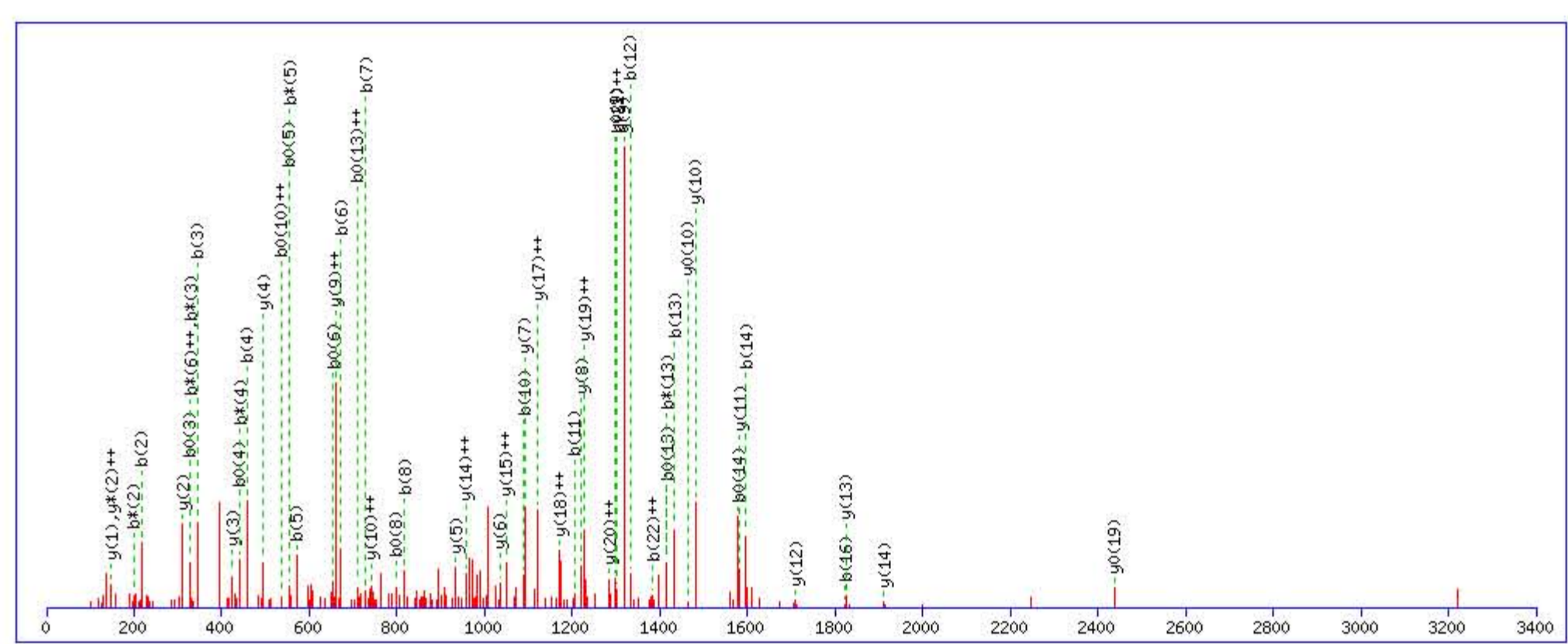
MASCOT Mascot Search Results

Peptide View

MS/MS Fragmentation of **NTEILTGSWSDQTYPEGTQAIYK**
 Found in **CFAH_HUMAN**, Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

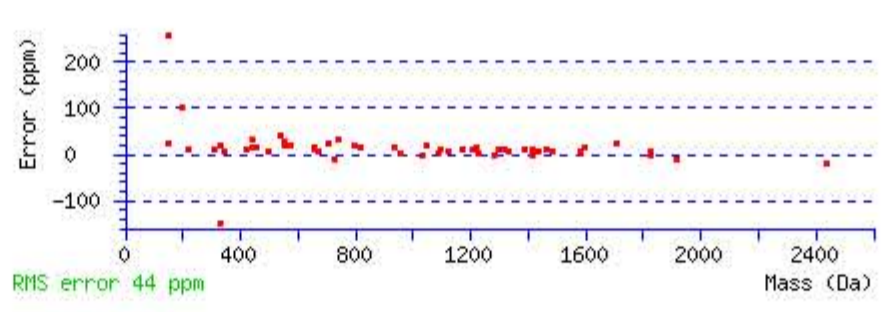
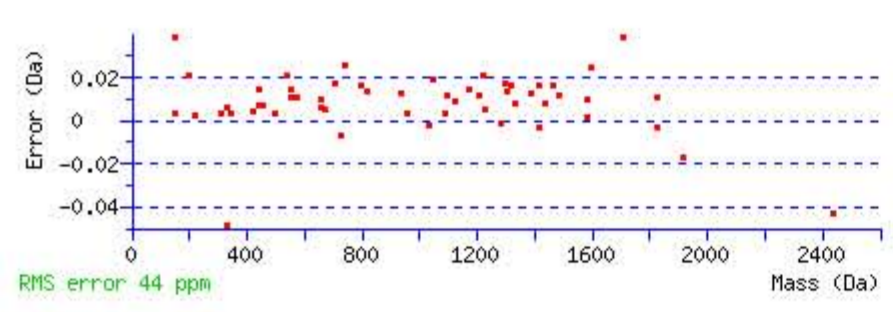
Match to Query 60932: 2912.406852 from(971.809560,3+) rtinseconds(2376) index(23845)
 Title: Locus:1.1.1.829.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2912.390213
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications: Q19 : Biotin:Thermo-21345 (Q)
 Ions Score: 86 Expect: 6.5e-008
 Matches : 56/252 fragment ions using 105 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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
86.0	2912.390213	0.016639	NTEILTGSWSDQTYPEGTQAIYK
23.0	2912.390213	0.016639	NTEILTGSWSDQTYPEGTQAIYK

MASCOT Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFCQPWQR**

Found in **CFAL_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

Match to Query 31931: 1430.693868 from(716.354210,2+) rtinseconds(2057) index(69149)

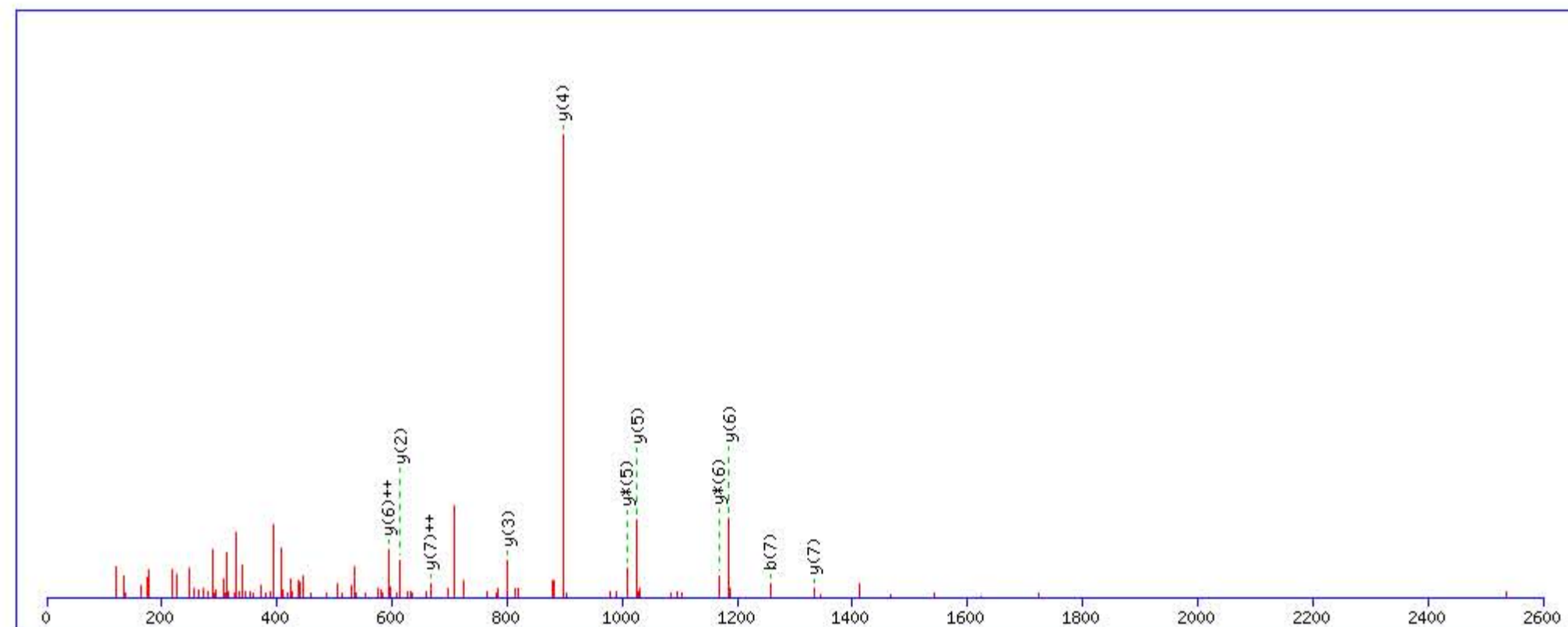
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1430.695145

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

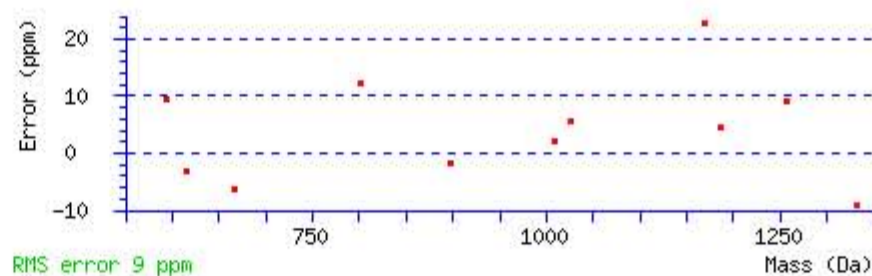
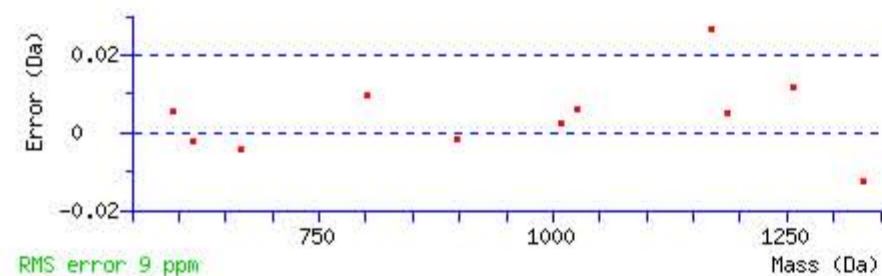
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.01

Matches : 11/50 fragment ions using 25 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
26.2	1430.695145	-0.001277	VFCQPWQR
4.7	1430.700989	-0.007121	NMPQADAMVLVAR
2.1	1430.695145	-0.001277	VFCQPWQR
0.5	1430.711319	-0.017451	RAKAEDENETLR
0.2	1430.693619	0.000249	QLQTLSPGGGGNR

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

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFPTYCQQK**

Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

Match to Query 32978: 1468.681388 from(735.347970,2+) rtinseconds(1835) index(67639)

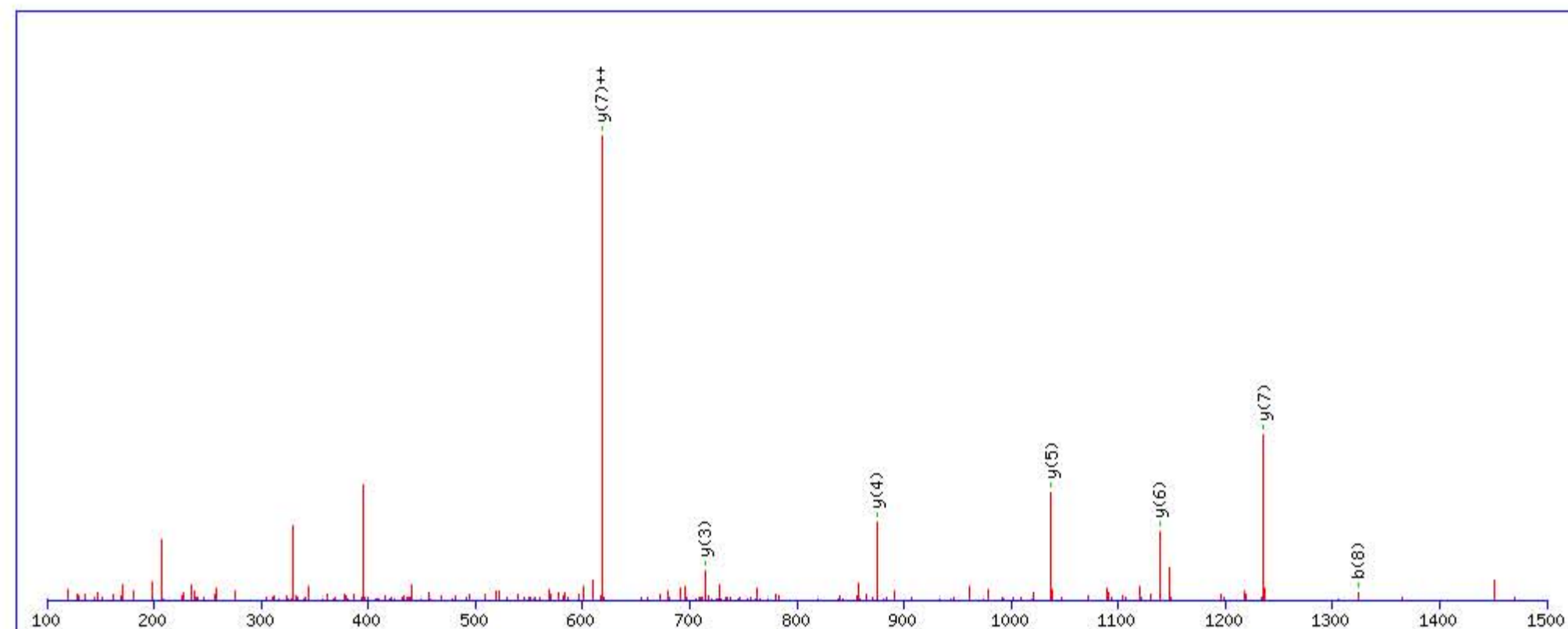
Title: Locus:1.1.1.1576.9 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1468.684296

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

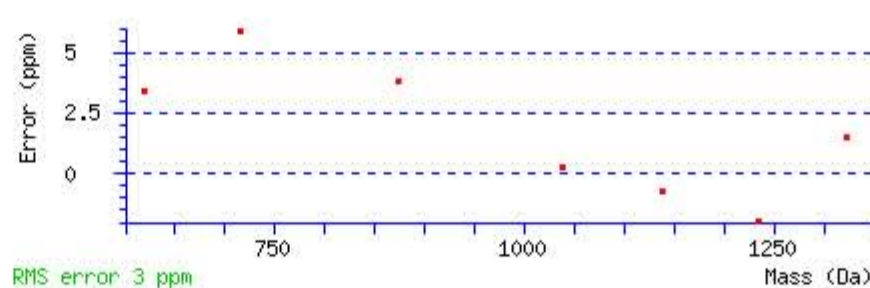
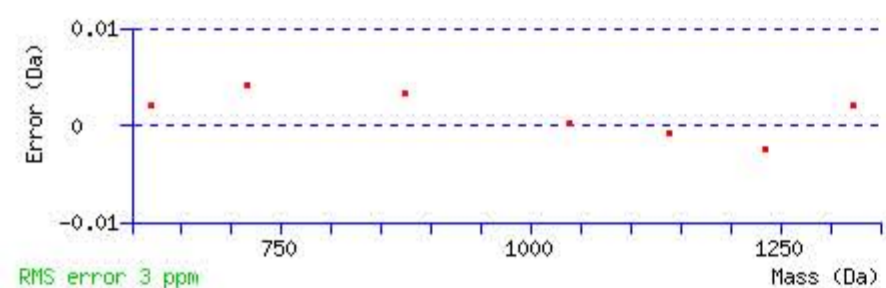
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.0066

Matches : 7/74 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							9
2	235.107718	118.057497			217.097153	109.052214	F	1382.659543	691.833410	1365.632994	683.320135	1364.648978	682.828127	8
3	332.160482	166.583879			314.149917	157.578596	P	1235.591129	618.299203	1218.564580	609.785928	1217.580564	609.293920	7
4	433.208161	217.107718			415.197596	208.102436	T	1138.538365	569.772821	1121.511816	561.259546	1120.527800	560.767538	6
5	596.271490	298.639383			578.260925	289.634101	Y	1037.490686	519.248981	1020.464137	510.735707			5
6	756.302139	378.654708			738.291574	369.649425	C	874.427357	437.717317	857.400808	429.204042			4
7	884.360717	442.683997	867.334168	434.170722	866.350152	433.678714	Q	714.396708	357.701992	697.370159	349.188718			3
8	1323.586043	662.296660	1306.559494	653.783385	1305.575478	653.291377	Q	586.338130	293.672703	569.311581	285.159428			2
9							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **SFPTYCQQK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.5	1468.684296	-0.002908	SFPTYCQQK
28.5	1468.684296	-0.002908	SFPTYCQQK
4.9	1468.671524	0.009864	MEAETGSSVETGKK
1.4	1468.688126	-0.006738	FSIPSMTEHHAGR
0.8	1468.680252	0.001136	YAKGNDCALLCK

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 40928: 1721.853882 from(574.958570,3+) rtinseconds(1894) index(67929)

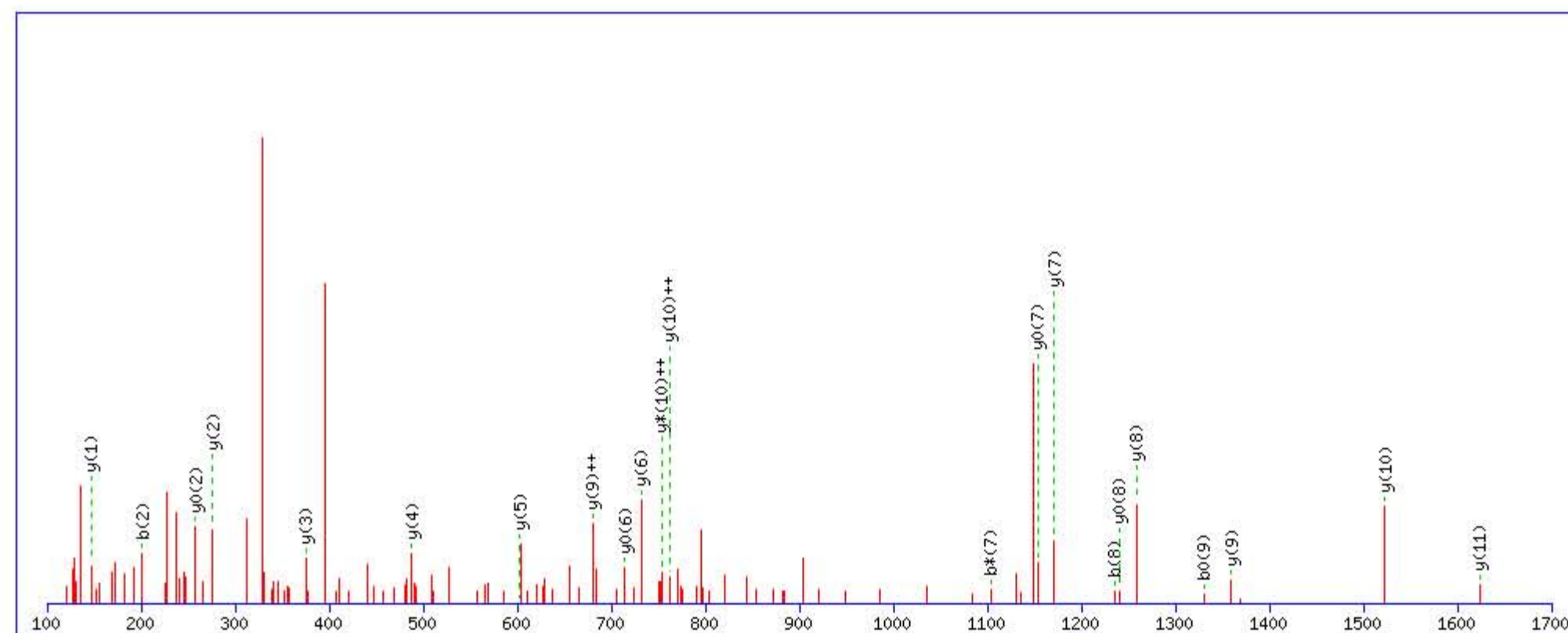
Title: Locus:1.1.1.1597.19 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1721.854584

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

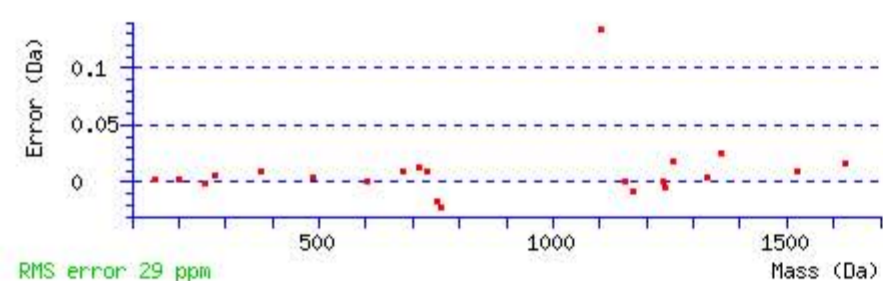
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

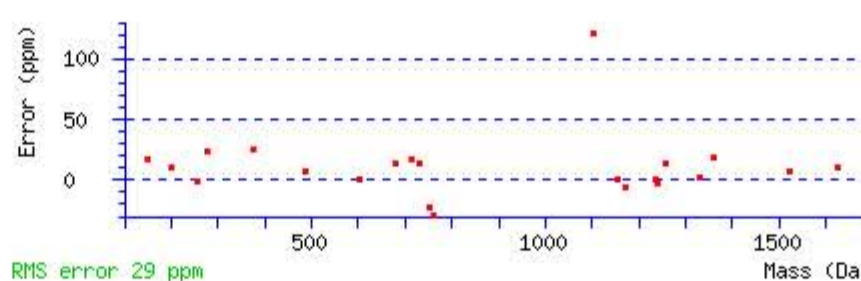
Ions Score: 49 Expect: 0.00033

Matches : 22/118 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	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



RMS error 29 ppm



RMS error 29 ppm

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
48.6	1721.854584	-0.000702	VTYTSQEDLVEK

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

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 54461: 2403.146562 from(802.056130,3+) rtinseconds(2280) index(70432)

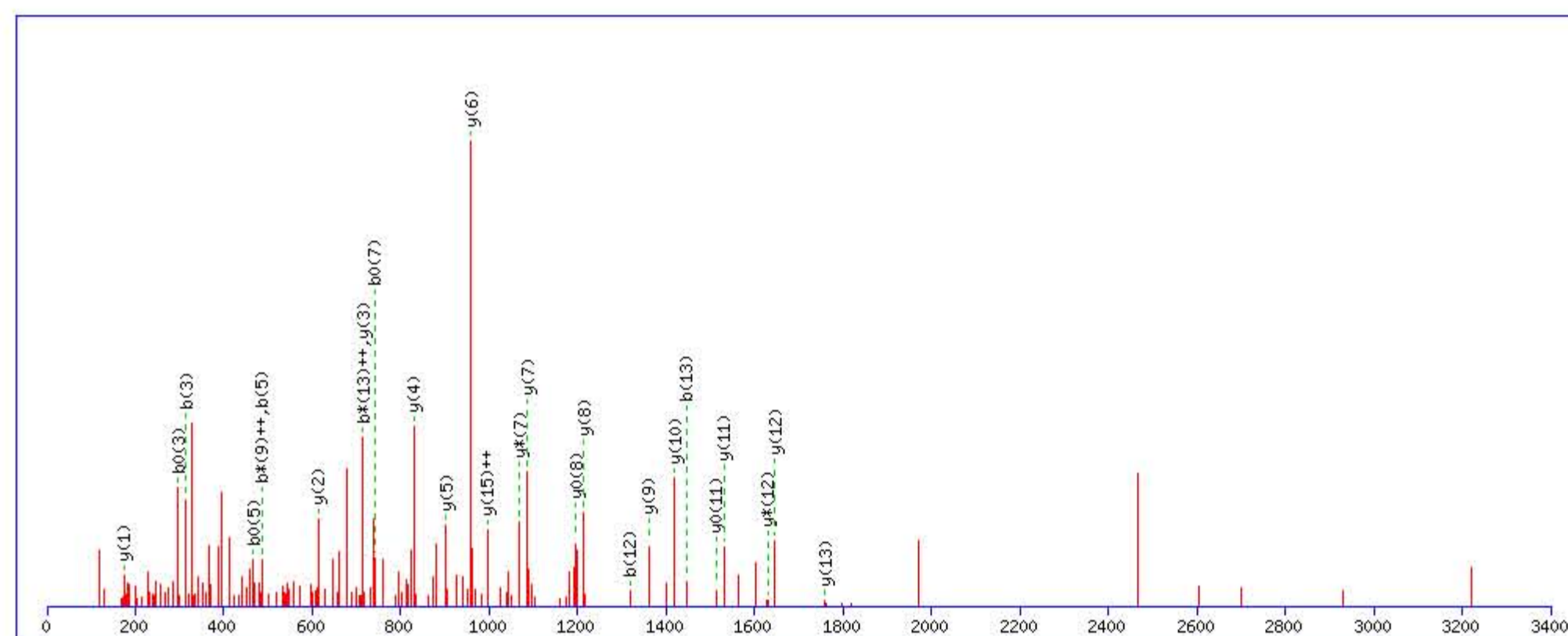
Title: Locus:1.1.1.1731.8 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2403.131119

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

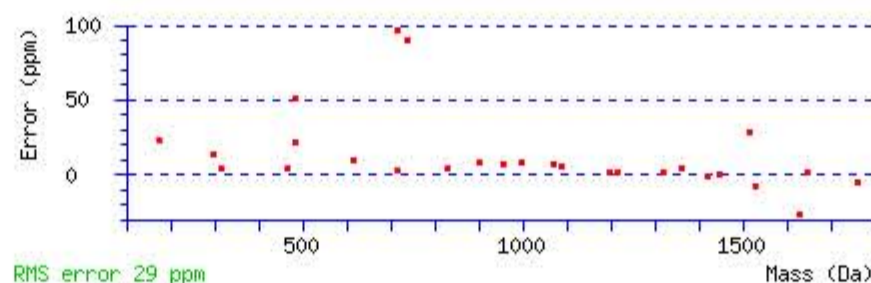
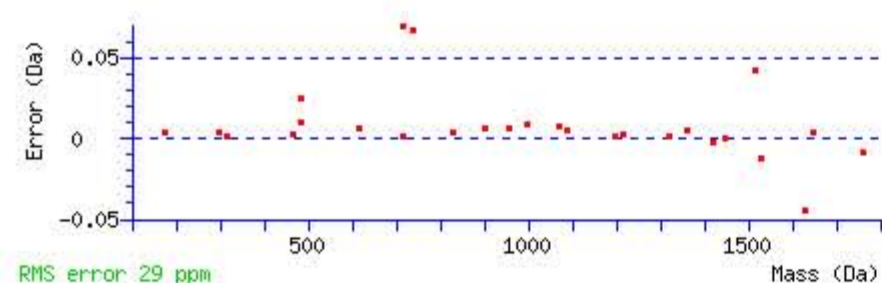
Variable modifications:

Q18 : Biotin:Thermo-21345 (Q)

Ions Score: 99 Expect: 7.5e-010

Matches : 27/208 fragment ions using 34 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							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
99.2	2403.131119	0.015443	EANVACLDLGFQQGADTQR
43.3	2403.131119	0.015443	EANVACLDLGFQQGADTQR
37.0	2403.131119	0.015443	EANVACLDLGFQQGADTQR
1.8	2403.157135	-0.010573	QAMMKTDFPGDLGSQR
0.6	2403.175339	-0.028777	AAEPLVGQRWEAFDVADAMRR

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **HLQEALGLPAGR**

Found in **CLC11_HUMAN**, C-type lectin domain family 11 member A OS=Homo sapiens GN=CLEC11A PE=1 SV=1

Match to Query 35764: 1571.860902 from(524.960910,3+) rtinseconds(1972) index(52657)

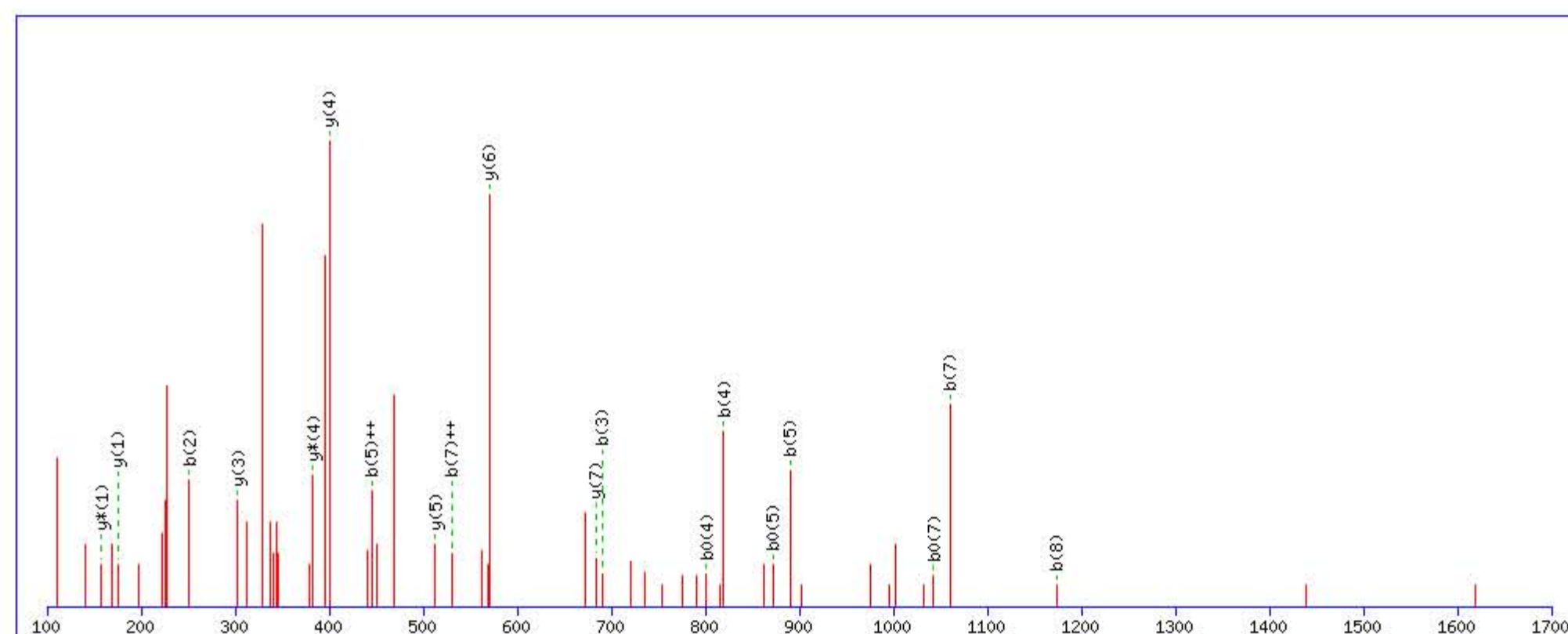
Title: Locus:1.1.1.1302.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1571.860596

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

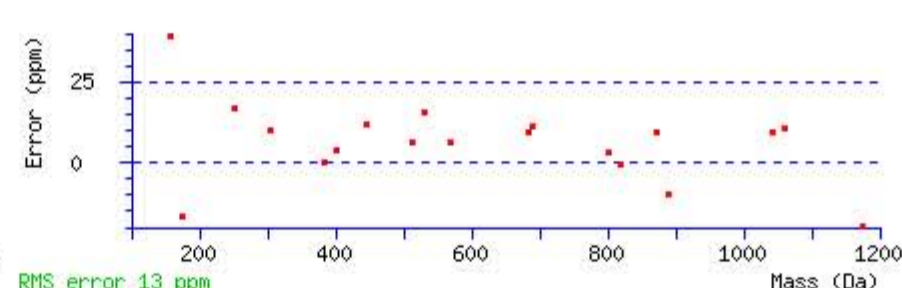
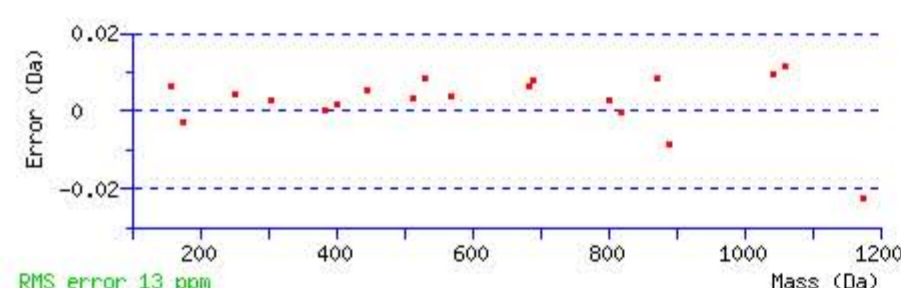
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.0036

Matches : 19/106 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	138.066188	69.536732					H							12
2	251.150252	126.078764					L	1435.808983	718.408129	1418.782434	709.894855	1417.798418	709.402847	11
3	690.375578	345.691427	673.349029	337.178153			Q	1322.724919	661.866098	1305.698370	653.352823	1304.714354	652.860815	10
4	819.418171	410.212724	802.391622	401.699449	801.407606	401.207441	E	883.499593	442.253434	866.473044	433.740160	865.489028	433.248152	9
5	890.455285	445.731281	873.428736	437.218006	872.444720	436.725998	A	754.457000	377.732138	737.430451	369.218863			8
6	1003.539349	502.273313	986.512800	493.760038	985.528784	493.268030	L	683.419886	342.213581	666.393337	333.700306			7
7	1060.560813	530.784045	1043.534264	522.270770	1042.550248	521.778762	G	570.335822	285.671549	553.309273	277.158274			6
8	1173.644877	587.326077	1156.618328	578.812802	1155.634312	578.320794	L	513.314358	257.160817	496.287809	248.647542			5
9	1270.697641	635.852459	1253.671092	627.339184	1252.687076	626.847176	P	400.230294	200.618785	383.203745	192.105510			4
10	1341.734755	671.371016	1324.708206	662.857741	1323.724190	662.365733	A	303.177530	152.092403	286.150981	143.579128			3
11	1398.756219	699.881747	1381.729670	691.368473	1380.745654	690.876465	G	232.140416	116.573846	215.113867	108.060571			2
12							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **HLQEALGLPAGR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.8	1571.860596	0.000306	HLQEALGLPAGR
1.6	1571.857224	0.003678	VNWLGSKEGLRWK
0.8	1571.863098	-0.002196	IQQLINGALNKTINK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **NEQESAVHPR**

Found in **DBNL_HUMAN**, Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1

Match to Query 33212: 1476.719592 from(493.247140,3+) rtinseconds(1312) index(48324)

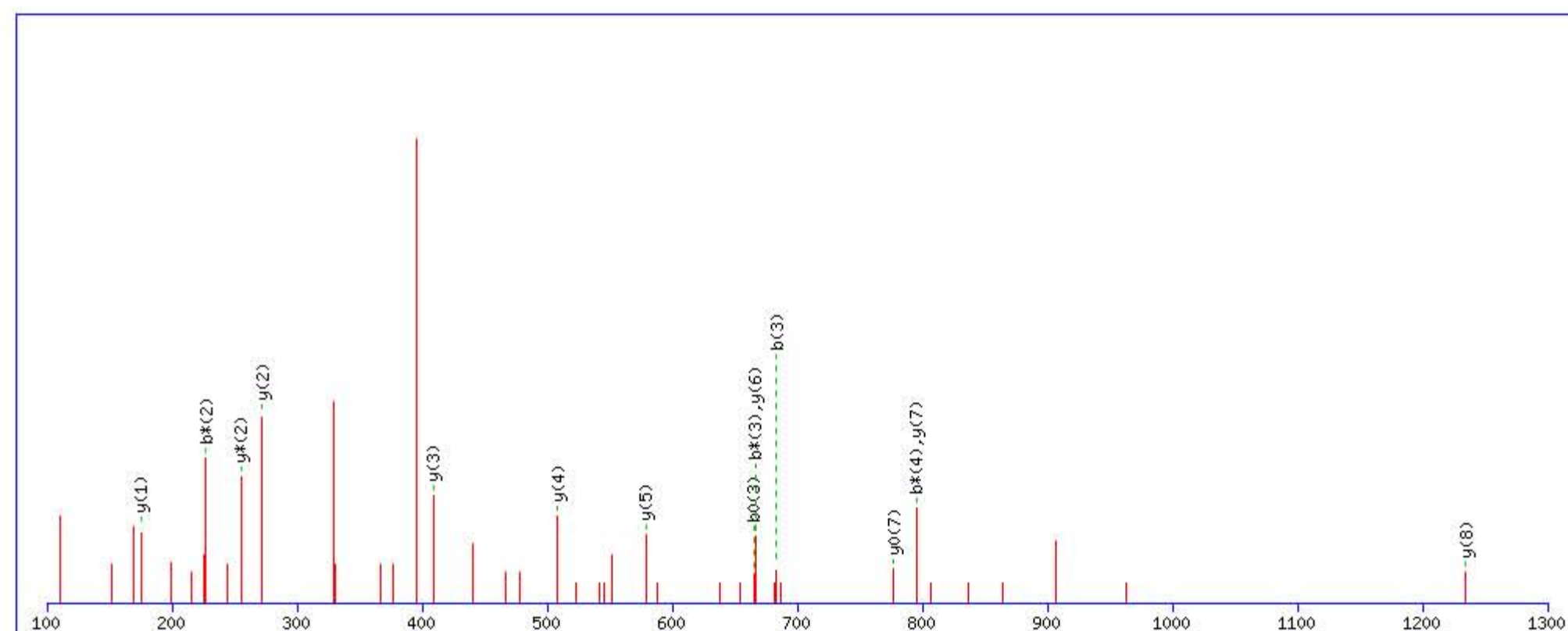
Title: Locus:1.1.1.1072.17 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1476.714325

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

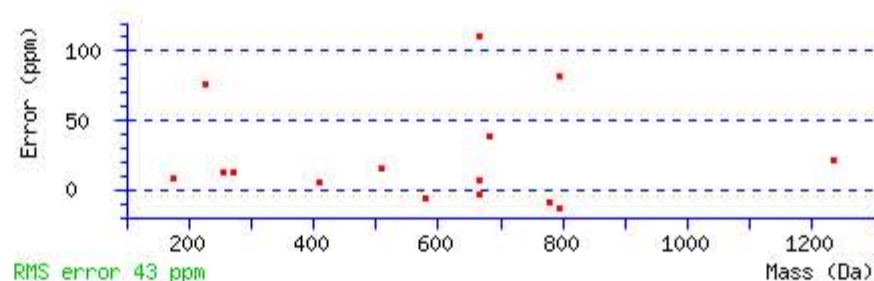
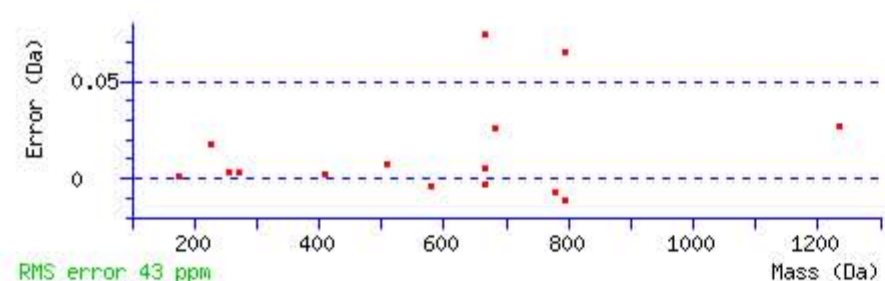
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.0002

Matches : 15/96 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	115.050203	58.028740	98.023654	49.515465			N							10
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	E	1363.678696	682.342986	1346.652147	673.829712	1345.668131	673.337704	9
3	683.318122	342.162699	666.291573	333.649425	665.307557	333.157417	Q	1234.636103	617.821690	1217.609554	609.308415	1216.625538	608.816407	8
4	812.360715	406.683996	795.334166	398.170721	794.350150	397.678713	E	795.410777	398.209027	778.384228	389.695752	777.400212	389.203744	7
5	899.392743	450.200010	882.366194	441.686735	881.382178	441.194727	S	666.368184	333.687730	649.341635	325.174456	648.357619	324.682448	6
6	970.429857	485.718567	953.403308	477.205292	952.419292	476.713284	A	579.336156	290.171716	562.309607	281.658442			5
7	1069.498271	535.252774	1052.471722	526.739499	1051.487706	526.247491	V	508.299042	254.653159	491.272493	246.139884			4
8	1206.557183	603.782230	1189.530634	595.268955	1188.546618	594.776947	H	409.230628	205.118952	392.204079	196.605677			3
9	1303.609947	652.308612	1286.583398	643.795337	1285.599382	643.303329	P	272.171716	136.589496	255.145167	128.076221			2
10							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **NEQESAVHPR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
40.3	1476.714325	0.005267	NEQESAVHPR
0.9	1476.712982	0.006610	DQDAIETDAMIKK

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 59972: 2843.261736 from(711.822710,4+) rtinseconds(1760) index(34832)

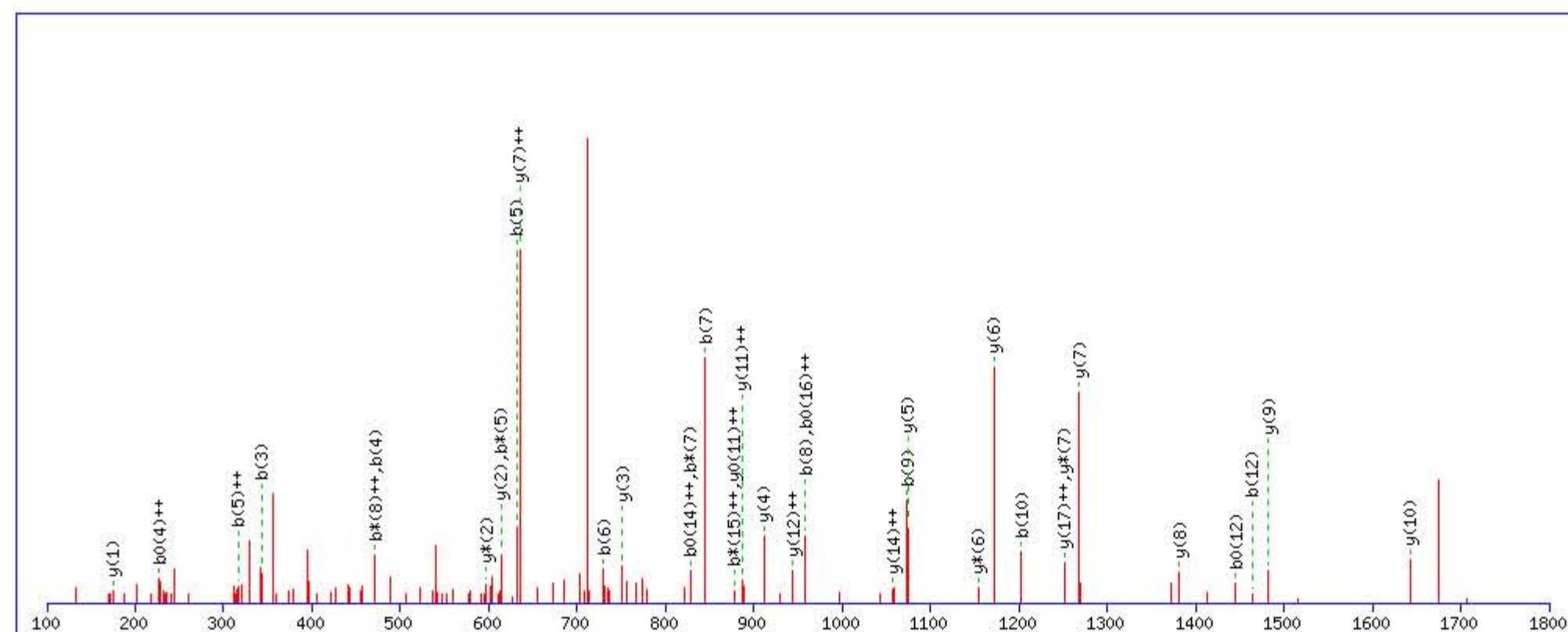
Title: Locus:1.1.1.3032.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2843.261169

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

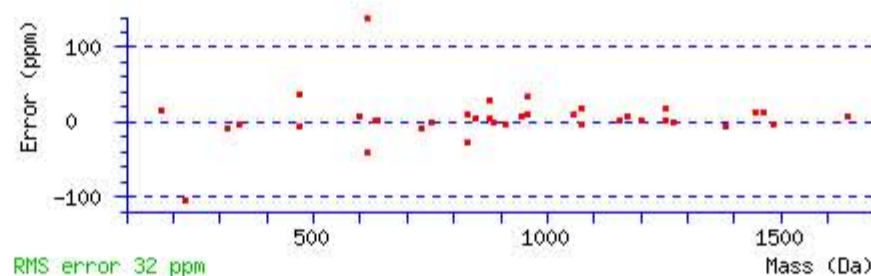
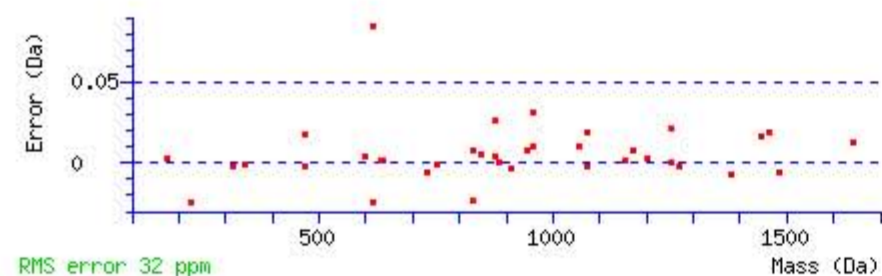
Variable modifications:

Q19 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 1.1e-005

Matches : 37/208 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	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
57.5	2843.261169	0.000567	RGEQCVDIDECTIPPYCHQR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **IQCAAGYEQSEHNCQDIDECTAGTHNCR**

Found in **FBLN3_HUMAN**, EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2

Match to Query 68555: 3733.547456 from(934.394140,4+) rtinseconds(1738) index(34682)

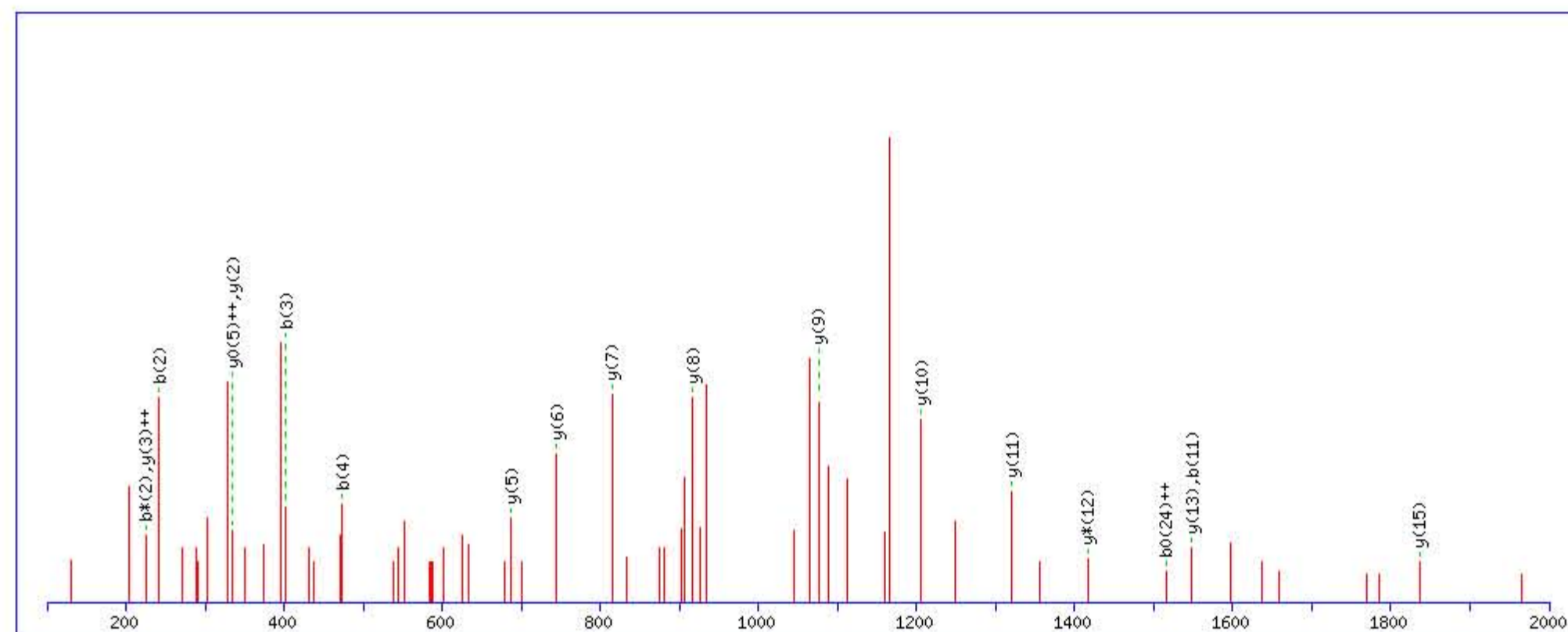
Title: Locus:1.1.1.3024.23 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3733.543625

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

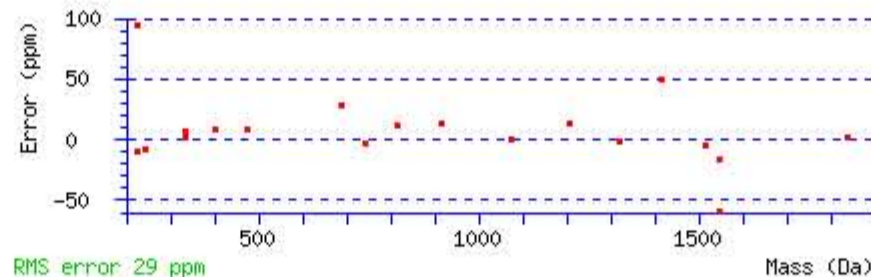
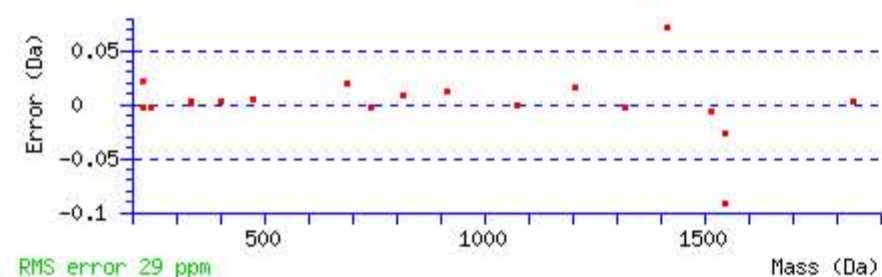
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.0014

Matches : 19/312 fragment ions using 43 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					I							29
2	242.149918	121.578597	225.123369	113.065323			Q	3621.466836	1811.237056	3604.440287	1802.723781	3603.456271	1802.231773	28
3	402.180567	201.593922	385.154018	193.080647			C	3493.408258	1747.207767	3476.381709	1738.694492	3475.397693	1738.202484	27
4	473.217681	237.112479	456.191132	228.599204			A	3333.377609	1667.192442	3316.351060	1658.679168	3315.367044	1658.187160	26
5	544.254795	272.631036	527.228246	264.117761			A	3262.340495	1631.673885	3245.313946	1623.160611	3244.329930	1622.668603	25
6	601.276259	301.141768	584.249710	292.628493			G	3191.303381	1596.155328	3174.276832	1587.642054	3173.292816	1587.150046	24
7	764.339588	382.673432	747.313039	374.160158			Y	3134.281917	1567.644596	3117.255368	1559.131322	3116.271352	1558.639314	23
8	893.382181	447.194729	876.355632	438.681454	875.371616	438.189446	E	2971.218588	1486.112932	2954.192039	1477.599657	2953.208023	1477.107649	22
9	1332.607507	666.807391	1315.580958	658.294117	1314.596942	657.802109	Q	2842.175995	1421.591635	2825.149446	1413.078361	2824.165430	1412.586353	21
10	1419.639535	710.323406	1402.612986	701.810131	1401.628970	701.318123	S	2402.950669	1201.978972	2385.924120	1193.465698	2384.940104	1192.973690	20
11	1548.682128	774.844702	1531.655579	766.331428	1530.671563	765.839420	E	2315.918641	1158.462958	2298.892092	1149.949684	2297.908076	1149.457676	19
12	1685.741040	843.374158	1668.714491	834.860884	1667.730475	834.368876	H	2186.876048	1093.941662	2169.849499	1085.428387	2168.865483	1084.936379	18
13	1799.783967	900.395622	1782.757418	891.882347	1781.773402	891.390339	N	2049.817136	1025.412206	2032.790587	1016.898931	2031.806571	1016.406923	17
14	1898.852381	949.929829	1881.825832	941.416554	1880.841816	940.924546	V	1935.774209	968.390742	1918.747660	959.877468	1917.763644	959.385460	16
15	2058.883030	1029.945153	2041.856481	1021.431879	2040.872465	1020.939871	C	1836.705795	918.856535	1819.679246	910.343261	1818.695230	909.851253	15
16	2186.941608	1093.974442	2169.915059	1085.461167	2168.931043	1084.969159	Q	1676.675146	838.841211	1659.648597	830.327936	1658.664581	829.835928	14
17	2301.968551	1151.487913	2284.942002	1142.974639	2283.957986	1142.482631	D	1548.616568	774.811922	1531.590019	766.298647	1530.606003	765.806639	13
18	2415.052615	1208.029945	2398.026066	1199.516671	2397.042050	1199.024663	I	1433.589625	717.298450	1416.563076	708.785176	1415.579060	708.293168	12
19	2530.079558	1265.543417	2513.053009	1257.030142	2512.068993	1256.538134	D	1320.505561	660.756418	1303.479012	652.243144	1302.494996	651.751136	11
20	2659.122151	1330.064713	2642.095602	1321.551439	2641.111586	1321.059431	E	1205.478618	603.242947	1188.452069	594.729672	1187.468053	594.237664	10
21	2819.152800	1410.080038	2802.126251	1401.566763	2801.142235	1401.074755	C	1076.436025	538.721650	1059.409476	530.208376	1058.425460	529.716368	9
22	2920.200479	1460.603877	2903.173930	1452.090603	2902.189914	1451.598595	T	916.405376	458.706326	899.378827	450.193051	898.394811	449.701043	8
23	2991.237593	1496.122434	2974.211044	1487.609160	2973.227028	1487.117152	A	815.357697	408.182486	798.331148	399.669212	797.347132	399.177204	7
24	3048.259057	1524.633166	3031.232508	1516.119892	3030.248492	1515.627884	G	744.320583	372.663929	727.294034	364.150655	726.310018	363.658647	6
25	3149.306736	1575.157006	3132.280187	1566.643731	3131.296171	1566.151723	T	687.299119	344.153197	670.272570	335.639923	669.288554	335.147915	5
26	3286.365648	1643.686462	3269.339099	1635.173187	3268.355083	1634.681179	H	586.251440	293.629358	569.224891	285.116083			4
27	3400.408575	1700.707925	3383.382026	1692.194651	3382.398010	1691.702643	N	449.192528	225.099902	432.165979	216.586627			3
28	3560.439224	1780.723250	3543.412675	1772.209975	3542.428659	1771.717967	C	335.149601	168.078438	318.123052	159.565164			2
29							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **IQCAAGYEQSEHNCQDIDECTAGTHNCR**

(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	3733.543625	0.003831	IQCAAGYEQSEHNCQDIDECTAGTHNCR
23.2	3733.543625	0.003831	IQCAAGYEQSEHNCQDIDECTAGTHNCR
22.1	3733.543625	0.003831	IQCAAGYEQSEHNCQDIDECTAGTHNCR

MASCOT 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 32096: 1434.769908 from(718.392230,2+) rtinseconds(1979) index(5751)

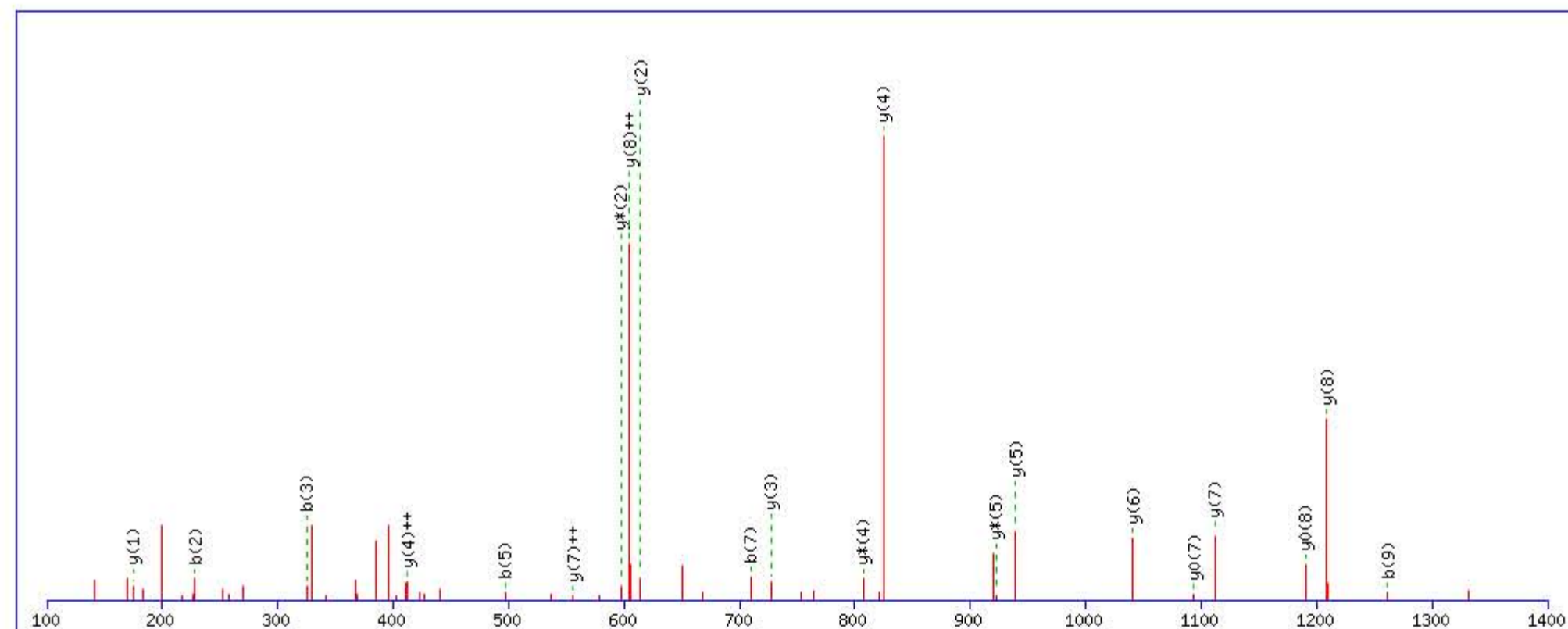
Title: Locus:1.1.1.1498.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1434.765305

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

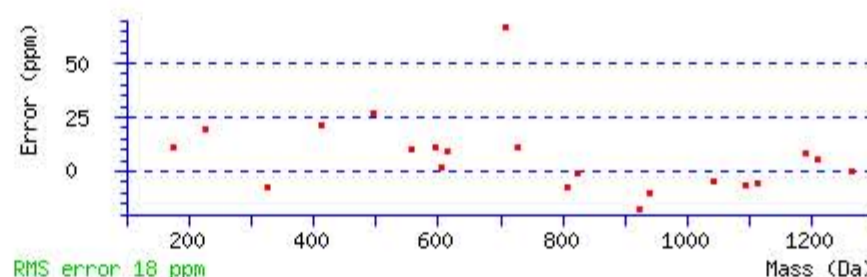
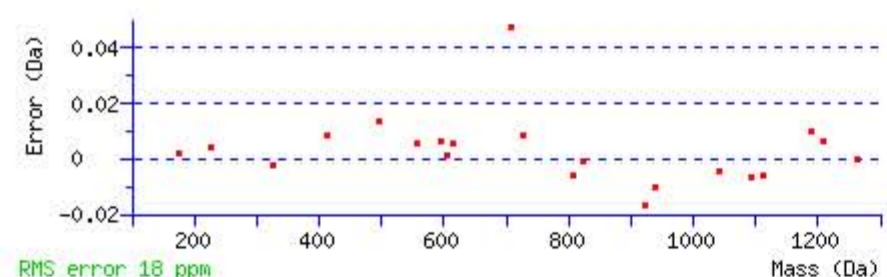
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 44 Expect: 0.00044

Matches : 21/92 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	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
44.1	1434.765305	0.004603	NLPATDPLQR
7.8	1434.757889	0.012019	NLIRQISSGEYR
4.2	1434.757919	0.011989	VQQAELHTGSLPR
0.5	1434.754074	0.015834	VKPFMTGAAEQIK

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

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 44693: 1906.928322 from(636.650050,3+) rtinseconds(1892) index(35592)

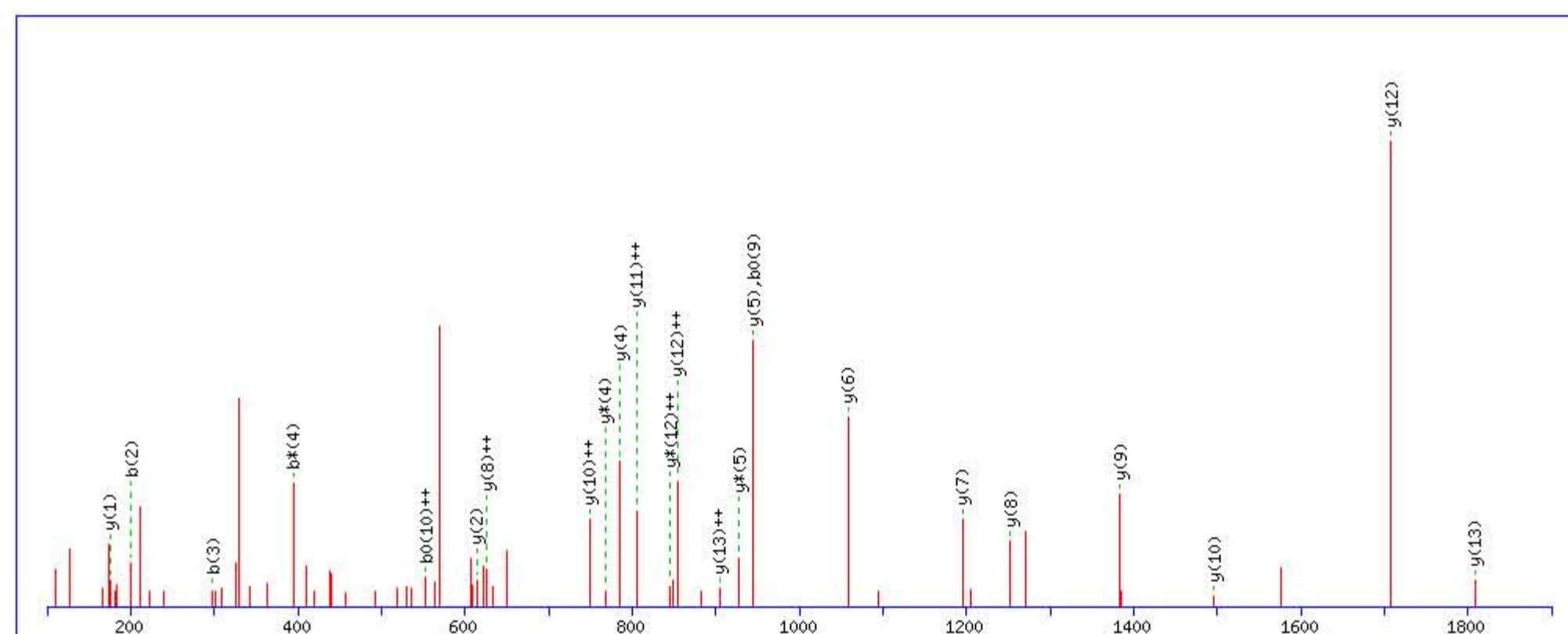
Title: Locus:1.1.1.3078.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1906.932816

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

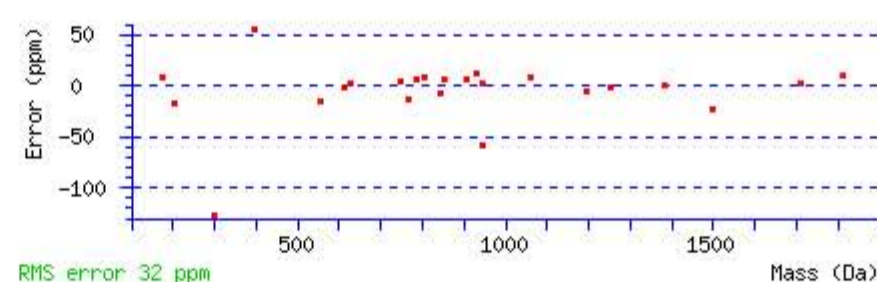
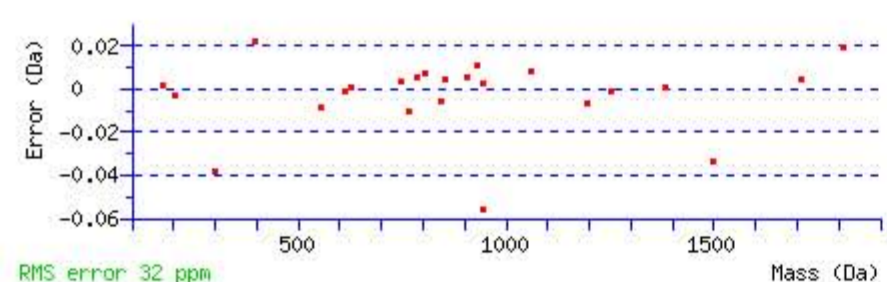
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 53 Expect: 0.00011

Matches : 24/124 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							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
52.9	1906.932816	-0.004494	VTPNLMGHLCGNQR

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

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 44850: 1912.053552 from(638.358460,3+) rtinseconds(2213) index(7086)

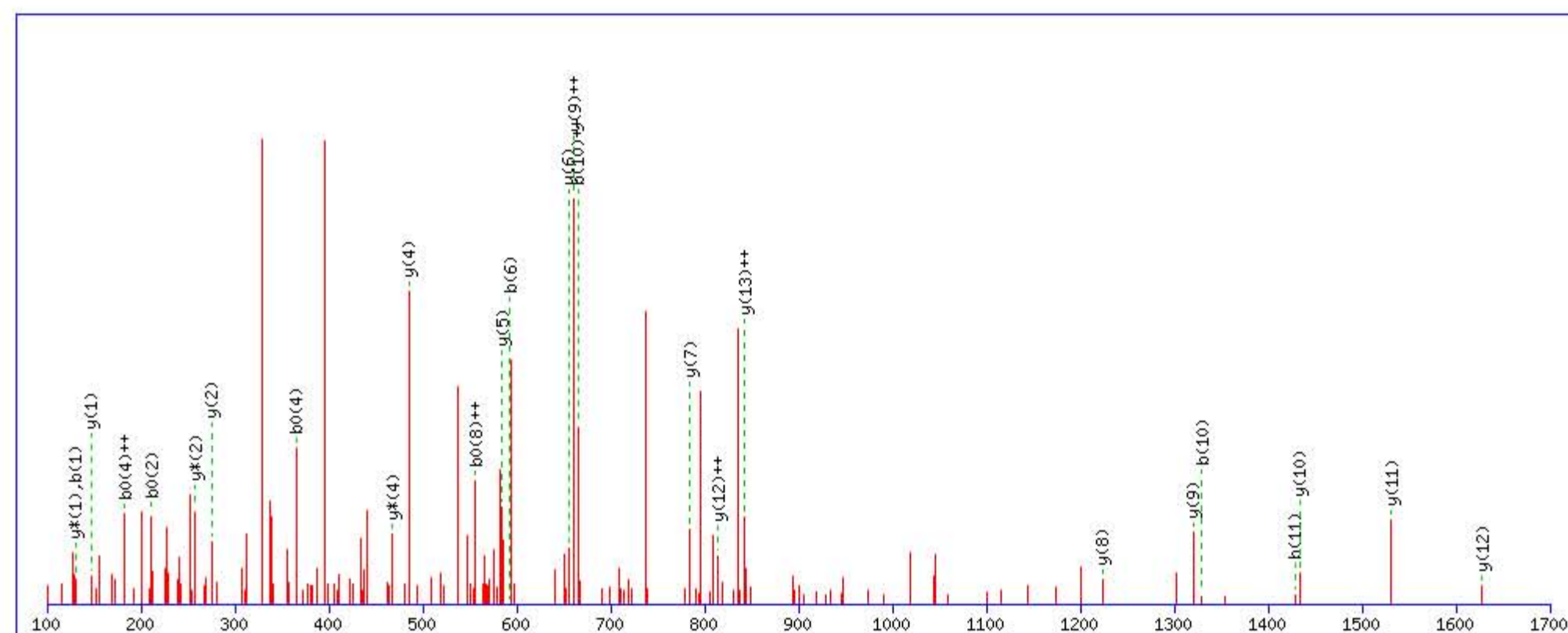
Title: Locus:1.1.1.1580.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1912.049194

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

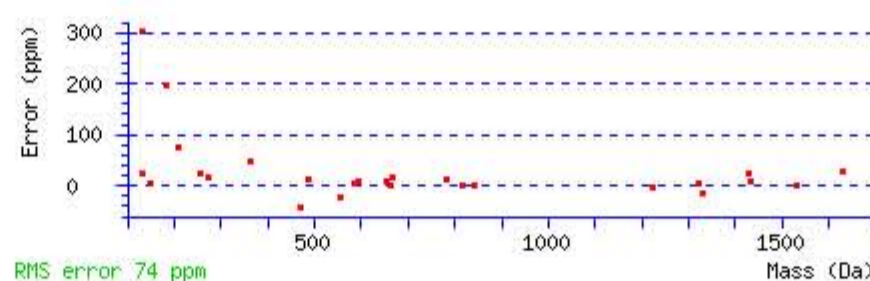
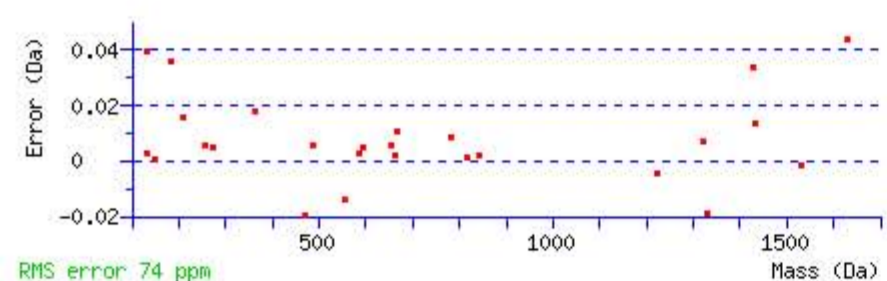
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 34 Expect: 0.0064

Matches : 26/142 fragment ions using 82 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							15
2	229.118283	115.062780			211.107718	106.057497	V	1784.013891	892.510583	1766.987342	883.997309	1766.003326	883.505301	14
3	286.139747	143.573512			268.129182	134.568229	G	1684.945477	842.976377	1667.918928	834.463102	1666.934912	833.971094	13
4	383.192511	192.099894			365.181946	183.094611	P	1627.924013	814.465645	1610.897464	805.952370	1609.913448	805.460362	12
5	480.245275	240.626276			462.234710	231.620993	P	1530.871249	765.939263	1513.844700	757.425988	1512.860684	756.933980	11
6	593.329339	297.168308			575.318774	288.163025	L	1433.818485	717.412881	1416.791936	708.899606	1415.807920	708.407598	10
7	690.382103	345.694690			672.371538	336.689407	P	1320.734421	660.870848	1303.707872	652.357574	1302.723856	651.865566	9
8	1129.607429	565.307353	1112.580880	556.794078	1111.596864	556.302070	Q	1223.681657	612.344466	1206.655108	603.831192	1205.671092	603.339184	8
9	1258.650022	629.828649	1241.623473	621.315375	1240.639457	620.823367	E	784.456331	392.731803	767.429782	384.218529	766.445766	383.726521	7
10	1329.687136	665.347206	1312.660587	656.833932	1311.676571	656.341924	A	655.413738	328.210507	638.387189	319.697232			6
11	1428.755550	714.881413	1411.729001	706.368139	1410.744985	705.876131	V	584.376624	292.691950	567.350075	284.178676			5
12	1525.808314	763.407795	1508.781765	754.894521	1507.797749	754.402513	P	485.308210	243.157743	468.281661	234.644468			4
13	1638.892378	819.949827	1621.865829	811.436553	1620.881813	810.944545	L	388.255446	194.631361	371.228897	186.118086			3
14	1766.950956	883.979116	1749.924407	875.465842	1748.940391	874.973833	Q	275.171382	138.089329	258.144833	129.576054			2
15							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **EVGPPLPQEAVPLQK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.2	1912.049194	0.004358	EVGPPLPQEAVPLQK
21.6	1912.049194	0.004358	EVGPPLPQEAVPLQK

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

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 51543: 2223.225068 from(1112.619810,2+) rtinseconds(2442) index(24155)

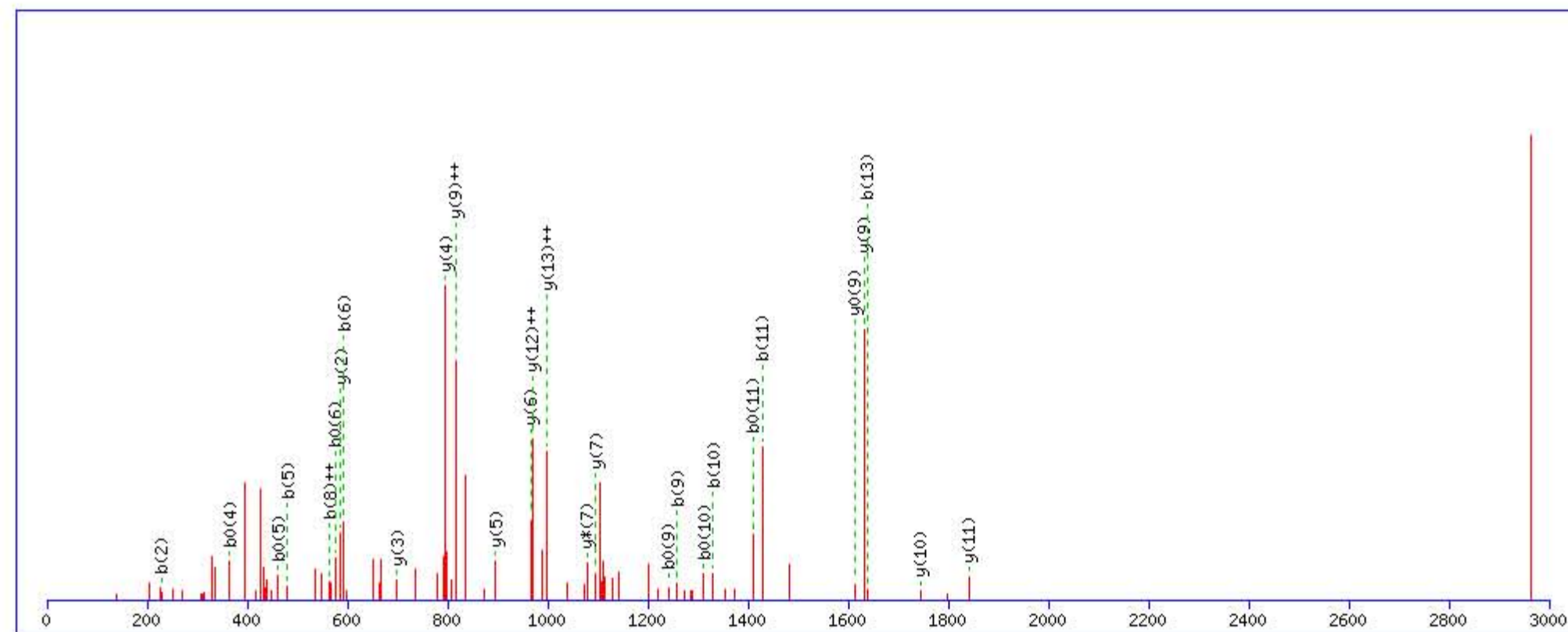
Title: Locus:1.1.1.852.8 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2223.215942

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

Variable modifications:

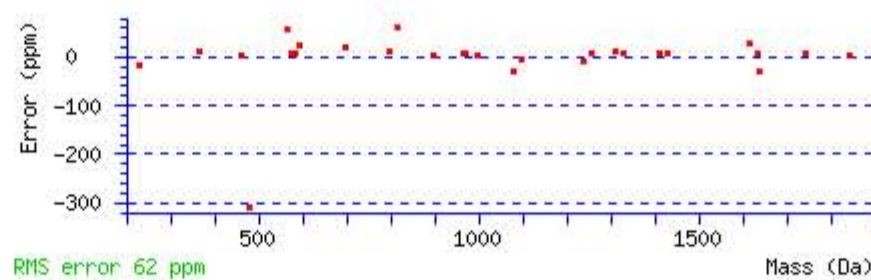
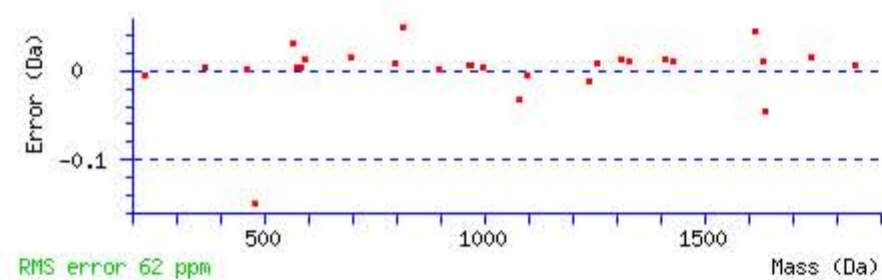
Q8 : Biotin:Thermo-21345 (Q)

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.0081

Matches : 28/142 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	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
32.6	2223.215942	0.009126	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 53728: 2347.088202 from(783.370010,3+) rtinseconds(1939) index(5537)

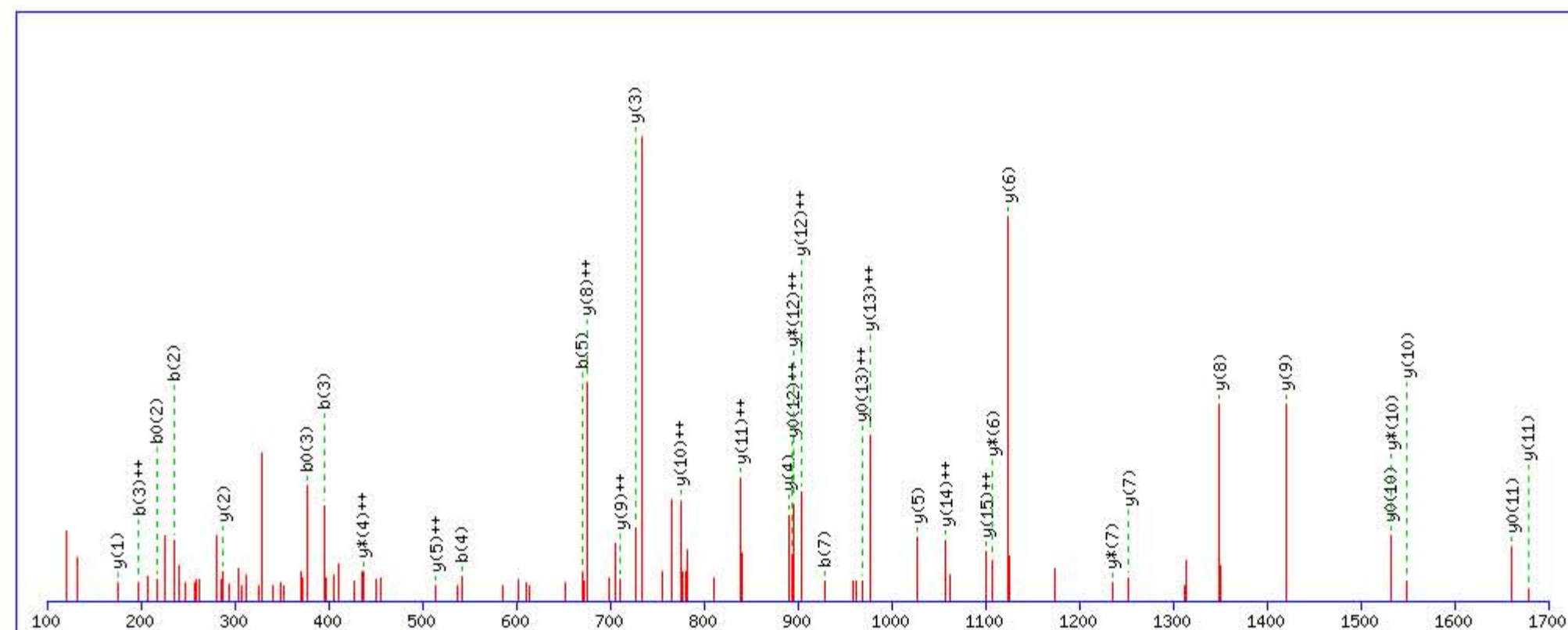
Title: Locus:1.1.1.1484.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2347.087784

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

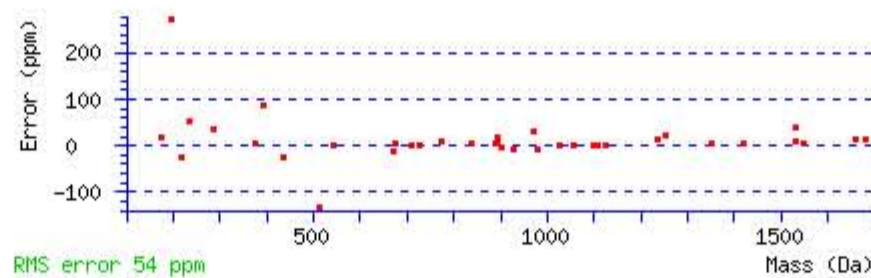
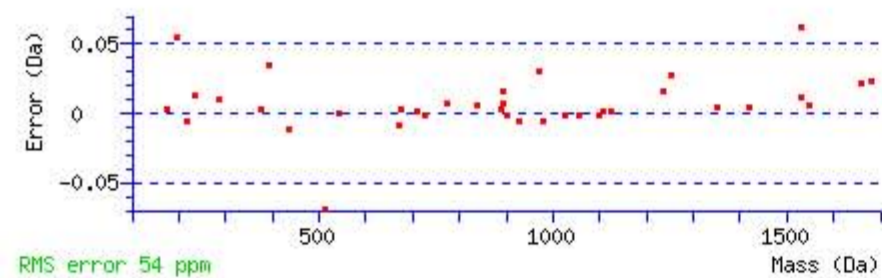
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 54 Expect: 9.8e-006

Matches : 37/152 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	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
53.9	2347.087784	0.000418	FSCFQEEAPQPHYQLR
26.8	2347.087784	0.000418	FSCFQEEAPQPHYQLR
0.5	2347.077271	0.010931	RCPCCAVIDTTQAPGKVVWWR
0.2	2347.087784	0.000418	FSCFQEEAPQPHYQLR

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 40215: 1687.814788 from(844.914670,2+) rtinseconds(2332) index(70692)

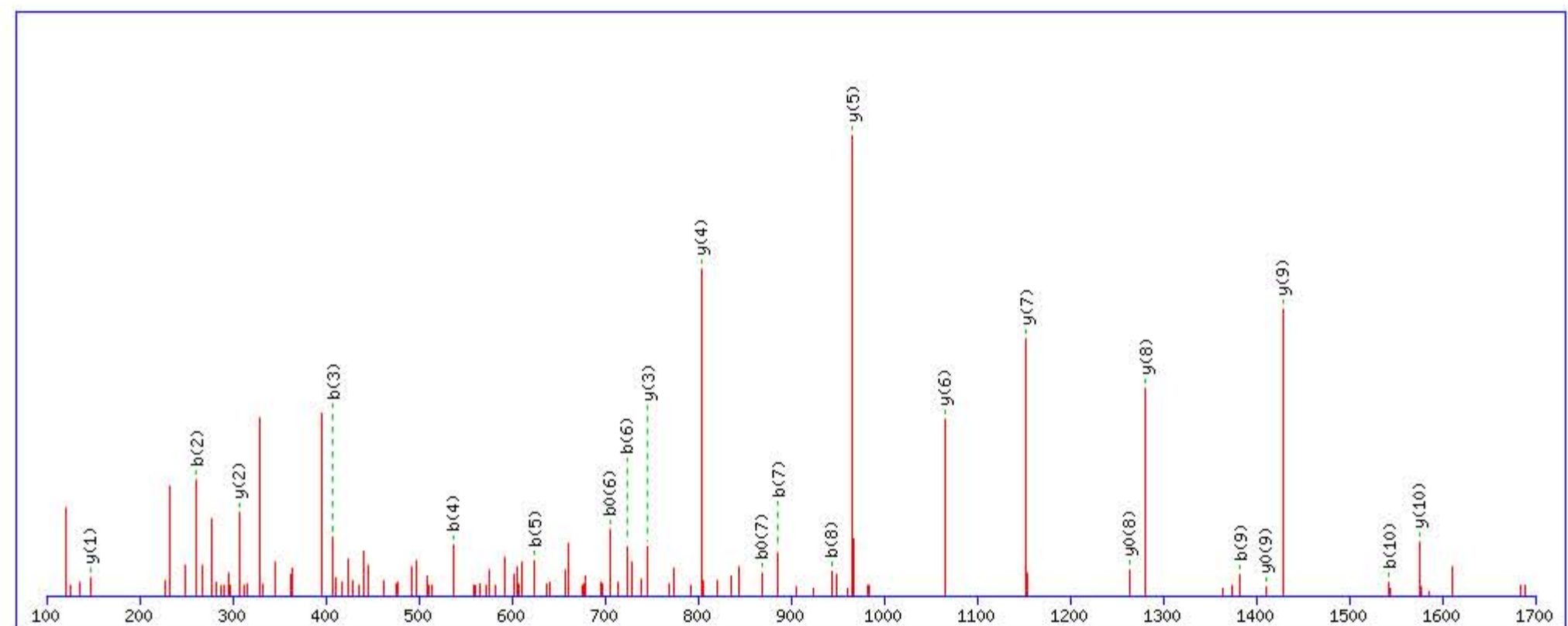
Title: Locus:1.1.1.1749.18 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1687.810226

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

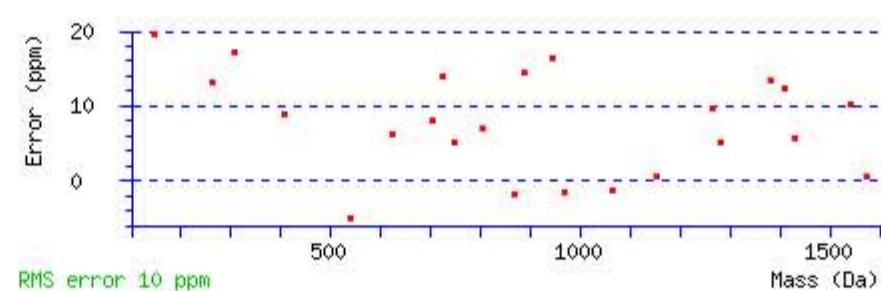
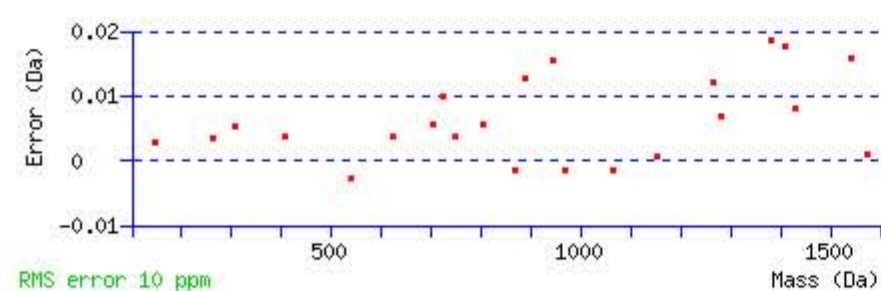
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 63 Expect: 1e-005

Matches : 23/86 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	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
63.0	1687.810226	0.004562	IFFESVYGQCK

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

MASCOT SCIENCE 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 24327: 1238.703788 from(620.359170,2+) rtinseconds(1748) index(20039)

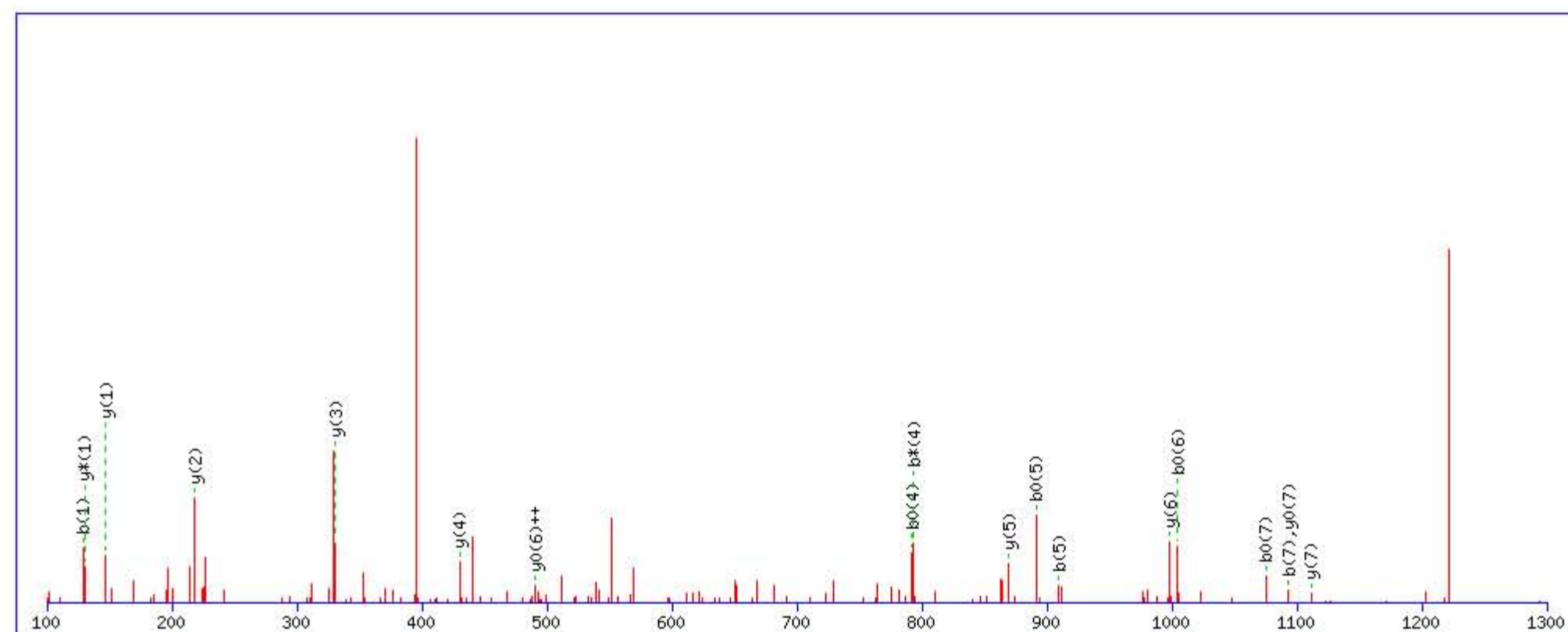
Title: Locus:1.1.1.611.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1238.705658

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

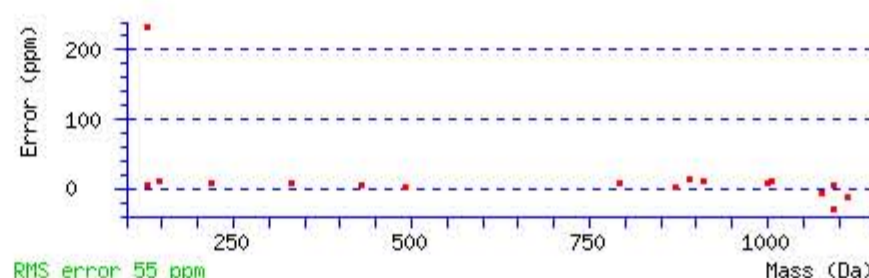
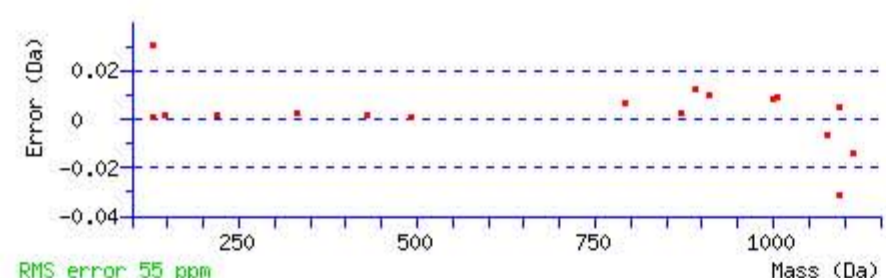
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 38 Expect: 0.0025

Matches : 18/70 fragment ions using 36 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.065854	65.036565	112.039305	56.523291			Q							8
2	242.149918	121.578597	225.123369	113.065323			L	1111.654379	556.330828	1094.627830	547.817553	1093.643814	547.325545	7
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	E	998.570315	499.788796	981.543766	491.275521	980.559750	490.783513	6
4	810.417837	405.712557	793.391288	397.199282	792.407272	396.707274	Q	869.527722	435.267499	852.501173	426.754225			5
5	909.486251	455.246764	892.459702	446.733489	891.475686	446.241481	V	430.302396	215.654836	413.275847	207.141562			4
6	1022.570315	511.788796	1005.543766	503.275521	1004.559750	502.783513	I	331.233982	166.120629	314.207433	157.607355			3
7	1093.607429	547.307353	1076.580880	538.794078	1075.596864	538.302070	A	218.149918	109.578597	201.123369	101.065323			2
8							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [QLEQVIAK](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.1	1238.705658	-0.001870	QLEQVIAK
16.4	1238.698257	0.005531	IHADASSKVLAK
14.8	1238.705658	-0.001870	QLEQVIAK
13.1	1238.687027	0.016761	KEETQPPVALK
8.4	1238.716904	-0.013116	DRVQVAIK
7.5	1238.691040	0.012748	LYKEFIDLAK
5.6	1238.702301	0.001487	DVFKKGFSLAK
5.2	1238.716888	-0.013100	KRILCPLDPK
3.7	1238.695572	0.008216	SHSRVRAIASR
3.3	1238.709473	-0.005685	NDLRPANKLAK

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 26939: 1338.666948 from(670.340750,2+) rtinseconds(2062) index(6226)

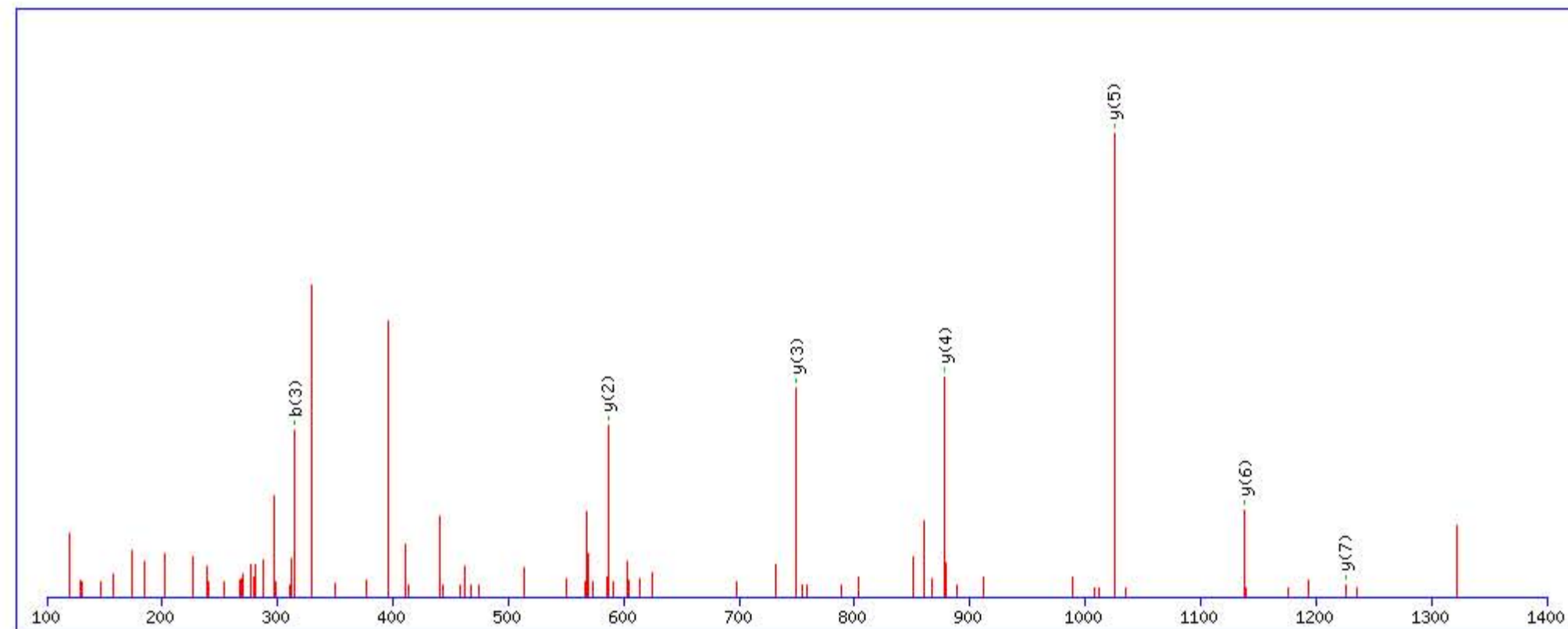
Title: Locus:1.1.1.1527.17 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1338.664185

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

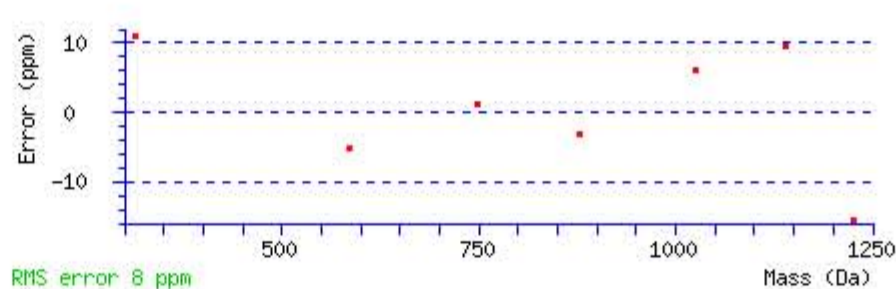
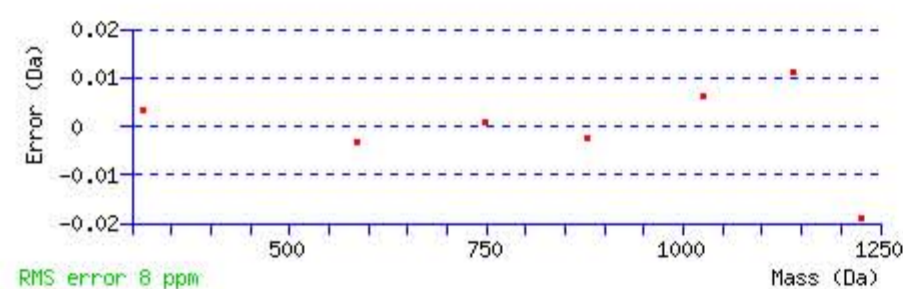
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.0018

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
39.9	1338.664185	0.002763	NSLFEYQK
12.3	1338.660172	0.006776	NSMFTAGKGVAEK
7.4	1338.660172	0.006776	BTVYVLQMBSLR
5.3	1338.686188	-0.019240	TVKMMYQK
3.8	1338.682632	-0.015684	NLSRMQSRFGK
1.2	1338.666672	0.000276	ESIKDLADYASK
0.9	1338.652283	0.014665	DAKSLAEMLSK
0.8	1338.652283	0.014665	DAKSLAEMLSK

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 29637: 1388.657228 from(695.335890,2+) rtinseconds(1677) index(3911)

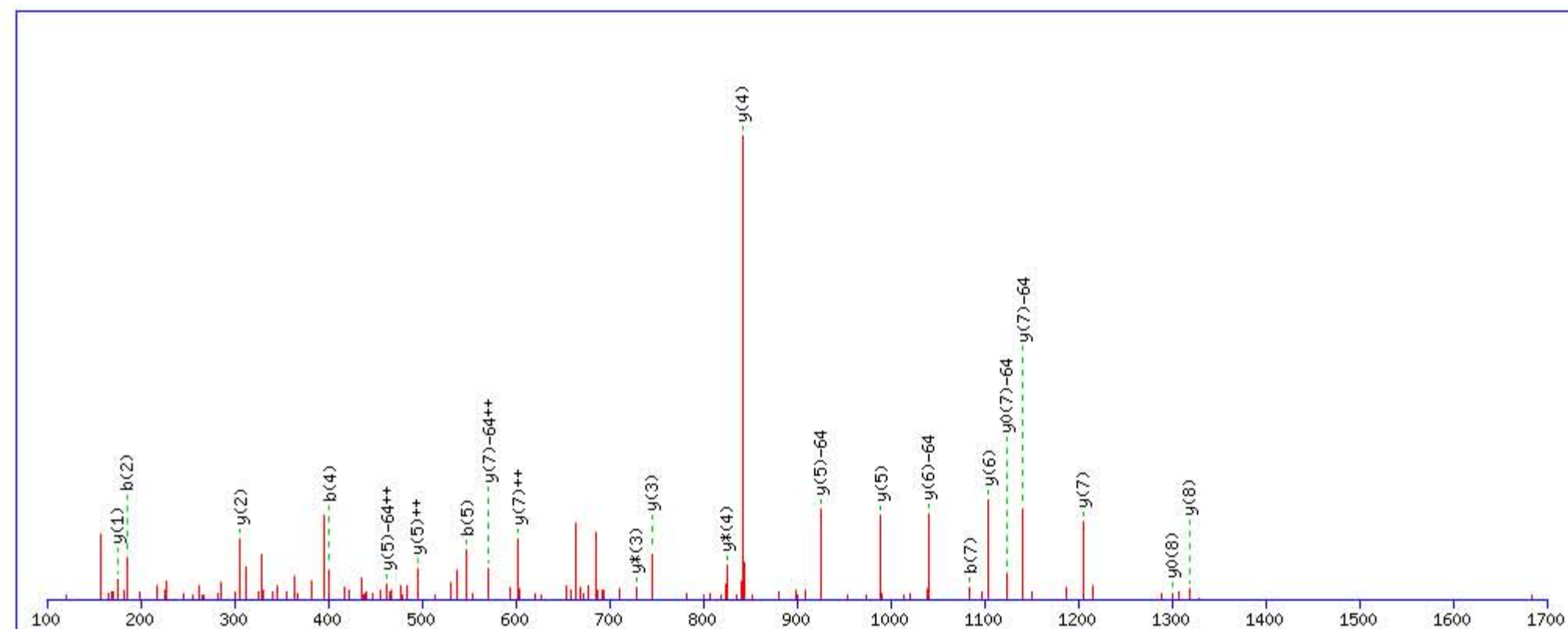
Title: Locus:1.1.1.1393.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1388.661438

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

Variable modifications:

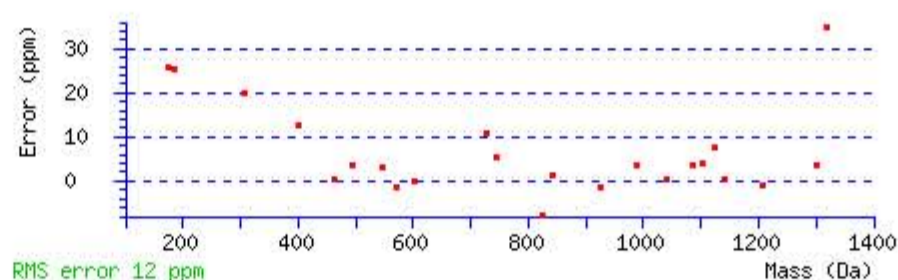
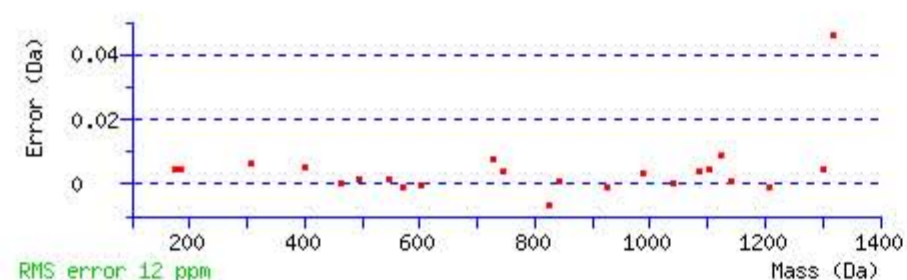
M5 : Oxidation (M), with neutral losses 0.000000 (shown in table), 63.998285

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 58 Expect: 1.1e-005

Matches : 23/112 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	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
58.0	1388.661438	-0.004210	ALTDMPQMR
20.2	1388.661438	-0.004210	ALTDMPQMR
4.8	1388.660568	-0.003340	SEMTASPLVGPER
0.8	1388.646637	0.010591	DREAGSMLPAGNR

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 33800: 1500.697808 from(751.356180,2+) rtinseconds(1583) index(66376)

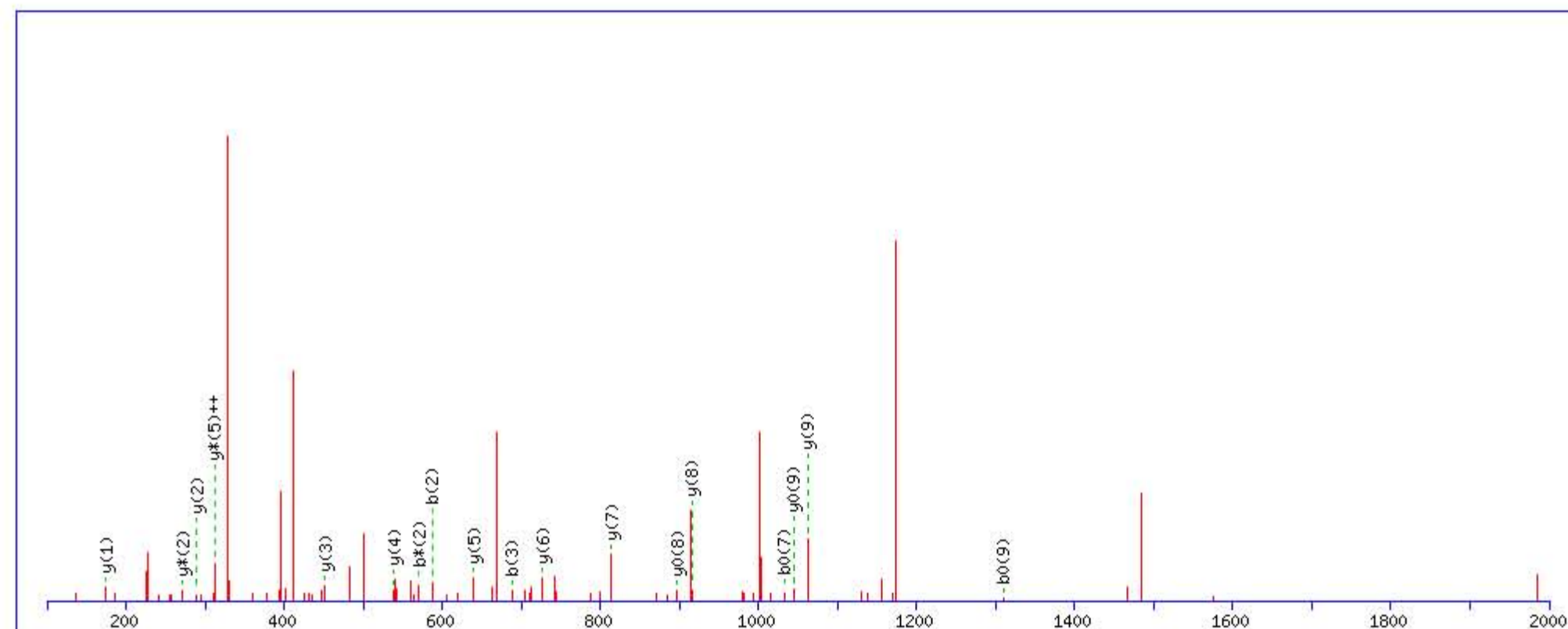
Title: Locus:1.1.1.1488.16 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1500.703110

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

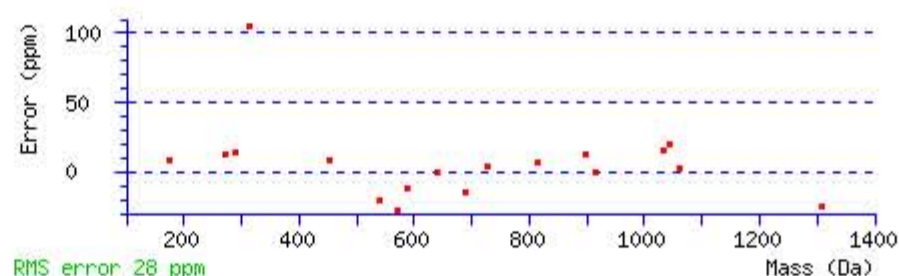
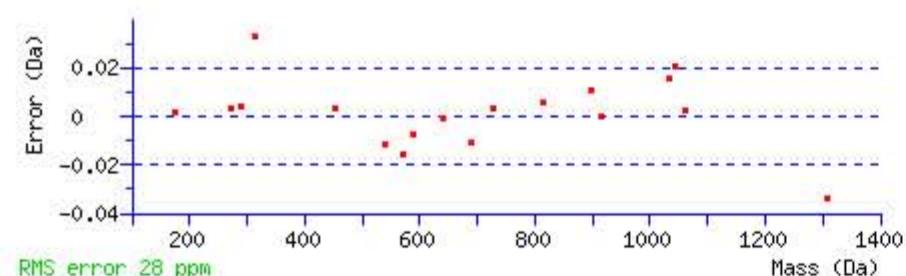
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 29 Expect: 0.017

Matches : 18/98 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	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
28.5	1500.703110	-0.005302	QFTSSTSYNR

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

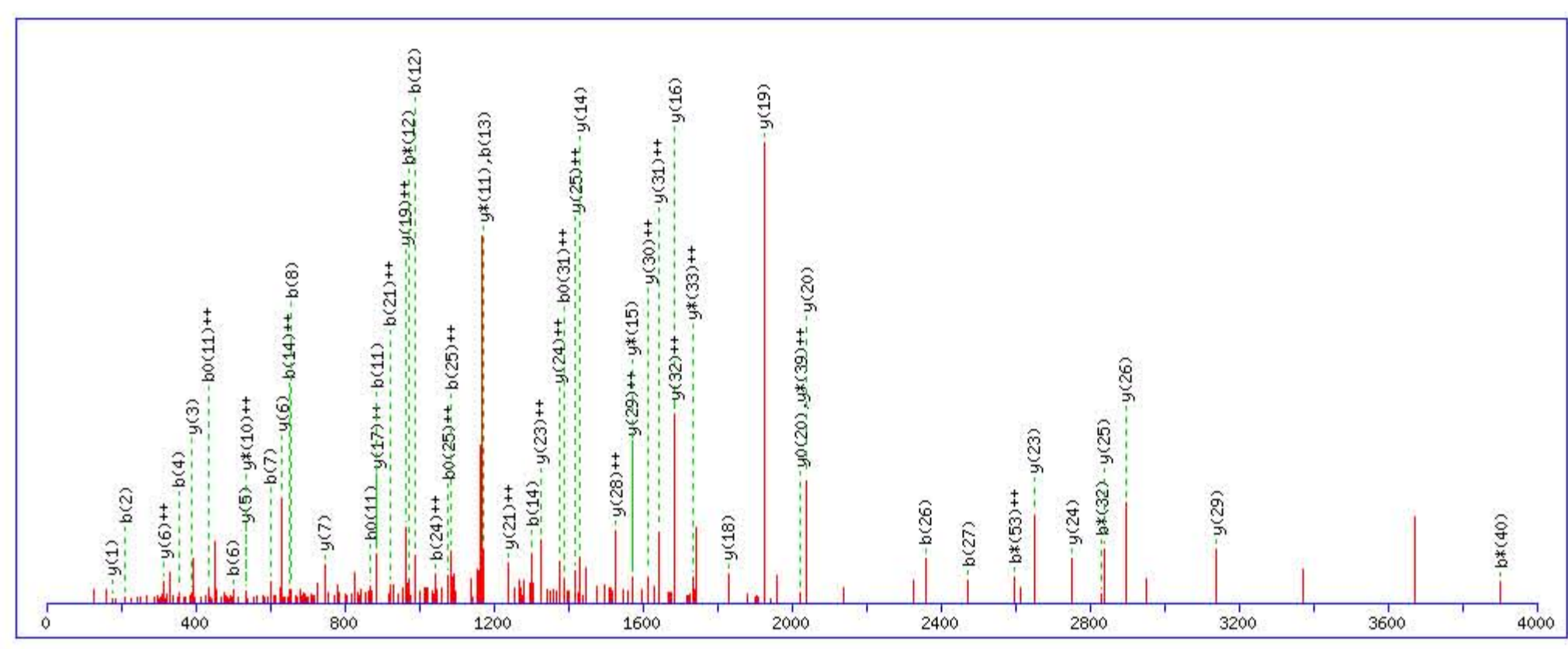
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPSSSGTGGTATWKPSSSGPGSTGSWNSGSSGTGSGTGNQNPSPRPGSTGTWNPSSER**
 Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

Match to Query 76594: 5844.577670 from(1169.922810,5+) rtinseconds(1798) index(4642)
 Title: Locus:1.1.1.1435.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to 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: 81 Expect: 2.3e-008
 Matches : 56/688 fragment ions using 95 most intense peaks [\(help\)](#)

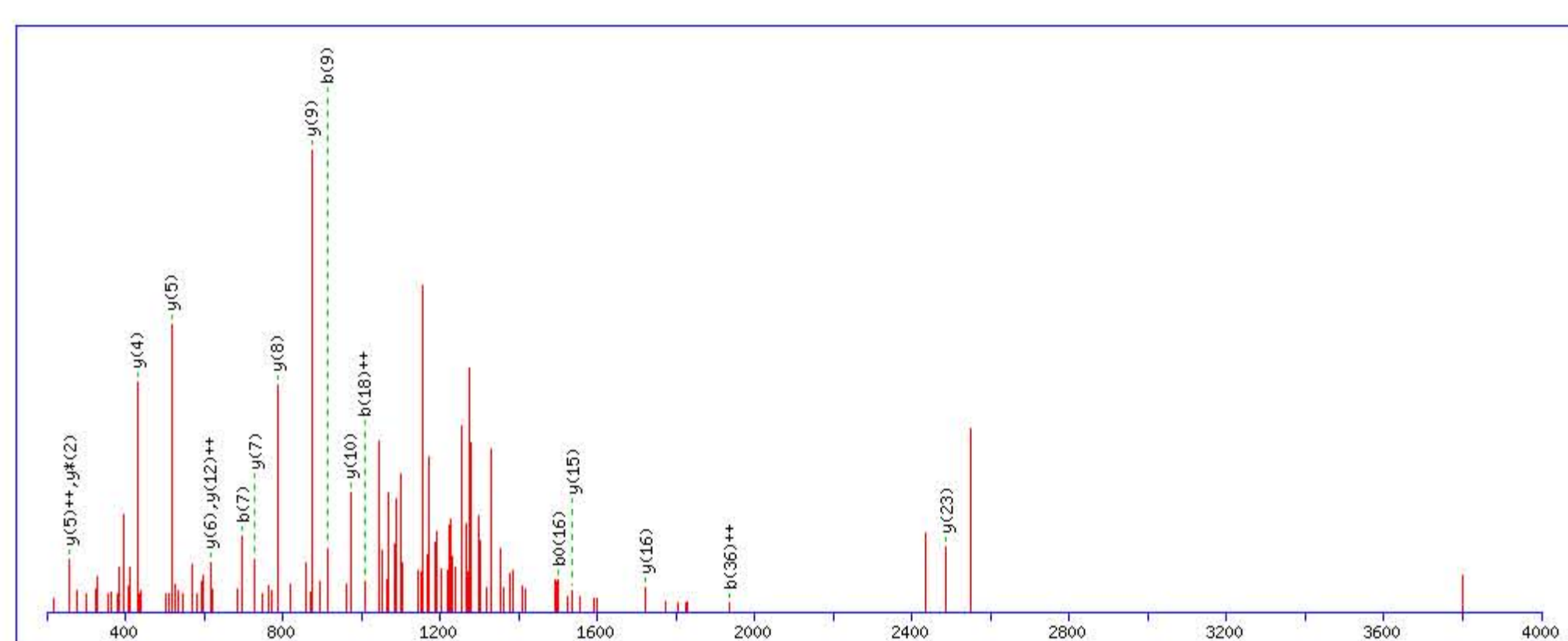
#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.050203	58.028740	98.023654	49.515465			N							59
2	212.102967	106.555121	195.076418	98.041847			P	5731.572302	2866.289789	5714.545753	2857.776515	5713.561737	2857.284507	58
3	269.124431	135.065853	252.097882	126.552579			G	5634.519538	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			

Peptide View

MS/MS Fragmentation of **GSAGHWTSESSVSGSTGQWHSESGSFRPDSPGSGNARPNPDWGTFFEEVSGNVSPGTR**
 Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

Match to Query 76912: 6284.810244 from(1048.475650,6+) rtinseconds(2112) index(6520)
 Title: Locus:1.1.1.1544.26 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 6284.792847
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q18 : Biotin:Thermo-21345 (Q)
 Ions Score: 29 Expect: 0.0051
 Matches : 18/646 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	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						

{MATRIX} SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDGSVDFGR**

Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

Match to Query 26036: 1290.608908 from(646.311730,2+) rtinseconds(1802) index(51546)

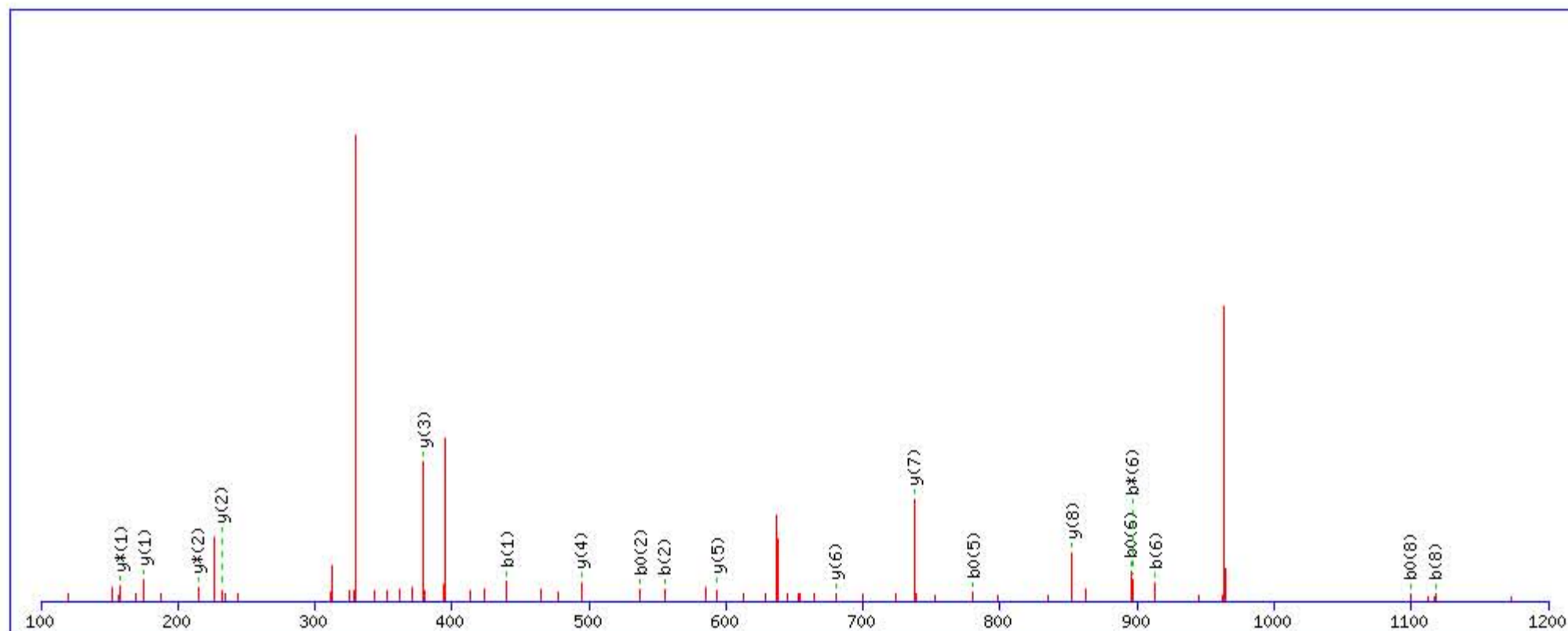
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1290.602692

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

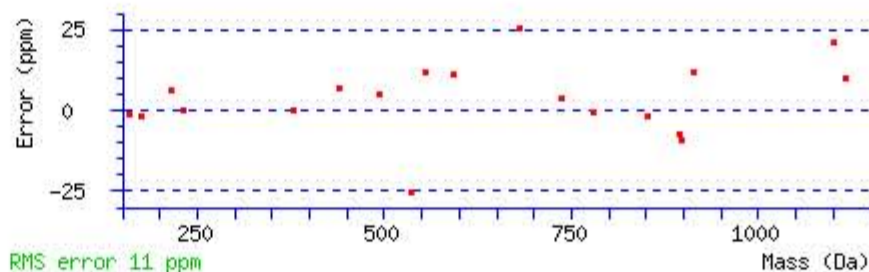
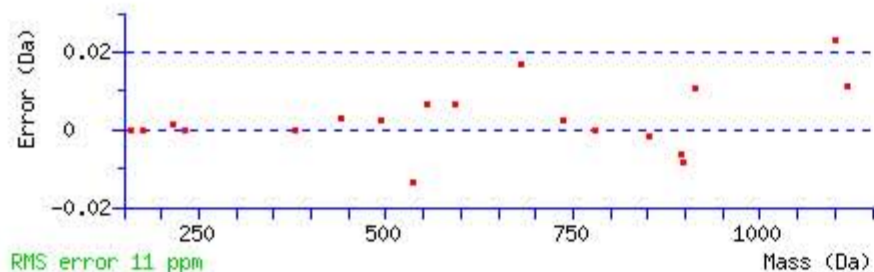
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 0.00036

Matches : 19/88 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	440.232602	220.619939	423.206053	212.106664			Q							9
2	555.259545	278.133411	538.232996	269.620136	537.248980	269.128128	D	852.384622	426.695949	835.358073	418.182674	834.374057	417.690666	8
3	612.281009	306.644143	595.254460	298.130868	594.270444	297.638860	G	737.357679	369.182477	720.331130	360.669203	719.347114	360.177195	7
4	699.313037	350.160157	682.286488	341.646882	681.302472	341.154874	S	680.336215	340.671745	663.309666	332.158471	662.325650	331.666463	6
5	798.381451	399.694364	781.354902	391.181089	780.370886	390.689081	V	593.304187	297.155731	576.277638	288.642457	575.293622	288.150449	5
6	913.408394	457.207835	896.381845	448.694560	895.397829	448.202552	D	494.235773	247.621524	477.209224	239.108250	476.225208	238.616242	4
7	1060.476808	530.742042	1043.450259	522.228768	1042.466243	521.736759	F	379.208830	190.108053	362.182281	181.594778			3
8	1117.498272	559.252774	1100.471723	550.739499	1099.487707	550.247491	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 [QDGSVDFGR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.1	1290.602692	0.006216	QDGSVDFGR

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 43235: 1823.893272 from(608.971700,3+) rtinseconds(1894) index(52045)

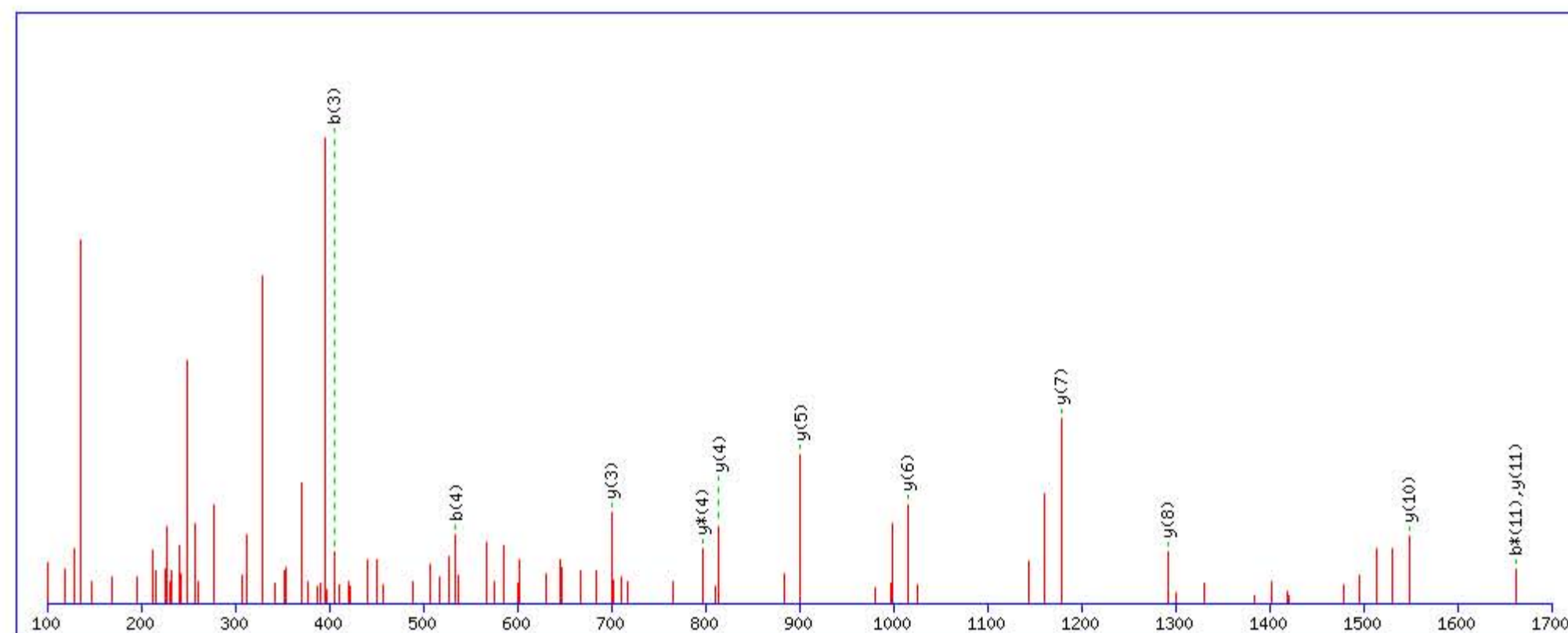
Title: Locus:1.1.1.1275.8 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1823.887573

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

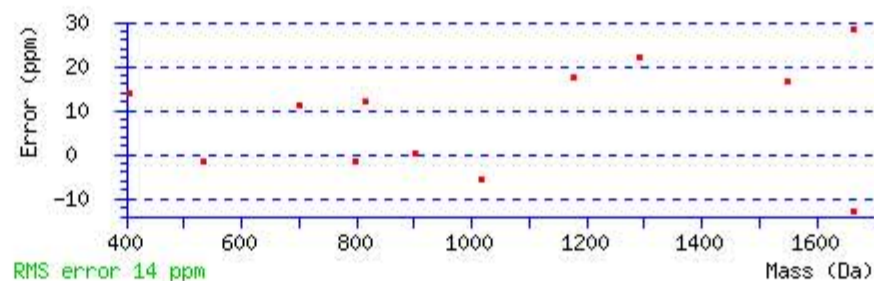
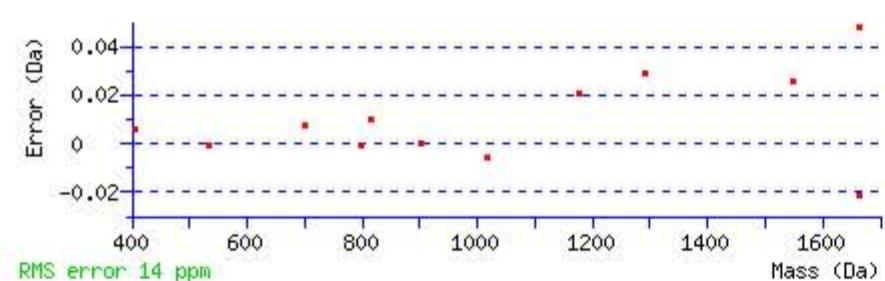
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 55 Expect: 7.1e-005

Matches : 12/114 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	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	$M_r(\text{calc})$:	Delta	Sequence
54.8	1823.887573	0.005699	YLQEIYNSNNQK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**

Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

Match to Query 43917: 1855.966696 from(464.998950,4+) rtinseconds(1510) index(2980)

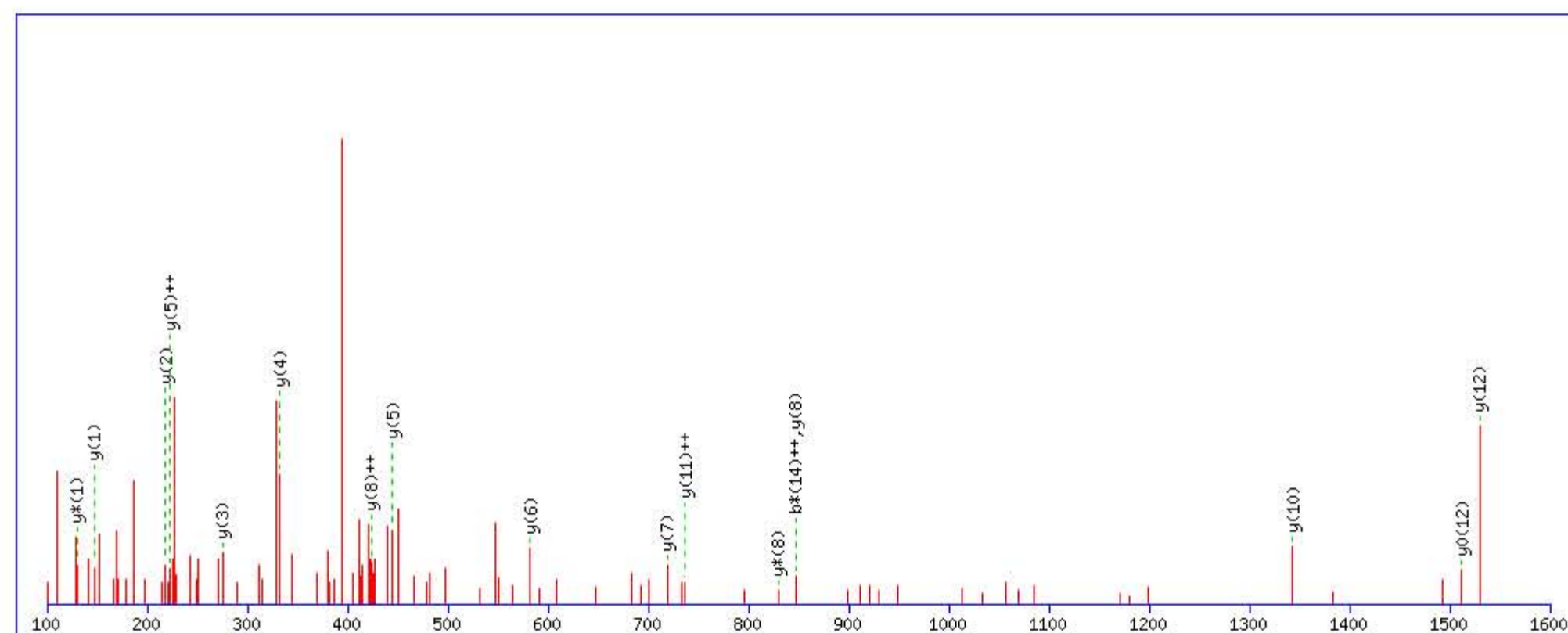
Title: Locus:1.1.1.1335.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1855.972687

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

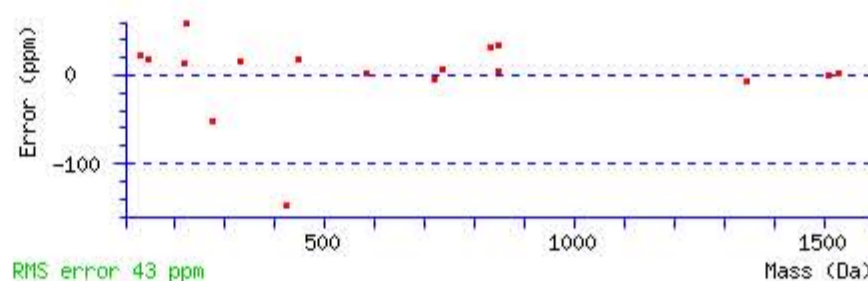
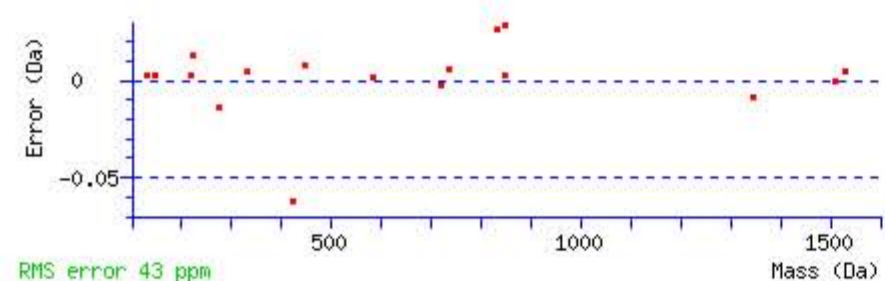
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.064

Matches : 17/134 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	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
26.4	1855.972687	-0.005991	LTIGEGQQHHLGGAK
16.4	1855.972687	-0.005991	LTIGEGQQHHLGGAK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**

Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

Match to Query 43927: 1855.968132 from(619.663320,3+) rtinseconds(1466) index(33059)

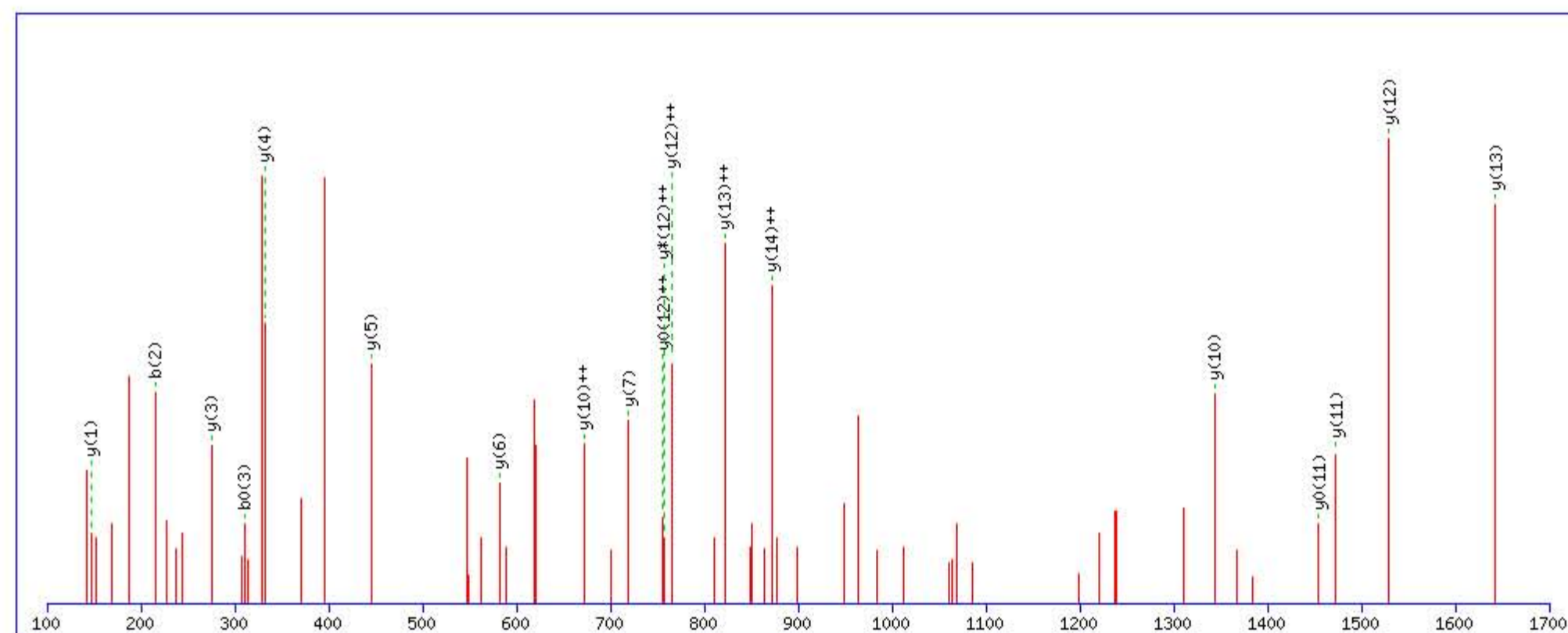
Title: Locus:1.1.1.2929.25 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1855.972687

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

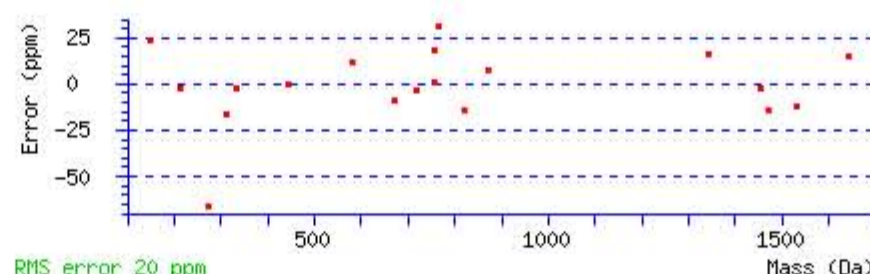
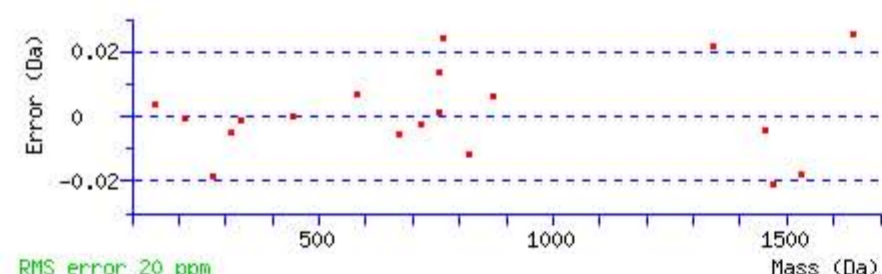
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.0012

Matches : 19/134 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	215.139019	108.073147			197.128454	99.067865	T	1743.895902	872.451589	1726.869353	863.938314	1725.885337	863.446306	14
3	328.223083	164.615179			310.212518	155.609897	I	1642.848223	821.927749	1625.821674	813.414475	1624.837658	812.922467	13
4	385.244547	193.125911			367.233982	184.120629	G	1529.764159	765.385717	1512.737610	756.872443	1511.753594	756.380435	12
5	514.287140	257.647208			496.276575	248.641926	E	1472.742695	736.874985	1455.716146	728.361711	1454.732130	727.869703	11
6	571.308604	286.157940			553.298039	277.152658	G	1343.700102	672.353689	1326.673553	663.840414			10
7	699.367182	350.187229	682.340633	341.673955	681.356617	341.181947	Q	1286.678638	643.842957	1269.652089	635.329682			9
8	1138.592508	569.799892	1121.565959	561.286618	1120.581943	560.794609	Q	1158.620060	579.813668	1141.593511	571.300393			8
9	1275.651420	638.329348	1258.624871	629.816074	1257.640855	629.324065	H	719.394734	360.201005	702.368185	351.687730			7
10	1412.710332	706.858804	1395.683783	698.345530	1394.699767	697.853521	H	582.335822	291.671549	565.309273	283.158274			6
11	1525.794396	763.400836	1508.767847	754.887561	1507.783831	754.395553	L	445.276910	223.142093	428.250361	214.628818			5
12	1582.815860	791.911568	1565.789311	783.398293	1564.805295	782.906285	G	332.192846	166.600061	315.166297	158.086786			4
13	1639.837324	820.422300	1622.810775	811.909025	1621.826759	811.417017	G	275.171382	138.089329	258.144833	129.576054			3
14	1710.874438	855.940857	1693.847889	847.427582	1692.863873	846.935574	A	218.149918	109.578597	201.123369	101.065322			2
15							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **LTIGEGQQHHLGGAK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.2	1855.972687	-0.004555	LTIGEGQQHHLGGAK
36.2	1855.972687	-0.004555	LTIGEGQQHHLGGAK
5.2	1855.979202	-0.011070	ITIVENVGSVEGLAYHR

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

MASCOT 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 50353: 2167.131896 from(542.790250,4+) rtinseconds(1777) index(34926)

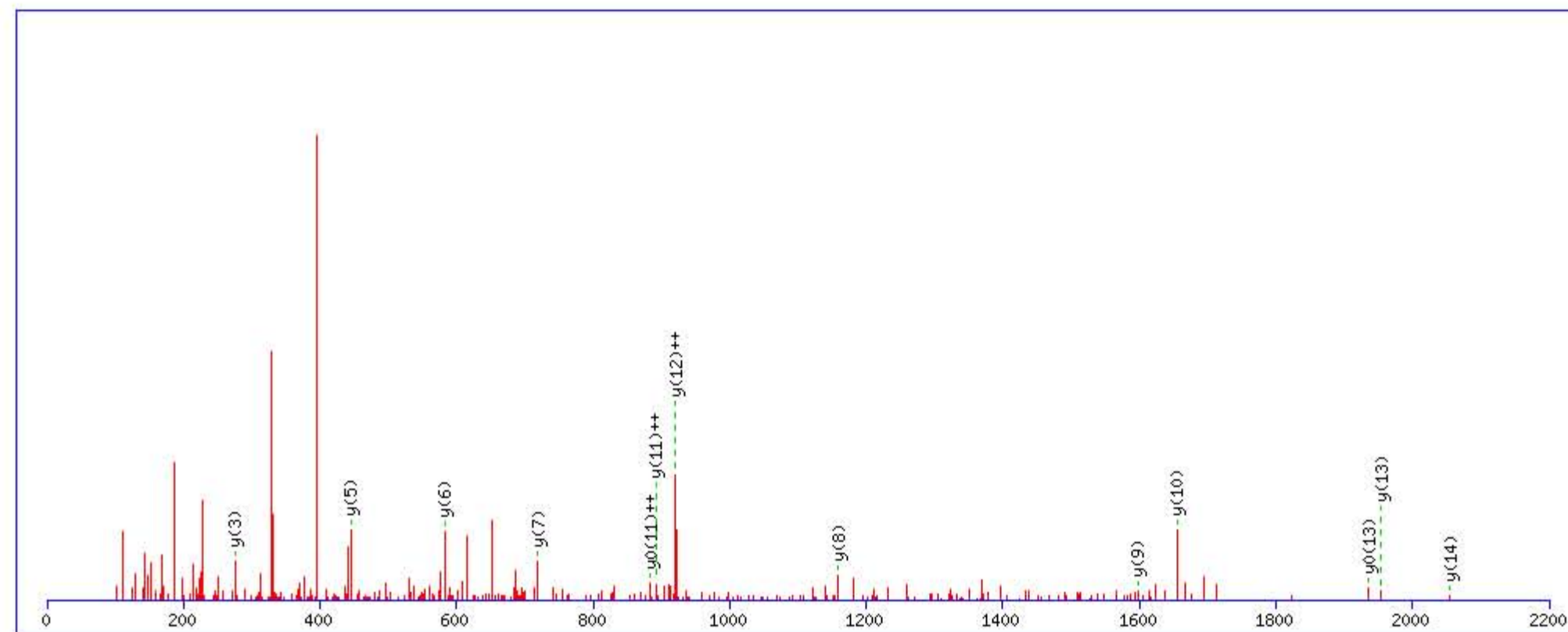
Title: Locus:1.1.1.3038.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2167.139435

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

Variable modifications:

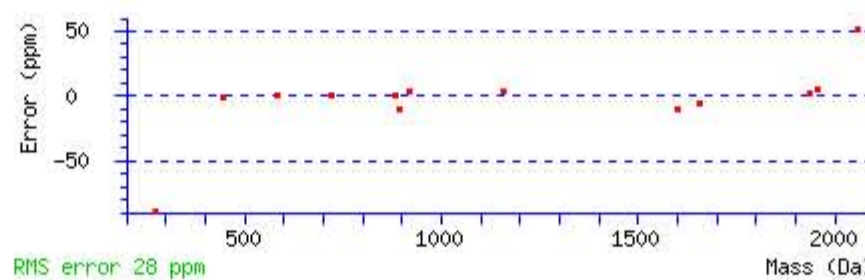
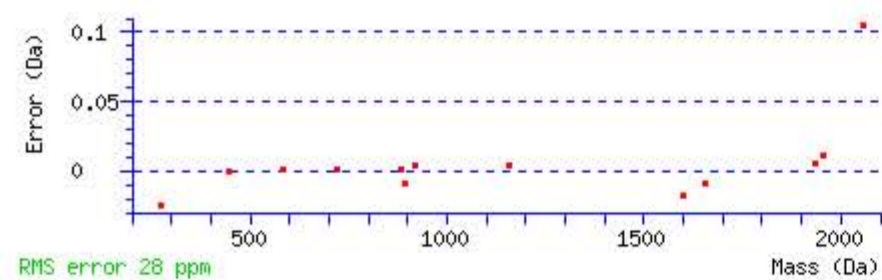
Q7 : Biotin:Thermo-21345 (Q)

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 31 Expect: 0.023

Matches : 13/134 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							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
30.5	2167.139435	-0.007539	LTIGEGQQHHLGGAK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VAQLEAQCQEPCKDTVQIHDITGK**

Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

Match to Query 62242: 3078.512536 from(770.635410,4+) rtinseconds(1903) index(52091)

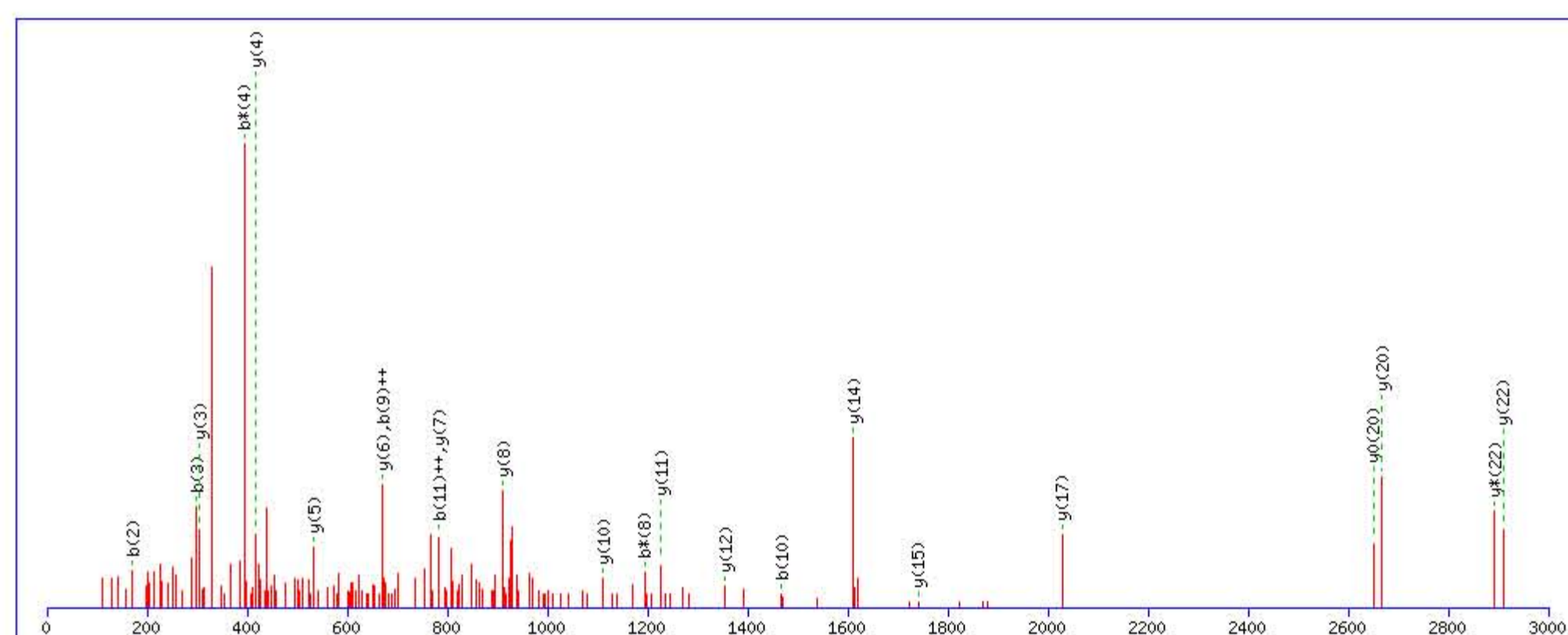
Title: Locus:1.1.1.1278.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3078.493668

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

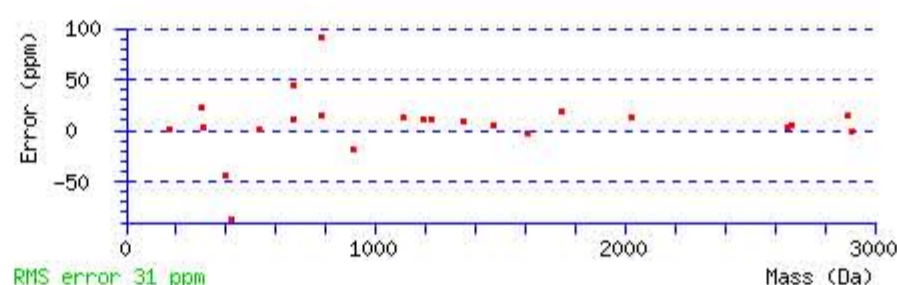
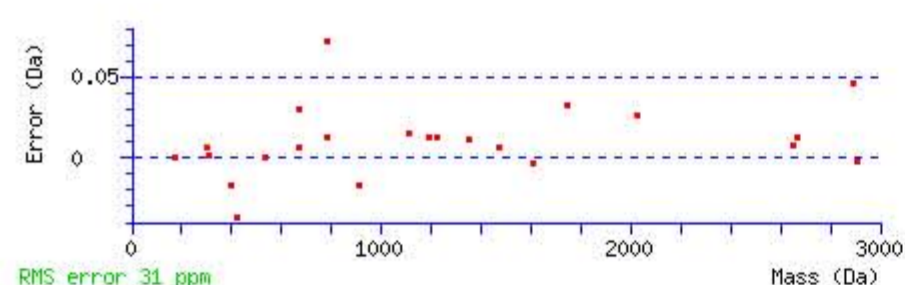
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 79 Expect: 3.8e-007

Matches : 23/260 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	100.075690	50.541483					V							24
2	171.112804	86.060040					A	2980.432529	1490.719902	2963.405980	1482.206628	2962.421964	1481.714620	23
3	299.171382	150.089329	282.144833	141.576055			Q	2909.395415	1455.201345	2892.368866	1446.688071	2891.384850	1446.196063	22
4	412.255446	206.631361	395.228897	198.118087			L	2781.336837	1391.172056	2764.310288	1382.658782	2763.326272	1382.166774	21
5	541.298039	271.152658	524.271490	262.639383	523.287474	262.147375	E	2668.252773	1334.630024	2651.226224	1326.116750	2650.242208	1325.624742	20
6	612.335153	306.671215	595.308604	298.157940	594.324588	297.665932	A	2539.210180	1270.108728	2522.183631	1261.595453	2521.199615	1261.103445	19
7	1051.560479	526.283878	1034.533930	517.770603	1033.549914	517.278595	Q	2468.173066	1234.590171	2451.146517	1226.076896	2450.162501	1225.584888	18
8	1211.591128	606.299202	1194.564579	597.785928	1193.580563	597.293920	C	2028.947740	1014.977508	2011.921191	1006.464234	2010.937175	1005.972225	17
9	1339.649706	670.328491	1322.623157	661.815217	1321.639141	661.323208	Q	1868.917091	934.962183	1851.890542	926.448909	1850.906526	925.956901	16
10	1468.692299	734.849788	1451.665750	726.336513	1450.681734	725.844505	E	1740.858513	870.932894	1723.831964	862.419620	1722.847948	861.927612	15
11	1565.745063	783.376170	1548.718514	774.862895	1547.734498	774.370887	P	1611.815920	806.411598	1594.789371	797.898323	1593.805355	797.406315	14
12	1725.775712	863.391494	1708.749163	854.878220	1707.765147	854.386212	C	1514.763156	757.885216	1497.736607	749.371941	1496.752591	748.879933	13
13	1853.870675	927.438976	1836.844126	918.925701	1835.860110	918.433693	K	1354.732507	677.869891	1337.705958	669.356617	1336.721942	668.864609	12
14	1968.897618	984.952447	1951.871069	976.439173	1950.887053	975.947165	D	1226.637544	613.822410	1209.610995	605.309135	1208.626979	604.817127	11
15	2069.945297	1035.476286	2052.918748	1026.963012	2051.934732	1026.471004	T	1111.610601	556.308938	1094.584052	547.795664	1093.600036	547.303656	10
16	2169.013711	1085.010493	2151.987162	1076.497219	2151.003146	1076.005211	V	1010.562922	505.785099	993.536373	497.271824	992.552357	496.779816	9
17	2297.072289	1149.039782	2280.045740	1140.526508	2279.061724	1140.034500	Q	911.494508	456.250892	894.467959	447.737618	893.483943	447.245610	8
18	2410.156353	1205.581814	2393.129804	1197.068540	2392.145788	1196.576532	I	783.435930	392.221603	766.409381	383.708328	765.425365	383.216320	7
19	2547.215265	1274.111270	2530.188716	1265.597996	2529.204700	1265.105988	H	670.351866	335.679571	653.325317	327.166296	652.341301	326.674288	6
20	2662.242208	1331.624742	2645.215659	1323.111467	2644.231643	1322.619459	D	533.292954	267.150115	516.266405	258.636840	515.282389	258.144832	5
21	2775.326272	1388.166774	2758.299723	1379.653499	2757.315707	1379.161491	I	418.266011	209.636643	401.239462	201.123369	400.255446	200.631361	4
22	2876.373951	1438.690613	2859.347402	1430.177339	2858.363386	1429.685331	T	305.181947	153.094611	288.155398	144.581337	287.171382	144.089329	3
23	2933.395415	1467.201345	2916.368866	1458.688071	2915.384850	1458.196063	G	204.134268	102.570772	187.107719	94.057497			2
24							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **VAQLEAQCQEPCKDTVQIHDITGK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
78.9	3078.493668	0.018868	VAQLEAQCQEPCKDTVQIHDITGK
65.1	3078.493668	0.018868	VAQLEAQCQEPCKDTVQIHDITGK
61.0	3078.493668	0.018868	VAQLEAQCQEPCKDTVQIHDITGK
15.2	3078.493668	0.018868	VAQLEAQCQEPCKDTVQIHDITGK

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 22388: 1171.566708 from(586.790630,2+) rtinseconds(1800) index(35054)

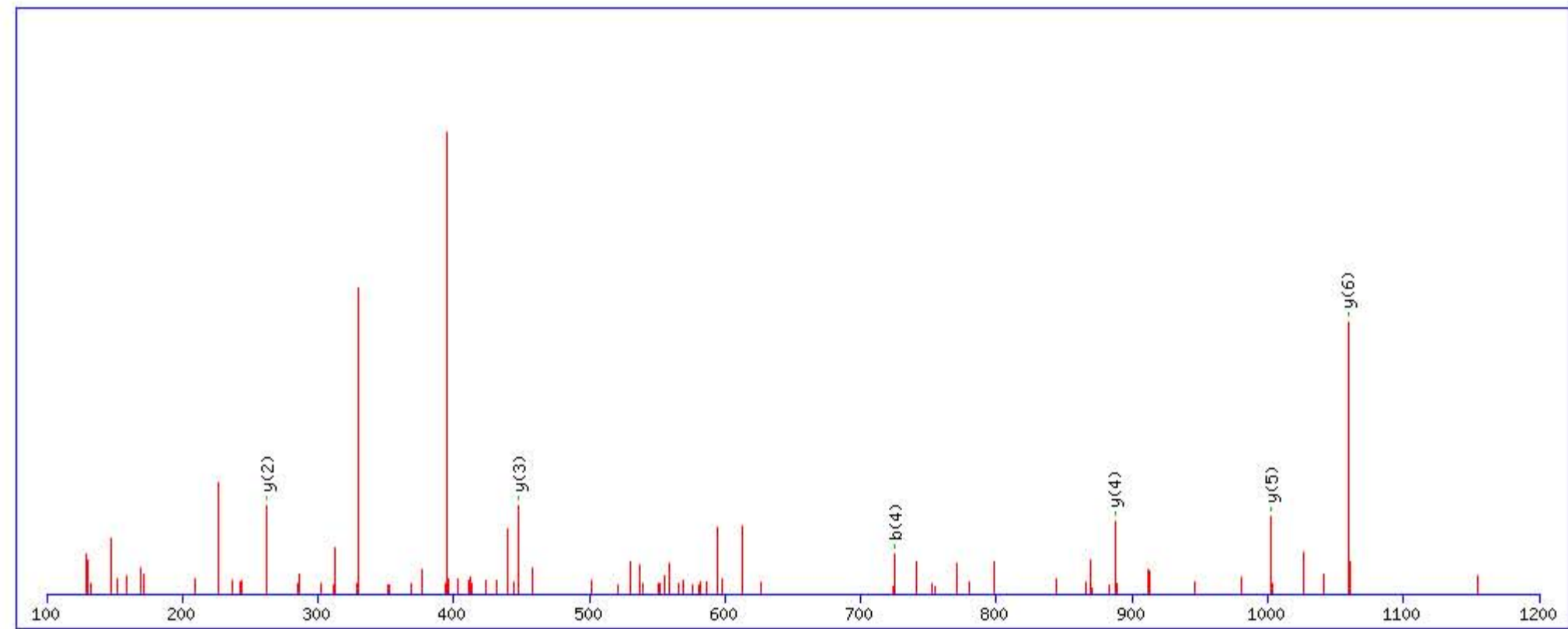
Title: Locus:1.1.1.3046.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1171.569580

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

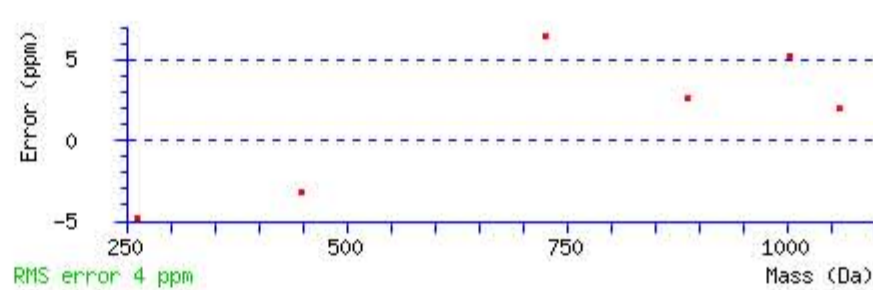
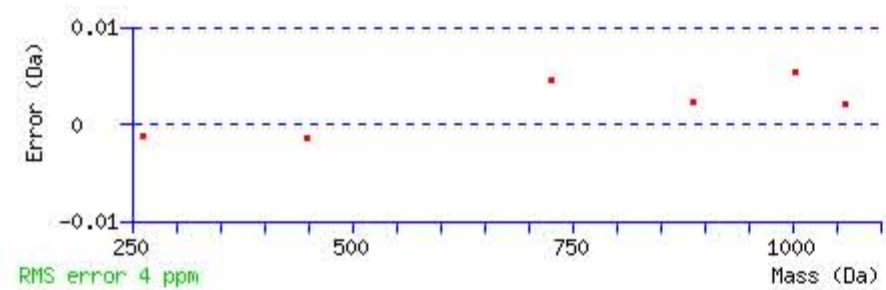
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 31 Expect: 0.006

Matches : 6/60 fragment ions using 11 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					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
31.4	1171.569580	-0.002872	IGDQWDK
7.2	1171.583328	-0.016620	GEVGDPGQKGTK
6.7	1171.572067	-0.005359	LGSGPDGAEIHK
6.2	1171.576096	-0.009388	LYFSDATLDK
5.2	1171.569565	-0.002857	LGPEWSQPMK
4.1	1171.573410	-0.006702	RAPDPGFQER
1.9	1171.559021	0.007687	SQLHCRMPK
1.2	1171.554337	0.012371	ALCDTPGVDPK
0.4	1171.577438	-0.010730	NDVLHNFVK
0.2	1171.562134	0.004574	RYEEERK

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **WCGTTQNYDADQK**

Found in **FN1C_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

Match to Query 44456: 1896.807132 from(633.276320,3+) rtinseconds(1654) index(34120)

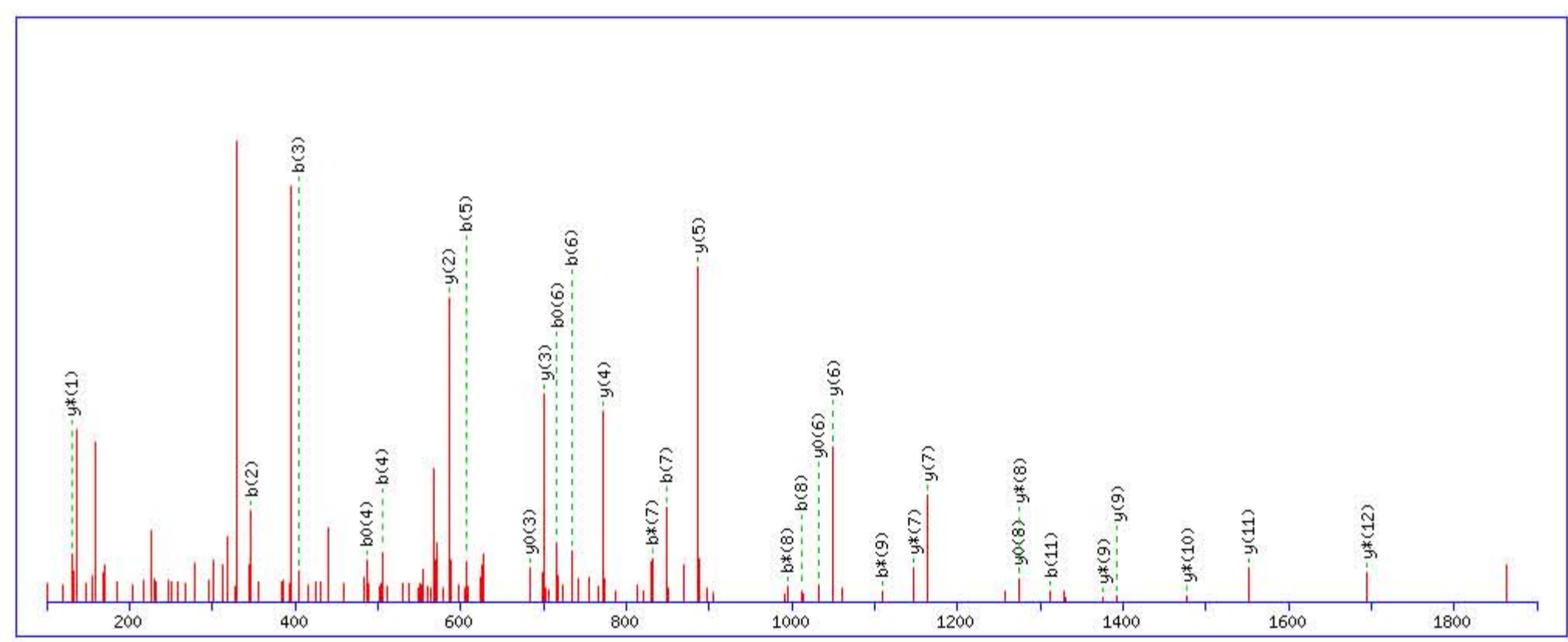
Title: Locus:1.1.1.2995.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1896.813477

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

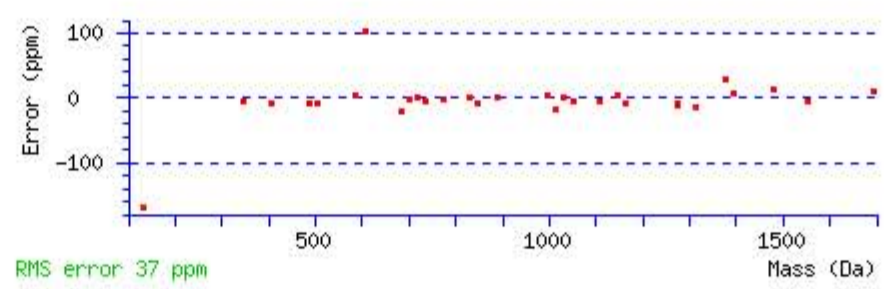
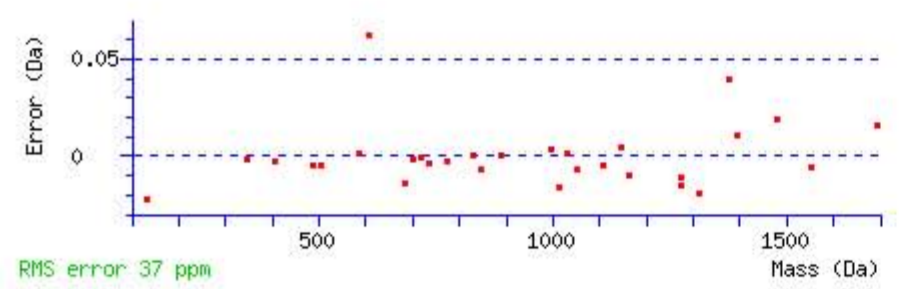
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 45 Expect: 0.00011

Matches : 30/124 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	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
44.7	1896.813477	-0.006345	WCGTTQNYDADQK

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 50535: 2174.039652 from(725.687160,3+) rtinseconds(1662) index(34170)

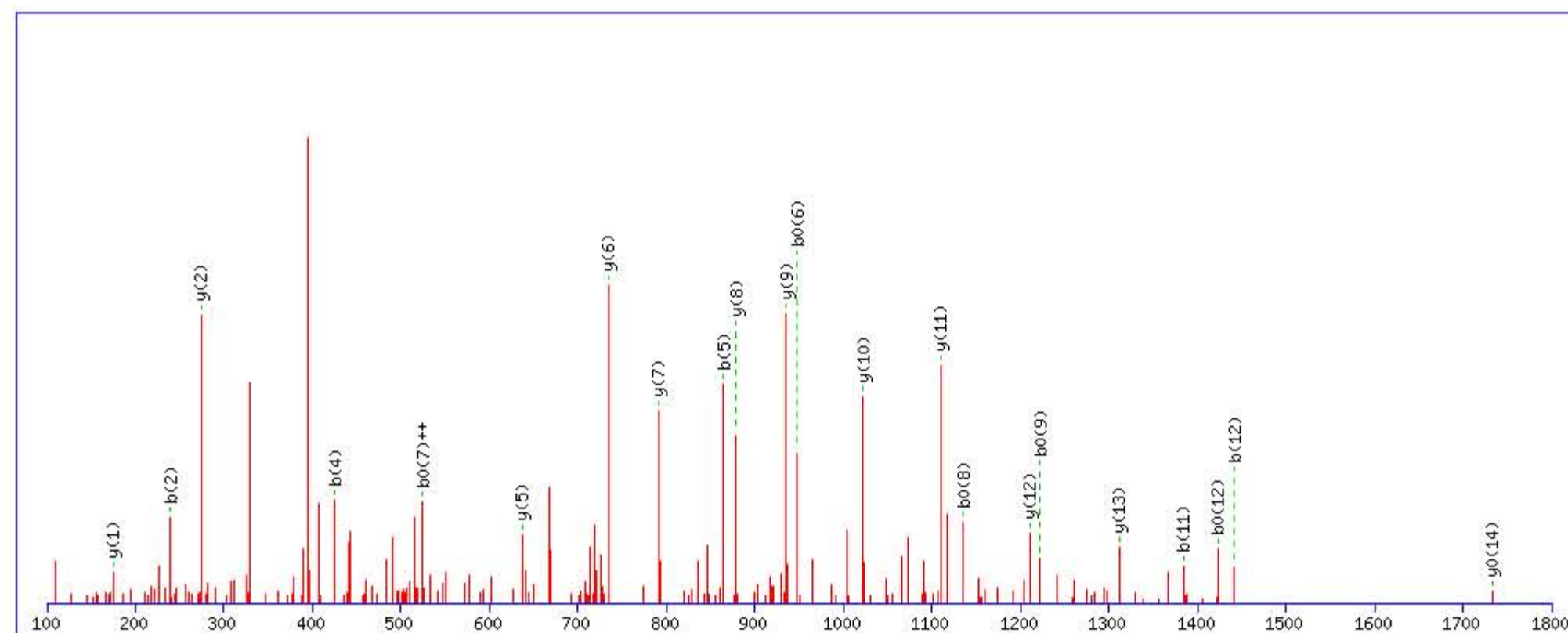
Title: Locus:1.1.1.2998.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2174.042664

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

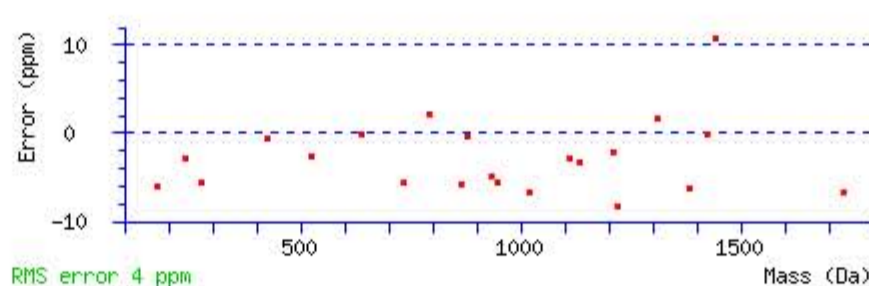
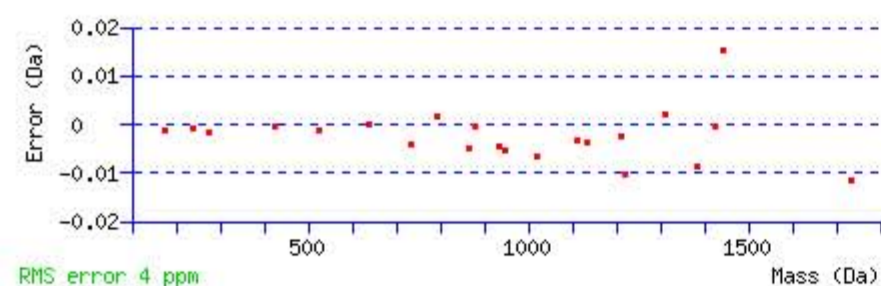
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 86 Expect: 4.6e-008

Matches : 22/190 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	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
86.3	2174.042664	-0.003012	HTSVQTTSSGSGPFTDVR

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

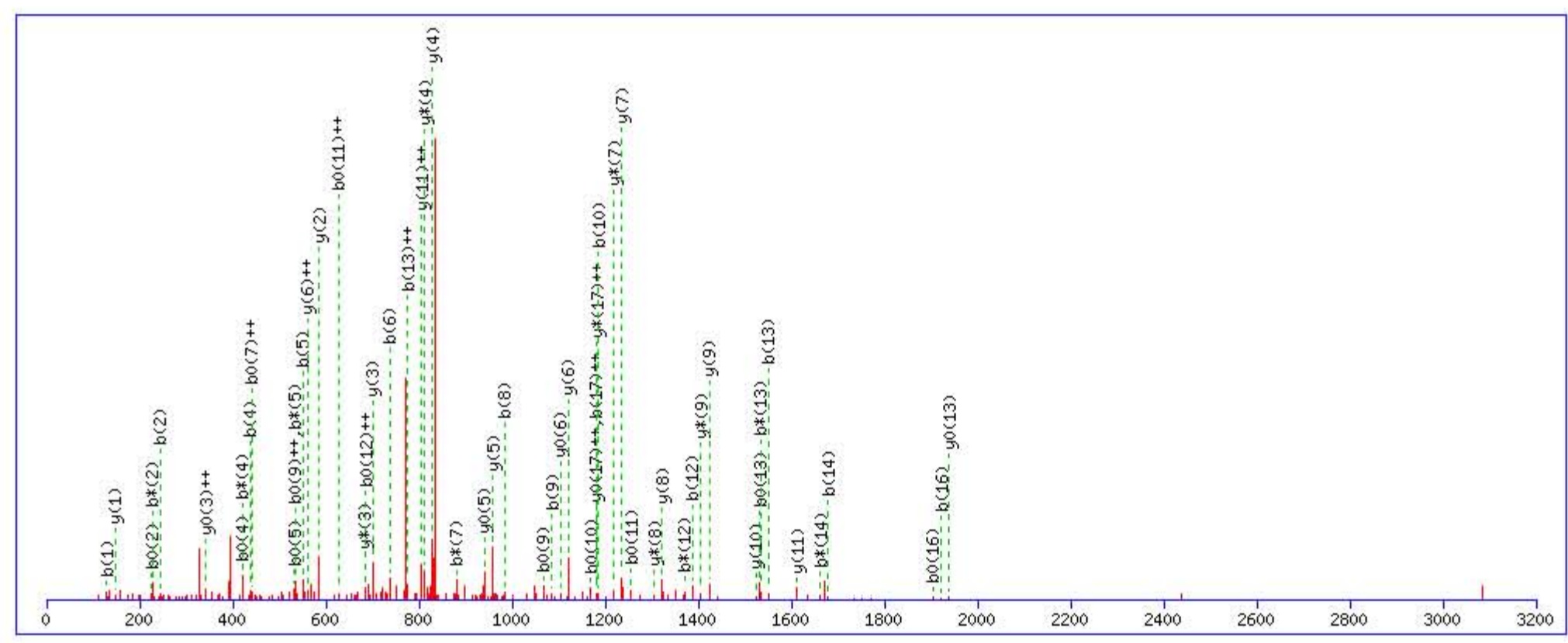
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **QDGHLWCSTTSNYEQDQK**
 Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

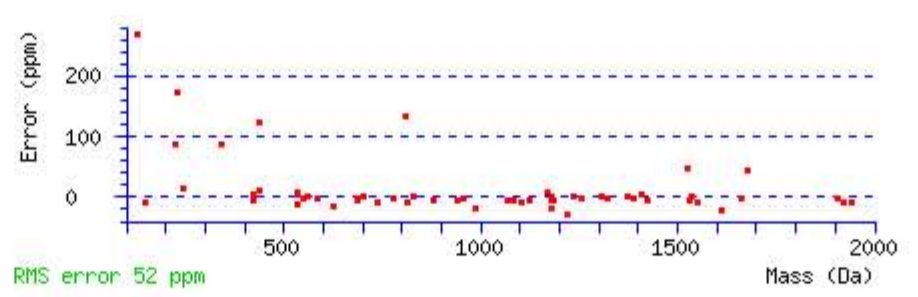
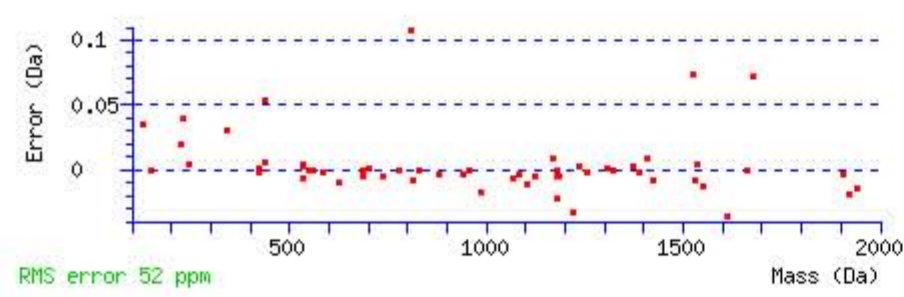
Match to Query 56805: 2507.089572 from(836.703800,3+) rtinseconds(1763) index(34845)
 Title: Locus:1.1.1.3033.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2507.084564
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q17 : Biotin:Thermo-21345 (Q)
 Ions Score: 66 Expect: 1.3e-006
 Matches : 57/198 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	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
65.8	2507.084564	0.005008	QDGHLWCSTTSNYEQDQK
47.4	2507.084564	0.005008	QDGHLWCSTTSNYEQDQK
0.1	2507.119598	-0.030026	KYGAAMVVMAFDEEGQATETDK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPGTTGQSYNQYSQR**

Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

Match to Query 58350: 2706.246372 from(903.089400,3+) rtinseconds(1488) index(33199)

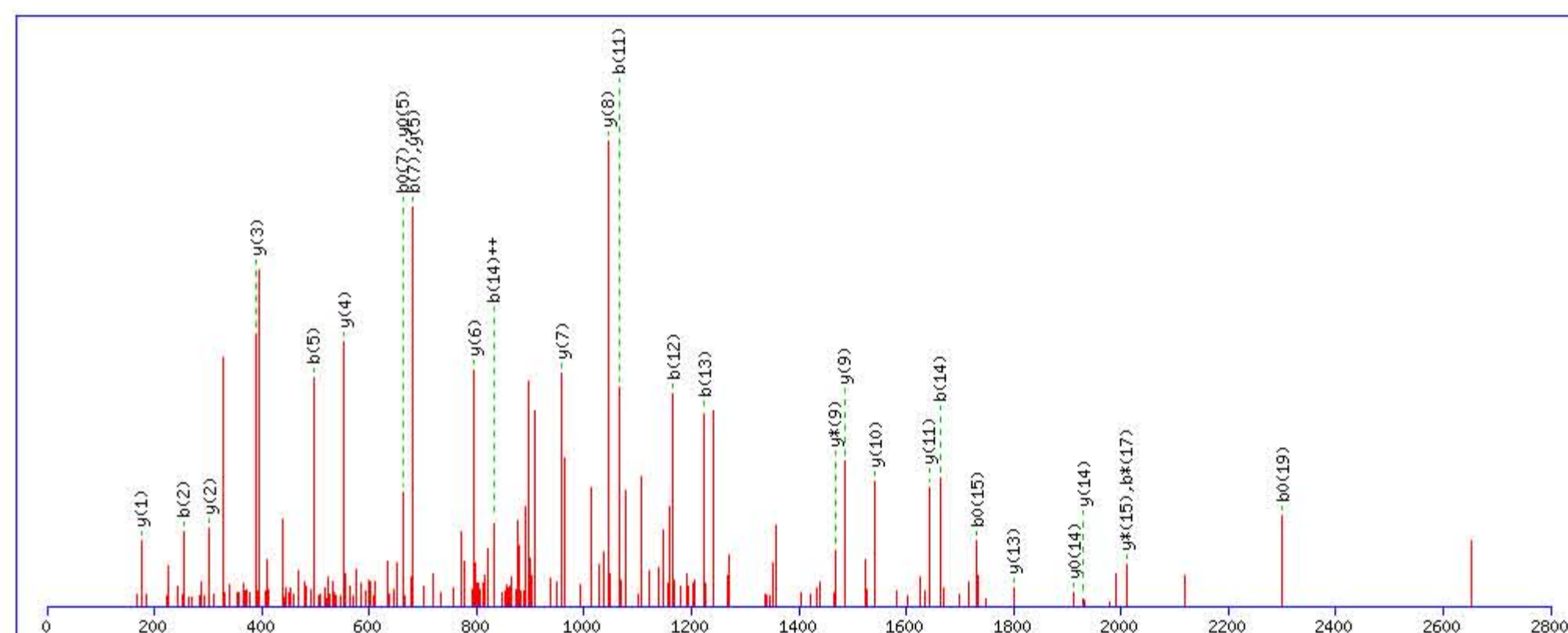
Title: Locus:1.1.1.2937.15 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2706.245621

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

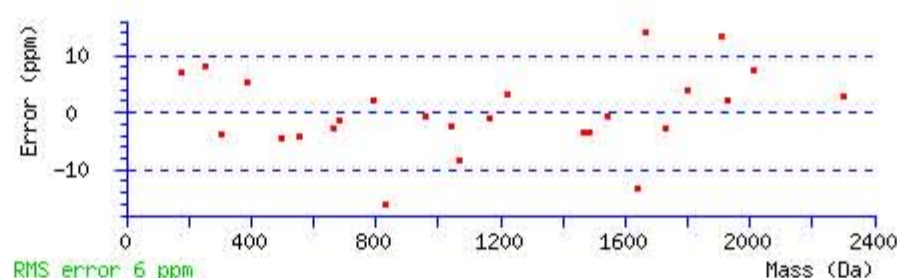
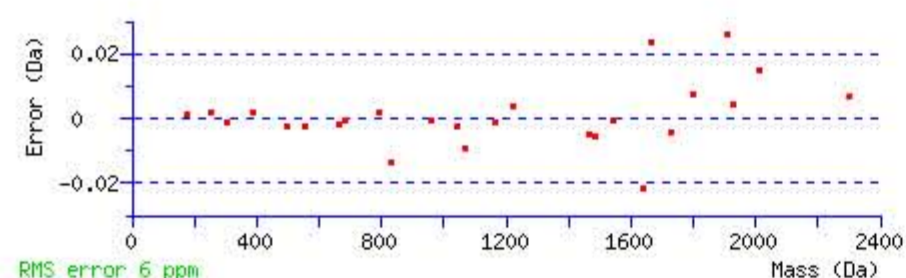
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 83 Expect: 7.6e-008

Matches : 29/240 fragment ions using 41 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	157.108387	79.057831	140.081838	70.544557			R							22
2	254.161151	127.584213	237.134602	119.070939			P	2551.151795	1276.079535	2534.125246	1267.566261	2533.141230	1267.074253	21
3	311.182615	156.094945	294.156066	147.581671			G	2454.099031	1227.553153	2437.072482	1219.039879	2436.088466	1218.547871	20
4	368.204079	184.605677	351.177530	176.092403			G	2397.077567	1199.042421	2380.051018	1190.529147	2379.067002	1190.037139	19
5	497.246672	249.126974	480.220123	240.613700	479.236107	240.121692	E	2340.056103	1170.531689	2323.029554	1162.018415	2322.045538	1161.526407	18
6	594.299436	297.653356	577.272887	289.140082	576.288871	288.648074	P	2211.013510	1106.010393	2193.986961	1097.497118	2193.002945	1097.005110	17
7	681.331464	341.169370	664.304915	332.656095	663.320899	332.164087	S	2113.960746	1057.484011	2096.934197	1048.970736	2095.950181	1048.478728	16
8	778.384228	389.695752	761.357679	381.182478	760.373663	380.690470	P	2026.928718	1013.967997	2009.902169	1005.454723	2008.918153	1004.962715	15
9	907.426821	454.217049	890.400272	445.703774	889.416256	445.211766	E	1929.875954	965.441615	1912.849405	956.928341	1911.865389	956.436333	14
10	964.448285	482.727781	947.421736	474.214506	946.437720	473.722498	G	1800.833361	900.920319	1783.806812	892.407044	1782.822796	891.915036	13
11	1065.495964	533.251620	1048.469415	524.738346	1047.485399	524.246337	T	1743.811897	872.409587	1726.785348	863.896312	1725.801332	863.404304	12
12	1166.543643	583.775460	1149.517094	575.262185	1148.533078	574.770177	T	1642.764218	821.885747	1625.737669	813.372473	1624.753653	812.880465	11
13	1223.565107	612.286191	1206.538558	603.772917	1205.554542	603.280909	G	1541.716539	771.361908	1524.689990	762.848633	1523.705974	762.356625	10
14	1662.790433	831.898854	1645.763884	823.385580	1644.779868	822.893572	Q	1484.695075	742.851176	1467.668526	734.337901	1466.684510	733.845893	9
15	1749.822461	875.414869	1732.795912	866.901594	1731.811896	866.409586	S	1045.469749	523.238513	1028.443200	514.725238	1027.459184	514.233230	8
16	1912.885790	956.946533	1895.859241	948.433259	1894.875225	947.941251	Y	958.437721	479.722499	941.411172	471.209224	940.427156	470.717216	7
17	2026.928717	1013.967997	2009.902168	1005.454722	2008.918152	1004.962714	N	795.374392	398.190834	778.347843	389.677560	777.363827	389.185552	6
18	2154.987295	1077.997285	2137.960746	1069.484011	2136.976730	1068.992003	Q	681.331465	341.169371	664.304916	332.656096	663.320900	332.164088	5
19	2318.050624	1159.528950	2301.024075	1151.015675	2300.040059	1150.523667	Y	553.272887	277.140082	536.246338	268.626807	535.262322	268.134799	4
20	2405.082652	1203.044964	2388.056103	1194.531689	2387.072087	1194.039681	S	390.209558	195.608417	373.183009	187.095143	372.198993	186.603135	3
21	2533.141230	1267.074253	2516.114681	1258.560978	2515.130665	1258.068971	Q	303.177530	152.092403	286.150981	143.579129			2
22							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **RPGGEPSPGTTGQSYNQYSQR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.5	2706.245621	0.000751	RPGGEPSPGTTGQSYNQYSQR
67.4	2706.245621	0.000751	RPGGEPSPGTTGQSYNQYSQR
48.1	2706.245621	0.000751	RPGGEPSPGTTGQSYNQYSQR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPGTTGQSYNQYSQR**

Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

Match to Query 58351: 2706.246372 from(903.089400,3+) rtinseconds(1480) index(33151)

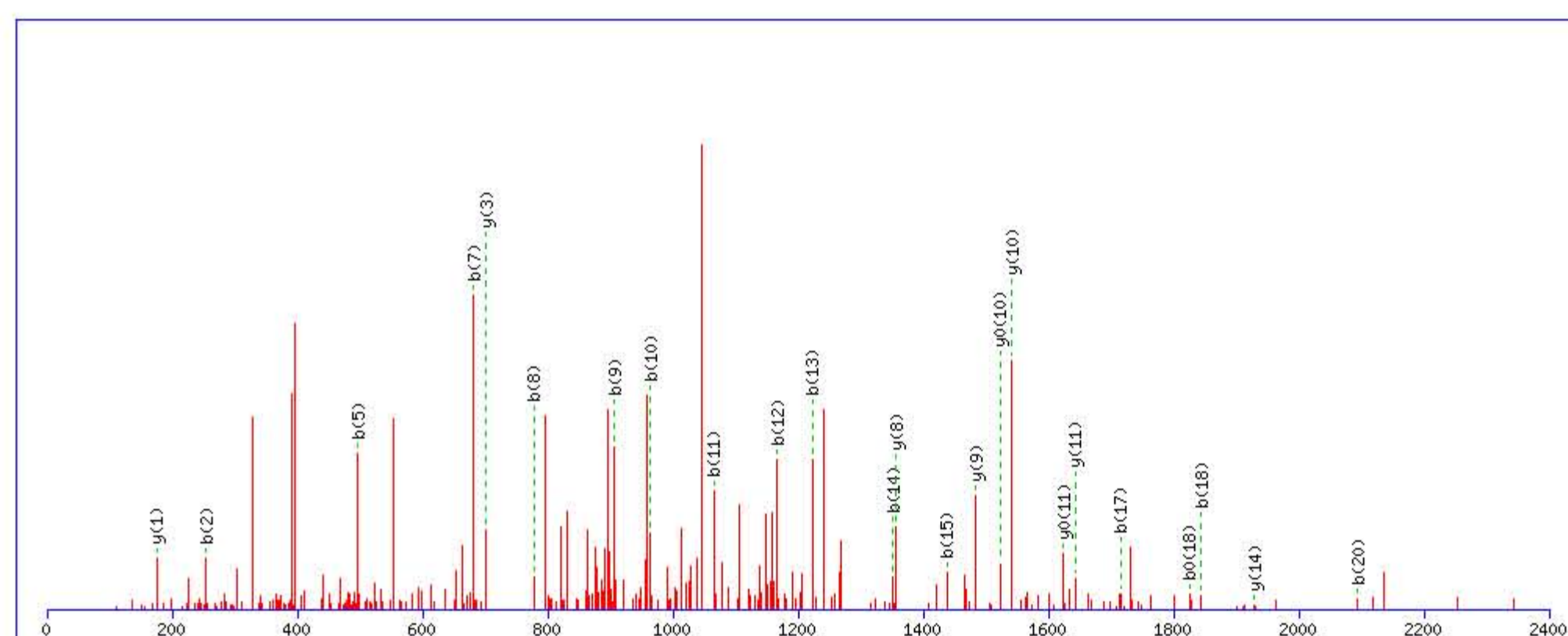
Title: Locus:1.1.1.2934.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2706.245621

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

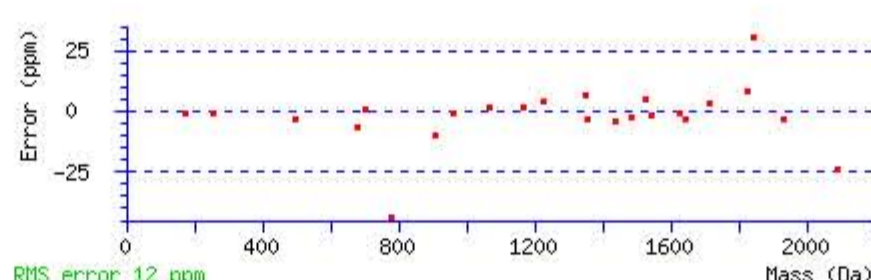
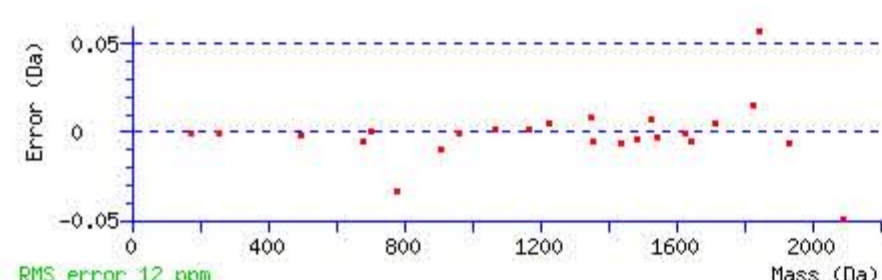
Variable modifications:

Q21 : Biotin:Thermo-21345 (Q)

Ions Score: 85 Expect: 4.1e-008

Matches : 24/240 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	157.108387	79.057831	140.081838	70.544557			R							22
2	254.161151	127.584213	237.134602	119.070939			P	2551.151795	1276.079535	2534.125246	1267.566261	2533.141230	1267.074253	21
3	311.182615	156.094945	294.156066	147.581671			G	2454.099031	1227.553153	2437.072482	1219.039879	2436.088466	1218.547871	20
4	368.204079	184.605677	351.177530	176.092403			G	2397.077567	1199.042421	2380.051018	1190.529147	2379.067002	1190.037139	19
5	497.246672	249.126974	480.220123	240.613700	479.236107	240.121692	E	2340.056103	1170.531689	2323.029554	1162.018415	2322.045538	1161.526407	18
6	594.299436	297.653356	577.272887	289.140082	576.288871	288.648074	P	2211.013510	1106.010393	2193.986961	1097.497118	2193.002945	1097.005110	17
7	681.331464	341.169370	664.304915	332.656095	663.320899	332.164087	S	2113.960746	1057.484011	2096.934197	1048.970736	2095.950181	1048.478728	16
8	778.384228	389.695752	761.357679	381.182478	760.373663	380.690470	P	2026.928718	1013.967997	2009.902169	1005.454723	2008.918153	1004.962715	15
9	907.426821	454.217049	890.400272	445.703774	889.416256	445.211766	E	1929.875954	965.441615	1912.849405	956.928341	1911.865389	956.436333	14
10	964.448285	482.727781	947.421736	474.214506	946.437720	473.722498	G	1800.833361	900.920319	1783.806812	892.407044	1782.822796	891.915036	13
11	1065.495964	533.251620	1048.469415	524.738346	1047.485399	524.246337	T	1743.811897	872.409587	1726.785348	863.896312	1725.801332	863.404304	12
12	1166.543643	583.775460	1149.517094	575.262185	1148.533078	574.770177	T	1642.764218	821.885747	1625.737669	813.372473	1624.753653	812.880465	11
13	1223.565107	612.286191	1206.538558	603.772917	1205.554542	603.280909	G	1541.716539	771.361908	1524.689990	762.848633	1523.705974	762.356625	10
14	1351.623685	676.315480	1334.597136	667.802206	1333.613120	667.310198	Q	1484.695075	742.851176	1467.668526	734.337901	1466.684510	733.845893	9
15	1438.655713	719.831494	1421.629164	711.318220	1420.645148	710.826212	S	1356.636497	678.821887	1339.609948	670.308612	1338.625932	669.816604	8
16	1601.719042	801.363159	1584.692493	792.849885	1583.708477	792.357876	Y	1269.604469	635.305873	1252.577920	626.792598	1251.593904	626.300590	7
17	1715.761969	858.384622	1698.735420	849.871348	1697.751404	849.379340	N	1106.541140	553.774208	1089.514591	545.260934	1088.530575	544.768926	6
18	1843.820547	922.413912	1826.793998	913.900637	1825.809982	913.408629	Q	992.498213	496.752745	975.471664	488.239470	974.487648	487.747462	5
19	2006.883876	1003.945576	1989.857327	995.432302	1988.873311	994.940294	Y	864.439635	432.723456	847.413086	424.210181	846.429070	423.718173	4
20	2093.915904	1047.461590	2076.889355	1038.948315	2075.905339	1038.456307	S	701.376306	351.191791	684.349757	342.678517	683.365741	342.186509	3
21	2533.141230	1267.074253	2516.114681	1258.560978	2515.130665	1258.068971	Q	614.344278	307.675777	597.317729	299.162503			2
22							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **RPGGEPSPGTTGQSYNQYSQR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
85.2	2706.245621	0.000751	RPGGEPSPGTTGQSYNQYSQR
76.6	2706.245621	0.000751	RPGGEPSPGTTGQSYNQYSQR
76.3	2706.245621	0.000751	RPGGEPSPGTTGQSYNQYSQR

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

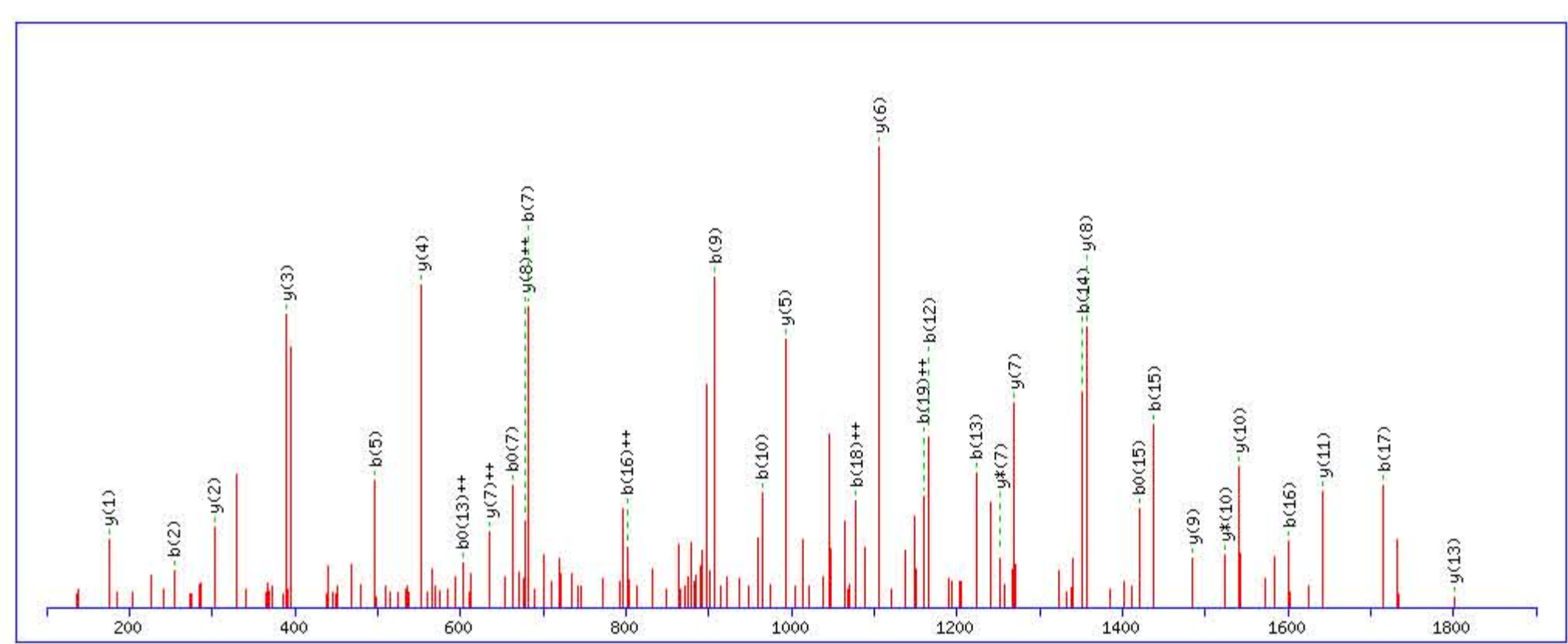
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPGTTGQSYNQYSQR**
 Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

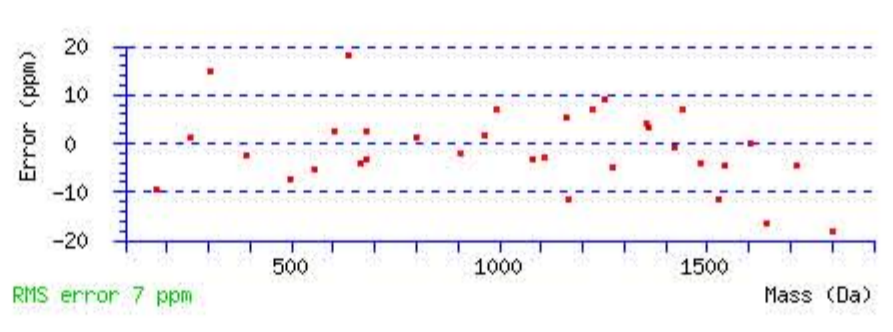
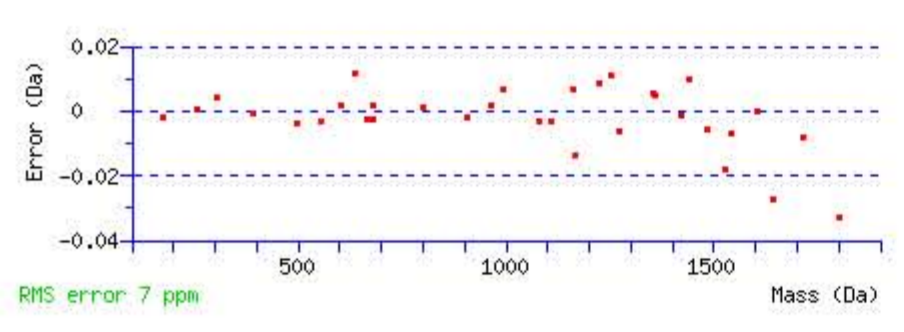
Match to Query 58352: 2706.246792 from(903.089540,3+) rtinseconds(1472) index(33109)
 Title: Locus:1.1.1.2931.25 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2706.245621
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q18 : Biotin:Thermo-21345 (Q)
 Ions Score: 91 Expect: 1.1e-008
 Matches : 33/240 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	157.108387	79.057831	140.081838	70.544557			R							22
2	254.161151	127.584213	237.134602	119.070939			P	2551.151795	1276.079535	2534.125246	1267.566261	2533.141230	1267.074253	21
3	311.182615	156.094945	294.156066	147.581671			G	2454.099031	1227.553153	2437.072482	1219.039879	2436.088466	1218.547871	20
4	368.204079	184.605677	351.177530	176.092403			G	2397.077567	1199.042421	2380.051018	1190.529147	2379.067002	1190.037139	19
5	497.246672	249.126974	480.220123	240.613700	479.236107	240.121692	E	2340.056103	1170.531689	2323.029554	1162.018415	2322.045538	1161.526407	18
6	594.299436	297.653356	577.272887	289.140082	576.288871	288.648074	P	2211.013510	1106.010393	2193.986961	1097.497118	2193.002945	1097.005110	17
7	681.331464	341.169370	664.304915	332.656095	663.320899	332.164087	S	2113.960746	1057.484011	2096.934197	1048.970736	2095.950181	1048.478728	16
8	778.384228	389.695752	761.357679	381.182478	760.373663	380.690470	P	2026.928718	1013.967997	2009.902169	1005.454723	2008.918153	1004.962715	15
9	907.426821	454.217049	890.400272	445.703774	889.416256	445.211766	E	1929.875954	965.441615	1912.849405	956.928341	1911.865389	956.436333	14
10	964.448285	482.727781	947.421736	474.214506	946.437720	473.722498	G	1800.833361	900.920319	1783.806812	892.407044	1782.822796	891.915036	13
11	1065.495964	533.251620	1048.469415	524.738346	1047.485399	524.246337	T	1743.811897	872.409587	1726.785348	863.896312	1725.801332	863.404304	12
12	1166.543643	583.775460	1149.517094	575.262185	1148.533078	574.770177	T	1642.764218	821.885747	1625.737669	813.372473	1624.753653	812.880465	11
13	1223.565107	612.286191	1206.538558	603.772917	1205.554542	603.280909	G	1541.716539	771.361908	1524.689990	762.848633	1523.705974	762.356625	10
14	1351.623685	676.315480	1334.597136	667.802206	1333.613120	667.310198	Q	1484.695075	742.851176	1467.668526	734.337901	1466.684510	733.845893	9
15	1438.655713	719.831494	1421.629164	711.318220	1420.645148	710.826212	S	1356.636497	678.821887	1339.609948	670.308612	1338.625932	669.816604	8
16	1601.719042	801.363159	1584.692493	792.849885	1583.708477	792.357876	Y	1269.604469	635.305873	1252.577920	626.792598	1251.593904	626.300590	7
17	1715.761969	858.384622	1698.735420	849.871348	1697.751404	849.379340	N	1106.541140	553.774208	1089.514591	545.260934	1088.530575	544.768926	6
18	2154.987295	1077.997285	2137.960746	1069.484011	2136.976730	1068.992003	Q	992.498213	496.752745	975.471664	488.239470	974.487648	487.747462	5
19	2318.050624	1159.528950	2301.024075	1151.015675	2300.040059	1150.523667	Y	553.272887	277.140082	536.246338	268.626807	535.262322	268.134799	4
20	2405.082652	1203.044964	2388.056103	1194.531689	2387.072087	1194.039681	S	390.209558	195.608417	373.183009	187.095143	372.198993	186.603135	3
21	2533.141230	1267.074253	2516.114681	1258.560978	2515.130665	1258.068971	Q	303.177530	152.092403	286.150981	143.579129			2
22							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **RPGGEPSPGTTGQSYNQYSQR**
 (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	2706.245621	0.001171	RPGGEPSPGTTGQSYNQYSQR
63.5	2706.245621	0.001171	RPGGEPSPGTTGQSYNQYSQR
37.1	2706.245621	0.001171	RPGGEPSPGTTGQSYNQYSQR

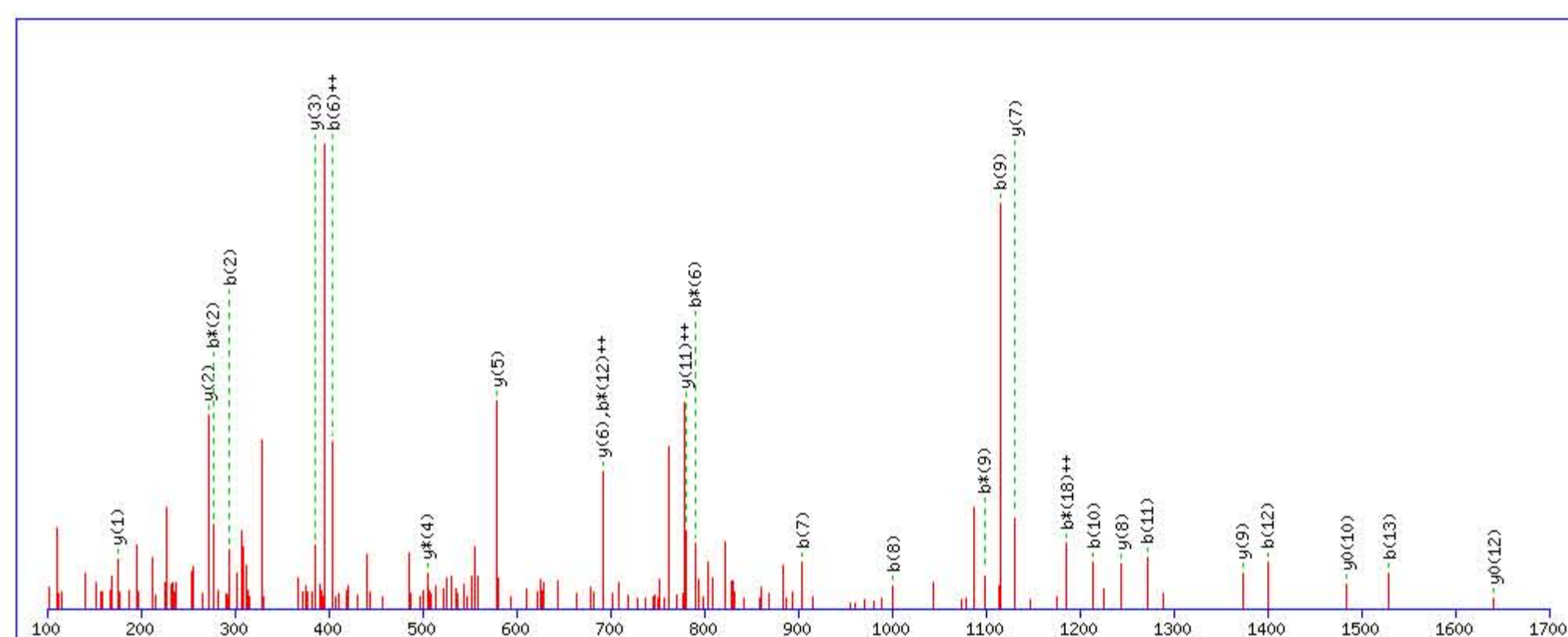
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **HRPRPYPPNVGEEIQIGHIPR**
 Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

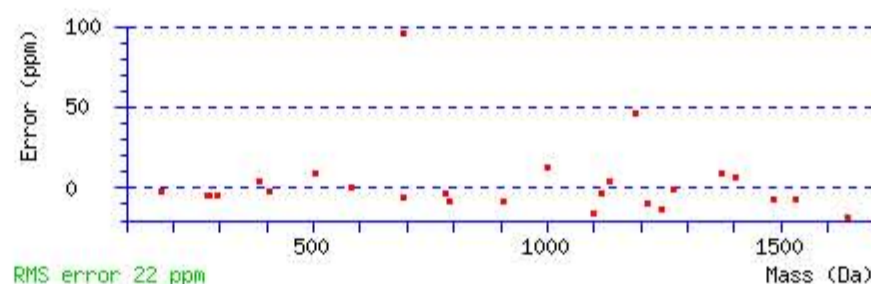
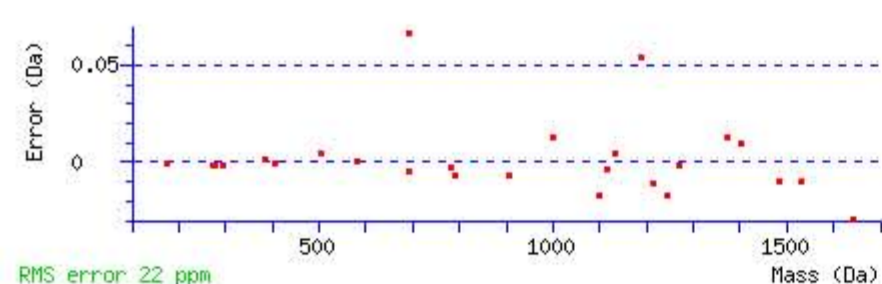
Match to Query 59121: 2772.465170 from(555.500310,5+) rtinseconds(1753) index(34787)
 Title: Locus:1.1.1.3030.8 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2772.475815
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q15 : Biotin:Thermo-21345 (Q)
 Ions Score: 42 Expect: 0.00014
 Matches : 26/200 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	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
41.9	2772.475815	-0.010645	HRPRPYPPNVGEEIQIGHIPR
0.7	2772.429306	0.035864	EKHLAILEKKNISEEVEAPEVEPR

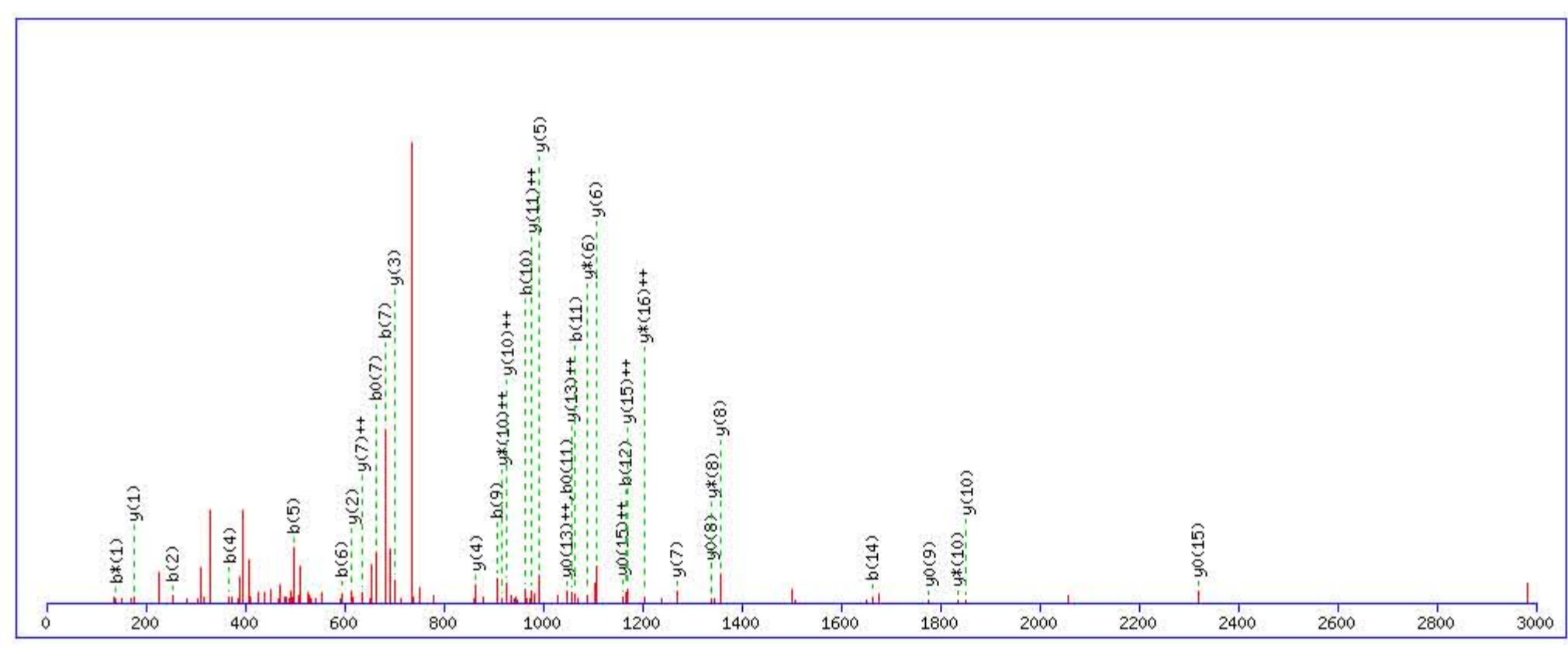
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPGTTGQSYNQYSQR**
 Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

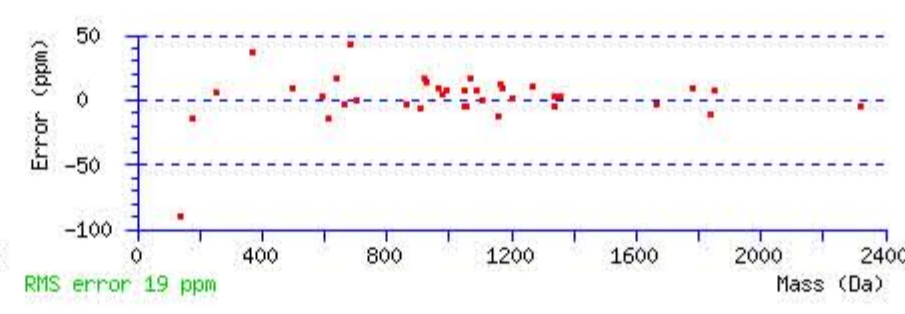
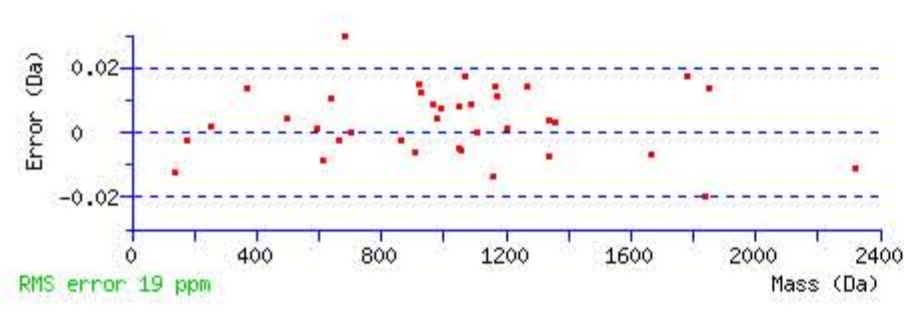
Match to Query 61828: 3017.416936 from(755.361510,4+) rtinseconds(1798) index(35044)
 Title: Locus:1.1.1.3045.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 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: 50 Expect: 0.00019
 Matches : 37/240 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	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 **RPGGEPSPGTTGQSYNQYSQR**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.6	3017.412369	0.004567	RPGGEPSPGTTGQSYNQYSQR
49.5	3017.412369	0.004567	RPGGEPSPGTTGQSYNQYSQR
22.1	3017.412369	0.004567	RPGGEPSPGTTGQSYNQYSQR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **RPGGEPSPGTTGQSYNQYSQR**

Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

Match to Query 61832: 3017.428182 from(1006.816670,3+) rtinseconds(1784) index(34978)

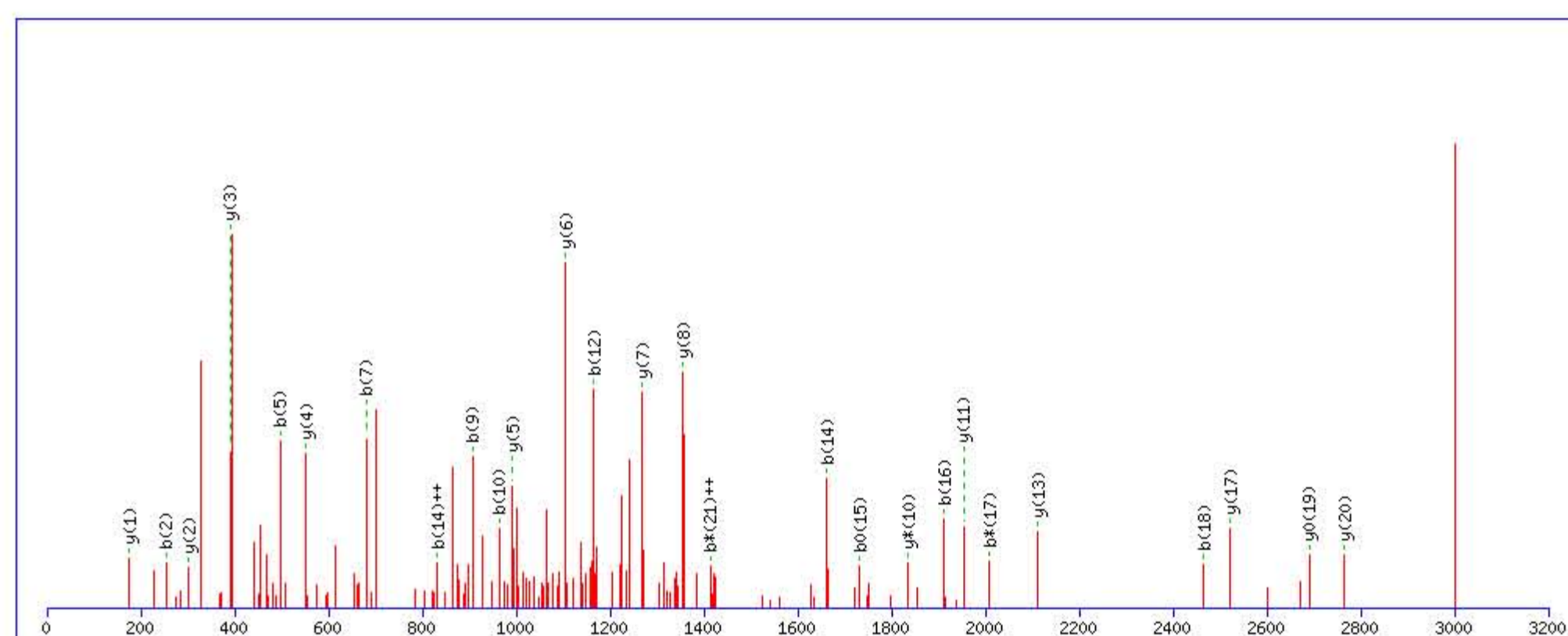
Title: Locus:1.1.1.3040.25 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3017.412369

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

Variable modifications:

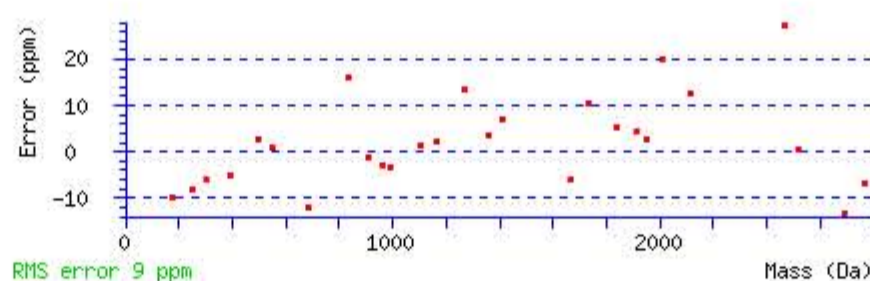
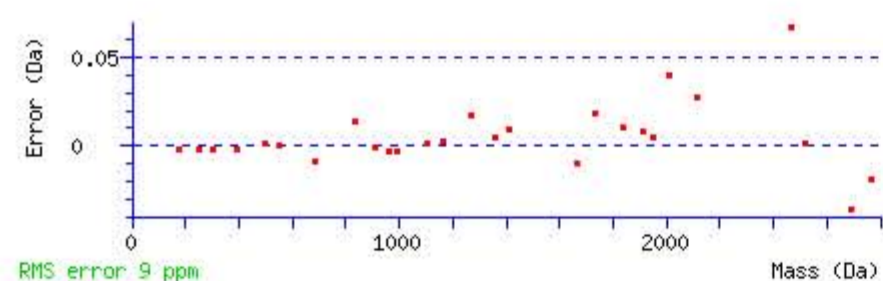
Q14 : Biotin:Thermo-21345 (Q)

Q18 : Biotin:Thermo-21345 (Q)

Ions Score: 72 Expect: 1.3e-006

Matches : 27/240 fragment ions using 45 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	157.108387	79.057831	140.081838	70.544557			R							22
2	254.161151	127.584213	237.134602	119.070939			P	2862.318543	1431.662909	2845.291994	1423.149635	2844.307978	1422.657627	21
3	311.182615	156.094945	294.156066	147.581671			G	2765.265779	1383.136527	2748.239230	1374.623253	2747.255214	1374.131245	20
4	368.204079	184.605677	351.177530	176.092403			G	2708.244315	1354.625795	2691.217766	1346.112521	2690.233750	1345.620513	19
5	497.246672	249.126974	480.220123	240.613700	479.236107	240.121692	E	2651.222851	1326.115063	2634.196302	1317.601789	2633.212286	1317.109781	18
6	594.299436	297.653356	577.272887	289.140082	576.288871	288.648074	P	2522.180258	1261.593767	2505.153709	1253.080492	2504.169693	1252.588484	17
7	681.331464	341.169370	664.304915	332.656095	663.320899	332.164087	S	2425.127494	1213.067385	2408.100945	1204.554110	2407.116929	1204.062102	16
8	778.384228	389.695752	761.357679	381.182478	760.373663	380.690470	P	2338.095466	1169.551371	2321.068917	1161.038096	2320.084901	1160.546088	15
9	907.426821	454.217049	890.400272	445.703774	889.416256	445.211766	E	2241.042702	1121.024989	2224.016153	1112.511714	2223.032137	1112.019706	14
10	964.448285	482.727781	947.421736	474.214506	946.437720	473.722498	G	2112.000109	1056.503692	2094.973560	1047.990418	2093.989544	1047.498410	13
11	1065.495964	533.251620	1048.469415	524.738346	1047.485399	524.246337	T	2054.978645	1027.992960	2037.952096	1019.479686	2036.968080	1018.987678	12
12	1166.543643	583.775460	1149.517094	575.262185	1148.533078	574.770177	T	1953.930966	977.469121	1936.904417	968.955847	1935.920401	968.463839	11
13	1223.565107	612.286191	1206.538558	603.772917	1205.554542	603.280909	G	1852.883287	926.945282	1835.856738	918.432007	1834.872722	917.939999	10
14	1662.790433	831.898854	1645.763884	823.385580	1644.779868	822.893572	Q	1795.861823	898.434550	1778.835274	889.921275	1777.851258	889.429267	9
15	1749.822461	875.414869	1732.795912	866.901594	1731.811896	866.409586	S	1356.636497	678.821887	1339.609948	670.308612	1338.625932	669.816604	8
16	1912.885790	956.946533	1895.859241	948.433259	1894.875225	947.941251	Y	1269.604469	635.305873	1252.577920	626.792598	1251.593904	626.300590	7
17	2026.928717	1013.967997	2009.902168	1005.454722	2008.918152	1004.962714	N	1106.541140	553.774208	1089.514591	545.260934	1088.530575	544.768926	6
18	2466.154043	1233.580659	2449.127494	1225.067385	2448.143478	1224.575377	Q	992.498213	496.752745	975.471664	488.239470	974.487648	487.747462	5
19	2629.217372	1315.112324	2612.190823	1306.599049	2611.206807	1306.107041	Y	553.272887	277.140082	536.246338	268.626807	535.262322	268.134799	4
20	2716.249400	1358.628338	2699.222851	1350.115063	2698.238835	1349.623056	S	390.209558	195.608417	373.183009	187.095143	372.198993	186.603135	3
21	2844.307978	1422.657627	2827.281429	1414.144353	2826.297413	1413.652345	Q	303.177530	152.092403	286.150981	143.579129			2
22							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [RPGGEPSPGTTGQSYNQYSQR](#)

(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	3017.412369	0.015813	RPGGEPSPGTTGQSYNQYSQR
70.8	3017.412369	0.015813	RPGGEPSPGTTGQSYNQYSQR
26.4	3017.412369	0.015813	RPGGEPSPGTTGQSYNQYSQR

MASCOT Search Results

Peptide View

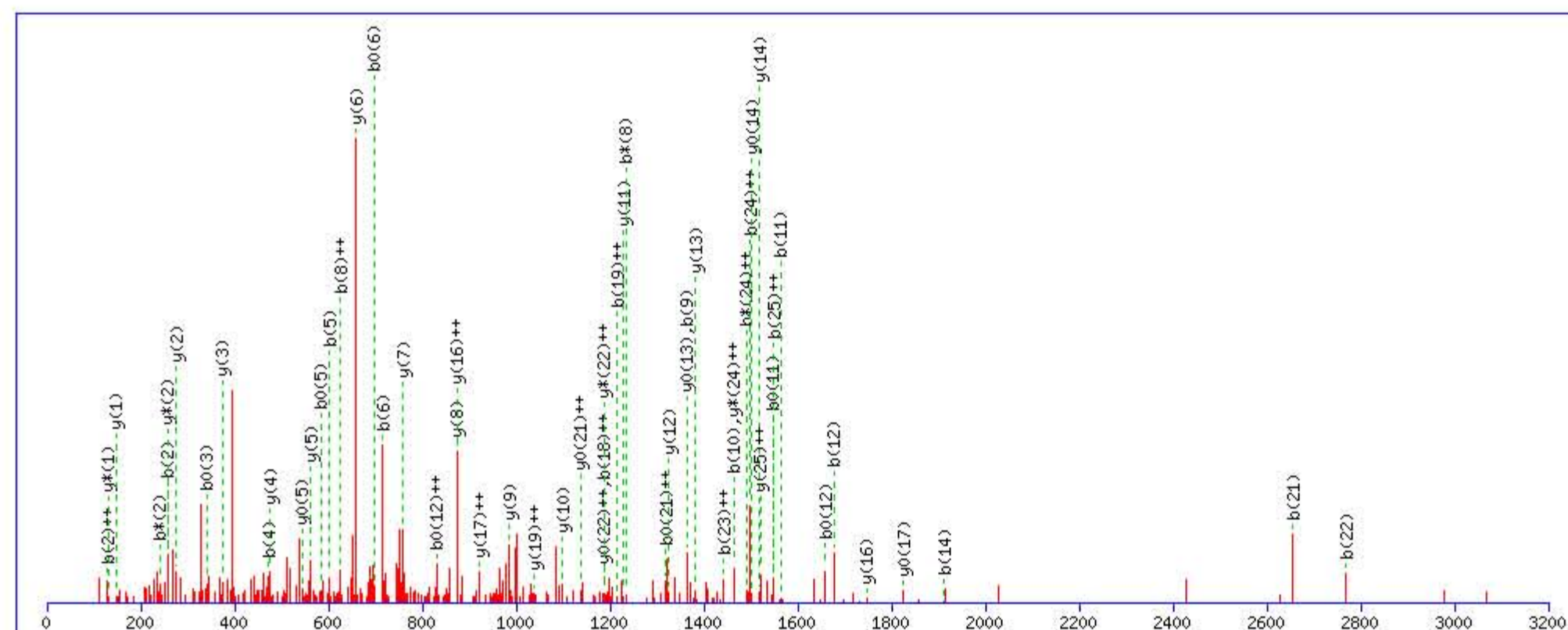
MS/MS Fragmentation of **KKTDELPLQLVTLPHPNLHGPEILDVPSTVQK**
 Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

Match to Query 68631: 3754.077420 from(751.822760,5+) rtinseconds(2331) index(38400)
 Title: Locus:1.1.1.3231.15 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

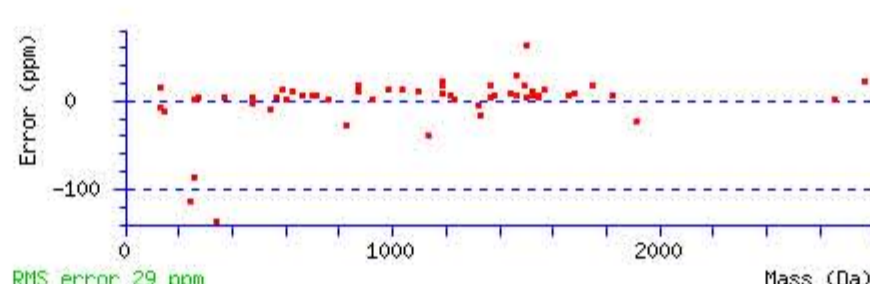
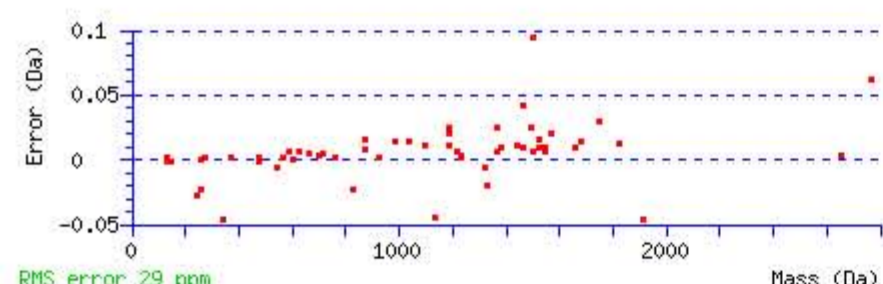
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3754.049149
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q8 : Biotin:Thermo-21345 (Q)
 Ions Score: 54 Expect: 1.9e-005
 Matches : 58/350 fragment ions using 172 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							31
2	257.197202	129.102239	240.170653	120.588965			K	3626.961469	1813.984372	3609.934920	1805.471098	3608.950904	1804.979090	30
3	358.244881	179.626079	341.218332	171.112804	340.234316	170.620796	T	3498.866506	1749.936891	3481.839957	1741.423616	3480.855941	1740.931608	29
4	473.271824	237.139550	456.245275	228.626276	455.261259	228.134268	D	3397.818827	1699.413051	3380.792278	1690.899777	3379.808262	1690.407769	28
5	602.314417	301.660847	585.287868	293.147572	584.303852	292.655564	E	3282.791884	1641.899580	3265.765335	1633.386305	3264.781319	1632.894297	27
6	715.398481	358.202879	698.371932	349.689604	697.387916	349.197596	L	3153.749291	1577.378283	3136.722742	1568.865009	3135.738726	1568.373001	26
7	812.451245	406.729261	795.424696	398.215986	794.440680	397.723978	P	3040.665227	1520.836251	3023.638678	1512.322977	3022.654662	1511.830969	25
8	1251.676571	626.341924	1234.650022	617.828649	1233.666006	617.336641	Q	2943.612463	1472.309869	2926.585914	1463.796595	2925.601898	1463.304587	24
9	1364.760635	682.883956	1347.734086	674.370681	1346.750070	673.878673	L	2504.387137	1252.697206	2487.360588	1244.183932	2486.376572	1243.691924	23
10	1463.829049	732.418163	1446.802500	723.904888	1445.818484	723.412880	V	2391.303073	1196.155174	2374.276524	1187.641900	2373.292508	1187.149892	22
11	1564.876728	782.942002	1547.850179	774.428728	1546.866163	773.936720	T	2292.234659	1146.620967	2275.208110	1138.107693	2274.224094	1137.615685	21
12	1677.960792	839.484034	1660.934243	830.970760	1659.950227	830.478752	L	2191.186980	1096.097128	2174.160431	1087.583853	2173.176415	1087.091845	20
13	1775.013556	888.010416	1757.987007	879.497142	1757.002991	879.005134	P	2078.102916	1039.555096	2061.076367	1031.041821	2060.092351	1030.549813	19
14	1912.072468	956.539872	1895.045919	948.026598	1894.061903	947.534590	H	1981.050152	991.028714	1964.023603	982.515440	1963.039587	982.023432	18
15	2009.125232	1005.066254	1992.098683	996.552980	1991.114667	996.060972	P	1843.991240	922.499258	1826.964691	913.985984	1825.980675	913.493976	17
16	2123.168159	1062.087717	2106.141610	1053.574443	2105.157594	1053.082435	N	1746.938476	873.972876	1729.911927	865.459602	1728.927911	864.967594	16
17	2236.252223	1118.629749	2219.225674	1110.116475	2218.241658	1109.624467	L	1632.895549	816.951413	1615.869000	808.438138	1614.884984	807.946130	15
18	2373.311135	1187.159205	2356.284586	1178.645931	2355.300570	1178.153923	H	1519.811485	760.409381	1502.784936	751.896106	1501.800920	751.404098	14
19	2430.332599	1215.669937	2413.306050	1207.156663	2412.322034	1206.664655	G	1382.752573	691.879925	1365.726024	683.366650	1364.742008	682.874642	13
20	2527.385363	1264.196319	2510.358814	1255.683045	2509.374798	1255.191037	P	1325.731109	663.369193	1308.704560	654.855918	1307.720544	654.363910	12
21	2656.427956	1328.717616	2639.401407	1320.204341	2638.417391	1319.712333	E	1228.678345	614.842811	1211.651796	606.329536	1210.667780	605.837528	11
22	2769.512020	1385.259648	2752.485471	1376.746373	2751.501455	1376.254365	I	1099.635752	550.321514	1082.609203	541.808240	1081.625187	541.316231	10
23	2882.596084	1441.801680	2865.569535	1433.288406	2864.585519	1432.796398	L	986.551688	493.779482	969.525139	485.266207	968.541123	484.774199	9
24	2997.623027	1499.315152	2980.596478	1490.801877	2979.612462	1490.309869	D	873.467624	437.237450	856.441075	428.724175	855.457059	428.232167	8
25	3096.691441	1548.849358	3079.664892	1540.336084	3078.680876	1539.844076	V	758.440681	379.723978	741.414132	371.210704	740.430116	370.718696	7
26	3193.744205	1597.375740	3176.717656	1588.862466	3175.733640	1588.370458	P	659.372267	330.189772	642.345718	321.676497	641.361702	321.184489	6
27	3280.776233	1640.891754	3263.749684	1632.378480	3262.765668	1631.886472	S	562.319503	281.663389	545.292954	273.150115	544.308938	272.658107	5
28	3381.823912	1691.415594	3364.797363	1682.902319	3363.813347	1682.410311	T	475.287475	238.147375	458.260926	229.634101	457.276910	229.142093	4
29	3480.892326	1740.949801	3463.865777	1732.436526	3462.881761	1731.944518	V	374.239796	187.623536	357.213247	179.110261			3
30	3608.950904	1804.979090	3591.924355	1796.465815	3590.940339	1795.973807	Q	275.171382	138.089329	258.144833	129.576055			2
31							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **KKTDELPLQLVTLPHPNLHGPEILDVPSTVQK**
 (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	3754.049149	0.028271	KKTDELPLQLVTLPHPNLHGPEILDVPSTVQK

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 25910: 1285.668608 from(643.841580,2+) rtinseconds(1468) index(33079)

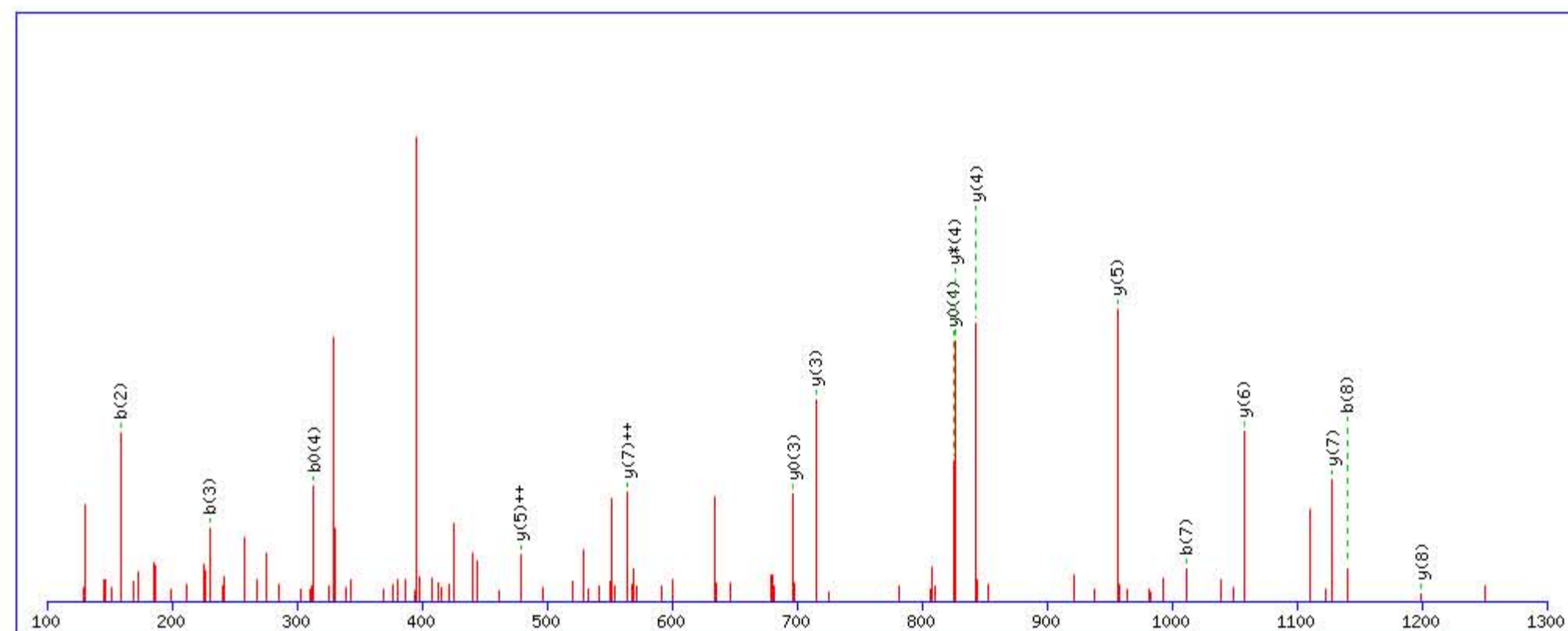
Title: Locus:1.1.1.2930.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1285.669998

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

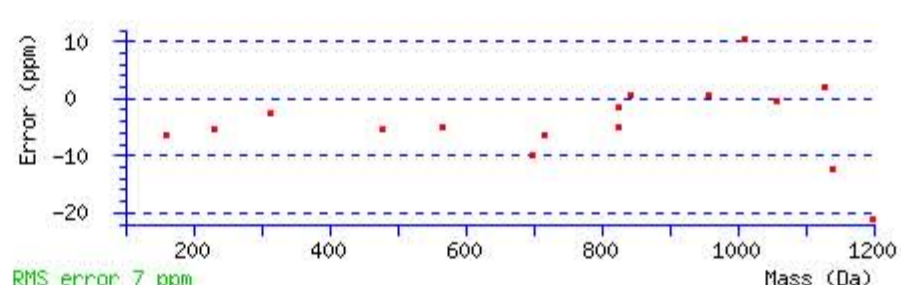
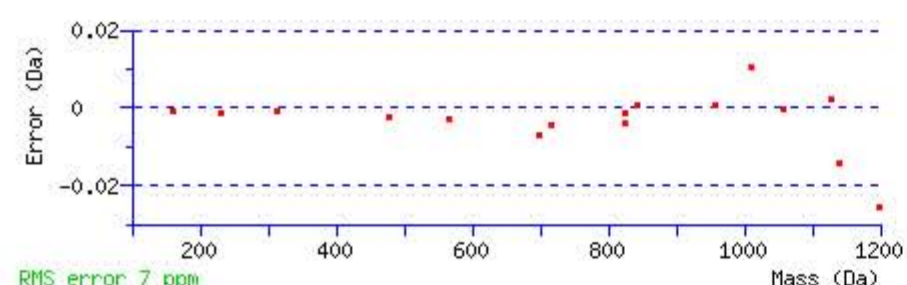
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 0.00044

Matches : 16/84 fragment ions using 23 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							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
45.8	1285.669998	-0.001390	SAATLQQEK
34.7	1285.669998	-0.001390	SAATLQQEK
9.4	1285.652237	0.016371	AMQIQEQK
6.8	1285.669998	-0.001390	ASLDQGKEK
6.2	1285.651367	0.017241	LLQAVENGDAEK
4.9	1285.658752	0.009856	IESLEQEK
4.9	1285.658768	0.009840	VTELEQEK
4.2	1285.649582	0.019026	SVPCPRCVR
3.4	1285.673859	-0.005251	NDVGGQRSLV
1.5	1285.687759	-0.019151	LKTGPEGALGSEK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SQETGDLVGGGLQETDK**

Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

Match to Query 49236: 2101.994322 from(701.672050,3+) rtinseconds(2020) index(36509)

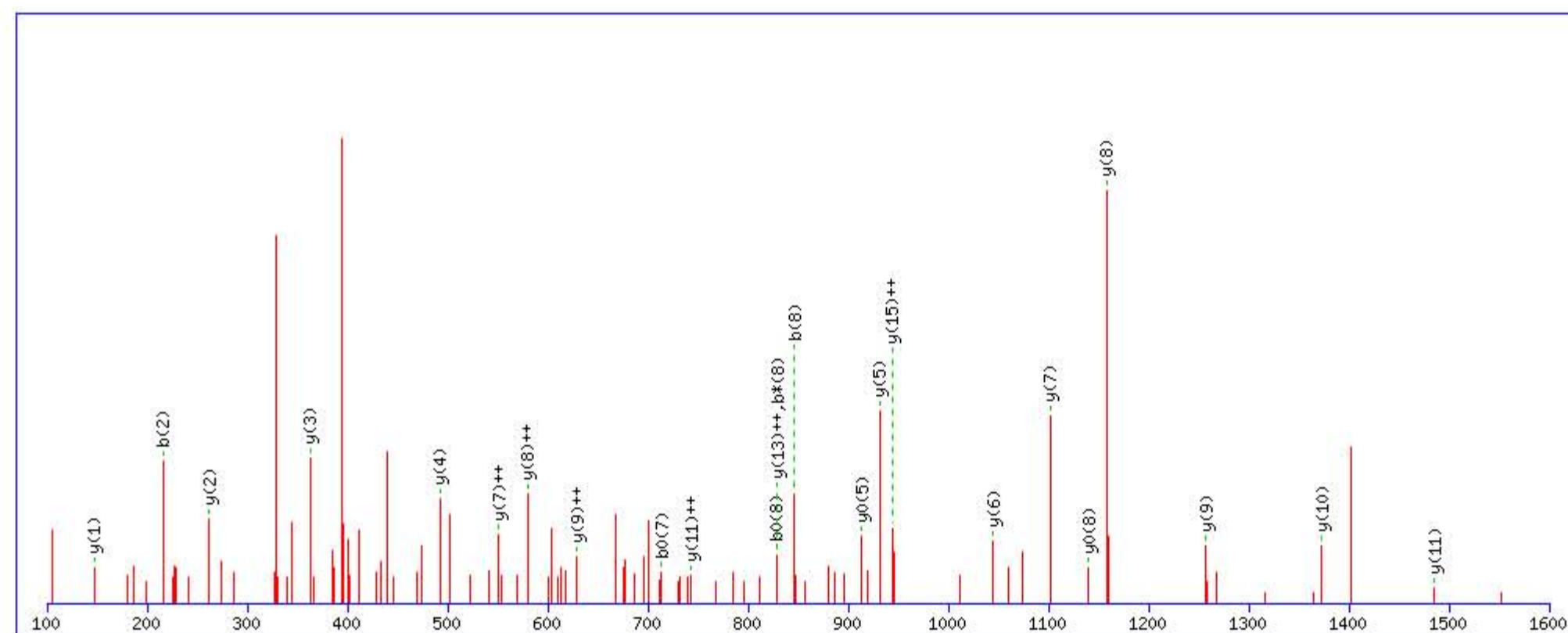
Title: Locus:1.1.1.3123.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2101.983780

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

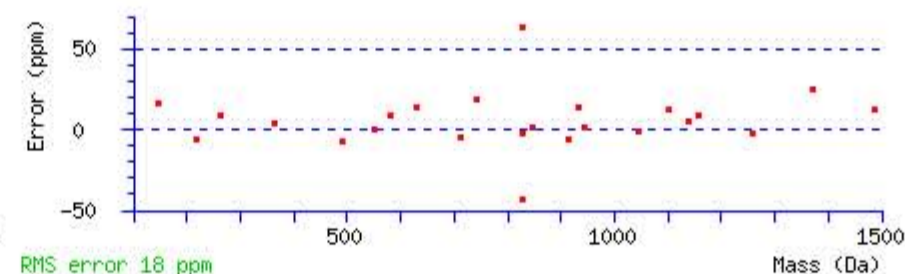
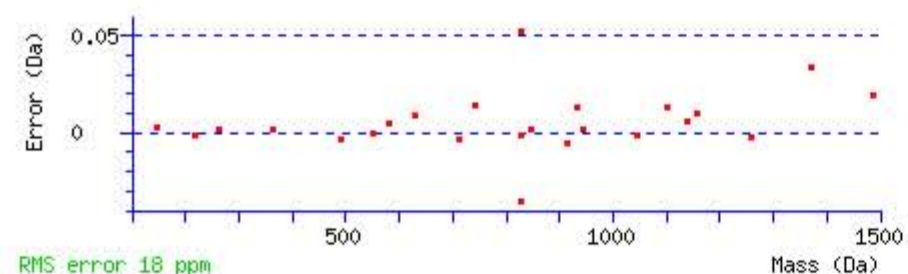
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 4e-006

Matches : 24/188 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 [SQETGDLVGGGLQETDK](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.5	2101.983780	0.010542	SQETGDLVGGGLQETDK

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

MASCOT Search Results

Peptide View

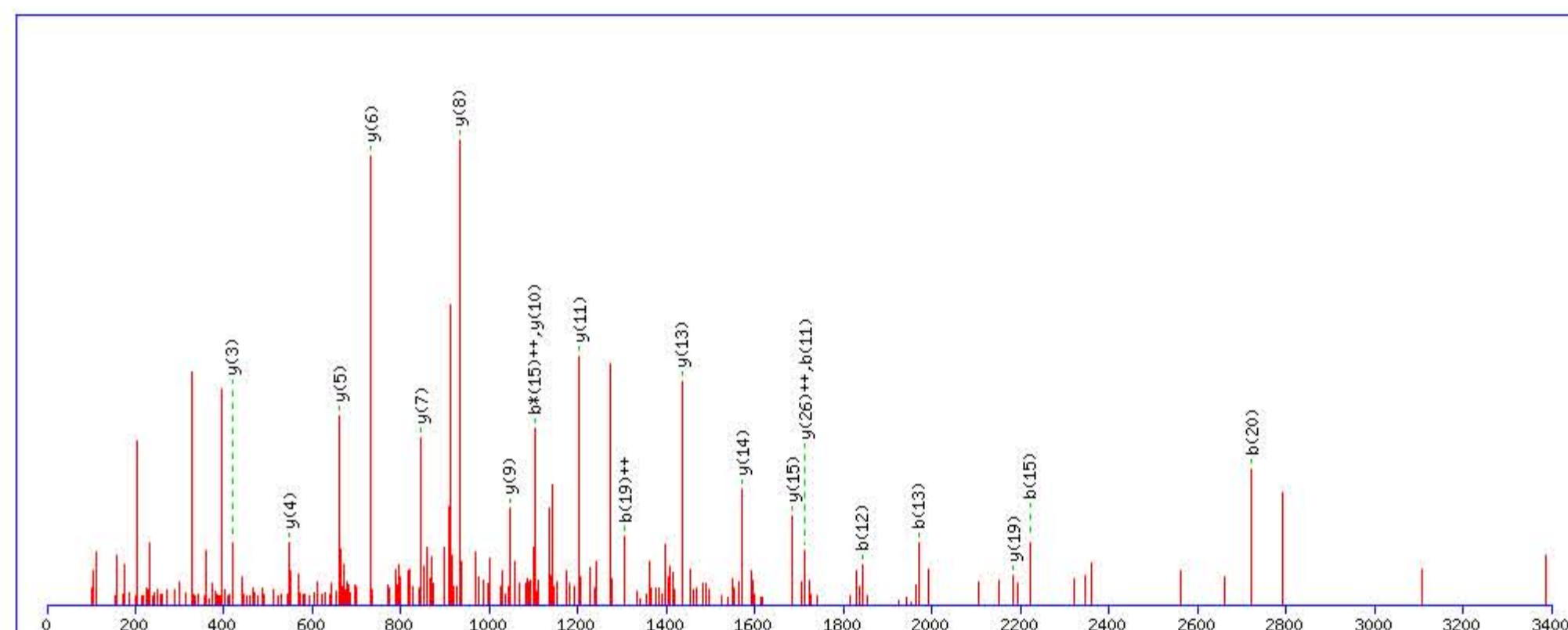
MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
 Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

Match to Query 68188: 3653.633456 from(914.415640,4+) rtinseconds(1976) index(36275)
 Title: Locus:1.1.1.3107.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

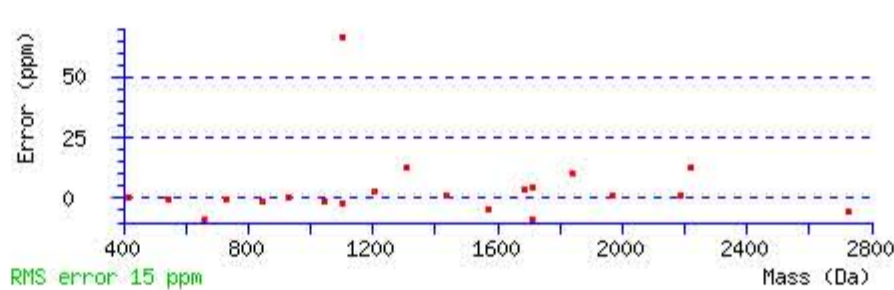
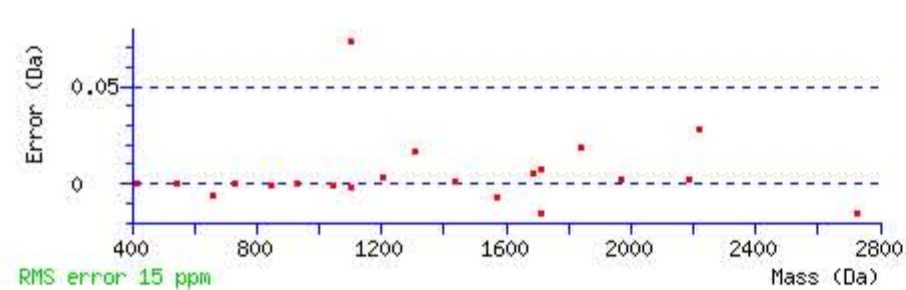
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3653.615311
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q5 : Biotin:Thermo-21345 (Q)
 Ions Score: 85 Expect: 2.9e-008
 Matches : 21/312 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	132.047761	66.527518					M							28
2	231.116175	116.061725					V	3523.582122	1762.294699	3506.555573	1753.781424	3505.571557	1753.289416	27
3	359.174753	180.091015	342.148204	171.577740			Q	3424.513708	1712.760492	3407.487159	1704.247217	3406.503143	1703.755209	26
4	488.217346	244.612311	471.190797	236.099037	470.206781	235.607029	E	3296.455130	1648.731203	3279.428581	1640.217928	3278.444565	1639.725920	25
5	927.442672	464.224974	910.416123	455.711700	909.432107	455.219692	Q	3167.412537	1584.209906	3150.385988	1575.696632	3149.401972	1575.204624	24
6	1087.473321	544.240298	1070.446772	535.727024	1069.462756	535.235016	C	2728.187211	1364.597243	2711.160662	1356.083969	2710.176646	1355.591961	23
7	1247.503970	624.255623	1230.477421	615.742349	1229.493405	615.250340	C	2568.156562	1284.581919	2551.130013	1276.068644	2550.145997	1275.576636	22
8	1384.562882	692.785079	1367.536333	684.271805	1366.552317	683.779796	H	2408.125913	1204.566594	2391.099364	1196.053320	2390.115348	1195.561312	21
9	1471.594910	736.301093	1454.568361	727.787819	1453.584345	727.295811	S	2271.067001	1136.037138	2254.040452	1127.523864	2253.056436	1127.031856	20
10	1599.653488	800.330382	1582.626939	791.817108	1581.642923	791.325100	Q	2184.034973	1092.521124	2167.008424	1084.007850	2166.024408	1083.515842	19
11	1712.737552	856.872414	1695.711003	848.359140	1694.726987	847.867132	L	2055.976395	1028.491835	2038.949846	1019.978561	2037.965830	1019.486553	18
12	1841.780145	921.393711	1824.753596	912.880436	1823.769580	912.388428	E	1942.892331	971.949804	1925.865782	963.436529	1924.881766	962.944521	17
13	1970.822738	985.915007	1953.796189	977.401733	1952.812173	976.909725	E	1813.849738	907.428507	1796.823189	898.915233	1795.839173	898.423225	16
14	2083.906802	1042.457039	2066.880253	1033.943764	2065.896237	1033.451756	L	1684.807145	842.907211	1667.780596	834.393936	1666.796580	833.901928	15
15	2220.965714	1110.986495	2203.939165	1102.473220	2202.955149	1101.981212	H	1571.723081	786.365179	1554.696532	777.851904	1553.712516	777.359896	14
16	2380.996363	1191.001819	2363.969814	1182.488545	2362.985798	1181.996537	C	1434.664169	717.835723	1417.637620	709.322448	1416.653604	708.830440	13
17	2452.033477	1226.520376	2435.006928	1218.007102	2434.022912	1217.515094	A	1274.633520	637.820398	1257.606971	629.307124	1256.622955	628.815116	12
18	2553.081156	1277.044216	2536.054607	1268.530941	2535.070591	1268.038933	T	1203.596406	602.301841	1186.569857	593.788567	1185.585841	593.296559	11
19	2610.102620	1305.554948	2593.076071	1297.041673	2592.092055	1296.549665	G	1102.548727	551.778002	1085.522178	543.264727	1084.538162	542.772719	10
20	2723.186684	1362.096980	2706.160135	1353.583705	2705.176119	1353.091697	I	1045.527263	523.267270	1028.500714	514.753995	1027.516698	514.261987	9
21	2810.218712	1405.612994	2793.192163	1397.099719	2792.208147	1396.607711	S	932.443199	466.725238	915.416650	458.211963	914.432634	457.719955	8
22	2923.302776	1462.155026	2906.276227	1453.641751	2905.292211	1453.149743	L	845.411171	423.209224	828.384622	414.695949	827.400606	414.203941	7
23	2994.339890	1497.673583	2977.313341	1489.160308	2976.329325	1488.668301	A	732.327107	366.667192	715.300558	358.153917	714.316542	357.661909	6
24	3108.382817	1554.695047	3091.356268	1546.181772	3090.372252	1545.689764	N	661.289993	331.148635	644.263444	322.635360	643.279428	322.143352	5
25	3237.425410	1619.216343	3220.398861	1610.703069	3219.414845	1610.211061	E	547.247066	274.127171	530.220517	265.613897	529.236501	265.121889	4
26	3365.483988	1683.245632	3348.457439	1674.732358	3347.473423	1674.240350	Q	418.204473	209.605874	401.177924	201.092600	400.193908	200.600592	3
27	3480.510931	1740.759104	3463.484382	1732.245829	3462.500366	1731.753821	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
28							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
84.9	3653.615311	0.018145	MVQEQCCHSQLEELHCATGISLANEQDR
84.9	3653.615311	0.018145	MVQEQCCHSQLEELHCATGISLANEQDR
72.2	3653.615311	0.018145	MVQEQCCHSQLEELHCATGISLANEQDR

MASCOT Search Results

Peptide View

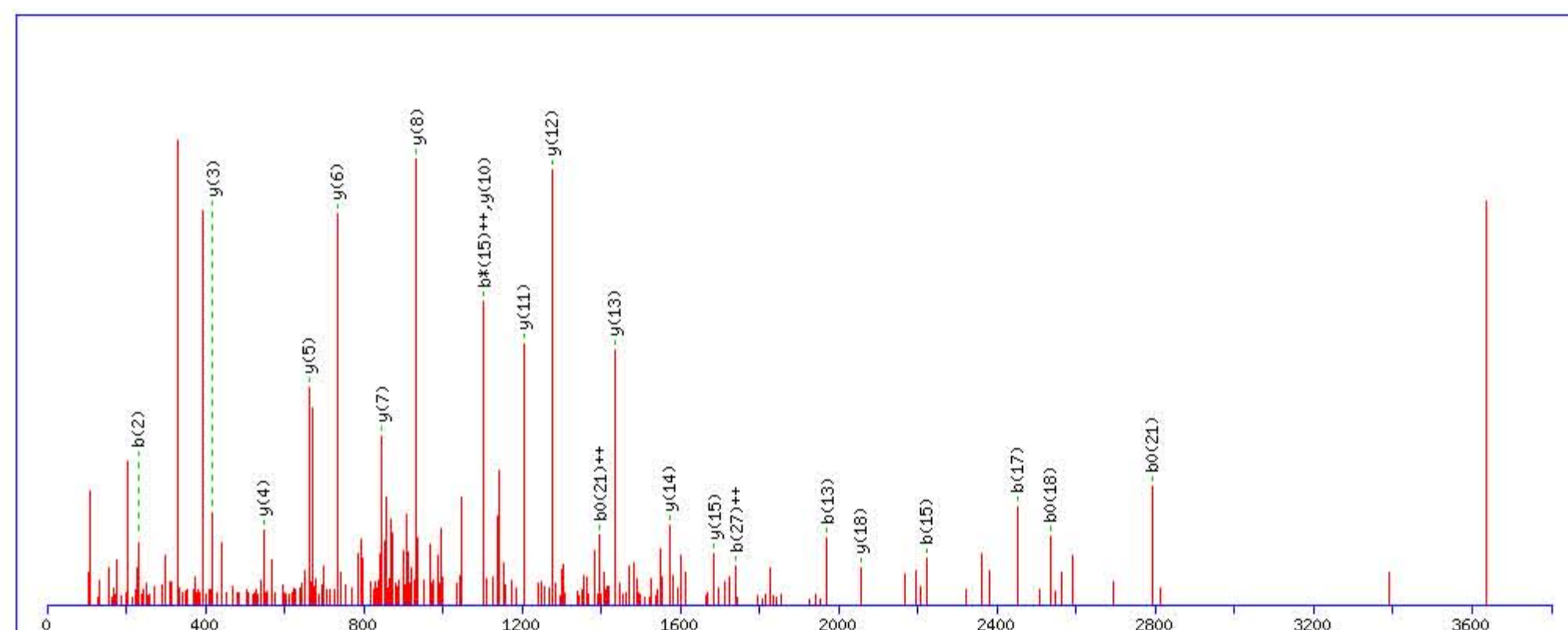
MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
 Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

Match to Query 68189: 3653.633456 from(914.415640,4+) rtinseconds(1985) index(36317)
 Title: Locus:1.1.1.3110.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

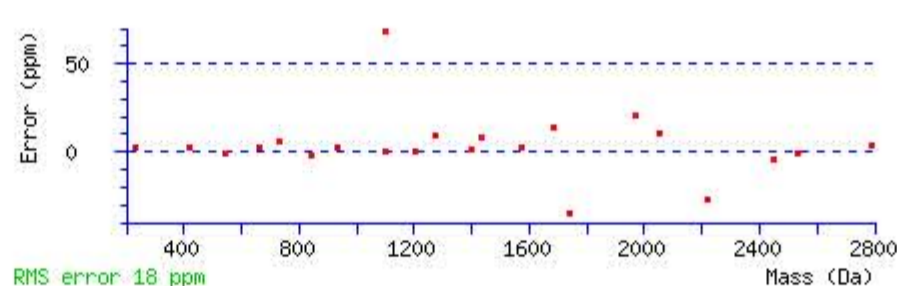
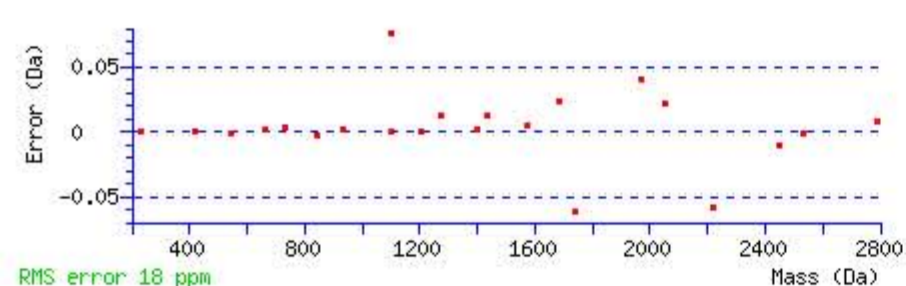
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3653.615311
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q10 : Biotin:Thermo-21345 (Q)
 Ions Score: 87 Expect: 2e-008
 Matches : 22/312 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	132.047761	66.527518					M							28
2	231.116175	116.061725					V	3523.582122	1762.294699	3506.555573	1753.781424	3505.571557	1753.289416	27
3	359.174753	180.091015	342.148204	171.577740			Q	3424.513708	1712.760492	3407.487159	1704.247217	3406.503143	1703.755209	26
4	488.217346	244.612311	471.190797	236.099037	470.206781	235.607029	E	3296.455130	1648.731203	3279.428581	1640.217928	3278.444565	1639.725920	25
5	616.275924	308.641600	599.249375	300.128326	598.265359	299.636318	Q	3167.412537	1584.209906	3150.385988	1575.696632	3149.401972	1575.204624	24
6	776.306573	388.656925	759.280024	380.143650	758.296008	379.651642	C	3039.353959	1520.180617	3022.327410	1511.667343	3021.343394	1511.175335	23
7	936.337222	468.672249	919.310673	460.158975	918.326657	459.666967	C	2879.323310	1440.165293	2862.296761	1431.652018	2861.312745	1431.160010	22
8	1073.396134	537.201705	1056.369585	528.688431	1055.385569	528.196423	H	2719.292661	1360.149968	2702.266112	1351.636694	2701.282096	1351.144686	21
9	1160.428162	580.717719	1143.401613	572.204445	1142.417597	571.712437	S	2582.233749	1291.620512	2565.207200	1283.107238	2564.223184	1282.615230	20
10	1599.653488	800.330382	1582.626939	791.817108	1581.642923	791.325100	Q	2495.201721	1248.104498	2478.175172	1239.591224	2477.191156	1239.099216	19
11	1712.737552	856.872414	1695.711003	848.359140	1694.726987	847.867132	L	2055.976395	1028.491835	2038.949846	1019.978561	2037.965830	1019.486553	18
12	1841.780145	921.393711	1824.753596	912.880436	1823.769580	912.388428	E	1942.892331	971.949804	1925.865782	963.436529	1924.881766	962.944521	17
13	1970.822738	985.915007	1953.796189	977.401733	1952.812173	976.909725	E	1813.849738	907.428507	1796.823189	898.915233	1795.839173	898.423225	16
14	2083.906802	1042.457039	2066.880253	1033.943764	2065.896237	1033.451756	L	1684.807145	842.907211	1667.780596	834.393936	1666.796580	833.901928	15
15	2220.965714	1110.986495	2203.939165	1102.473220	2202.955149	1101.981212	H	1571.723081	786.365179	1554.696532	777.851904	1553.712516	777.359896	14
16	2380.996363	1191.001819	2363.969814	1182.488545	2362.985798	1181.996537	C	1434.664169	717.835723	1417.637620	709.322448	1416.653604	708.830440	13
17	2452.033477	1226.520376	2435.006928	1218.007102	2434.022912	1217.515094	A	1274.633520	637.820398	1257.606971	629.307124	1256.622955	628.815116	12
18	2553.081156	1277.044216	2536.054607	1268.530941	2535.070591	1268.038933	T	1203.596406	602.301841	1186.569857	593.788567	1185.585841	593.296559	11
19	2610.102620	1305.554948	2593.076071	1297.041673	2592.092055	1296.549665	G	1102.548727	551.778002	1085.522178	543.264727	1084.538162	542.772719	10
20	2723.186684	1362.096980	2706.160135	1353.583705	2705.176119	1353.091697	I	1045.527263	523.267270	1028.500714	514.753995	1027.516698	514.261987	9
21	2810.218712	1405.612994	2793.192163	1397.099719	2792.208147	1396.607711	S	932.443199	466.725238	915.416650	458.211963	914.432634	457.719955	8
22	2923.302776	1462.155026	2906.276227	1453.641751	2905.292211	1453.149743	L	845.411171	423.209224	828.384622	414.695949	827.400606	414.203941	7
23	2994.339890	1497.673583	2977.313341	1489.160308	2976.329325	1488.668301	A	732.327107	366.667192	715.300558	358.153917	714.316542	357.661909	6
24	3108.382817	1554.695047	3091.356268	1546.181772	3090.372252	1545.689764	N	661.289993	331.148635	644.263444	322.635360	643.279428	322.143352	5
25	3237.425410	1619.216343	3220.398861	1610.703069	3219.414845	1610.211061	E	547.247066	274.127171	530.220517	265.613897	529.236501	265.121889	4
26	3365.483988	1683.245632	3348.457439	1674.732358	3347.473423	1674.240350	Q	418.204473	209.605874	401.177924	201.092600	400.193908	200.600592	3
27	3480.510931	1740.759104	3463.484382	1732.245829	3462.500366	1731.753821	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
28							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
86.5	3653.615311	0.018145	MVQEQCCHSQLEELHCATGISLANEQDR
86.5	3653.615311	0.018145	MVQEQCCHSQLEELHCATGISLANEQDR
86.5	3653.615311	0.018145	MVQEQCCHSQLEELHCATGISLANEQDR

MASCOT Search Results

Peptide View

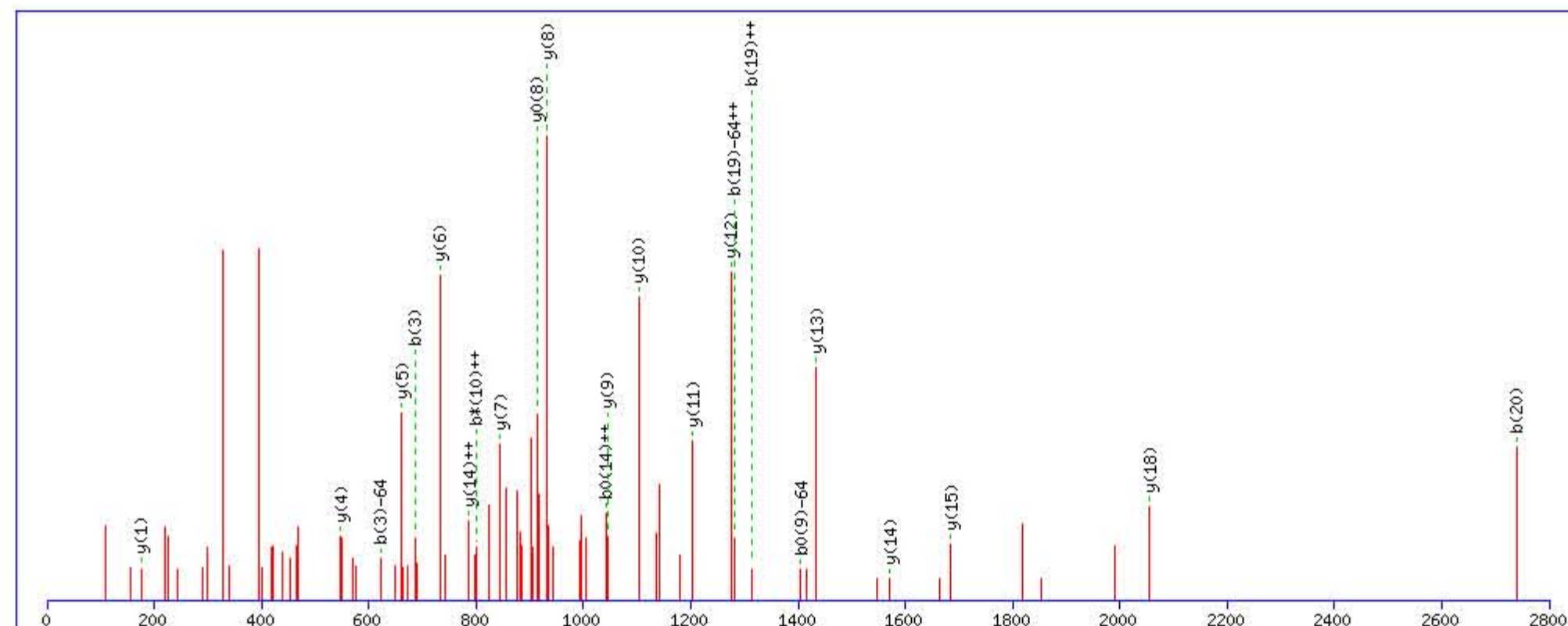
MS/MS Fragmentation of **MVQEQCCHSQLEELHLCATGISLANEQDR**
 Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

Match to Query 68294: 3669.620416 from(918.412380,4+) rtinseconds(1915) index(35793)
 Title: Locus:1.1.1.3086.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

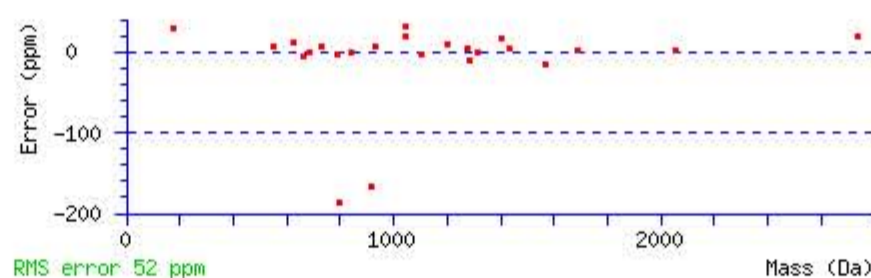
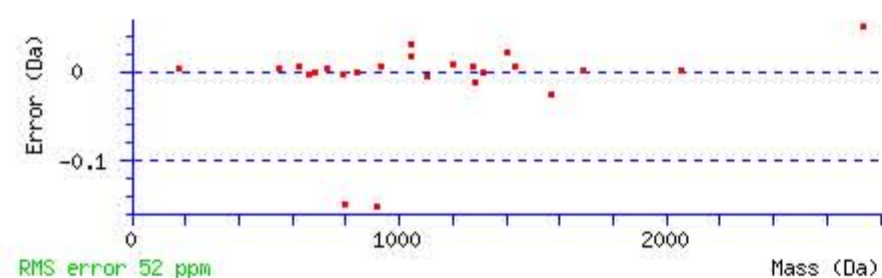
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3669.610229
 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: 63 Expect: 2.6e-006
 Matches : 24/464 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	148.042676	74.524976					M							28
2	247.111090	124.059183					V	3523.582122	1762.294699	3506.555573	1753.781425	3505.571557	1753.289417	27
3	686.336416	343.671846	669.309867	335.158572			Q	3424.513708	1712.760492	3407.487159	1704.247217	3406.503143	1703.755209	26
4	815.379009	408.193143	798.352460	399.679868	797.368444	399.187860	E	2985.288382	1493.147829	2968.261833	1484.634554	2967.277817	1484.142547	25
5	943.437587	472.222432	926.411038	463.709157	925.427022	463.217149	Q	2856.245789	1428.626532	2839.219240	1420.113258	2838.235224	1419.621250	24
6	1103.468236	552.237756	1086.441687	543.724482	1085.457671	543.232474	C	2728.187211	1364.597243	2711.160662	1356.083969	2710.176646	1355.591961	23
7	1263.498885	632.253081	1246.472336	623.739806	1245.488320	623.247798	C	2568.156562	1284.581919	2551.130013	1276.068644	2550.145997	1275.576636	22
8	1400.557797	700.782537	1383.531248	692.269262	1382.547232	691.777254	H	2408.125913	1204.566594	2391.099364	1196.053320	2390.115348	1195.561312	21
9	1487.589825	744.298551	1470.563276	735.785276	1469.579260	735.293268	S	2271.067001	1136.037138	2254.040452	1127.523864	2253.056436	1127.031856	20
10	1615.648403	808.327840	1598.621854	799.814565	1597.637838	799.322557	Q	2184.034973	1092.521124	2167.008424	1084.007850	2166.024408	1083.515842	19
11	1728.732467	864.869872	1711.705918	856.356597	1710.721902	855.864589	L	2055.976395	1028.491835	2038.949846	1019.978561	2037.965830	1019.486553	18
12	1857.775060	929.391168	1840.748511	920.877894	1839.764495	920.385886	E	1942.892331	971.949804	1925.865782	963.436529	1924.881766	962.944521	17
13	1986.817653	993.912465	1969.791104	985.399190	1968.807088	984.907182	E	1813.849738	907.428507	1796.823189	898.915233	1795.839173	898.423225	16
14	2099.901717	1050.454497	2082.875168	1041.941222	2081.891152	1041.449214	L	1684.807145	842.907211	1667.780596	834.393936	1666.796580	833.901928	15
15	2236.960629	1118.983953	2219.934080	1110.470678	2218.950064	1109.978670	H	1571.723081	786.365179	1554.696532	777.851904	1553.712516	777.359896	14
16	2396.991278	1198.999277	2379.964729	1190.486002	2378.980713	1189.993994	C	1434.664169	717.835723	1417.637620	709.322448	1416.653604	708.830440	13
17	2468.028392	1234.517834	2451.001843	1226.004559	2450.017827	1225.512552	A	1274.633520	637.820398	1257.606971	629.307124	1256.622955	628.815116	12
18	2569.076071	1285.041673	2552.049522	1276.528399	2551.065506	1276.036391	T	1203.596406	602.301841	1186.569857	593.788567	1185.585841	593.296559	11
19	2626.097535	1313.552405	2609.070986	1305.039131	2608.086970	1304.547123	G	1102.548727	551.778002	1085.522178	543.264727	1084.538162	542.772719	10
20	2739.181599	1370.094437	2722.155050	1361.581163	2721.171034	1361.089155	I	1045.527263	523.267270	1028.500714	514.753995	1027.516698	514.261987	9
21	2826.213627	1413.610452	2809.187078	1405.097177	2808.203062	1404.605169	S	932.443199	466.725238	915.416650	458.211963	914.432634	457.719955	8
22	2939.297691	1470.152484	2922.271142	1461.639209	2921.287126	1461.147201	L	845.411171	423.209224	828.384622	414.695949	827.400606	414.203941	7
23	3010.334805	1505.671041	2993.308256	1497.157766	2992.324240	1496.665758	A	732.327107	366.667192	715.300558	358.153917	714.316542	357.661909	6
24	3124.377732	1562.692504	3107.351183	1554.179230	3106.367167	1553.687222	N	661.289993	331.148635	644.263444	322.635360	643.279428	322.143352	5
25	3253.420325	1627.213801	3236.393776	1618.700526	3235.409760	1618.208518	E	547.247066	274.127171	530.220517	265.613897	529.236501	265.121889	4
26	3381.478903	1691.243090	3364.452354	1682.729815	3363.468338	1682.237807	Q	418.204473	209.605874	401.177924	201.092600	400.193908	200.600592	3
27	3496.505846	1748.756561	3479.479297	1740.243287	3478.495281	1739.751279	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 **MVQEQCCHSQLEELHLCATGISLANEQDR**
 (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	3669.610229	0.010187	MVQEQCCHSQLEELHLCATGISLANEQDR
61.3	3669.610229	0.010187	MVQEQCCHSQLEELHLCATGISLANEQDR
61.3	3669.610229	0.010187	MVQEQCCHSQLEELHLCATGISLANEQDR

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELSEALGQIFDSQR**

Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

Match to Query 25306: 1902.969342 from(635.330390,3+) rtinseconds(2718) index(57151)

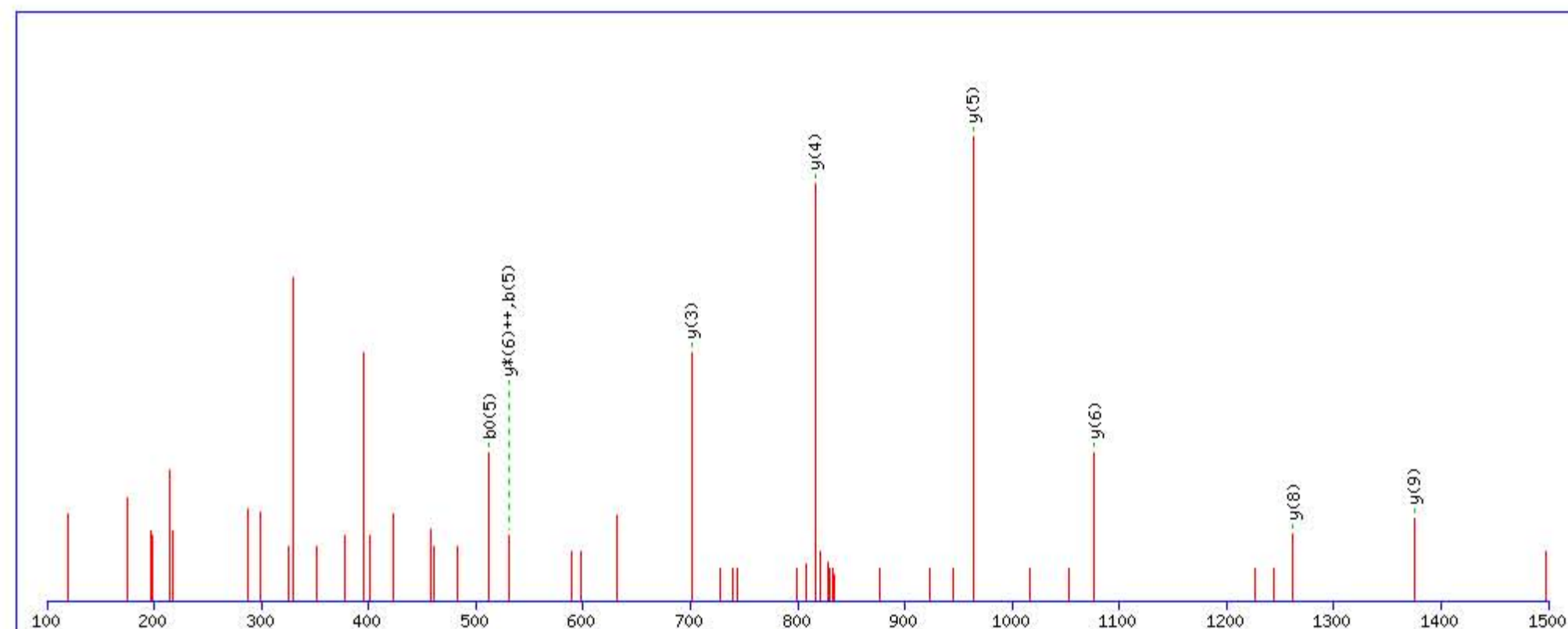
Title: Locus:1.1.1.1561.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1902.950928

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

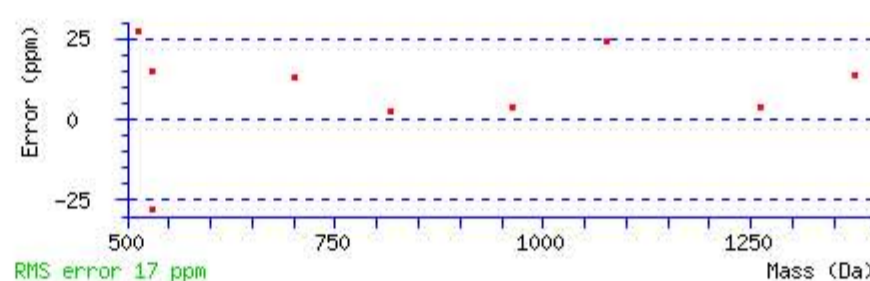
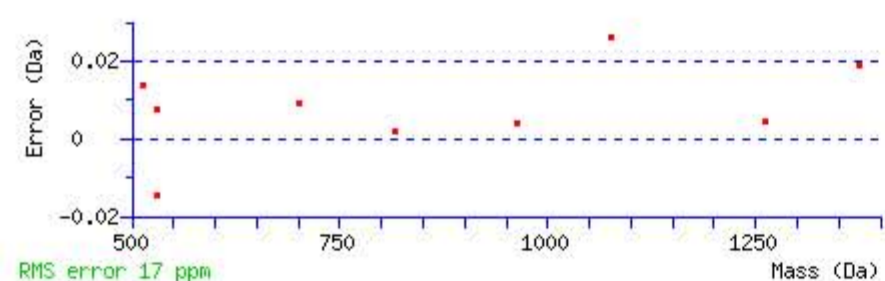
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.017

Matches : 9/138 fragment ions using 13 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							14
2	243.133933	122.070605			225.123368	113.065322	L	1774.915632	887.961454	1757.889083	879.448180	1756.905067	878.956172	13
3	330.165961	165.586618			312.155396	156.581336	S	1661.831568	831.419422	1644.805019	822.906148	1643.821003	822.414140	12
4	459.208554	230.107915			441.197989	221.102633	E	1574.799540	787.903408	1557.772991	779.390134	1556.788975	778.898126	11
5	530.245668	265.626472			512.235103	256.621190	A	1445.756947	723.382112	1428.730398	714.868837	1427.746382	714.376829	10
6	643.329732	322.168504			625.319167	313.163222	L	1374.719833	687.863555	1357.693284	679.350280	1356.709268	678.858272	9
7	700.351196	350.679236			682.340631	341.673954	G	1261.635769	631.321523	1244.609220	622.808248	1243.625204	622.316240	8
8	828.409774	414.708525	811.383225	406.195251	810.399209	405.703243	Q	1204.614305	602.810791	1187.587756	594.297516	1186.603740	593.805508	7
9	941.493838	471.250557	924.467289	462.737283	923.483273	462.245275	I	1076.555727	538.781502	1059.529178	530.268227	1058.545162	529.776219	6
10	1088.562252	544.784764	1071.535703	536.271490	1070.551687	535.779482	F	963.471663	482.239470	946.445114	473.726195	945.461098	473.234187	5
11	1203.589195	602.298236	1186.562646	593.784961	1185.578630	593.292953	D	816.403249	408.705263	799.376700	400.191988	798.392684	399.699980	4
12	1290.621223	645.814250	1273.594674	637.300975	1272.610658	636.808967	S	701.376306	351.191791	684.349757	342.678517	683.365741	342.186509	3
13	1729.846549	865.426913	1712.820000	856.913638	1711.835984	856.421630	Q	614.344278	307.675777	597.317729	299.162503			2
14							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **ELSEALGQIFDSQR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.6	1902.950928	0.018414	ELSEALGQIFDSQR
16.8	1902.947739	0.021603	MKEQLREMNLR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **KSQLVYQSR**

Found in **LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

Match to Query 31206: 1418.773788 from(710.394170,2+) rtinseconds(1542) index(49818)

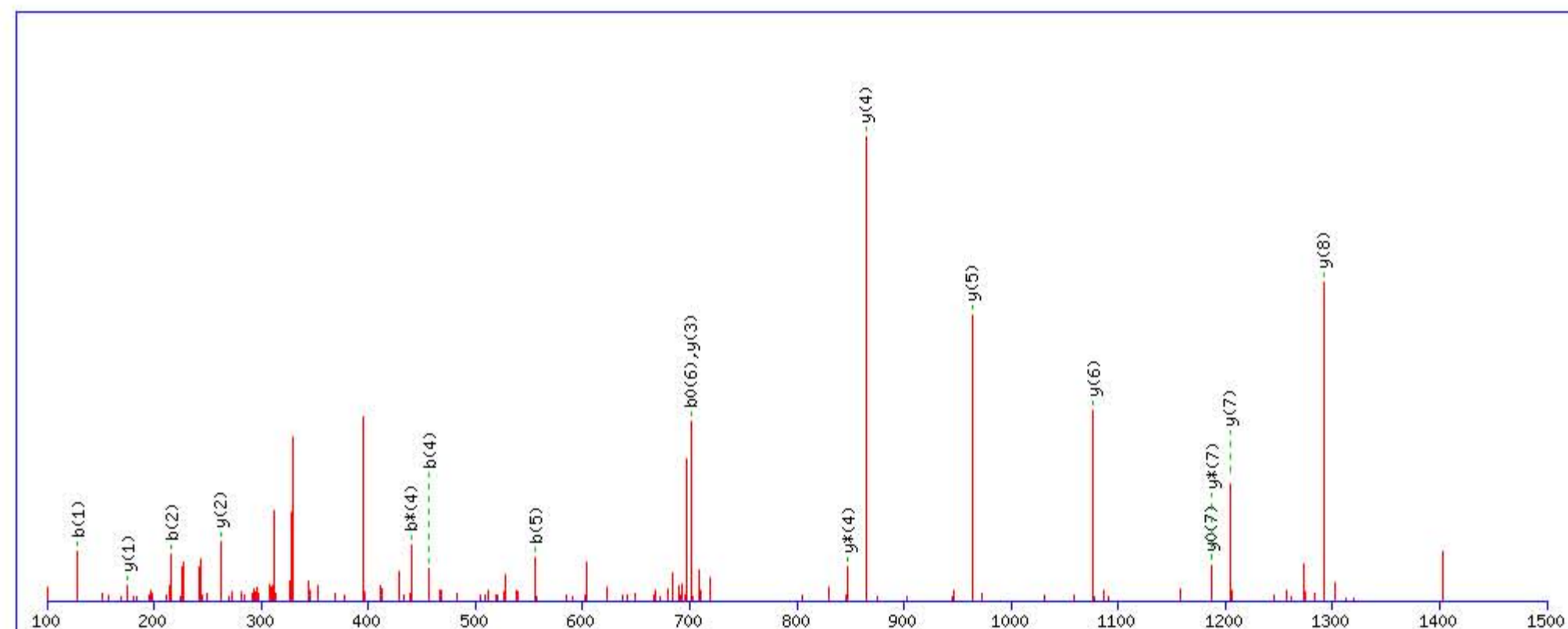
Title: Locus:1.1.1.1152.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1418.770386

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

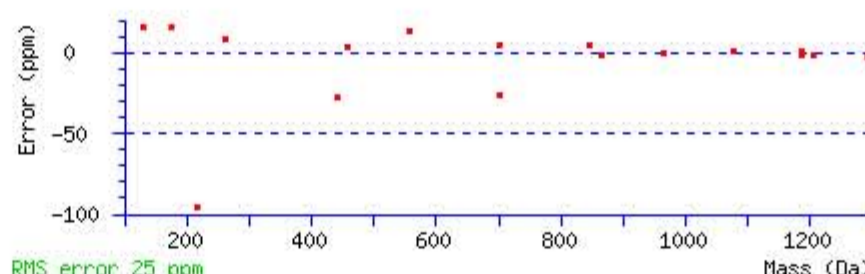
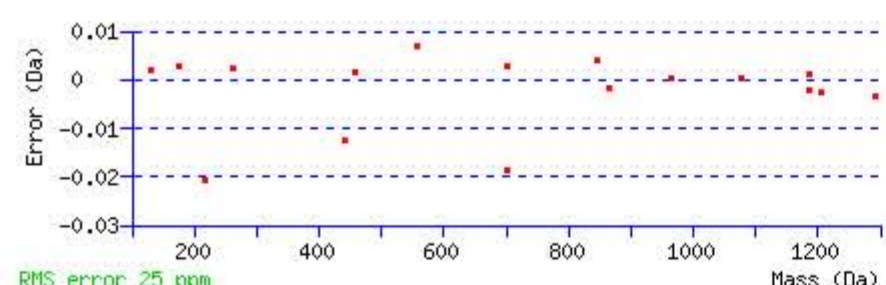
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 4e-005

Matches : 17/92 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	129.102239	65.054757	112.075690	56.541483			K							9
2	216.134267	108.570771	199.107718	100.057497	198.123702	99.565489	S	1291.682719	646.344998	1274.656170	637.831723	1273.672154	637.339715	8
3	344.192845	172.600060	327.166296	164.086786	326.182280	163.594778	Q	1204.650691	602.828984	1187.624142	594.315709	1186.640126	593.823701	7
4	457.276909	229.142092	440.250360	220.628818	439.266344	220.136810	L	1076.592113	538.799695	1059.565564	530.286420	1058.581548	529.794412	6
5	556.345323	278.676300	539.318774	270.163025	538.334758	269.671017	V	963.508049	482.257663	946.481500	473.744388	945.497484	473.252380	5
6	719.408652	360.207964	702.382103	351.694690	701.398087	351.202682	Y	864.439635	432.723456	847.413086	424.210181	846.429070	423.718173	4
7	1158.633978	579.820627	1141.607429	571.307353	1140.623413	570.815345	Q	701.376306	351.191791	684.349757	342.678517	683.365741	342.186509	3
8	1245.666006	623.336641	1228.639457	614.823367	1227.655441	614.331359	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
9							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **KSQLVYQSR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.5	1418.770386	0.003402	KSQLVYQSR
9.2	1418.780273	-0.006485	TNQLMETLKTIK
8.7	1418.770386	0.003402	KSQLVYQSR
4.9	1418.788147	-0.014359	QSQVDRLYVALK
4.6	1418.787659	-0.013871	KEILLAMLVVDK
2.6	1418.776886	-0.003098	EKAKALEDLAGFK
2.6	1418.787659	-0.013871	KEILLAMLVVDK

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

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 44729: 1908.850168 from(955.432360,2+) rtinseconds(2123) index(53719)

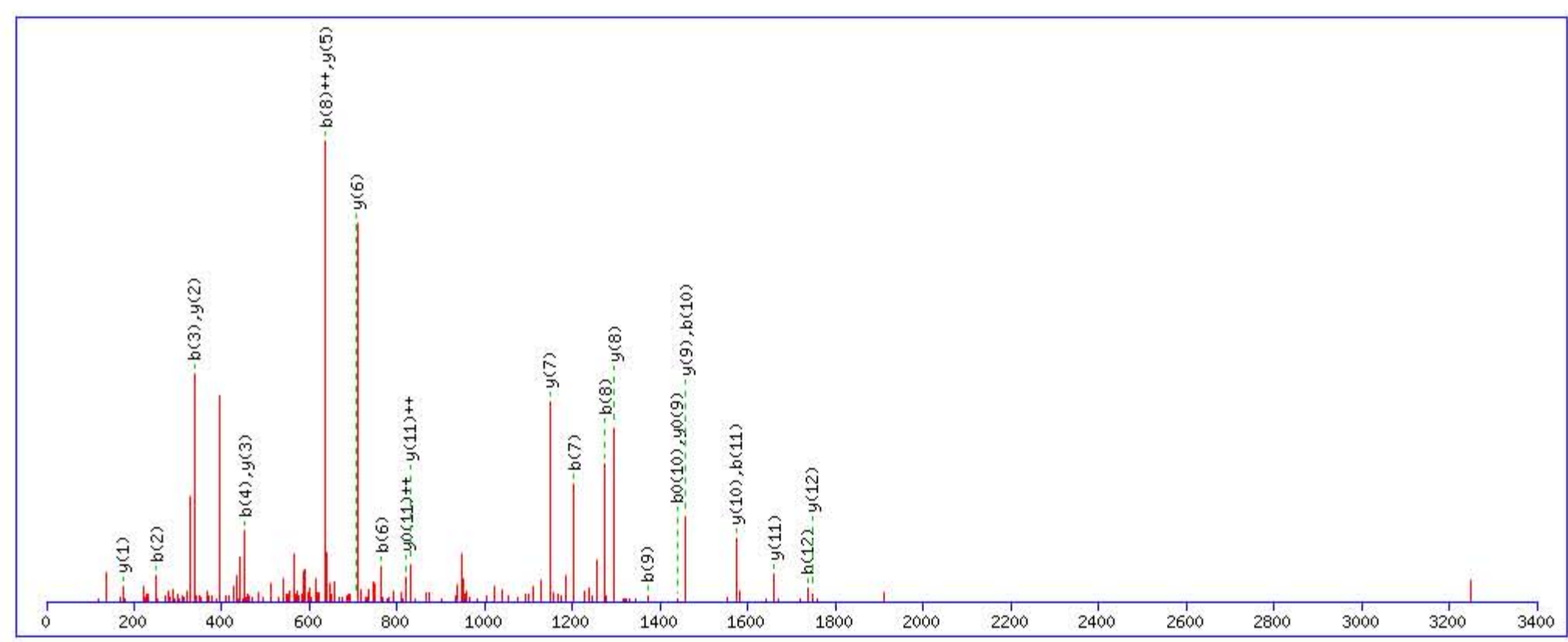
Title: Locus:1.1.1.1354.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1908.835236

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

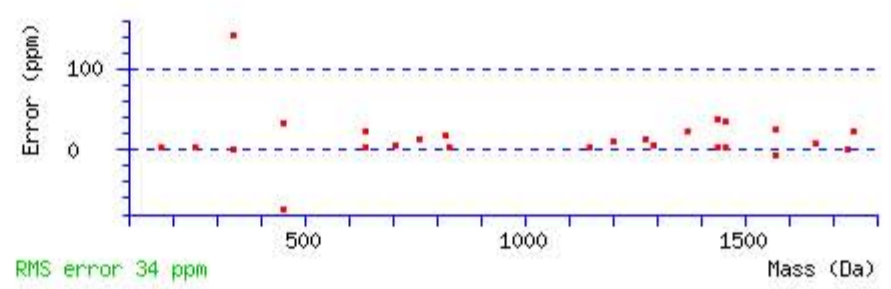
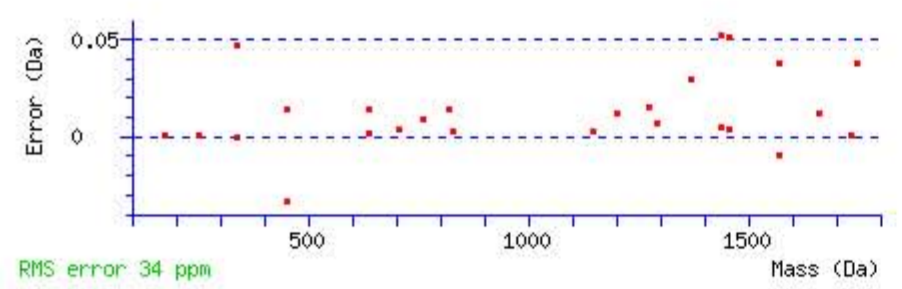
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 77 Expect: 1.5e-007

Matches : 26/126 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
76.9	1908.835236	0.014932	YSSDYFQAPSDYR

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **TGAQELLR**

Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

Match to Query 23272: 1197.656788 from(599.835670,2+) rtinseconds(1892) index(5149)

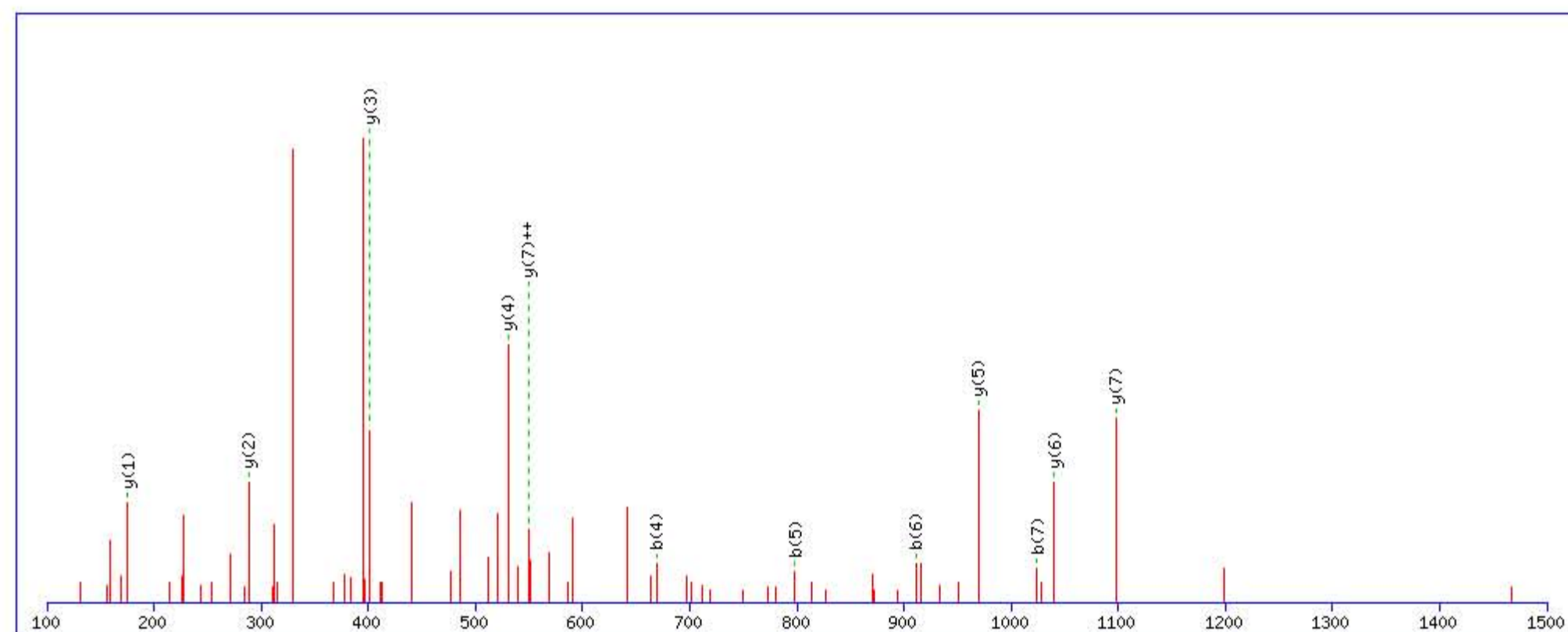
Title: Locus:1.1.1.1468.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1197.653961

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

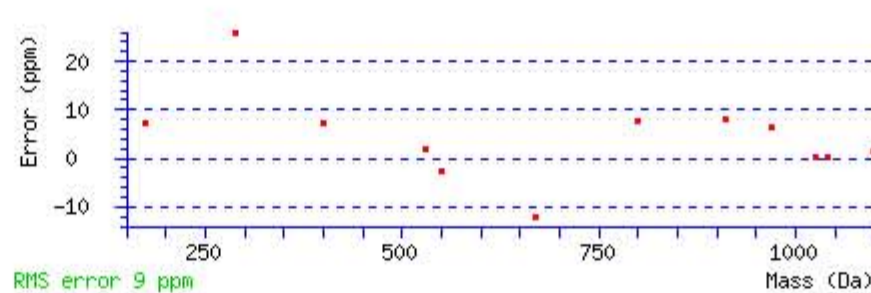
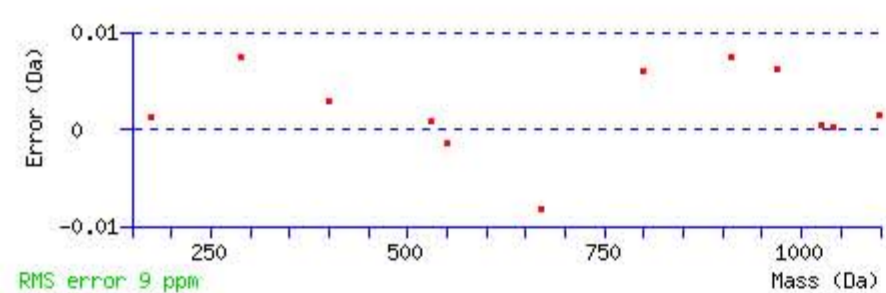
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 49 Expect: 0.00032

Matches : 12/72 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	102.054955	51.531116			84.044390	42.525833	T							8
2	159.076419	80.041847			141.065854	71.036565	G	1097.613577	549.310427	1080.587028	540.797152	1079.603012	540.305144	7
3	230.113533	115.560404			212.102968	106.555122	A	1040.592113	520.799695	1023.565564	512.286420	1022.581548	511.794412	6
4	669.338859	335.173068	652.312310	326.659793	651.328294	326.167785	Q	969.554999	485.281138	952.528450	476.767863	951.544434	476.275855	5
5	798.381452	399.694364	781.354903	391.181090	780.370887	390.689082	E	530.329673	265.668475	513.303124	257.155200	512.319108	256.663192	4
6	911.465516	456.236396	894.438967	447.723122	893.454951	447.231114	L	401.287080	201.147178	384.260531	192.633903			3
7	1024.549580	512.778428	1007.523031	504.265153	1006.539015	503.773145	L	288.203016	144.605146	271.176467	136.091871			2
8							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [TGAQELLR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.9	1197.653961	0.002827	TGAQELLR
25.2	1197.653961	0.002827	QTQEILR
23.5	1197.653961	0.002827	QTQEILR
18.2	1197.653961	0.002827	TQQLLR
16.0	1197.646545	0.010243	RSPQAEILR
15.6	1197.671692	-0.014904	LGLNAAEALIR
12.7	1197.653961	0.002827	QTEQLLR
11.8	1197.669220	-0.012432	TLWAQLR
11.5	1197.640045	0.016743	QCQLQRPLR
11.4	1197.653961	0.002827	QTEQLLR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GASQAGAPQGR**

Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

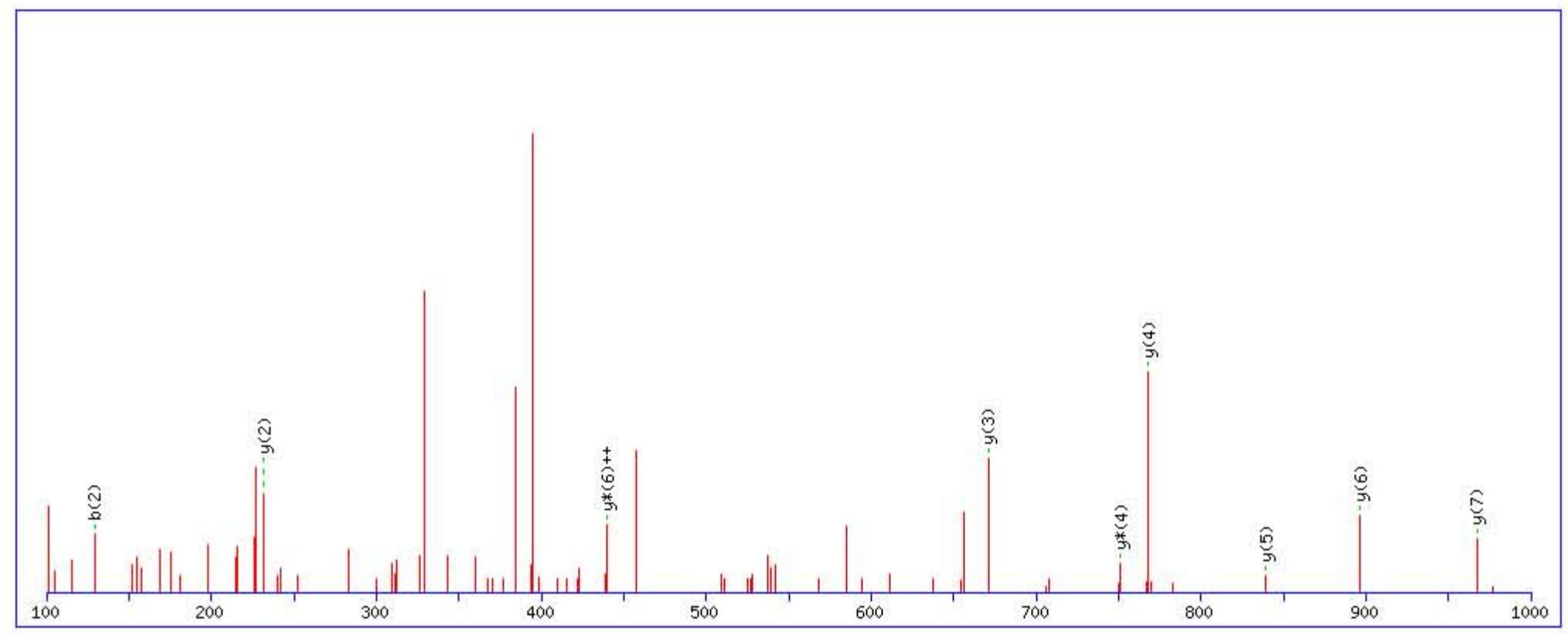
Match to Query 26389: 1309.653792 from(437.558540,3+) rtinseconds(1258) index(1377)
 Title: Locus:1.1.1.1247.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1309.656097

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

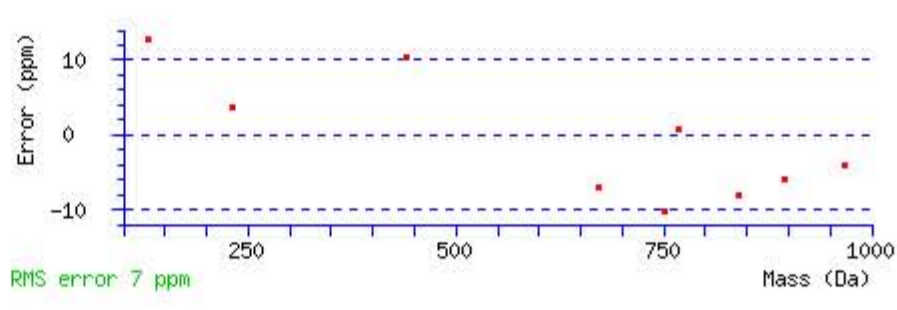
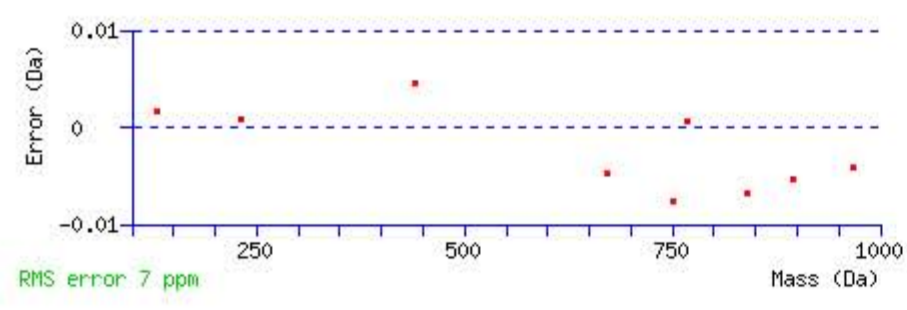
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 29 Expect: 0.0047

Matches : 9/94 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							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
29.3	1309.656097	-0.002305	GASQAGAPQGR
23.7	1309.656097	-0.002305	GASQAGAPQGR
4.5	1309.648682	0.005110	SLQAQEDARHR
4.4	1309.669998	-0.016206	LIETQMERFK

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 37959: 1620.817722 from(541.279850,3+) rtinseconds(1673) index(3883)

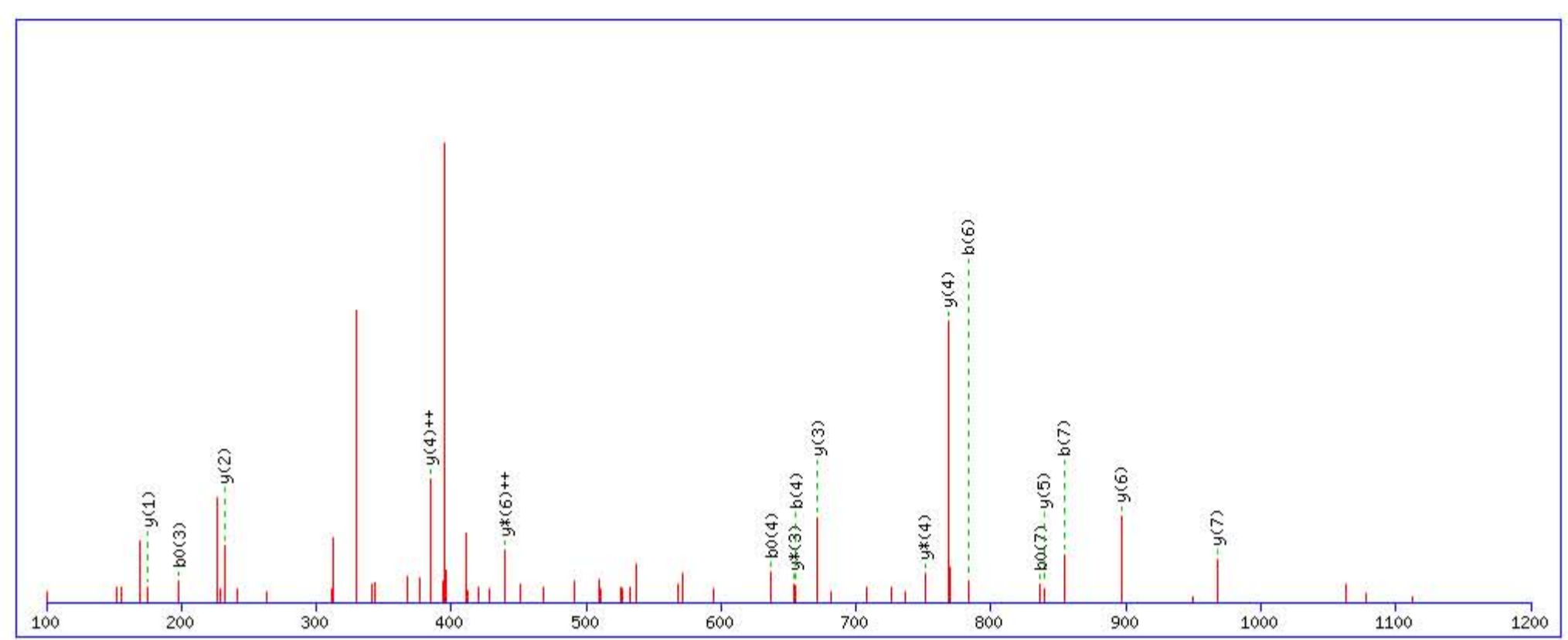
Title: Locus:1.1.1.1392.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1620.822845

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

Variable modifications:

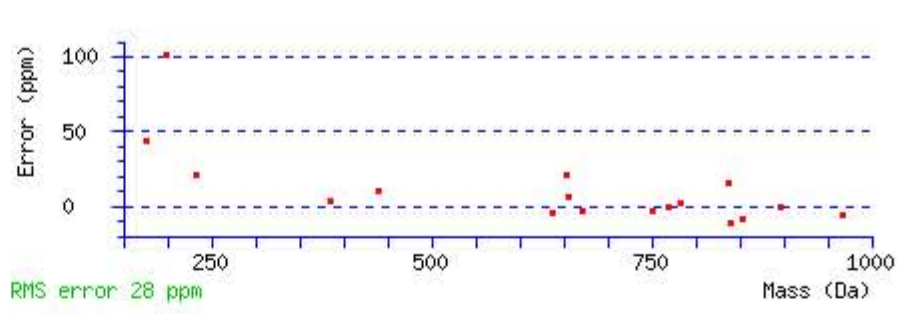
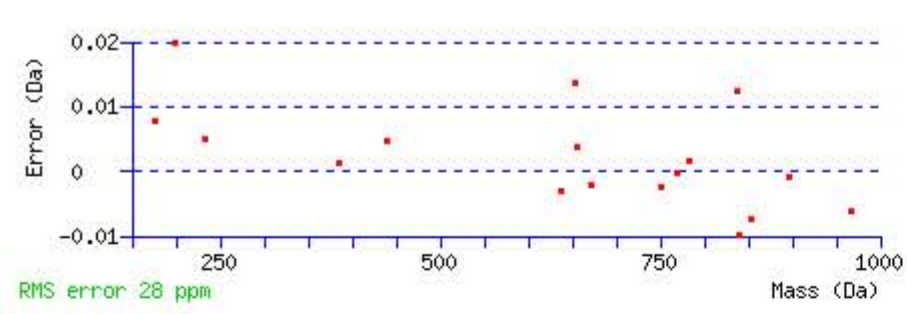
Q4 : Biotin:Thermo-21345 (Q)

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 29 Expect: 0.0074

Matches : 17/94 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	58.028740	29.518008					G							11
2	129.065854	65.036565					A	1564.808666	782.907971	1547.782117	774.394697	1546.798101	773.902689	10
3	216.097882	108.552579			198.087317	99.547296	S	1493.771552	747.389414	1476.745003	738.876140	1475.760987	738.384131	9
4	655.323208	328.165242	638.296659	319.651968	637.312643	319.159960	Q	1406.739524	703.873400	1389.712975	695.360126			8
5	726.360322	363.683799	709.333773	355.170525	708.349757	354.678517	A	967.514198	484.260737	950.487649	475.747463			7
6	783.381786	392.194531	766.355237	383.681257	765.371221	383.189249	G	896.477084	448.742180	879.450535	440.228906			6
7	854.418900	427.713088	837.392351	419.199814	836.408335	418.707806	A	839.455620	420.231448	822.429071	411.718174			5
8	951.471664	476.239470	934.445115	467.726196	933.461099	467.234188	P	768.418506	384.712891	751.391957	376.199617			4
9	1390.696990	695.852133	1373.670441	687.338859	1372.686425	686.846851	Q	671.365742	336.186509	654.339193	327.673235			3
10	1447.718454	724.362865	1430.691905	715.849591	1429.707889	715.357583	G	232.140416	116.573846	215.113867	108.060571			2
11							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **GASQAGAPQGR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.9	1620.822845	-0.005123	GASQAGAPQGR
5.8	1620.815430	0.002292	SLQAQEDARHR
0.2	1620.815430	0.002292	SLQAQEDARHR
0.0	1620.841232	-0.023510	YYFAVRAKDIYGR

MASCOT Search Results

Peptide View

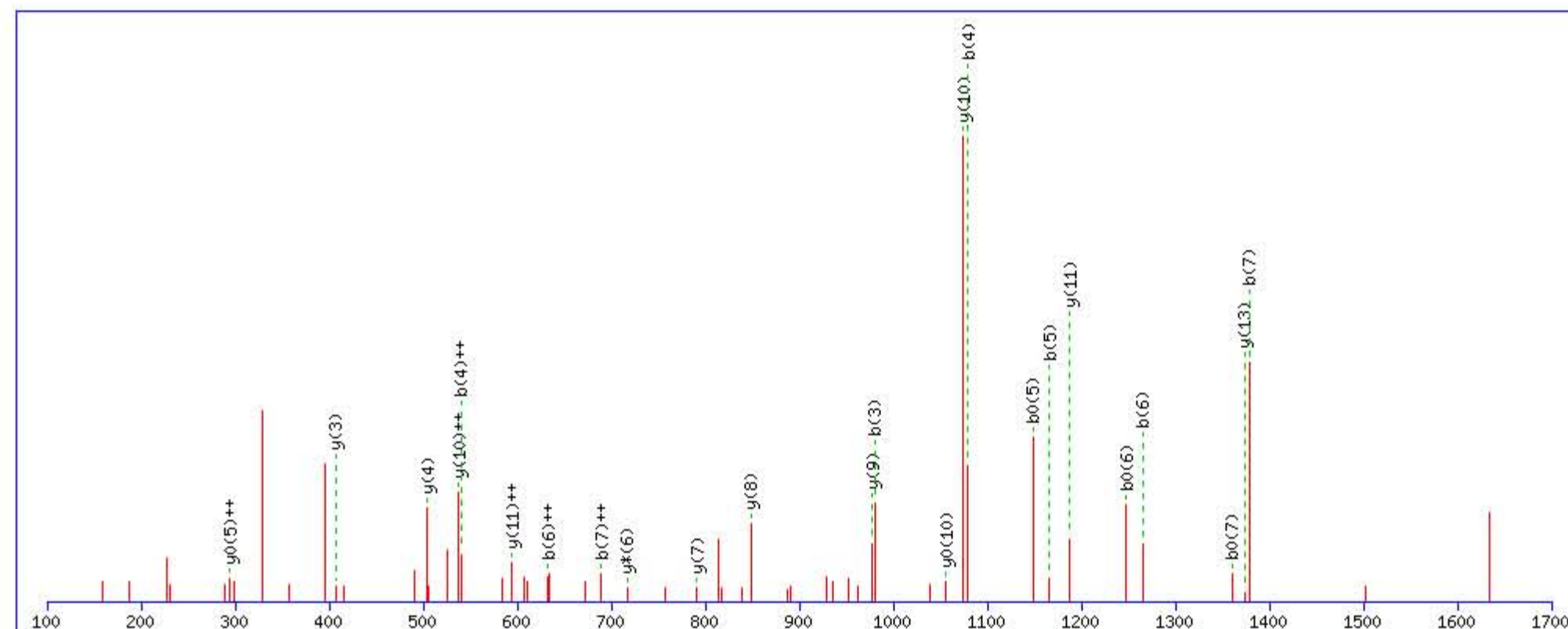
MS/MS Fragmentation of **QTQVSVLPEGGETPLFK**
 Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

Match to Query 55390: 2451.304362 from(818.108730,3+) rtinseconds(2612) index(40243)
 Title: Locus:1.1.1.3328.21 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

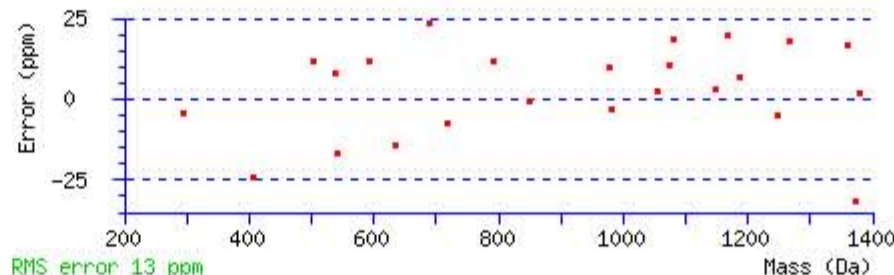
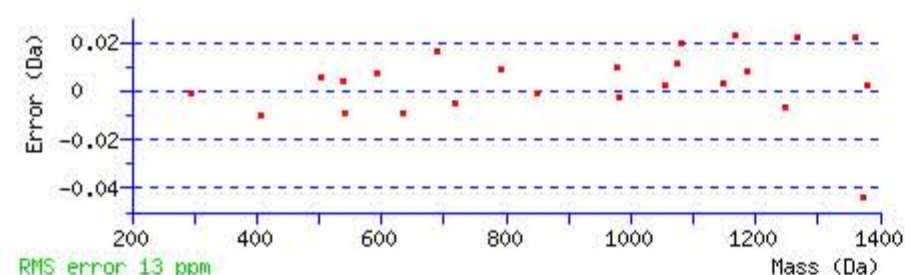
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 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: 41 Expect: 0.00076
 Matches : 25/182 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	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
40.9	2451.290588	0.013774	QTQVSVLPEGGETPLFK
7.3	2451.277130	0.027232	GFPSDTQLLDLRRNHFPSVPR
2.4	2451.330780	-0.026418	RQFQSQLADLQQLPDILK
2.4	2451.330780	-0.026418	RQFQSQLADLQQLPDILK

MASCOT Search Results

Peptide View

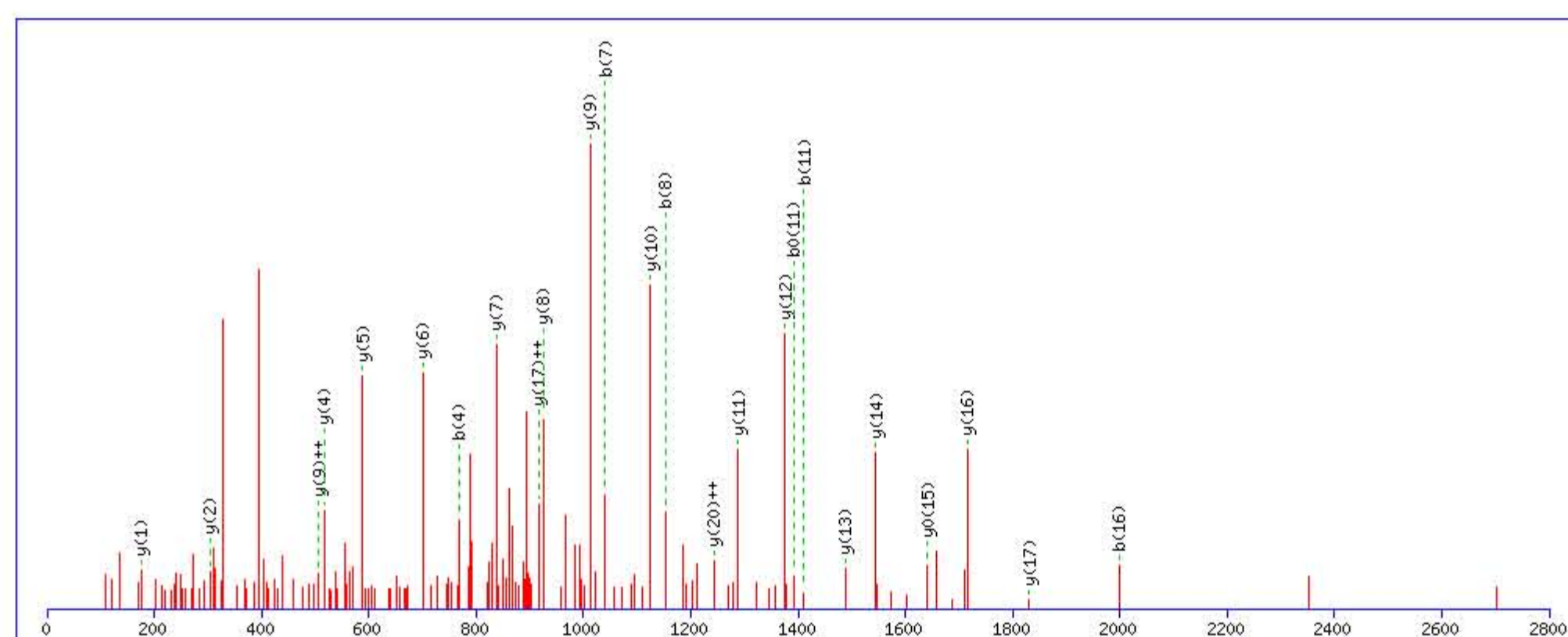
MS/MS Fragmentation of **DPDQTDGLGLSYLSSHIANVER**
 Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

Match to Query 58320: 2697.322722 from(900.114850,3+) rtinseconds(2556) index(24804)
 Title: Locus:1.1.1.892.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

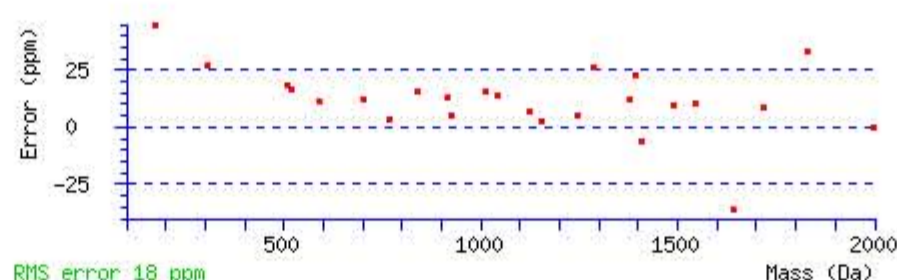
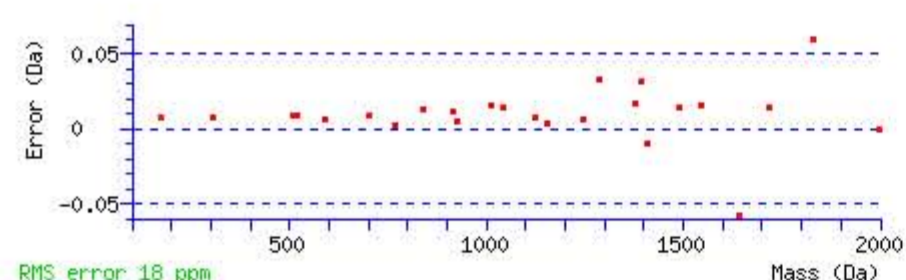
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2697.306824
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q4 : Biotin:Thermo-21345 (Q)
 Ions Score: 113 Expect: 1.5e-010
 Matches : 25/244 fragment ions using 37 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.034219	58.520748			98.023654	49.515465	D							22
2	213.086983	107.047129			195.076418	98.041847	P	2583.287164	1292.147220	2566.260615	1283.633945	2565.276599	1283.141937	21
3	328.113926	164.560601			310.103361	155.555319	D	2486.234400	1243.620838	2469.207851	1235.107563	2468.223835	1234.615555	20
4	767.339252	384.173264	750.312703	375.659989	749.328687	375.167982	Q	2371.207457	1186.107366	2354.180908	1177.594092	2353.196892	1177.102084	19
5	868.386931	434.697104	851.360382	426.183829	850.376366	425.691821	T	1931.982131	966.494704	1914.955582	957.981429	1913.971566	957.489421	18
6	983.413874	492.210575	966.387325	483.697300	965.403309	483.205292	D	1830.934452	915.970864	1813.907903	907.457590	1812.923887	906.965581	17
7	1040.435338	520.721307	1023.408789	512.208032	1022.424773	511.716025	G	1715.907509	858.457392	1698.880960	849.944118	1697.896944	849.452110	16
8	1153.519402	577.263339	1136.492853	568.750065	1135.508837	568.258056	L	1658.886045	829.946661	1641.859496	821.433386	1640.875480	820.941378	15
9	1210.540866	605.774071	1193.514317	597.260796	1192.530301	596.768788	G	1545.801981	773.404629	1528.775432	764.891354	1527.791416	764.399346	14
10	1323.624930	662.316103	1306.598381	653.802828	1305.614365	653.310820	L	1488.780517	744.893897	1471.753968	736.380622	1470.769952	735.888614	13
11	1410.656958	705.832117	1393.630409	697.318842	1392.646393	696.826834	S	1375.696453	688.351865	1358.669904	679.838590	1357.685888	679.346582	12
12	1573.720287	787.363781	1556.693738	778.850507	1555.709722	778.358499	Y	1288.664425	644.835851	1271.637876	636.322576	1270.653860	635.830568	11
13	1686.804351	843.905813	1669.777802	835.392539	1668.793786	834.900531	L	1125.601096	563.304186	1108.574547	554.790912	1107.590531	554.298904	10
14	1773.836379	887.421827	1756.809830	878.908553	1755.825814	878.416545	S	1012.517032	506.762154	995.490483	498.248880	994.506467	497.756872	9
15	1860.868407	930.937841	1843.841858	922.424567	1842.857842	921.932559	S	925.485004	463.246140	908.458455	454.732866	907.474439	454.240858	8
16	1997.927319	999.467297	1980.900770	990.954023	1979.916754	990.462015	H	838.452976	419.730126	821.426427	411.216852	820.442411	410.724844	7
17	2111.011383	1056.009329	2093.984834	1047.496055	2093.000818	1047.004047	I	701.394064	351.200670	684.367515	342.687396	683.383499	342.195388	6
18	2182.048497	1091.527886	2165.021948	1083.014612	2164.037932	1082.522604	A	588.310000	294.658638	571.283451	286.145364	570.299435	285.653356	5
19	2296.091424	1148.549350	2279.064875	1140.036075	2278.080859	1139.544067	N	517.272886	259.140081	500.246337	250.626806	499.262321	250.134798	4
20	2395.159838	1198.083557	2378.133289	1189.570282	2377.149273	1189.078274	V	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
21	2524.202431	1262.604853	2507.175882	1254.091579	2506.191866	1253.599571	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
22							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
112.7	2697.306824	0.015898	DPDQTDGLGLSYLSSHIANVER

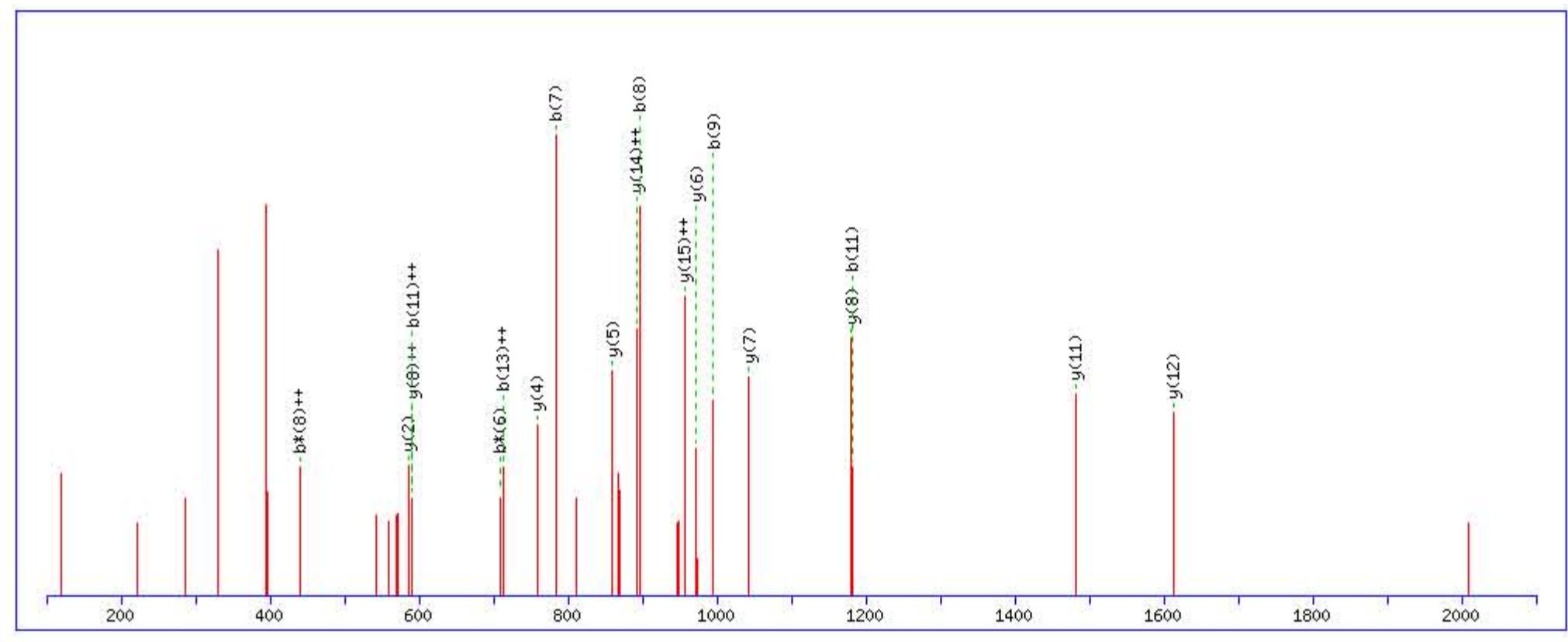
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VIHDNFGIVEGLMTTVHAIATQK**
 Found in **G3P_HUMAN**, Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3

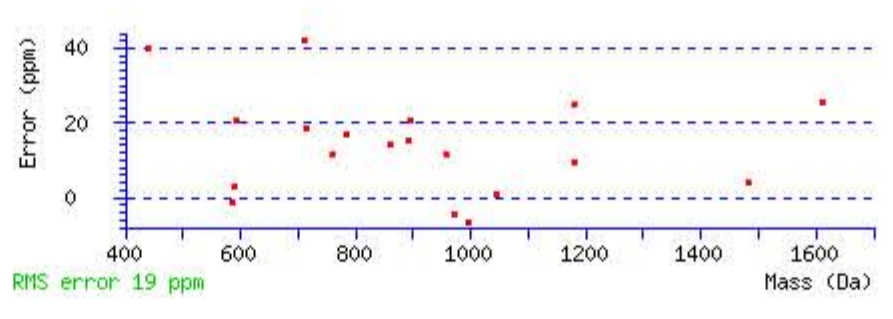
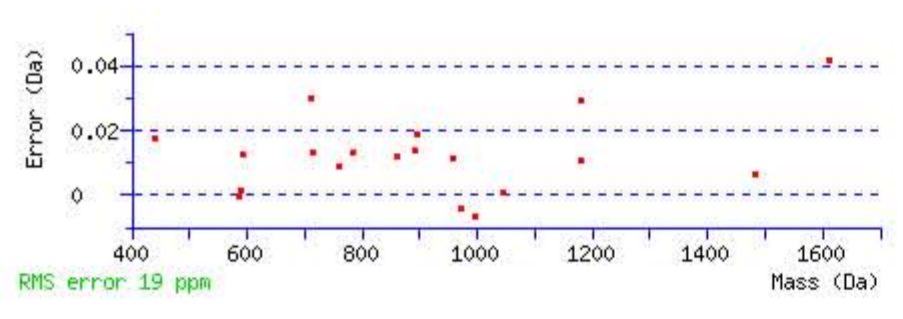
Match to Query 60892: 2905.548856 from(727.394490,4+) rtinseconds(3124) index(60325)
 Title: Locus:1.1.1.1699.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2905.519424
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q23 : Biotin:Thermo-21345 (Q)
 Ions Score: 43 Expect: 0.00013
 Matches : 19/258 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							24
2	213.159754	107.083515					I	2807.458272	1404.232774	2790.431723	1395.719499	2789.447707	1395.227491	23
3	350.218666	175.612971					H	2694.374208	1347.690742	2677.347659	1339.177467	2676.363643	1338.685459	22
4	465.245609	233.126443			447.235044	224.121160	D	2557.315296	1279.161286	2540.288747	1270.648011	2539.304731	1270.156003	21
5	579.288536	290.147906	562.261987	281.634632	561.277971	281.142624	N	2442.288353	1221.647814	2425.261804	1213.134540	2424.277788	1212.642532	20
6	726.356950	363.682113	709.330401	355.168838	708.346385	354.676830	F	2328.245426	1164.626351	2311.218877	1156.113076	2310.234861	1155.621068	19
7	783.378414	392.192845	766.351865	383.679571	765.367849	383.187563	G	2181.177012	1091.092144	2164.150463	1082.578869	2163.166447	1082.086861	18
8	896.462478	448.734877	879.435929	440.221603	878.451913	439.729595	I	2124.155548	1062.581412	2107.128999	1054.068137	2106.144983	1053.576129	17
9	995.530892	498.269084	978.504343	489.755810	977.520327	489.263802	V	2011.071484	1006.039380	1994.044935	997.526105	1993.060919	997.034097	16
10	1124.573485	562.790381	1107.546936	554.277106	1106.562920	553.785098	E	1912.003070	956.505173	1894.976521	947.991899	1893.992505	947.499890	15
11	1181.594949	591.301113	1164.568400	582.787838	1163.584384	582.295830	G	1782.960477	891.983876	1765.933928	883.470602	1764.949912	882.978594	14
12	1294.679013	647.843144	1277.652464	639.329870	1276.668448	638.837862	L	1725.939013	863.473144	1708.912464	854.959870	1707.928448	854.467862	13
13	1425.719498	713.363387	1408.692949	704.850113	1407.708933	704.358104	M	1612.854949	806.931113	1595.828400	798.417838	1594.844384	797.925830	12
14	1526.767177	763.887227	1509.740628	755.373952	1508.756612	754.881944	T	1481.814464	741.410870	1464.787915	732.897596	1463.803899	732.405588	11
15	1627.814856	814.411066	1610.788307	805.897792	1609.804291	805.405783	T	1380.766785	690.887031	1363.740236	682.373756	1362.756220	681.881748	10
16	1726.883270	863.945273	1709.856721	855.431999	1708.872705	854.939991	V	1279.719106	640.363191	1262.692557	631.849917	1261.708541	631.357909	9
17	1863.942182	932.474729	1846.915633	923.961455	1845.931617	923.469447	H	1180.650692	590.828984	1163.624143	582.315710	1162.640127	581.823701	8
18	1934.979296	967.993286	1917.952747	959.480012	1916.968731	958.988003	A	1043.591780	522.299528	1026.565231	513.786254	1025.581215	513.294245	7
19	2048.063360	1024.535318	2031.036811	1016.022044	2030.052795	1015.530036	I	972.554666	486.780971	955.528117	478.267697	954.544101	477.775689	6
20	2149.111039	1075.059157	2132.084490	1066.545883	2131.100474	1066.053875	T	859.470602	430.238939	842.444053	421.725665	841.460037	421.233657	5
21	2220.148153	1110.577714	2203.121604	1102.064440	2202.137588	1101.572432	A	758.422923	379.715100	741.396374	371.201825	740.412358	370.709817	4
22	2321.195832	1161.101554	2304.169283	1152.588279	2303.185267	1152.096271	T	687.385809	344.196543	670.359260	335.683268	669.375244	335.191260	3
23	2760.421158	1380.714217	2743.394609	1372.200942	2742.410593	1371.708934	Q	586.338130	293.672703	569.311581	285.159429			2
24							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **VIHDNFGIVEGLMTTVHAIATQK**
 (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	2905.519424	0.029432	VIHDNFGIVEGLMTTVHAIATQK
1.9	2905.511490	0.037366	TLQEIFQAENTIMLLERSIMAK
1.9	2905.511490	0.037366	TLQEIFQAENTIMLLERSIMAK

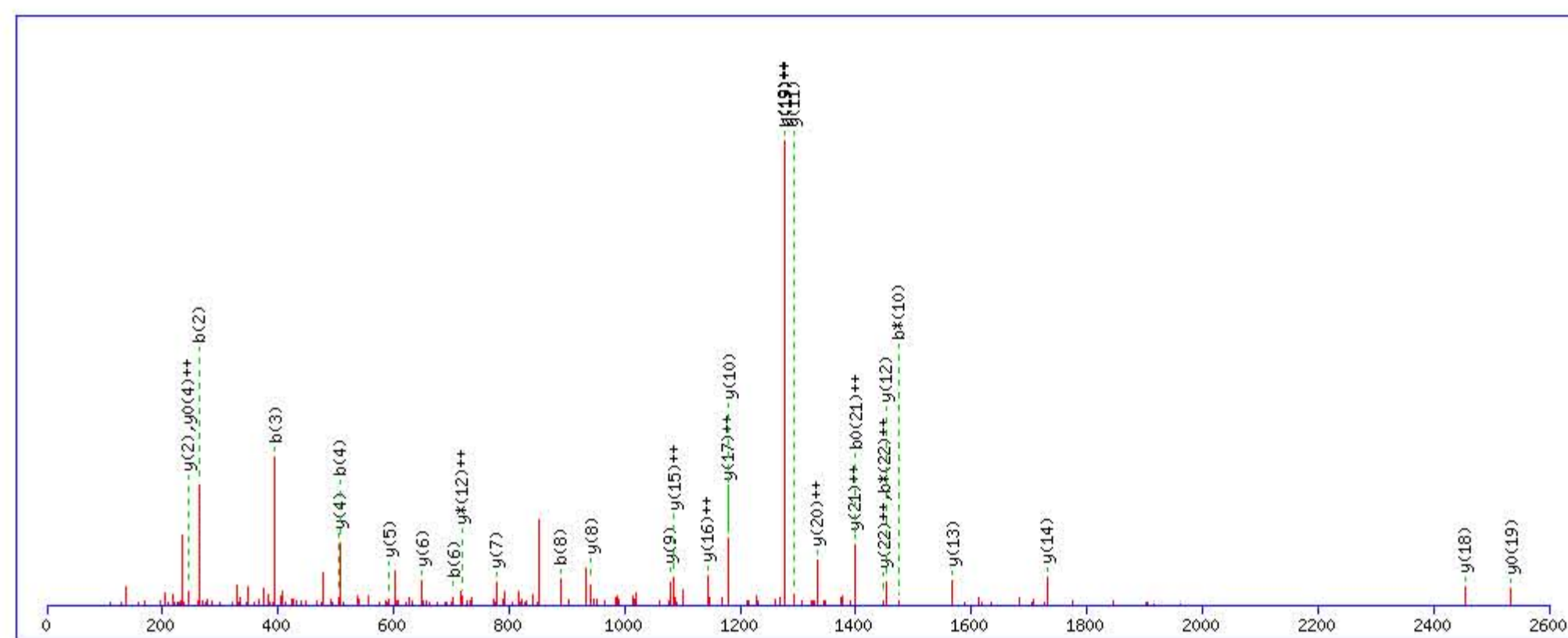
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **YVMLPVADQYDCITHYEGSTCPK**
 Found in **HPTR_HUMAN**, Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=1 SV=2

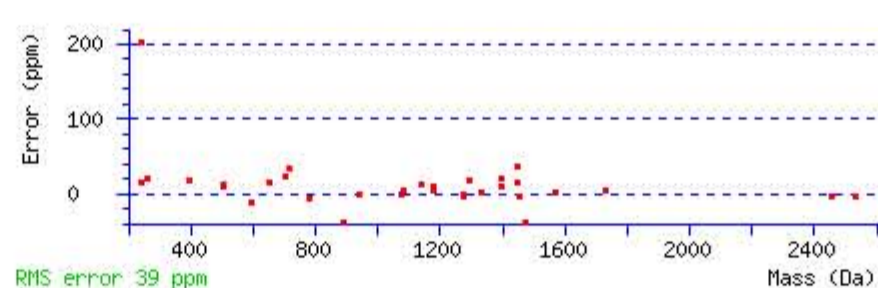
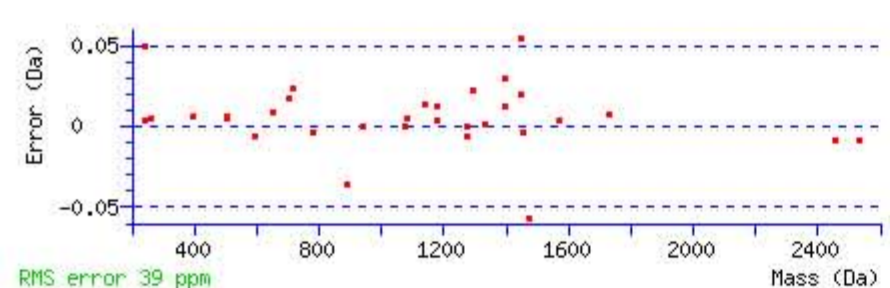
Match to Query 62112: 3057.388722 from(1020.136850,3+) rtinseconds(2453) index(24185)
 Title: Locus:1.1.1.856.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 3057.374466
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q9 : Biotin:Thermo-21345 (Q)
 Ions Score: 62 Expect: 6.9e-006
 Matches : 32/228 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	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	$M_r(\text{calc})$:	Delta	Sequence
61.8	3057.374466	0.014256	YVMLPVADQYDCITHYEGSTCPK

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYFPHFDSLHGSAQVK**

Found in **HBA_HUMAN**, Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2

Match to Query 49864: 2144.050976 from(537.020020,4+) rtinseconds(2067) index(6251)

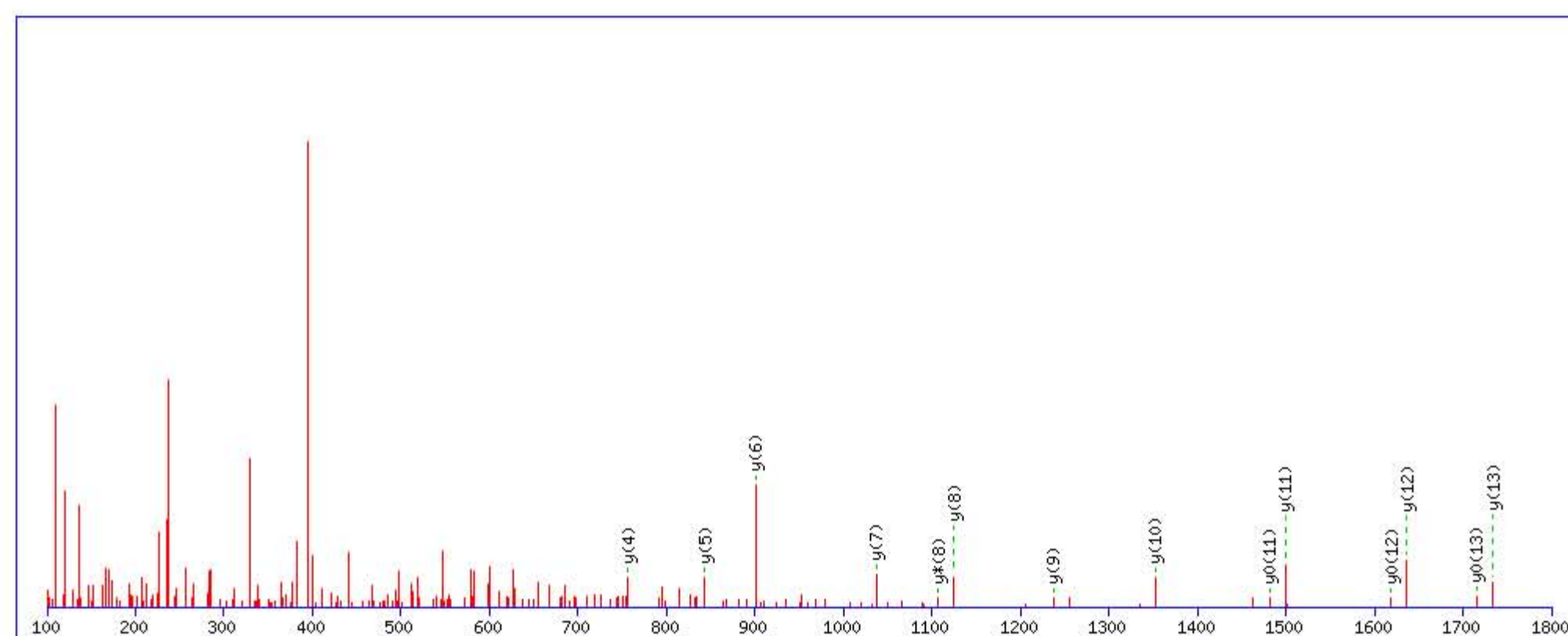
Title: Locus:1.1.1.1529.5 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2144.051346

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

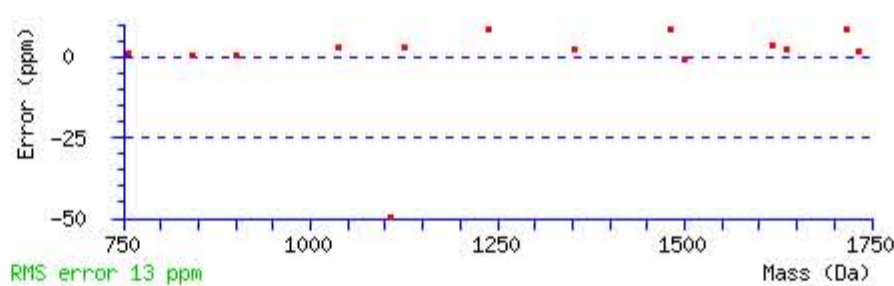
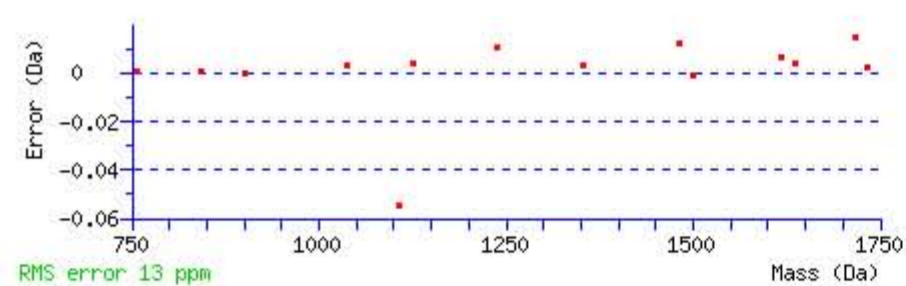
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 0.00064

Matches : 14/146 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	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 [TYFPHFDSLHGSAQVK](#)

(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	2144.051346	-0.000370	TYFPHFDSLHGSAQVK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **YYCFQGNQFLR**

Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

Match to Query 42788: 1805.838108 from(903.926330,2+) rtinseconds(2306) index(70568)

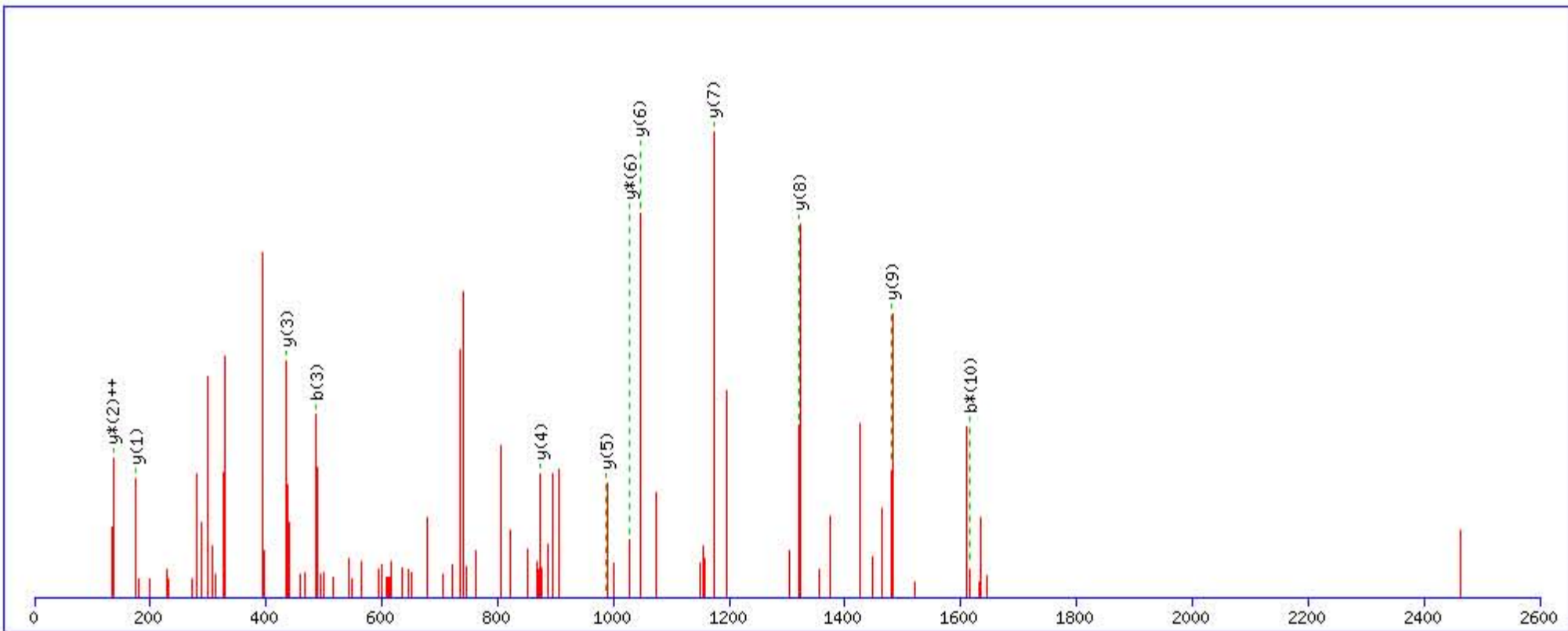
Title: Locus:1.1.1.1740.14 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1805.838165

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

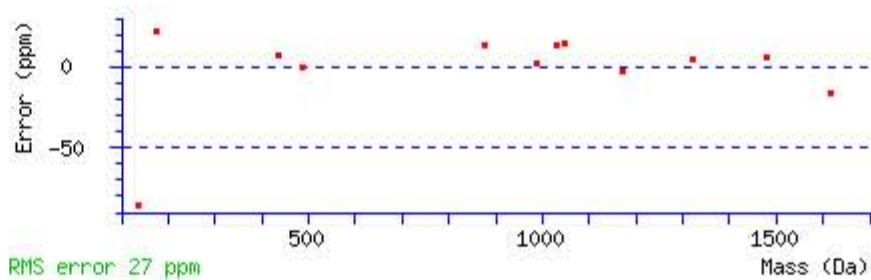
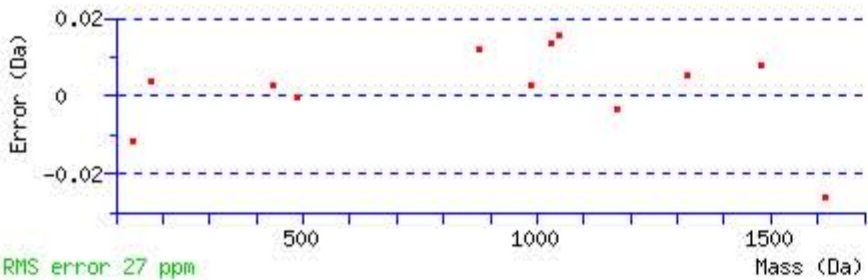
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.031

Matches : 12/72 fragment ions using 32 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	#
1	164.070605	82.538940			Y					11
2	327.133934	164.070605			Y	1643.782117	822.394697	1626.755568	813.881422	10
3	487.164583	244.085930			C	1480.718788	740.863032	1463.692239	732.349758	9
4	634.232997	317.620137			F	1320.688139	660.847708	1303.661590	652.334433	8
5	762.291575	381.649426	745.265026	373.136151	Q	1173.619725	587.313501	1156.593176	578.800226	7
6	819.313039	410.160158	802.286490	401.646883	G	1045.561147	523.284212	1028.534598	514.770937	6
7	933.355966	467.181621	916.329417	458.668347	N	988.539683	494.773480	971.513134	486.260205	5
8	1372.581292	686.794284	1355.554743	678.281010	Q	874.496756	437.752016	857.470207	429.238742	4
9	1519.649706	760.328491	1502.623157	751.815217	F	435.271430	218.139353	418.244881	209.626078	3
10	1632.733770	816.870523	1615.707221	808.357249	L	288.203016	144.605146	271.176467	136.091871	2
11					R	175.118952	88.063114	158.092403	79.549839	1



NCBI BLAST search of [YYCFQGNQFLR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.0	1805.838165	-0.000057	YYCFQGNQFLR
24.4	1805.838165	-0.000057	YYCFQGNQFLR

MASCOT 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 47745: 2022.931888 from(1012.473220,2+) rtinseconds(2415) index(71158)

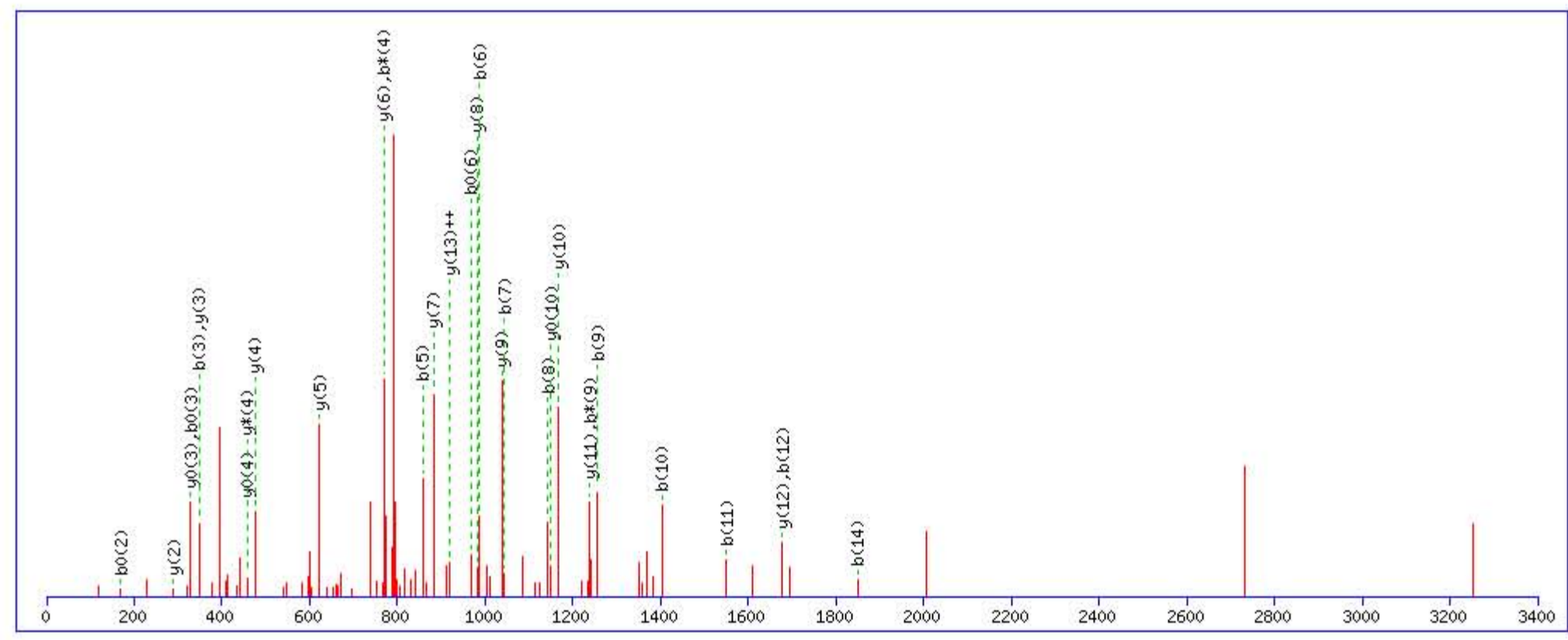
Title: Locus:1.1.1.1778.18 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2022.929184

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

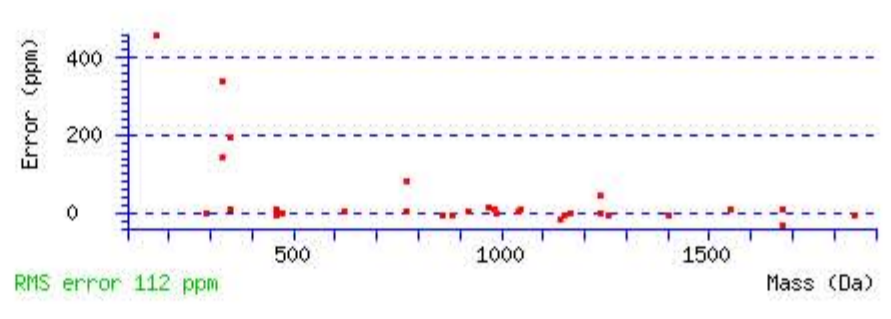
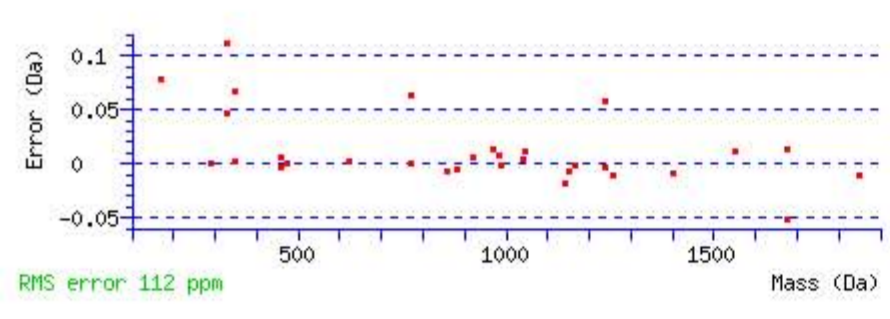
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 58 Expect: 2.3e-005

Matches : 31/158 fragment ions using 55 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							15
2	187.071333	94.039305			169.060768	85.034022	E	1966.914982	983.961129	1949.888433	975.447855	1948.904417	974.955847	14
3	347.101982	174.054629			329.091417	165.049347	C	1837.872389	919.439833	1820.845840	910.926558	1819.861824	910.434550	13
4	786.327308	393.667292	769.300759	385.154018	768.316743	384.662010	Q	1677.841740	839.424508	1660.815191	830.911234	1659.831175	830.419226	12
5	857.364422	429.185849	840.337873	420.672575	839.353857	420.180567	A	1238.616414	619.811845	1221.589865	611.298571	1220.605849	610.806563	11
6	986.407015	493.707146	969.380466	485.193871	968.396450	484.701863	E	1167.579300	584.293288	1150.552751	575.780014	1149.568735	575.288006	10
7	1043.428479	522.217878	1026.401930	513.704603	1025.417914	513.212595	G	1038.536707	519.771992	1021.510158	511.258717	1020.526142	510.766709	9
8	1142.496893	571.752085	1125.470344	563.238810	1124.486328	562.746802	V	981.515243	491.261260	964.488694	482.747985	963.504678	482.255977	8
9	1255.580957	628.294117	1238.554408	619.780842	1237.570392	619.288834	L	882.446829	441.727053	865.420280	433.213778	864.436264	432.721770	7
10	1402.649371	701.828324	1385.622822	693.315049	1384.638806	692.823041	F	769.362765	385.185021	752.336216	376.671746	751.352200	376.179738	6
11	1549.717785	775.362531	1532.691236	766.849256	1531.707220	766.357248	F	622.294351	311.650814	605.267802	303.137539	604.283786	302.645531	5
12	1677.776363	839.391820	1660.749814	830.878545	1659.765798	830.386537	Q	475.225937	238.116606	458.199388	229.603332	457.215372	229.111324	4
13	1734.797827	867.902552	1717.771278	859.389277	1716.787262	858.897269	G	347.167359	174.087317	330.140810	165.574043	329.156794	165.082035	3
14	1849.824770	925.416023	1832.798221	916.902749	1831.814205	916.410741	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
15							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.8	2022.929184	0.002704	GECQAEGVLFFQGDR
11.9	2022.929184	0.002704	GECQAEGVLFFQGDR

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 58136: 2674.329492 from(892.450440,3+) rtinseconds(2665) index(72484)

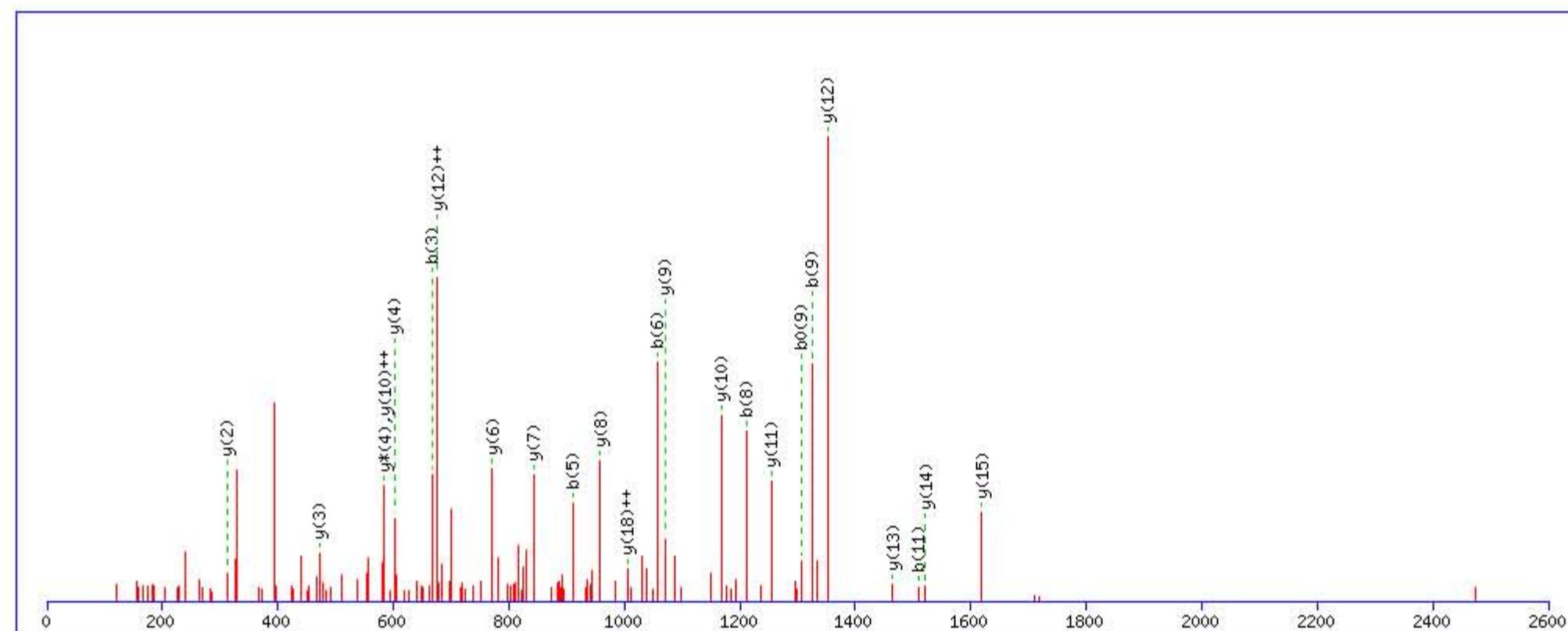
Title: Locus:1.1.1.1865.13 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2674.324722

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

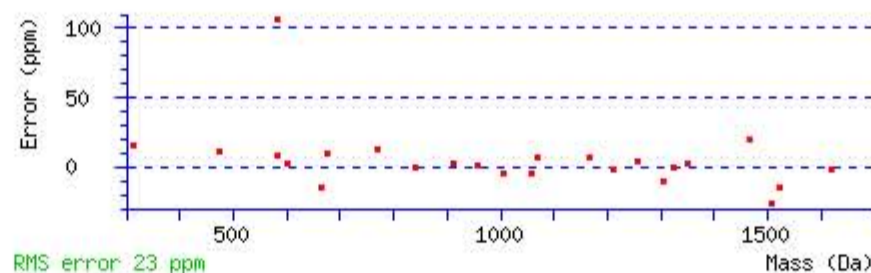
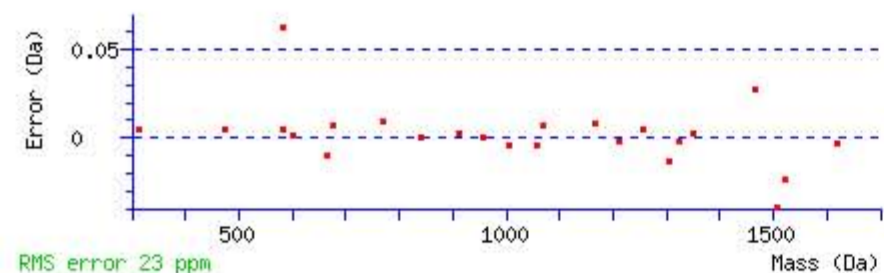
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 95 Expect: 7.9e-009

Matches : 24/224 fragment ions using 33 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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
95.4	2674.324722	0.004770	LLQDEFPGIPSPLDAAVECHR

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 26949: 1338.735848 from(670.375200,2+) rtinseconds(1940) index(36007)

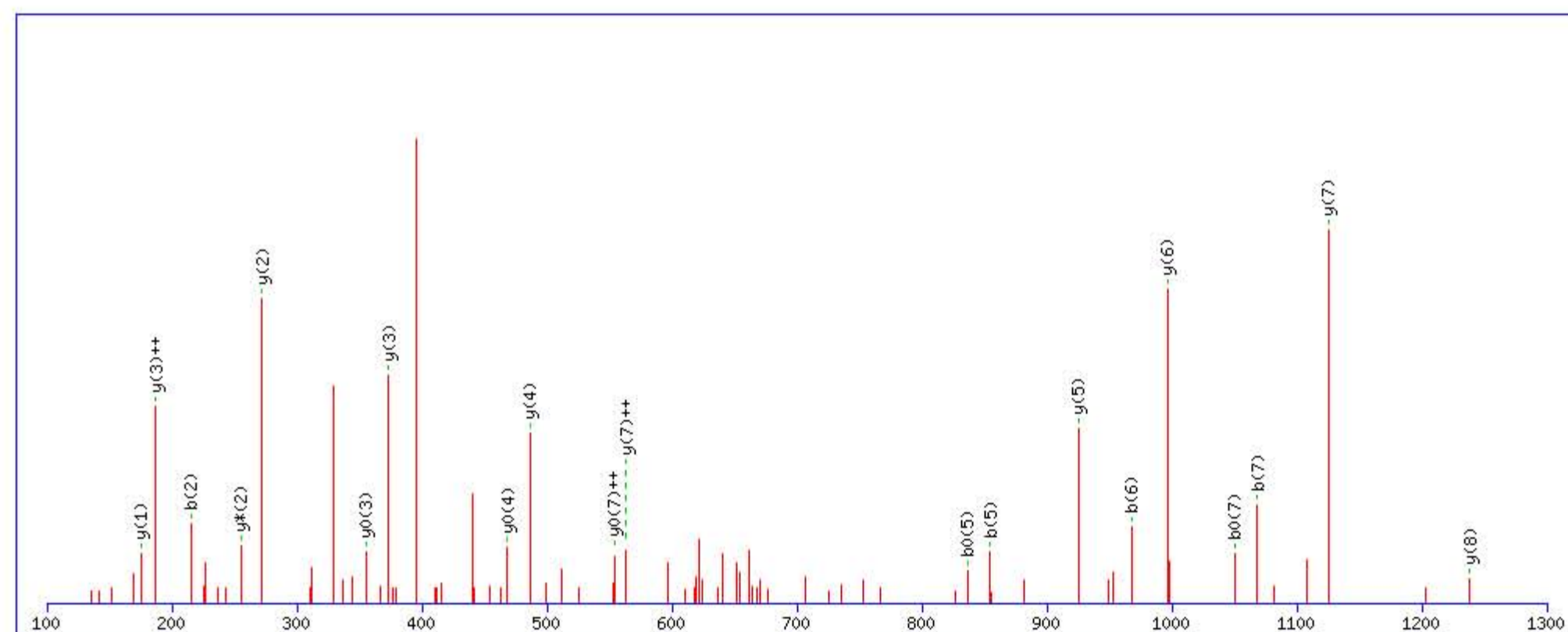
Title: Locus:1.1.1.3095.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1338.732941

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

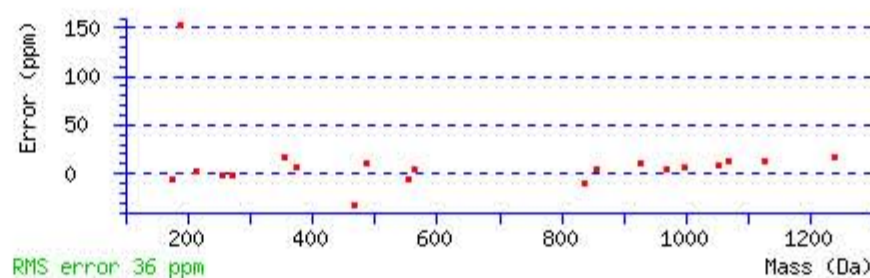
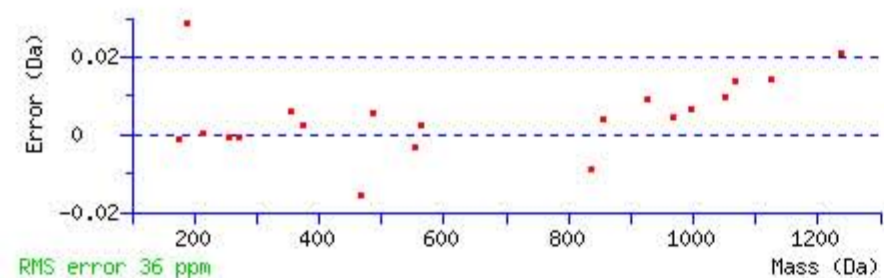
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 58 Expect: 2.7e-005

Matches : 20/84 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	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
58.3	1338.732941	0.002907	TLEAQLTPR
11.8	1338.732956	0.002892	VDLQSLPTR
5.9	1338.725555	0.010293	VDTVAAEHLTRK
2.5	1338.744171	-0.008323	MKEALHQIVVR
2.3	1338.725555	0.010293	RSPTVEPSTLPR

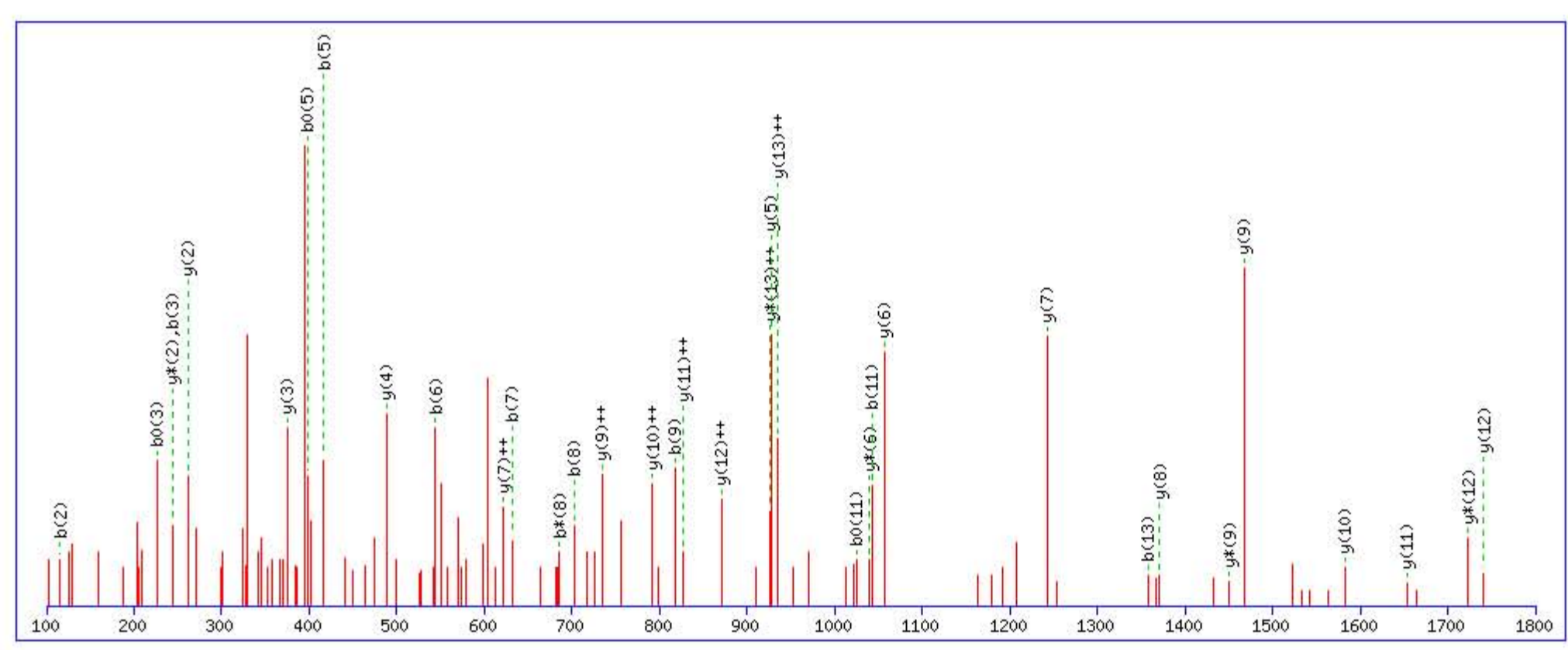
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNK**
 Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

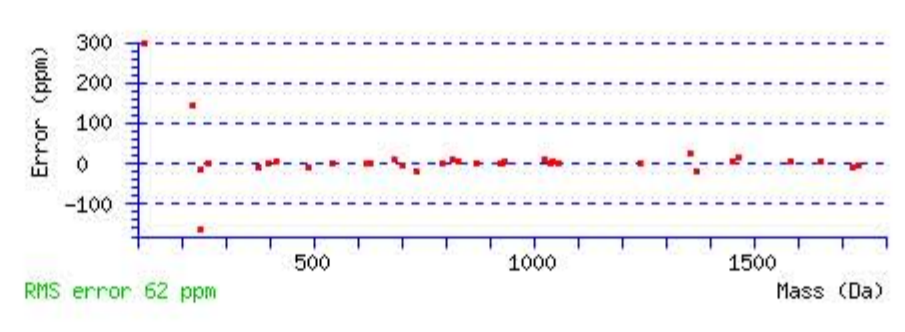
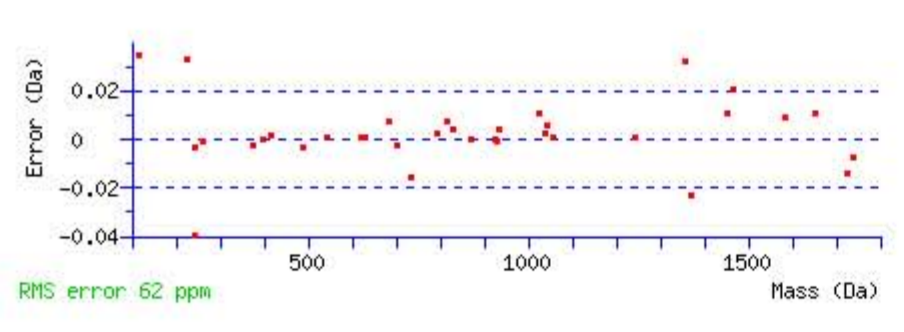
Match to Query 52730: 2283.056322 from(762.026050,3+) rtinseconds(1912) index(35769)
 Title: Locus:1.1.1.3085.21 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 2283.058975
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q14 : Biotin:Thermo-21345 (Q)
 Ions Score: 65 Expect: 4.1e-006
 Matches : 35/180 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	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
64.8	2283.058975	-0.002653	GGETAQSADPQWEQLNNK
32.9	2283.058975	-0.002653	GGETAQSADPQWEQLNNK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNKK**

Found in **HEP2_HUMAN**, Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

Match to Query 52731: 2283.062952 from(762.028260,3+) rtinseconds(1890) index(35573)

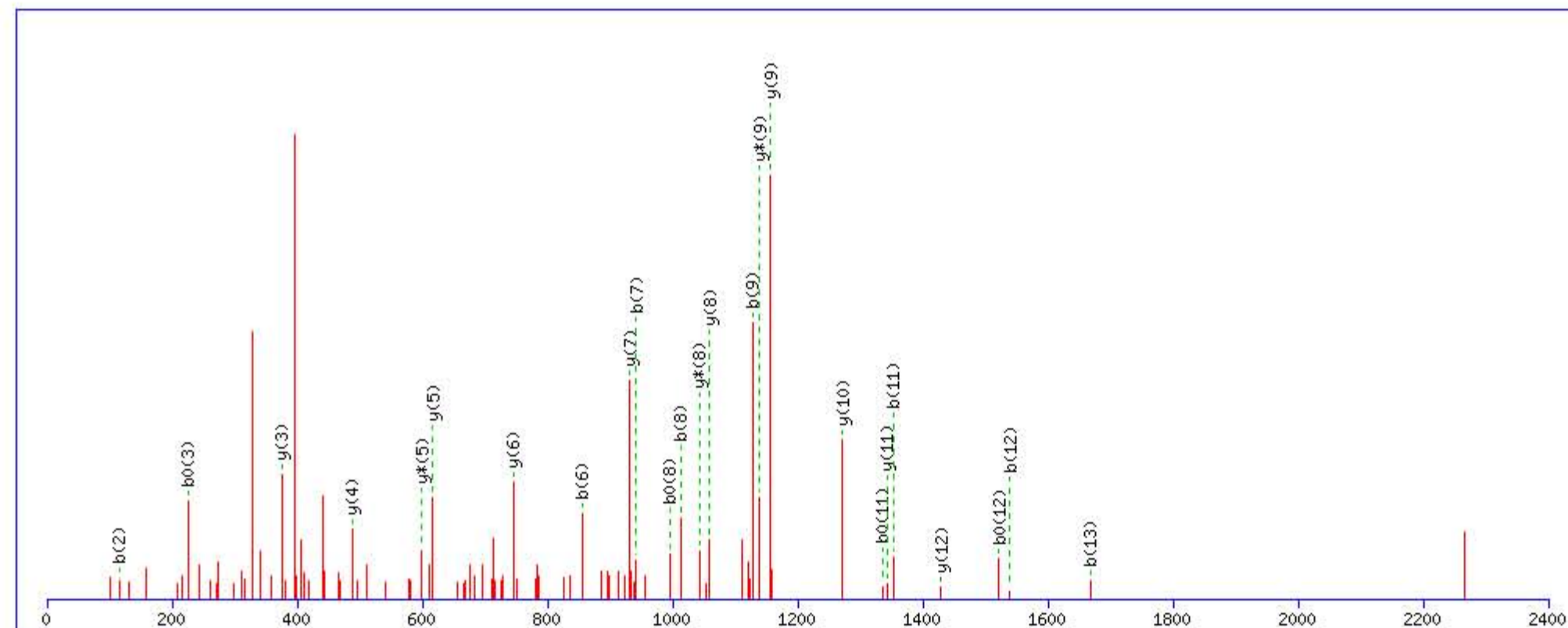
Title: Locus:1.1.1.3077.25 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2283.058975

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

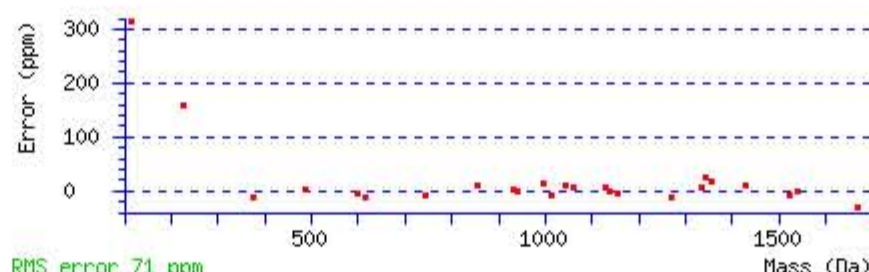
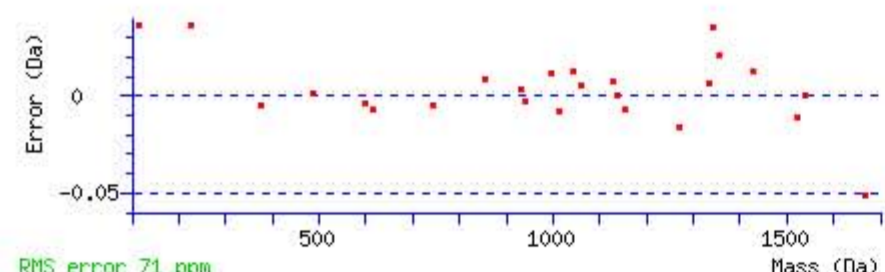
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 59 Expect: 1.8e-005

Matches : 25/180 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 [GGETAQSADPQWEQLNKK](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.9	2283.058975	0.003977	GGETAQSADPQWEQLNKK
14.5	2283.058975	0.003977	GGETAQSADPQWEQLNKK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VQLSPDLLATLPEPASPGR**

Found in **HGFA_HUMAN**, Hepatocyte growth factor activator OS=Homo sapiens GN=HGFAC PE=1 SV=1

Match to Query 52481: 2271.227832 from(758.083220,3+) rtinseconds(2669) index(9512)

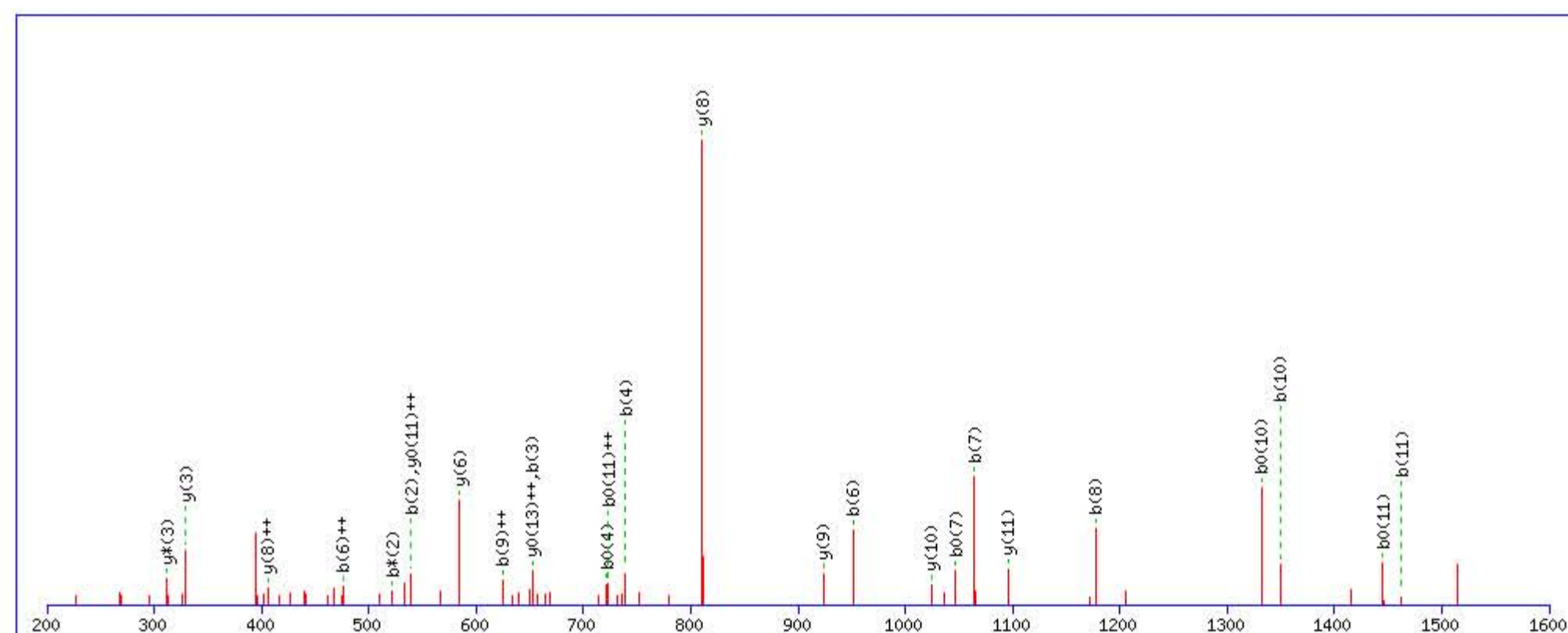
Title: Locus:1.1.1.1738.23 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2271.229675

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

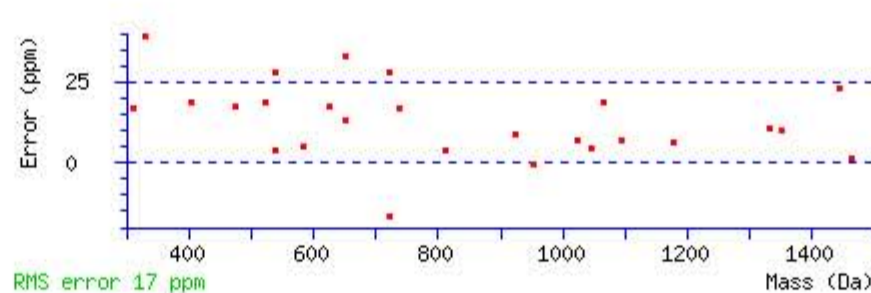
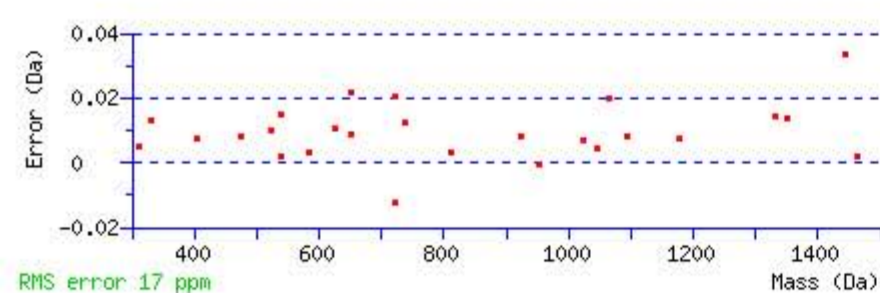
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 1.4e-005

Matches : 26/202 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							19
2	539.301016	270.154146	522.274467	261.640872			Q	2173.168553	1087.087914	2156.142004	1078.574640	2155.157988	1078.082632	18
3	652.385080	326.696178	635.358531	318.182904			L	1733.943227	867.475252	1716.916678	858.961977	1715.932662	858.469969	17
4	739.417108	370.212192	722.390559	361.698918	721.406543	361.206910	S	1620.859163	810.933219	1603.832614	802.419945	1602.848598	801.927937	16
5	836.469872	418.738574	819.443323	410.225300	818.459307	409.733292	P	1533.827135	767.417206	1516.800586	758.903931	1515.816570	758.411923	15
6	951.496815	476.252046	934.470266	467.738771	933.486250	467.246763	D	1436.774371	718.890824	1419.747822	710.377549	1418.763806	709.885541	14
7	1064.580879	532.794078	1047.554330	524.280803	1046.570314	523.788795	L	1321.747428	661.377352	1304.720879	652.864078	1303.736863	652.372069	13
8	1177.664943	589.336110	1160.638394	580.822835	1159.654378	580.330827	L	1208.663364	604.835320	1191.636815	596.322046	1190.652799	595.830038	12
9	1248.702057	624.854667	1231.675508	616.341392	1230.691492	615.849384	A	1095.579300	548.293288	1078.552751	539.780014	1077.568735	539.288006	11
10	1349.749736	675.378506	1332.723187	666.865232	1331.739171	666.373223	T	1024.542186	512.774731	1007.515637	504.261456	1006.531621	503.769448	10
11	1462.833800	731.920538	1445.807251	723.407264	1444.823235	722.915255	L	923.494507	462.250892	906.467958	453.737617	905.483942	453.245609	9
12	1559.886564	780.446920	1542.860015	771.933646	1541.875999	771.441637	P	810.410443	405.708860	793.383894	397.195585	792.399878	396.703577	8
13	1688.929157	844.968216	1671.902608	836.454942	1670.918592	835.962934	E	713.357679	357.182478	696.331130	348.669203	695.347114	348.177195	7
14	1785.981921	893.494598	1768.955372	884.981324	1767.971356	884.489316	P	584.315086	292.661181	567.288537	284.147907	566.304521	283.655899	6
15	1857.019035	929.013155	1839.992486	920.499881	1839.008470	920.007873	A	487.262322	244.134799	470.235773	235.621525	469.251757	235.129517	5
16	1944.051063	972.529169	1927.024514	964.015895	1926.040498	963.523887	S	416.225208	208.616242	399.198659	200.102968	398.214643	199.610960	4
17	2041.103827	1021.055552	2024.077278	1012.542277	2023.093262	1012.050269	P	329.193180	165.100228	312.166631	156.586954			3
18	2098.125291	1049.566283	2081.098742	1041.053009	2080.114726	1040.561001	G	232.140416	116.573846	215.113867	108.060572			2
19							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [VQLSPDLLATLPEPASPGR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.8	2271.229675	-0.001843	VQLSPDLLATLPEPASPGR
5.0	2271.226303	0.001529	IAKSDPPTLLTPSKWSVEFR

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 34167: 1508.710602 from(503.910810,3+) rtinseconds(1757) index(67243)

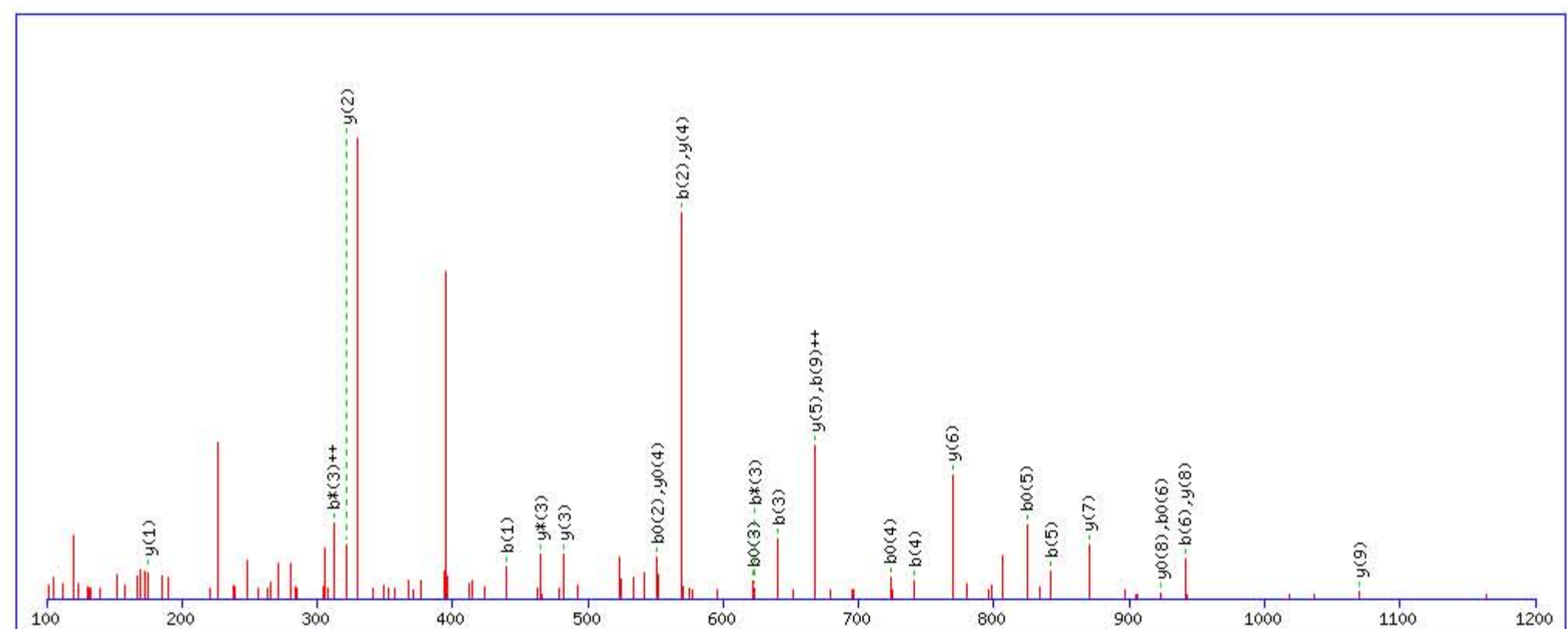
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1508.711578

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

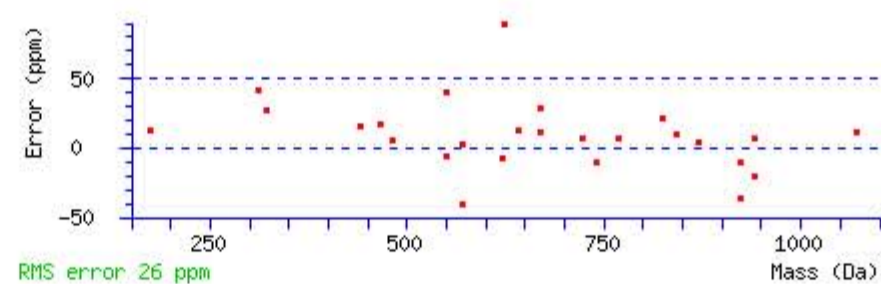
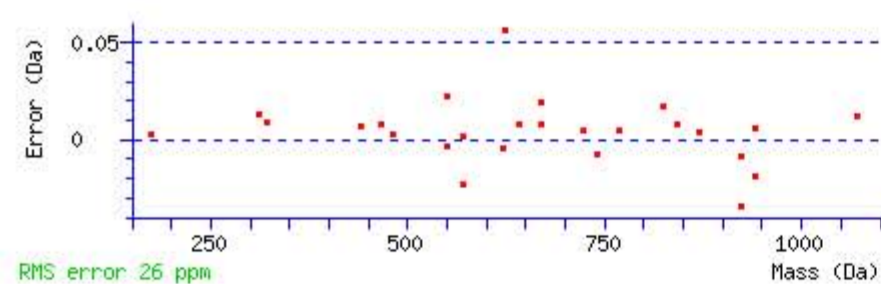
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 53 Expect: 1.2e-005

Matches : 26/100 fragment ions using 40 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	440.232602	220.619939	423.206053	212.106664			Q							10
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	E	1070.493522	535.750399	1053.466973	527.237125	1052.482957	526.745117	9
3	640.312309	320.659793	623.285760	312.146518	622.301744	311.654510	A	941.450929	471.229103	924.424380	462.715828	923.440364	462.223820	8
4	741.359988	371.183632	724.333439	362.670358	723.349423	362.178350	T	870.413815	435.710546	853.387266	427.197271	852.403250	426.705263	7
5	842.407667	421.707472	825.381118	413.194197	824.397102	412.702189	T	769.366136	385.186706	752.339587	376.673432	751.355571	376.181424	6
6	941.476081	471.241679	924.449532	462.728404	923.465516	462.236396	V	668.318457	334.662867	651.291908	326.149592	650.307892	325.657584	5
7	1028.508109	514.757693	1011.481560	506.244418	1010.497544	505.752410	S	569.250043	285.128660	552.223494	276.615385	551.239478	276.123377	4
8	1188.538758	594.773017	1171.512209	586.259743	1170.528193	585.767735	C	482.218015	241.612646	465.191466	233.099371			3
9	1335.607172	668.307224	1318.580623	659.793950	1317.596607	659.301942	F	322.187366	161.597321	305.160817	153.084047			2
10							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **QEATTVSCFR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
52.9	1508.711578	-0.000976	QEATTVSCFR
0.5	1508.692932	0.017670	THILSMEEDKFR

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 66936: 3494.682736 from(874.677960,4+) rtinseconds(2821) index(73773)

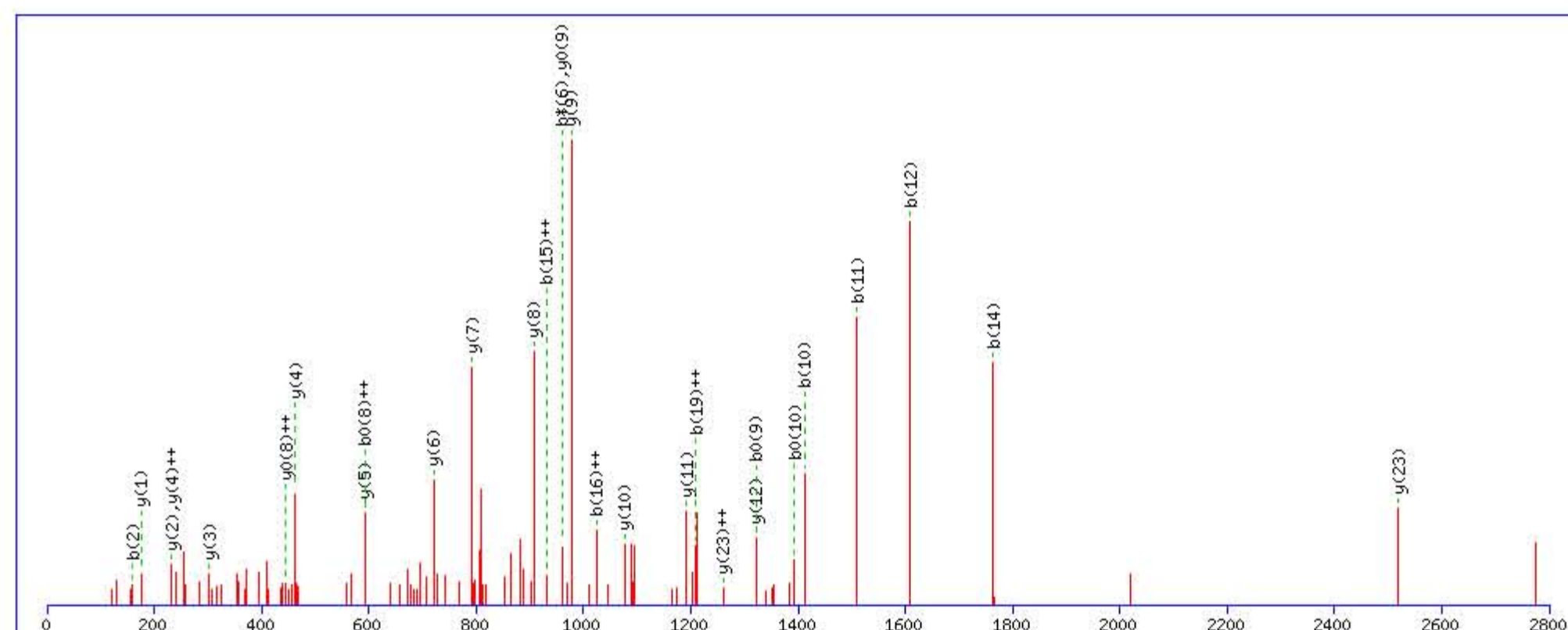
Title: Locus:1.1.1.1918.13 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3494.671112

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

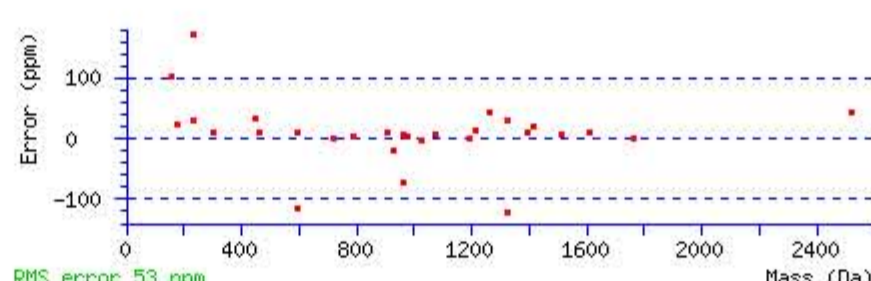
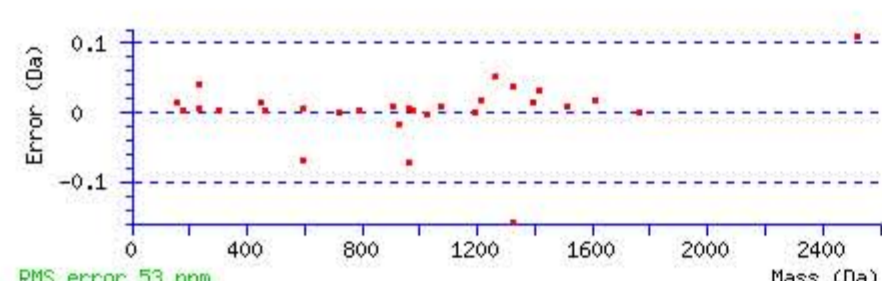
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 59 Expect: 2.7e-005

Matches : 29/318 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	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



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
59.0	3494.671112	0.011624	GTELQHLLHAVVPGPWQEDVADAEECAGR
29.8	3494.671112	0.011624	GTELQHLLHAVVPGPWQEDVADAEECAGR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **WSAETPHKQFTFTSEPHAQLEENFCR**

Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

Match to Query 67845: 3584.663820 from(717.940040,5+) rtinseconds(2036) index(69024)

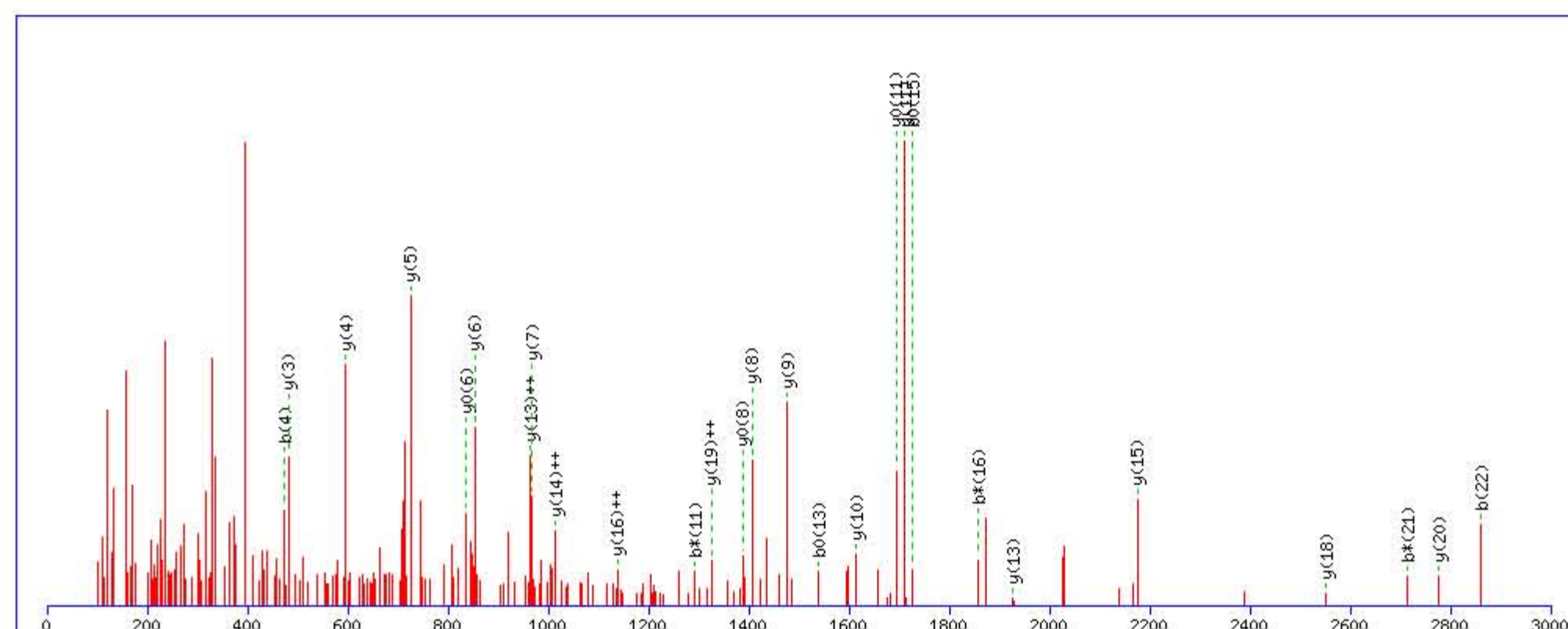
Title: Locus:1.1.1.1646.10 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3584.660538

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

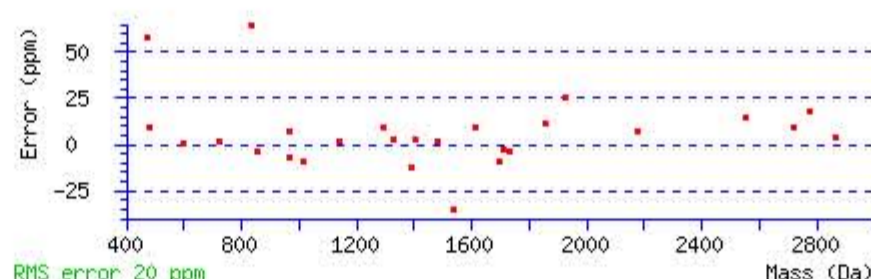
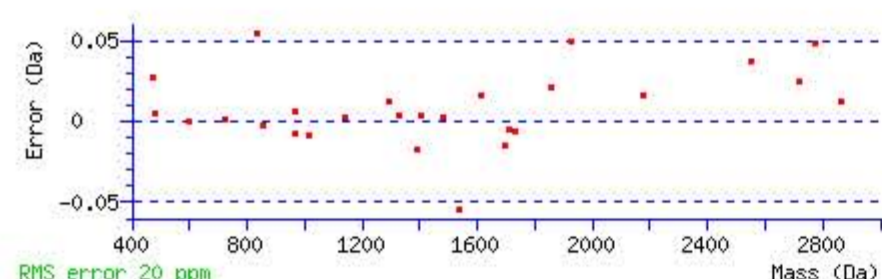
Variable modifications:

Q20 : Biotin:Thermo-21345 (Q)

Ions Score: 67 Expect: 3.1e-006

Matches : 27/288 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	187.086589	94.046932					W							27
2	274.118617	137.562947			256.108052	128.557664	S	3399.588510	1700.297893	3382.561961	1691.784618	3381.577945	1691.292610	26
3	345.155731	173.081504			327.145166	164.076221	A	3312.556482	1656.781879	3295.529933	1648.268605	3294.545917	1647.776597	25
4	474.198324	237.602800			456.187759	228.597518	E	3241.519368	1621.263322	3224.492819	1612.750047	3223.508803	1612.258040	24
5	575.246003	288.126640			557.235438	279.121357	T	3112.476775	1556.742026	3095.450226	1548.228751	3094.466210	1547.736743	23
6	672.298767	336.653022			654.288202	327.647739	P	3011.429096	1506.218186	2994.402547	1497.704912	2993.418531	1497.212904	22
7	809.357679	405.182478			791.347114	396.177195	H	2914.376332	1457.691804	2897.349783	1449.178530	2896.365767	1448.686522	21
8	937.452642	469.229959	920.426093	460.716685	919.442077	460.224677	K	2777.317420	1389.162348	2760.290871	1380.649074	2759.306855	1380.157066	20
9	1034.505406	517.756341	1017.478857	509.243067	1016.494841	508.751059	P	2649.222457	1325.114867	2632.195908	1316.601592	2631.211892	1316.109584	19
10	1162.563984	581.785630	1145.537435	573.272356	1144.553419	572.780348	Q	2552.169693	1276.588485	2535.143144	1268.075210	2534.159128	1267.583202	18
11	1309.632398	655.319837	1292.605849	646.806563	1291.621833	646.314555	F	2424.111115	1212.559196	2407.084566	1204.045921	2406.100550	1203.553913	17
12	1410.680077	705.843677	1393.653528	697.330402	1392.669512	696.838394	T	2277.042701	1139.024988	2260.016152	1130.511714	2259.032136	1130.019706	16
13	1557.748491	779.377884	1540.721942	770.864609	1539.737926	770.372601	F	2175.995022	1088.501149	2158.968473	1079.987874	2157.984457	1079.495866	15
14	1658.796170	829.901723	1641.769621	821.388449	1640.785605	820.896441	T	2028.926608	1014.966942	2011.900059	1006.453668	2010.916043	1005.961660	14
15	1745.828198	873.417737	1728.801649	864.904463	1727.817633	864.412455	S	1927.878929	964.443103	1910.852380	955.929828	1909.868364	955.437820	13
16	1874.870791	937.939034	1857.844242	929.425759	1856.860226	928.933751	E	1840.846901	920.927089	1823.820352	912.413814	1822.836336	911.921806	12
17	1971.923555	986.465416	1954.897006	977.952141	1953.912990	977.460133	P	1711.804308	856.405792	1694.777759	847.892518	1693.793743	847.400510	11
18	2108.982467	1054.994872	2091.955918	1046.481597	2090.971902	1045.989589	H	1614.751544	807.879410	1597.724995	799.366136	1596.740979	798.874128	10
19	2180.019581	1090.513429	2162.993032	1082.000154	2162.009016	1081.508146	A	1477.692632	739.349954	1460.666083	730.836680	1459.682067	730.344672	9
20	2619.244907	1310.126092	2602.218358	1301.612817	2601.234342	1301.120809	Q	1406.655518	703.831397	1389.628969	695.318123	1388.644953	694.826115	8
21	2732.328971	1366.668124	2715.302422	1358.154849	2714.318406	1357.662841	L	967.430192	484.218734	950.403643	475.705460	949.419627	475.213452	7
22	2861.371564	1431.189420	2844.345015	1422.676146	2843.360999	1422.184138	E	854.346128	427.676702	837.319579	419.163427	836.335563	418.671419	6
23	2990.414157	1495.710717	2973.387608	1487.197442	2972.403592	1486.705434	E	725.303535	363.155405	708.276986	354.642131	707.292970	354.150123	5
24	3104.457084	1552.732180	3087.430535	1544.218906	3086.446519	1543.726898	N	596.260942	298.634109	579.234393	290.120834			4
25	3251.525498	1626.266387	3234.498949	1617.753113	3233.514933	1617.261105	F	482.218015	241.612645	465.191466	233.099371			3
26	3411.556147	1706.281712	3394.529598	1697.768437	3393.545582	1697.276429	C	335.149601	168.078438	318.123052	159.565164			2
27							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [WSAETPHKQFTFTSEPHAQLEENFCR](#)

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.8	3584.660538	0.003282	WSAETPHKQFTFTSEPHAQLEENFCR
9.9	3584.660538	0.003282	WSAETPHKQFTFTSEPHAQLEENFCR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **FTCACPDQFK**

Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

Match to Query 36415: 1583.703568 from(792.859060,2+) rtinseconds(1921) index(52226)

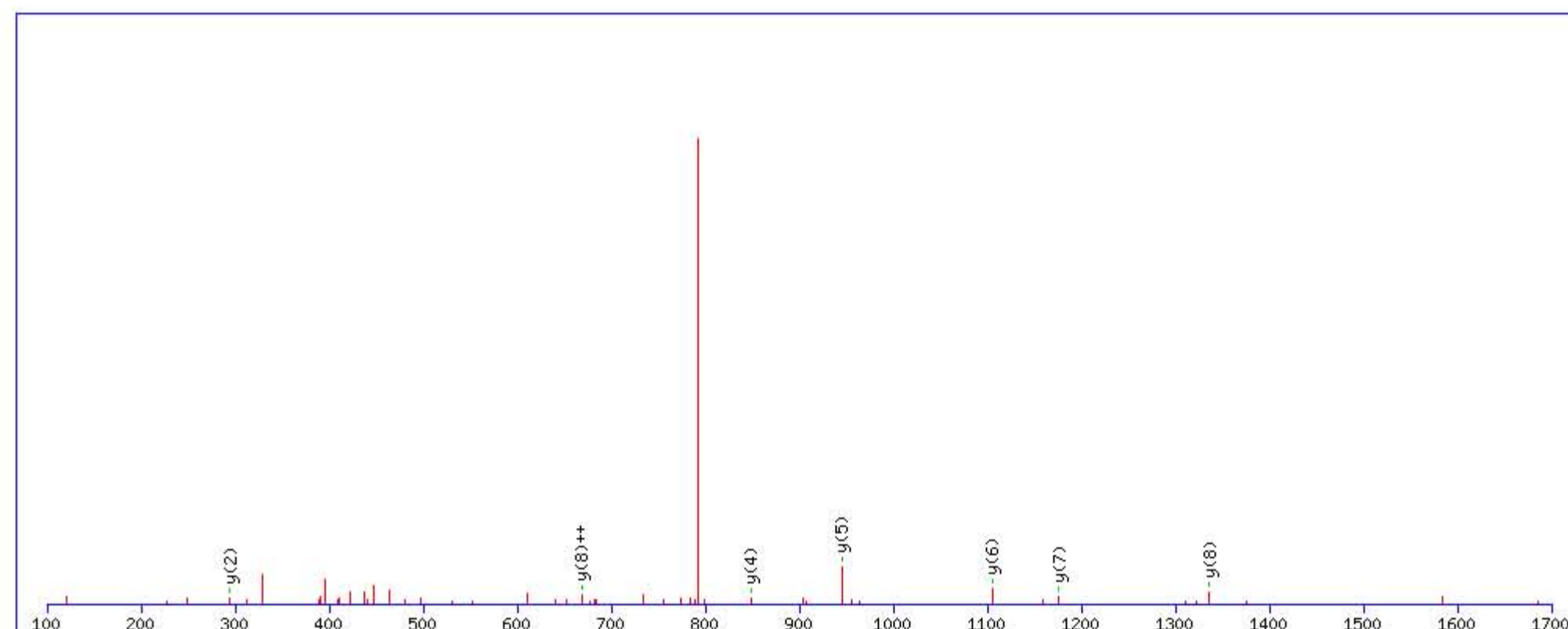
Title: Locus:1.1.1.1284.22 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1583.693497

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

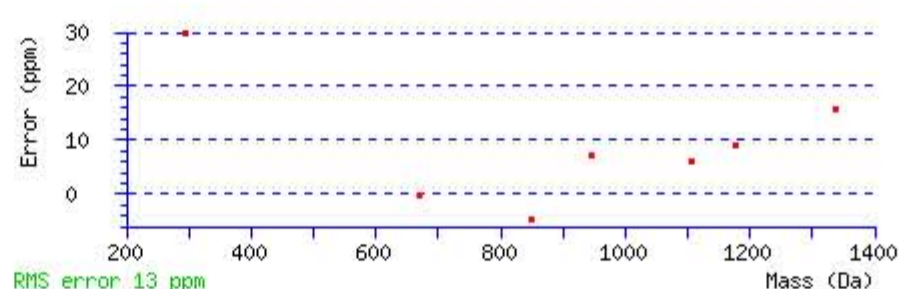
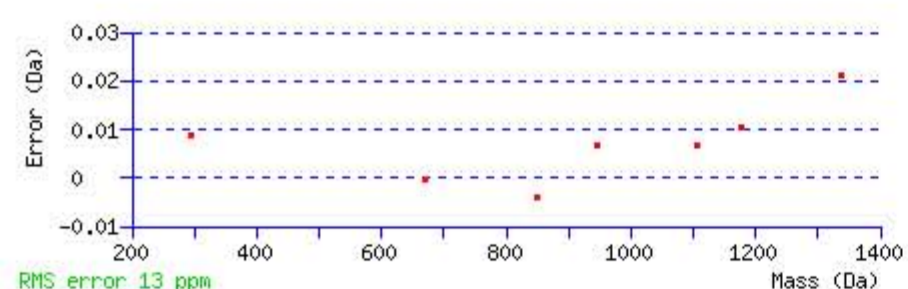
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.0086

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	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
29.5	1583.693497	0.010071	FTCACPDQFK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GQCLITQSPYYR**

Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

Match to Query 44417: 1892.934372 from(631.985400,3+) rtinseconds(2154) index(53925)

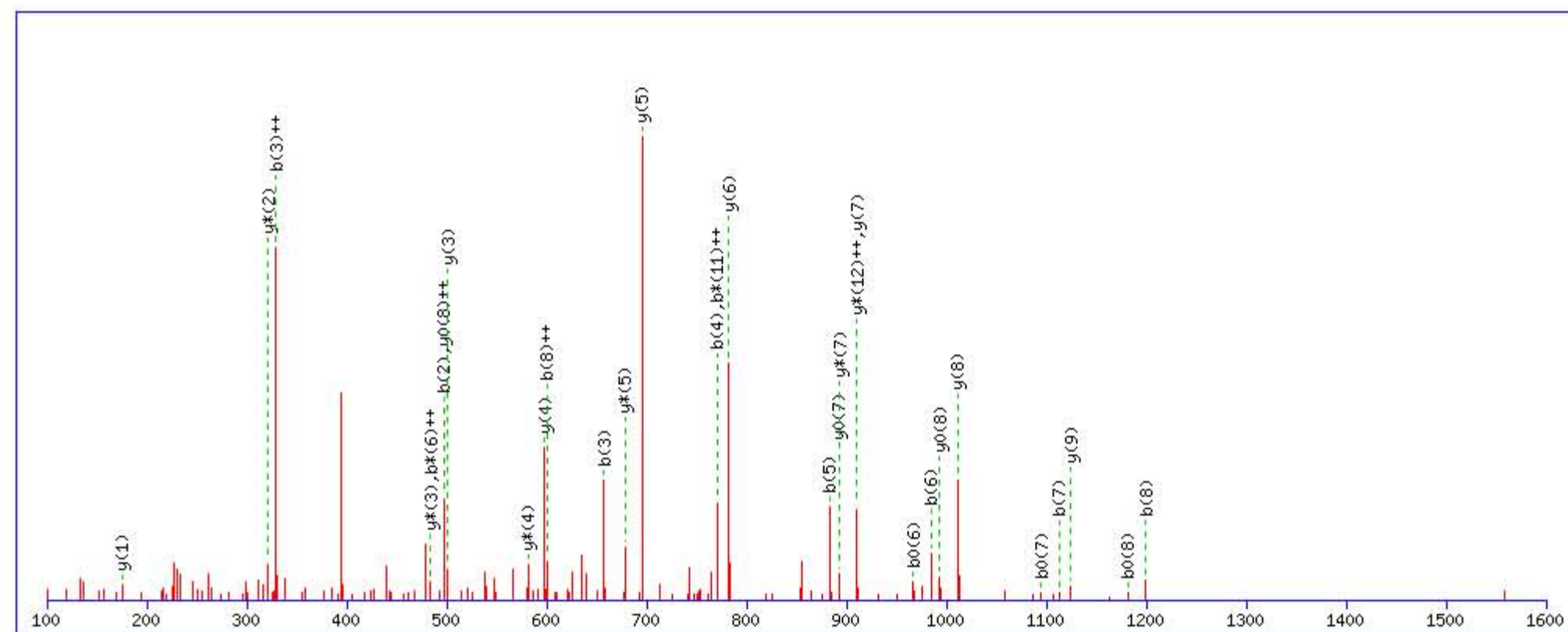
Title: Locus:1.1.1.1365.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1892.927704

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

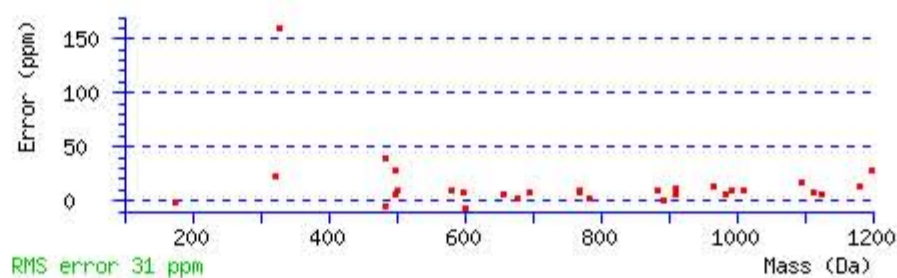
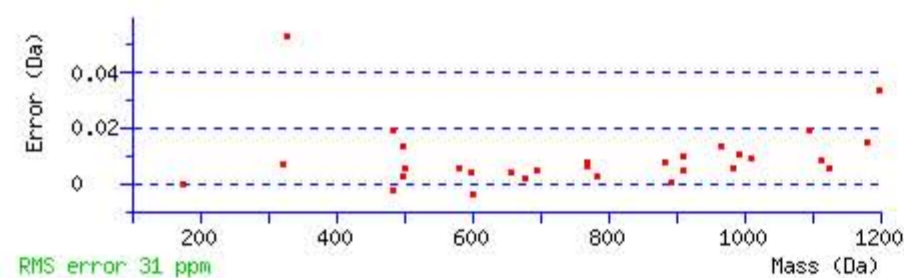
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 47 Expect: 6.5e-005

Matches : 31/122 fragment ions using 45 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							13
2	497.254066	249.130671	480.227517	240.617397			Q	1836.913526	918.960401	1819.886977	910.447127	1818.902961	909.955119	12
3	657.284715	329.145996	640.258166	320.632721			C	1397.688200	699.347738	1380.661651	690.834464	1379.677635	690.342456	11
4	770.368779	385.688028	753.342230	377.174753			L	1237.657551	619.332414	1220.631002	610.819139	1219.646986	610.327131	10
5	883.452843	442.230060	866.426294	433.716785			I	1124.573487	562.790382	1107.546938	554.277107	1106.562922	553.785099	9
6	984.500522	492.753899	967.473973	484.240625	966.489957	483.748617	T	1011.489423	506.248350	994.462874	497.735075	993.478858	497.243067	8
7	1112.559100	556.783188	1095.532551	548.269914	1094.548535	547.777906	Q	910.441744	455.724510	893.415195	447.211236	892.431179	446.719228	7
8	1199.591128	600.299202	1182.564579	591.785928	1181.580563	591.293920	S	782.383166	391.695221	765.356617	383.181947	764.372601	382.689939	6
9	1296.643892	648.825584	1279.617343	640.312310	1278.633327	639.820302	P	695.351138	348.179207	678.324589	339.665933			5
10	1393.696656	697.351966	1376.670107	688.838692	1375.686091	688.346684	P	598.298374	299.652825	581.271825	291.139551			4
11	1556.759985	778.883631	1539.733436	770.370356	1538.749420	769.878348	Y	501.245610	251.126443	484.219061	242.613169			3
12	1719.823314	860.415295	1702.796765	851.902021	1701.812749	851.410013	Y	338.182281	169.594778	321.155732	161.081504			2
13							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **GQCLITQSPYYR**

(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	1892.927704	0.006668	GQCLITQSPYYR
14.4	1892.927704	0.006668	GQCLITQSPYYR
2.8	1892.912445	0.021927	MAFAPPKNTDGPKMQTK

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

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 57961: 2647.304176 from(662.833320,4+) rtinseconds(2354) index(70792)

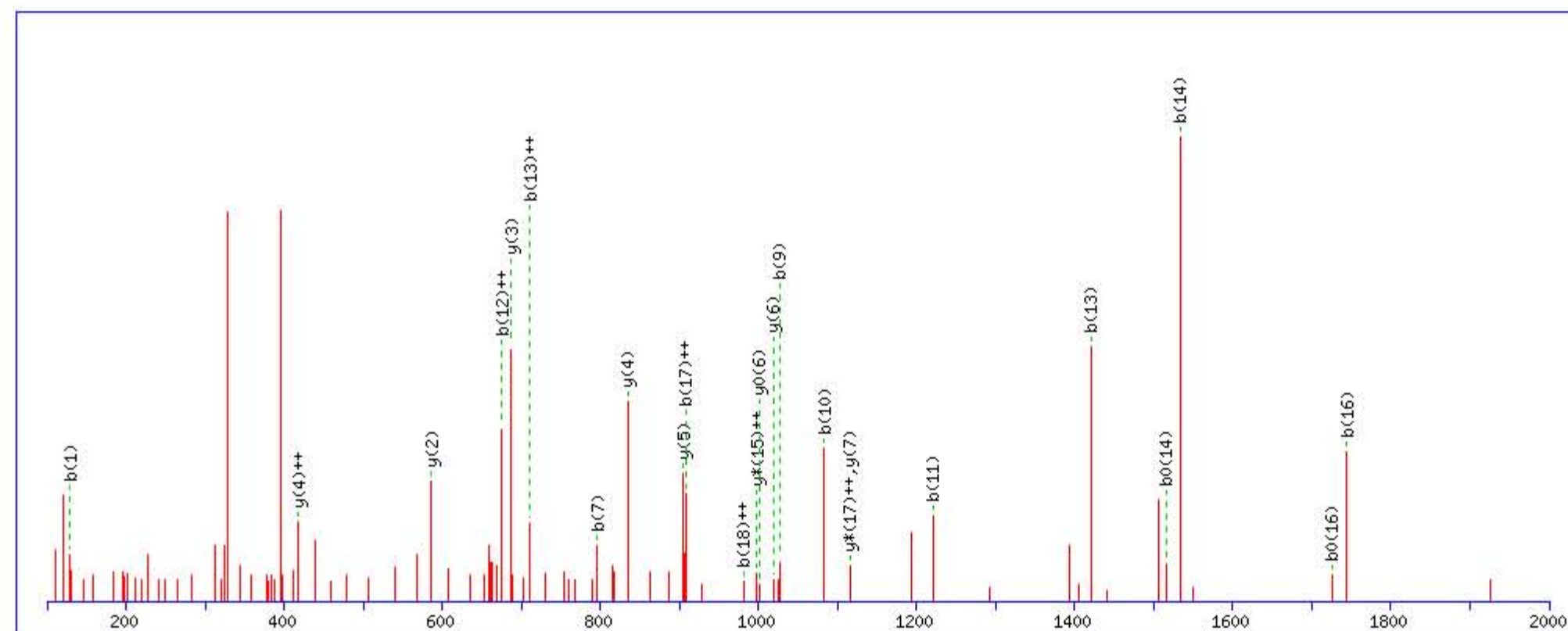
Title: Locus:1.1.1.1757.13 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2647.296082

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

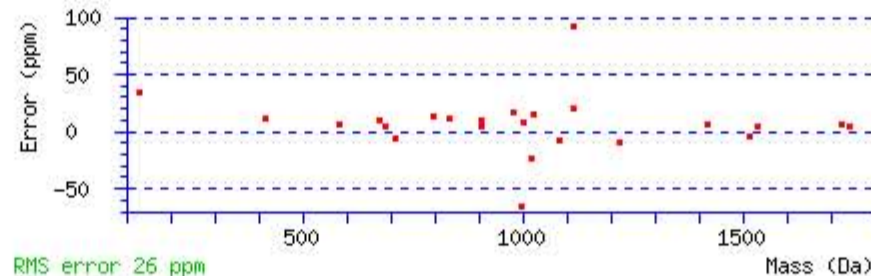
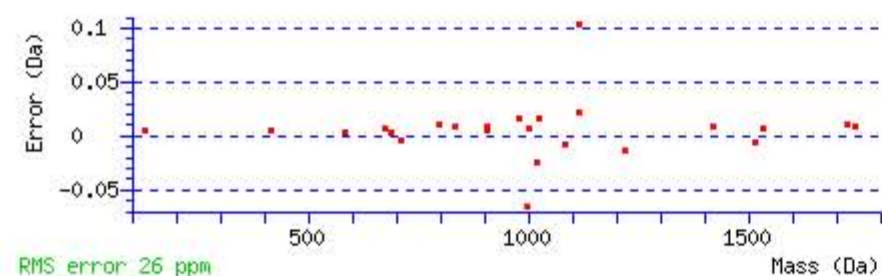
Variable modifications:

Q20 : Biotin:Thermo-21345 (Q)

Ions Score: 38 Expect: 0.0047

Matches : 24/232 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	129.102239	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
37.9	2647.296082	0.008094	KGDTFSCMVGHEALPLAFTQK

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

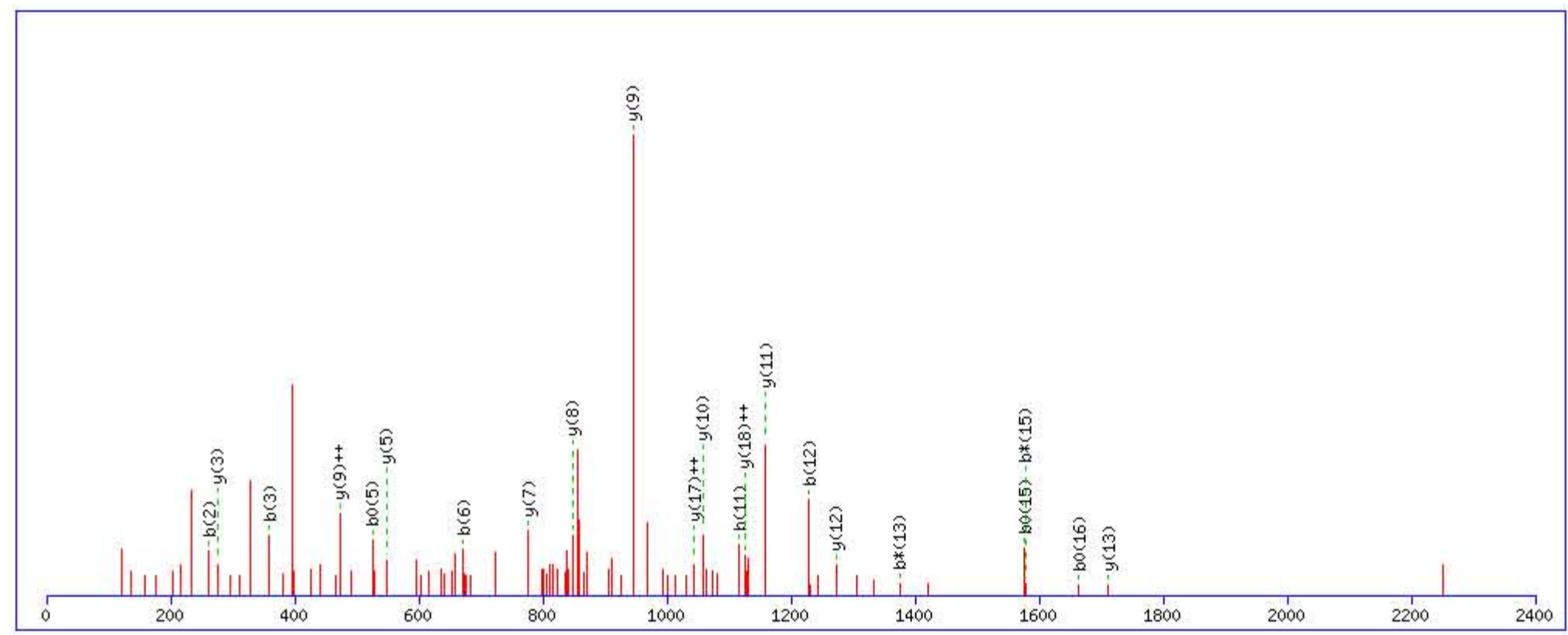
MASCOT Search Results

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

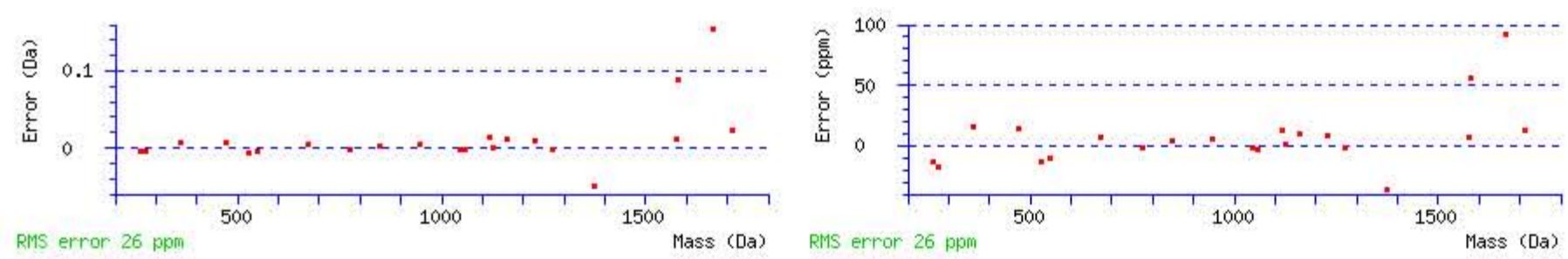
Match to Query 66792: 3478.695096 from(870.681050,4+) rtinseconds(2591) index(40067)
 Title: Locus:1.1.1.3321.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 3478.674866
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q18 : Biotin:Thermo-21345 (Q)
 Ions Score: 40 Expect: 0.0025
 Matches : 22/328 fragment ions using 44 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.050203	58.028740	98.023654	49.515465			N							30
2	262.118617	131.562946	245.092068	123.049672			F	3365.639210	1683.323243	3348.612661	1674.809968	3347.628645	1674.317960	29
3	359.171381	180.089328	342.144832	171.576054			P	3218.570796	1609.789036	3201.544247	1601.275761	3200.560231	1600.783753	28
4	456.224145	228.615710	439.197596	220.102436			P	3121.518032	1561.262654	3104.491483	1552.749379	3103.507467	1552.257371	27
5	543.256173	272.131725	526.229624	263.618450	525.245608	263.126442	S	3024.465268	1512.736272	3007.438719	1504.222997	3006.454703	1503.730989	26
6	671.314751	336.161014	654.288202	327.647739	653.304186	327.155731	Q	2937.433240	1469.220258	2920.406691	1460.706983	2919.422675	1460.214975	25
7	786.341694	393.674485	769.315145	385.161210	768.331129	384.669202	D	2809.374662	1405.190969	2792.348113	1396.677694	2791.364097	1396.185686	24
8	857.378808	429.193042	840.352259	420.679767	839.368243	420.187759	A	2694.347719	1347.677497	2677.321170	1339.164223	2676.337154	1338.672215	23
9	944.410836	472.709056	927.384287	464.195781	926.400271	463.703773	S	2623.310605	1312.158941	2606.284056	1303.645666	2605.300040	1303.153658	22
10	1001.432300	501.219788	984.405751	492.706513	983.421735	492.214505	G	2536.278577	1268.642926	2519.252028	1260.129652	2518.268012	1259.637644	21
11	1116.459243	558.733260	1099.432694	550.219985	1098.448678	549.727977	D	2479.257113	1240.132195	2462.230564	1231.618920	2461.246548	1231.126912	20
12	1229.543307	615.275291	1212.516758	606.762017	1211.532742	606.270009	L	2364.230170	1182.618723	2347.203621	1174.105448	2346.219605	1173.613440	19
13	1392.606636	696.806956	1375.580087	688.293682	1374.596071	687.801673	Y	2251.146106	1126.076691	2234.119557	1117.563416	2233.135541	1117.071408	18
14	1493.654315	747.330796	1476.627766	738.817521	1475.643750	738.325513	T	2088.082777	1044.545026	2071.056228	1036.031752	2070.072212	1035.539744	17
15	1594.701994	797.854635	1577.675445	789.341361	1576.691429	788.849353	T	1987.035098	994.021187	1970.008549	985.507913	1969.024533	985.015905	16
16	1681.734022	841.370649	1664.707473	832.857375	1663.723457	832.365367	S	1885.987419	943.497348	1868.960870	934.984073	1867.976854	934.492065	15
17	1768.766050	884.886663	1751.739501	876.373389	1750.755485	875.881381	S	1798.955391	899.981334	1781.928842	891.468059	1780.944826	890.976051	14
18	2207.991376	1104.499326	2190.964827	1095.986051	2189.980811	1095.494043	Q	1711.923363	856.465320	1694.896814	847.952045	1693.912798	847.460037	13
19	2321.075440	1161.041358	2304.048891	1152.528083	2303.064875	1152.036075	L	1272.698037	636.852657	1255.671488	628.339382	1254.687472	627.847374	12
20	2422.123119	1211.565197	2405.096570	1203.051923	2404.112554	1202.559915	T	1159.613973	580.310625	1142.587424	571.797350	1141.603408	571.305342	11
21	2535.207183	1268.107229	2518.180634	1259.593955	2517.196618	1259.101947	L	1058.566294	529.786785	1041.539745	521.273511	1040.555729	520.781503	10
22	2632.259947	1316.633611	2615.233398	1308.120337	2614.249382	1307.628329	P	945.482230	473.244753	928.455681	464.731479	927.471665	464.239471	9
23	2703.297061	1352.152169	2686.270512	1343.638894	2685.286496	1343.146886	A	848.429466	424.718371	831.402917	416.205097	830.418901	415.713089	8
24	2804.344740	1402.676008	2787.318191	1394.162733	2786.334175	1393.670725	T	777.392352	389.199814	760.365803	380.686540	759.381787	380.194532	7
25	2932.403318	1466.705297	2915.376769	1458.192022	2914.392753	1457.700015	Q	676.344673	338.675975	659.318124	330.162700			6
26	3092.433967	1546.720621	3075.407418	1538.207347	3074.423402	1537.715339	C	548.286095	274.646686	531.259546	266.133411			5
27	3205.518031	1603.262653	3188.491482	1594.749379	3187.507466	1594.257371	L	388.255446	194.631361	371.228897	186.118087			4
28	3276.555145	1638.781211	3259.528596	1630.267936	3258.544580	1629.775928	A	275.171382	138.089329	258.144833	129.576055			3
29	3333.576609	1667.291943	3316.550060	1658.778668	3315.566044	1658.286660	G	204.134268	102.570772	187.107719	94.057497			2
30							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.7	3478.674866	0.020230	NFPPSQDASGDLYTTSSQLTLPATQCLAGK
16.1	3478.674866	0.020230	NFPPSQDASGDLYTTSSQLTLPATQCLAGK
9.3	3478.674866	0.020230	NFPPSQDASGDLYTTSSQLTLPATQCLAGK

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 23790: 1220.655448 from(611.335000,2+) rtinseconds(1442) index(65416)

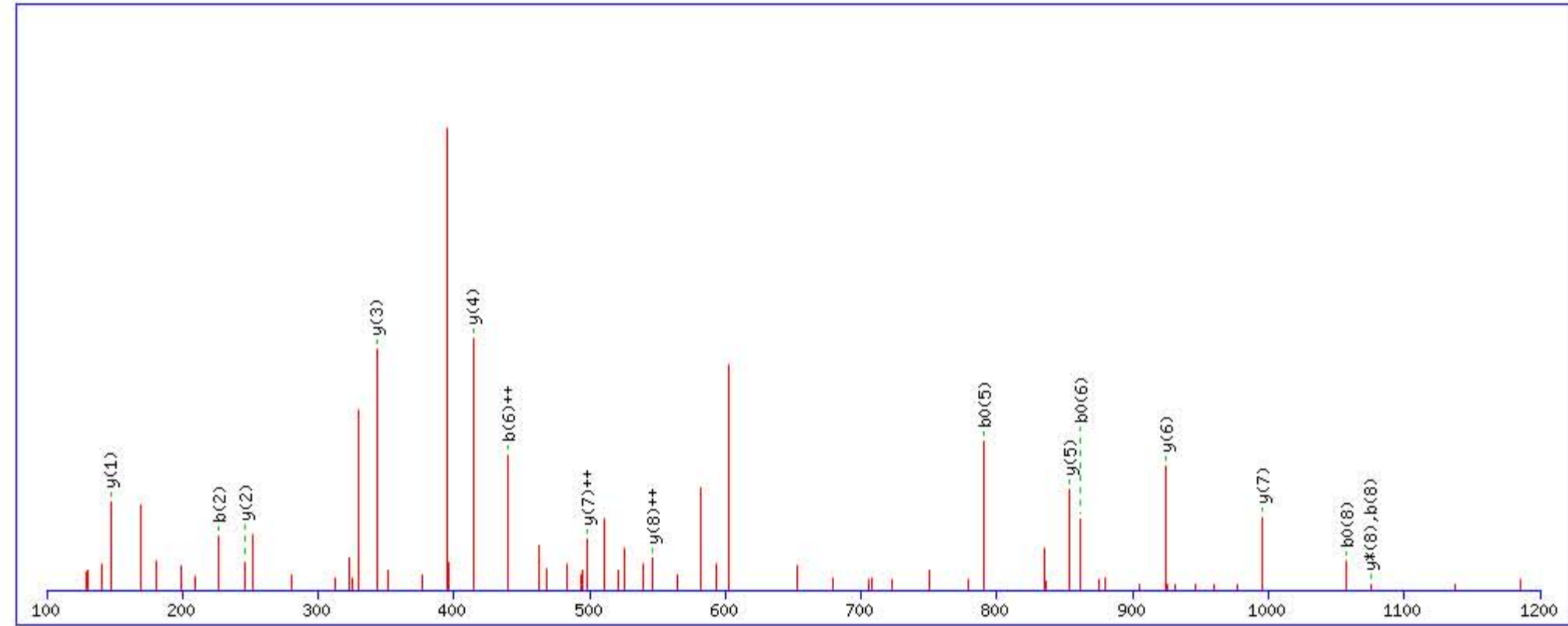
Title: Locus:1.1.1.1439.22 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1220.658707

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

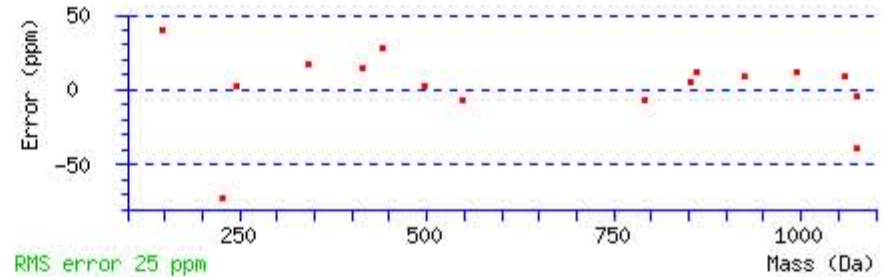
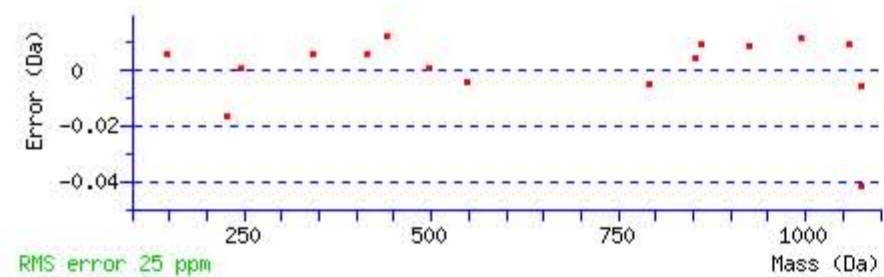
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 42 Expect: 0.0012

Matches : 16/72 fragment ions using 31 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
41.7	1220.658707	-0.003259	EPAAQAPVK
9.9	1220.658722	-0.003274	EQNVPPVK
8.9	1220.644806	0.010642	GGHVQREK
6.4	1220.669937	-0.014489	IIAHSNQK
6.4	1220.640076	0.015372	LLAEYTGAAQK
6.1	1220.669937	-0.014489	QELKHAGK
5.8	1220.637589	0.017859	NHMFFIAITK
3.3	1220.654678	0.000770	SVRMLSGSKEK
2.7	1220.658722	-0.003274	QPNLPDVK
2.0	1220.651306	0.004142	TRSSWKSLEK

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 58820: 2746.371642 from(916.464490,3+) rtinseconds(2252) index(70287)

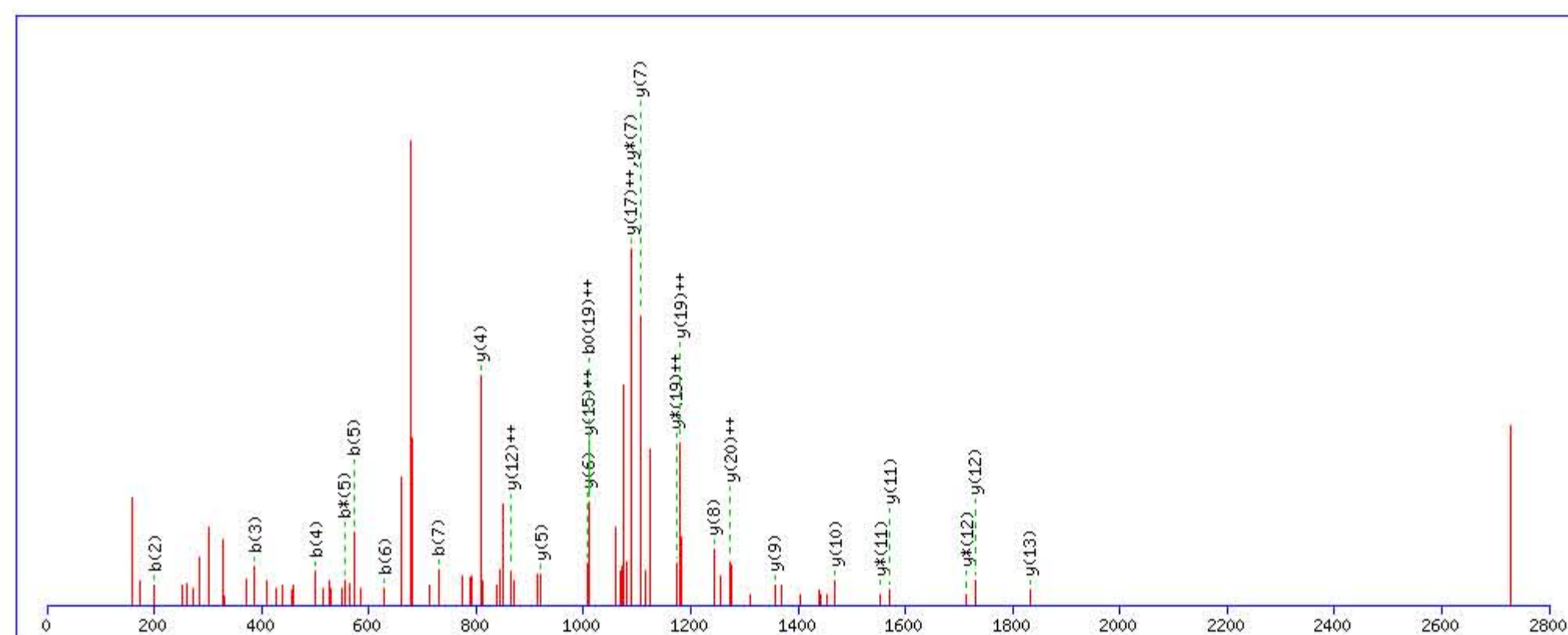
Title: Locus:1.1.1.1721.26 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2746.368332

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

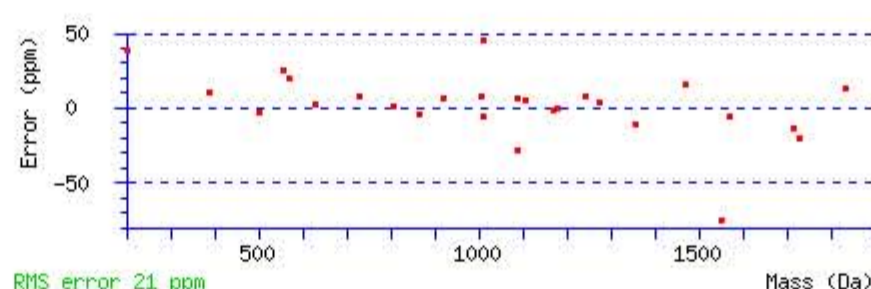
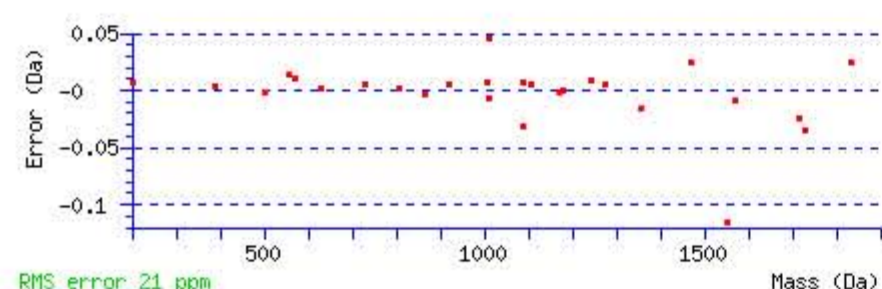
Variable modifications:

Q21 : Biotin:Thermo-21345 (Q)

Ions Score: 50 Expect: 2e-005

Matches : 27/236 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							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
50.5	2746.368332	0.003310	SLWNAGTSVTCTLNHPSLPPQR
0.3	2746.402496	-0.030854	ESLKRVTFALPDDAETEDTGVLNVK

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 33089: 1471.788588 from(736.901570,2+) rtinseconds(2245) index(70233)

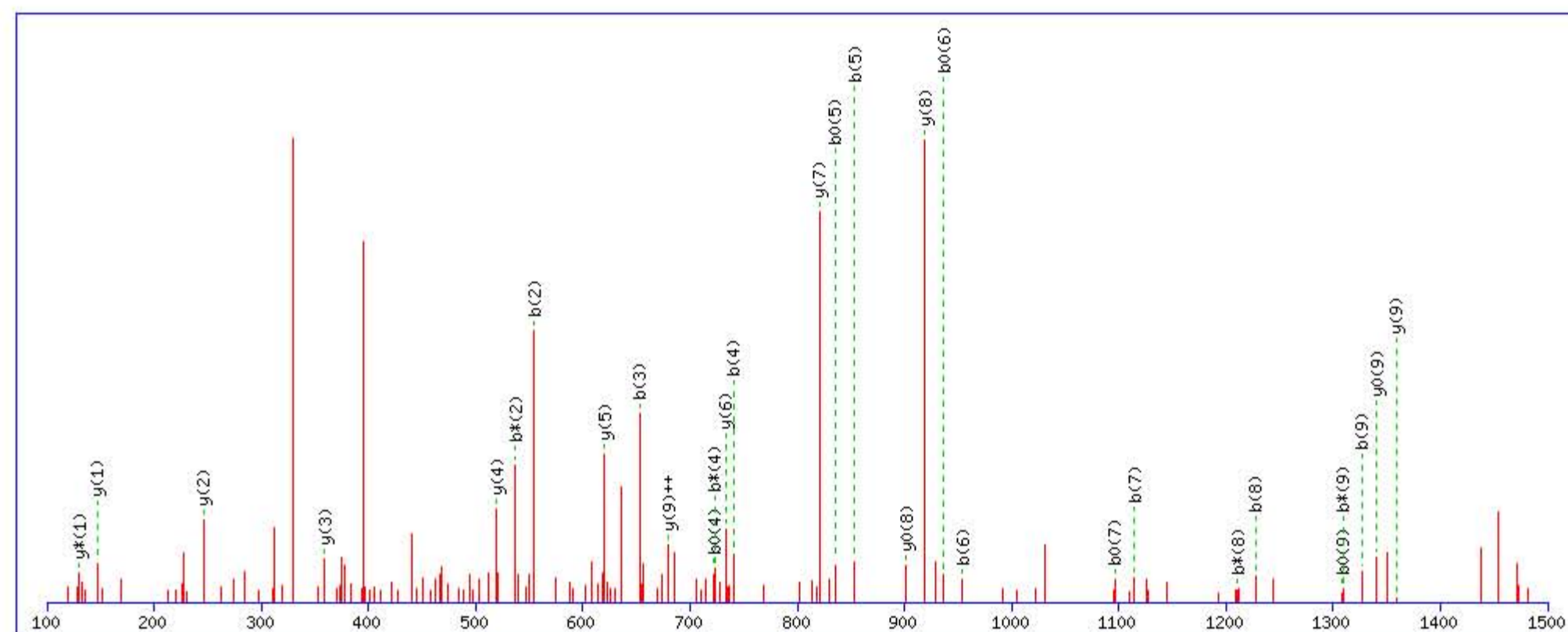
Title: Locus:1.1.1.1719.17 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1471.789093

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

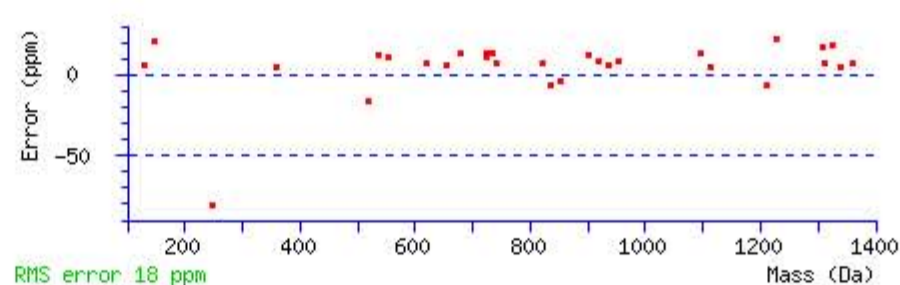
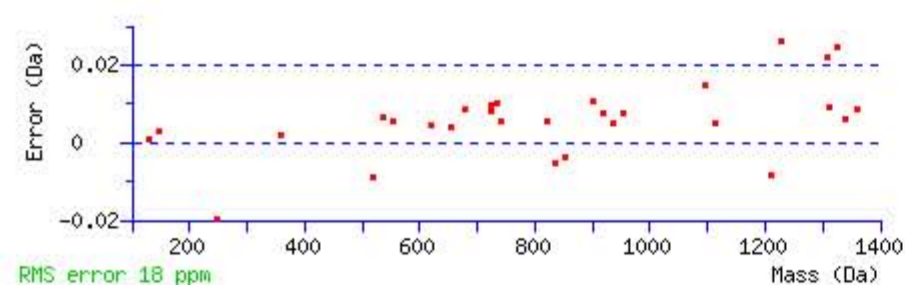
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 44 Expect: 0.00031

Matches : 30/94 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	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
43.5	1471.789093	-0.000505	NQVSLTCLVK
5.8	1471.806793	-0.018205	AAALLAKQAEMEVK
4.4	1471.797592	-0.009004	KYFWDR AFLVK
4.0	1471.803467	-0.014879	EKQG PLLDLFGQK
2.4	1471.799438	-0.010850	EVELDRLRDTVK
1.9	1471.792908	-0.004320	NITINCVKGINAR
1.9	1471.777847	0.010741	QLDMELVSVK
1.3	1471.792221	-0.003633	NESI IPLSPFEVK

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 37103: 1596.828222 from(533.283350,3+) rtinseconds(1978) index(68636)

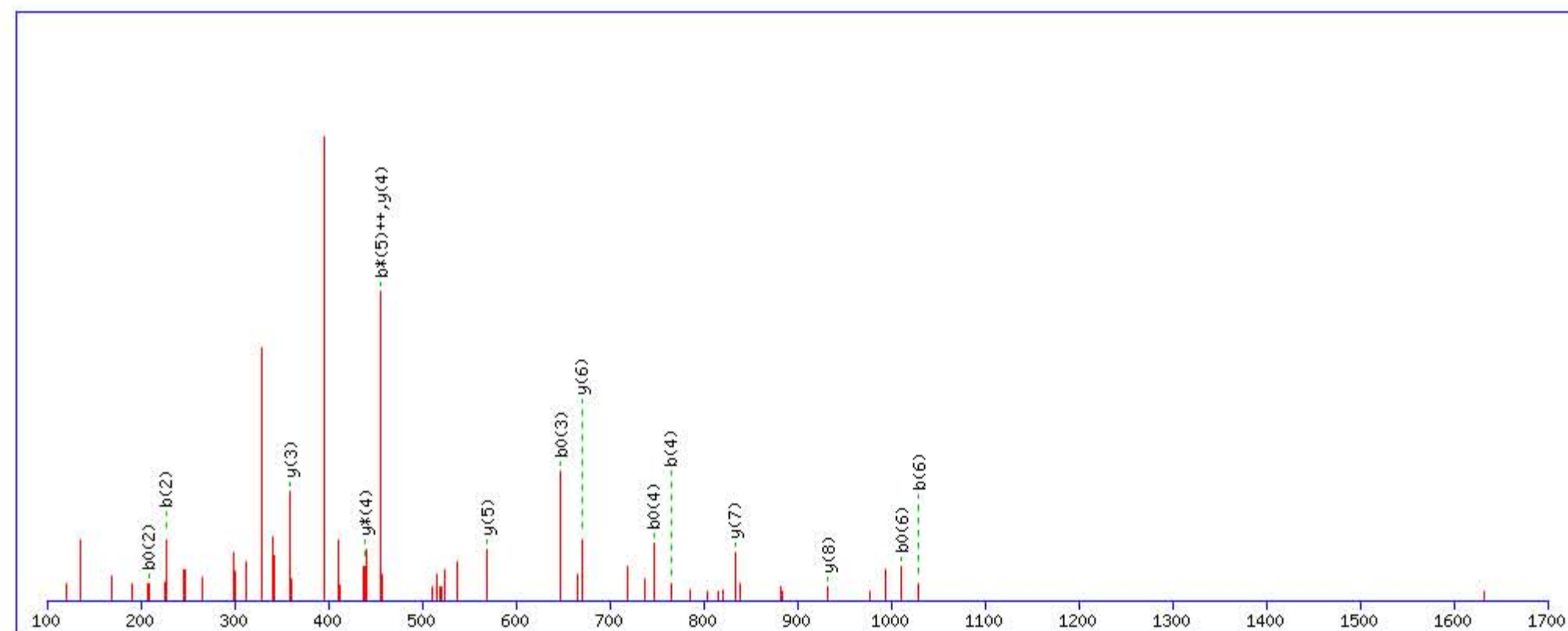
Title: Locus:1.1.1.1626.17 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf.5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1596.833389

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

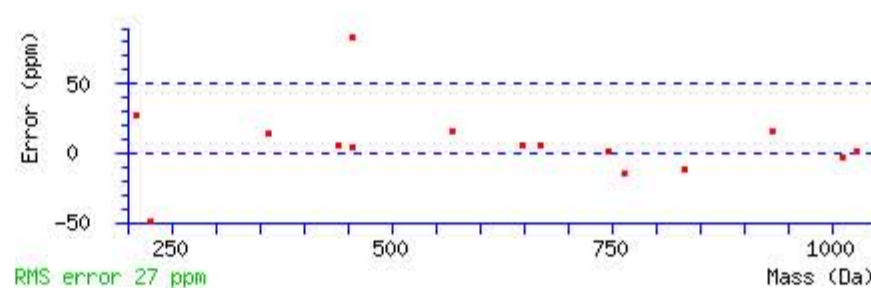
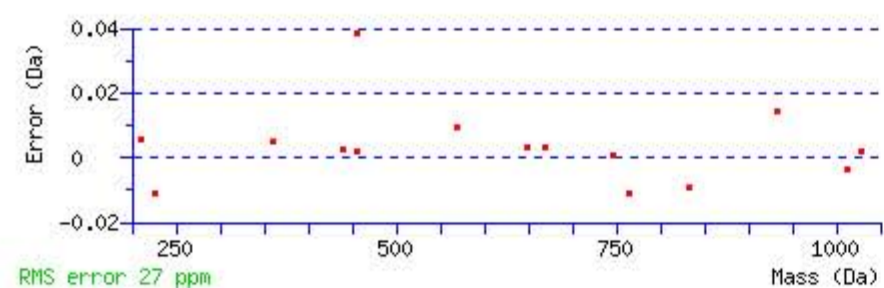
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.058

Matches : 15/114 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	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	$M_r(\text{calc})$:	Delta	Sequence
26.7	1596.833389	-0.005167	EPQVYTLPPSR

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **WQQGNVFSCSVMEALHNHYTQK**

Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

Match to Query 62423: 3111.433920 from(623.294060,5+) rtinseconds(2036) index(6027)

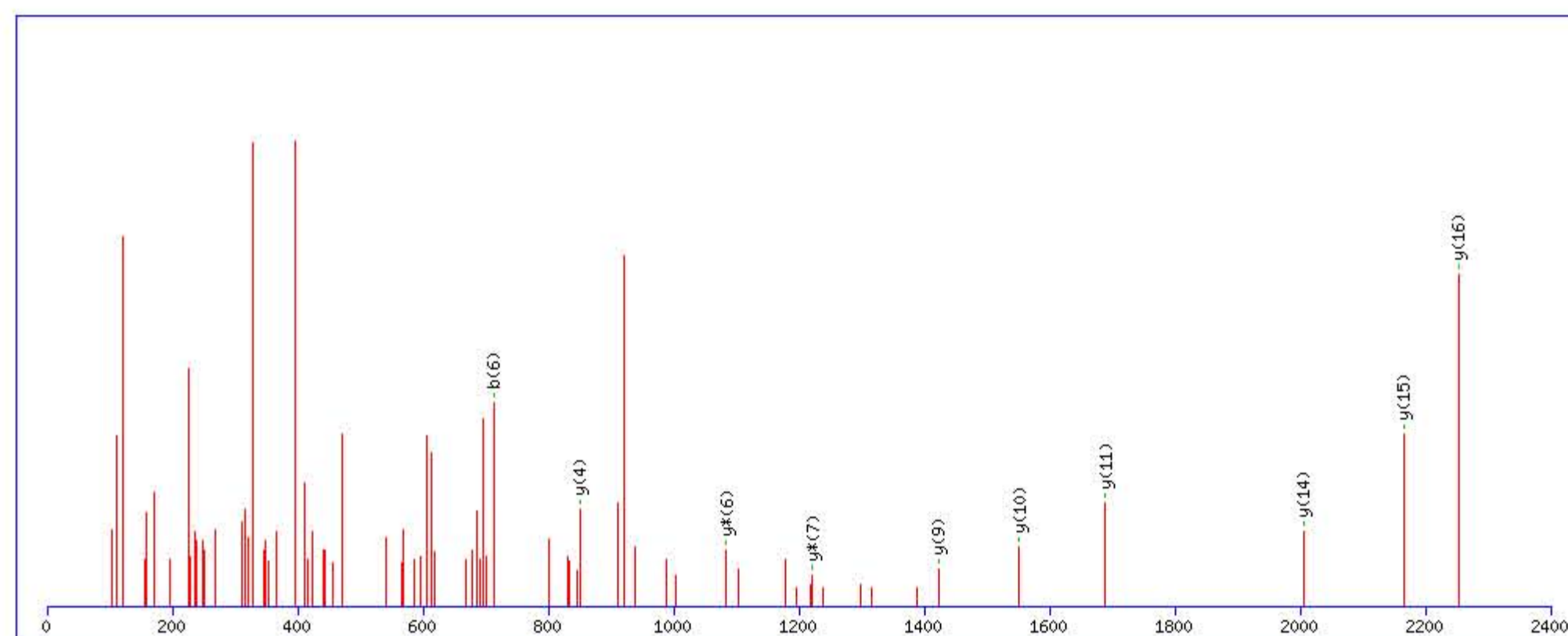
Title: Locus:1.1.1.1518.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3111.426590

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

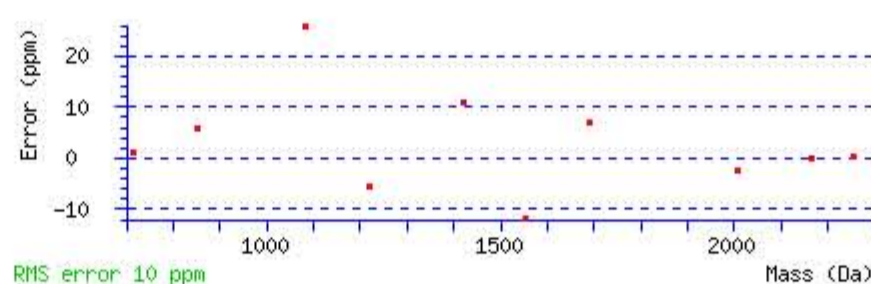
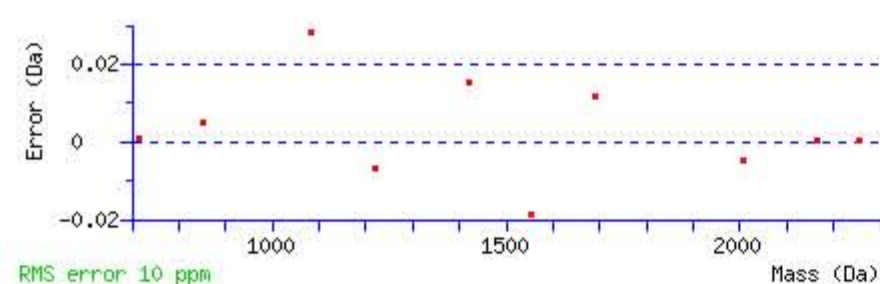
Variable modifications:

Q22 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.038

Matches : 10/244 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	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 **WQQGNVFSCSVMEALHNHYTQK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.7	3111.426590	0.007330	WQQGNVFSCSVMEALHNHYTQK

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 33089: 1471.788588 from(736.901570,2+) rtinseconds(2245) index(70233)

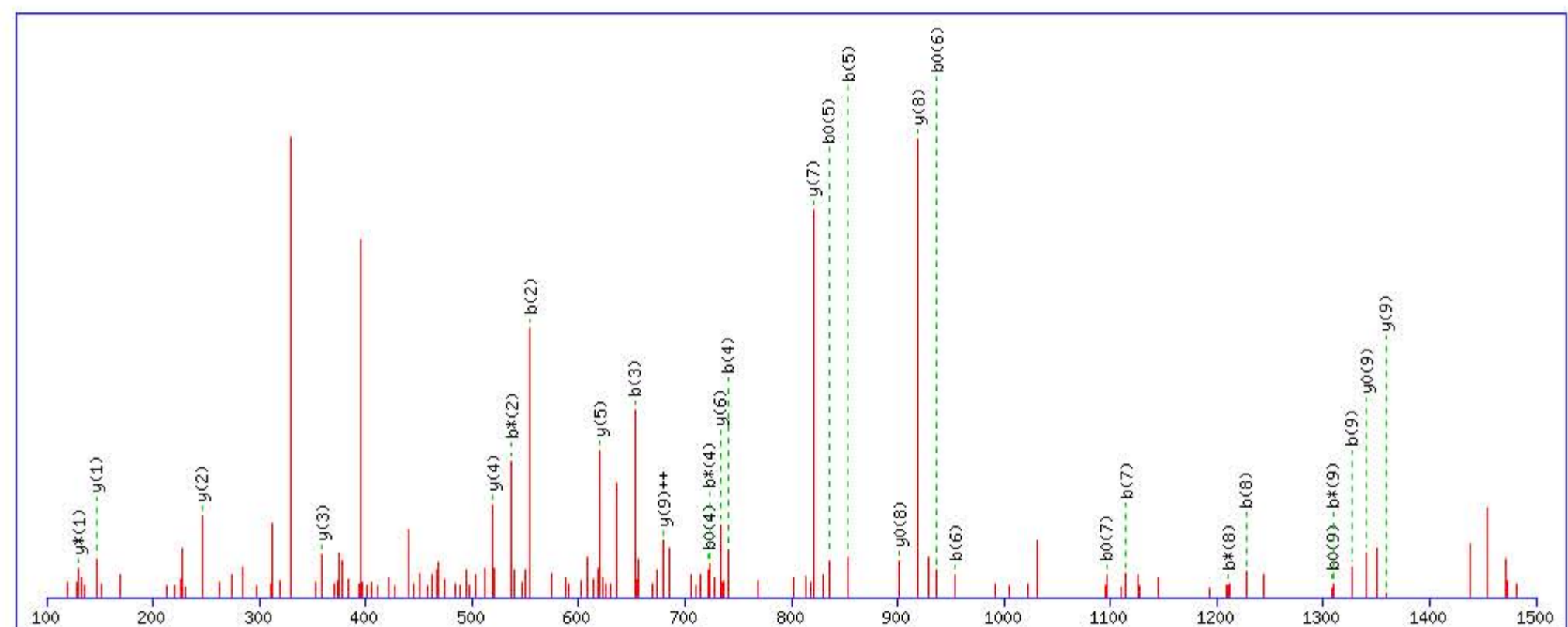
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1471.789093

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

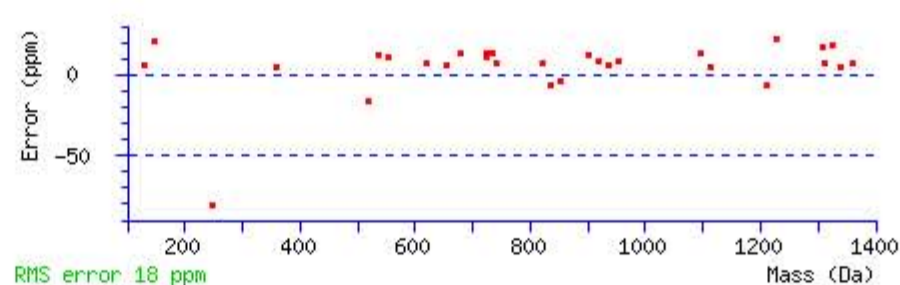
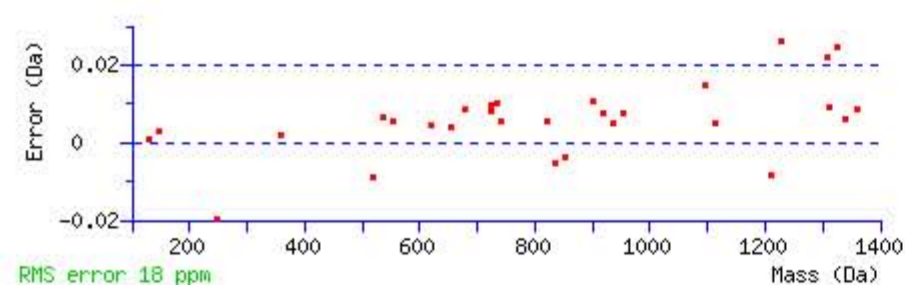
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 44 Expect: 0.00031

Matches : 30/94 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	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
43.5	1471.789093	-0.000505	NQVSLTCLVK
5.8	1471.806793	-0.018205	AAALLAKQAEMEVK
4.4	1471.797592	-0.009004	KYFWDR AFLVK
4.0	1471.803467	-0.014879	EKQG PLLDLFGQK
2.4	1471.799438	-0.010850	EVELDRLRDTVK
1.9	1471.792908	-0.004320	NITINCVKGINAR
1.9	1471.777847	0.010741	QLDMELVSVK
1.3	1471.792221	-0.003633	NESI IPLSPFEVK

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 37103: 1596.828222 from(533.283350,3+) rtinseconds(1978) index(68636)

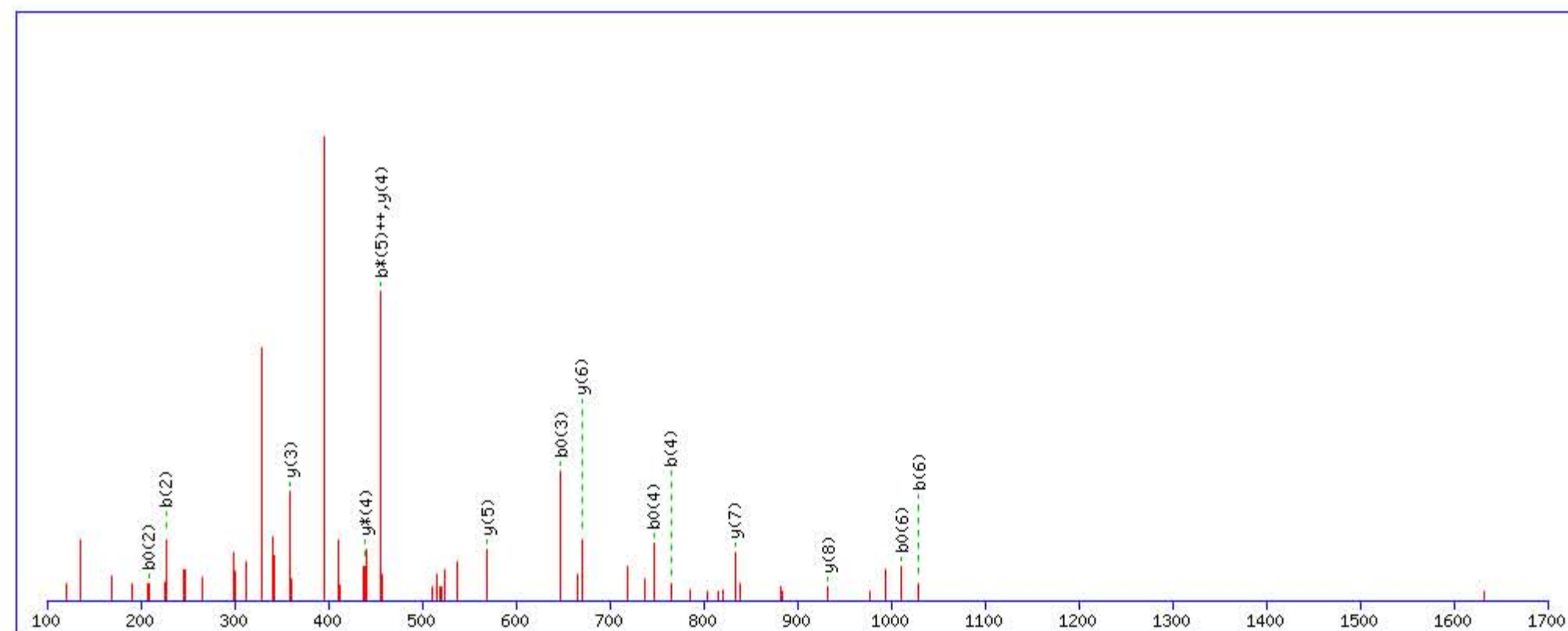
Title: Locus:1.1.1.1626.17 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf.5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1596.833389

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

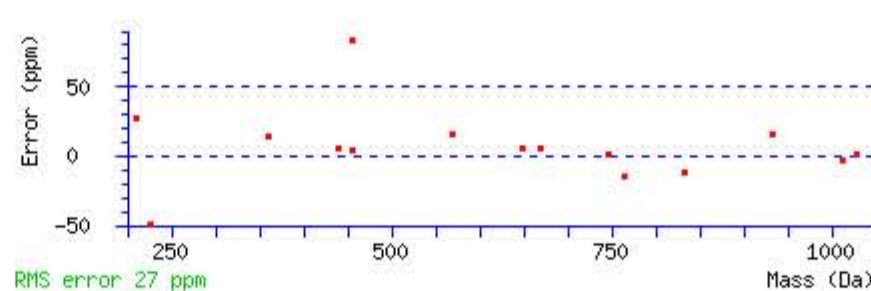
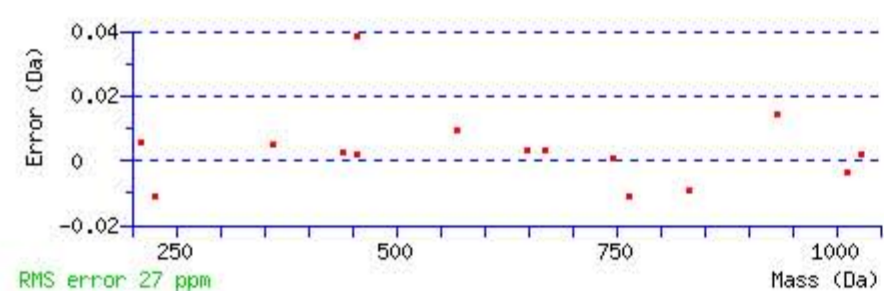
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.058

Matches : 15/114 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	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	$M_r(\text{calc})$:	Delta	Sequence
26.7	1596.833389	-0.005167	EPQVYTLPPSR

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **WQQGNVFSCSVMEALHNHYTQK**

Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

Match to Query 62423: 3111.433920 from(623.294060,5+) rtinseconds(2036) index(6027)

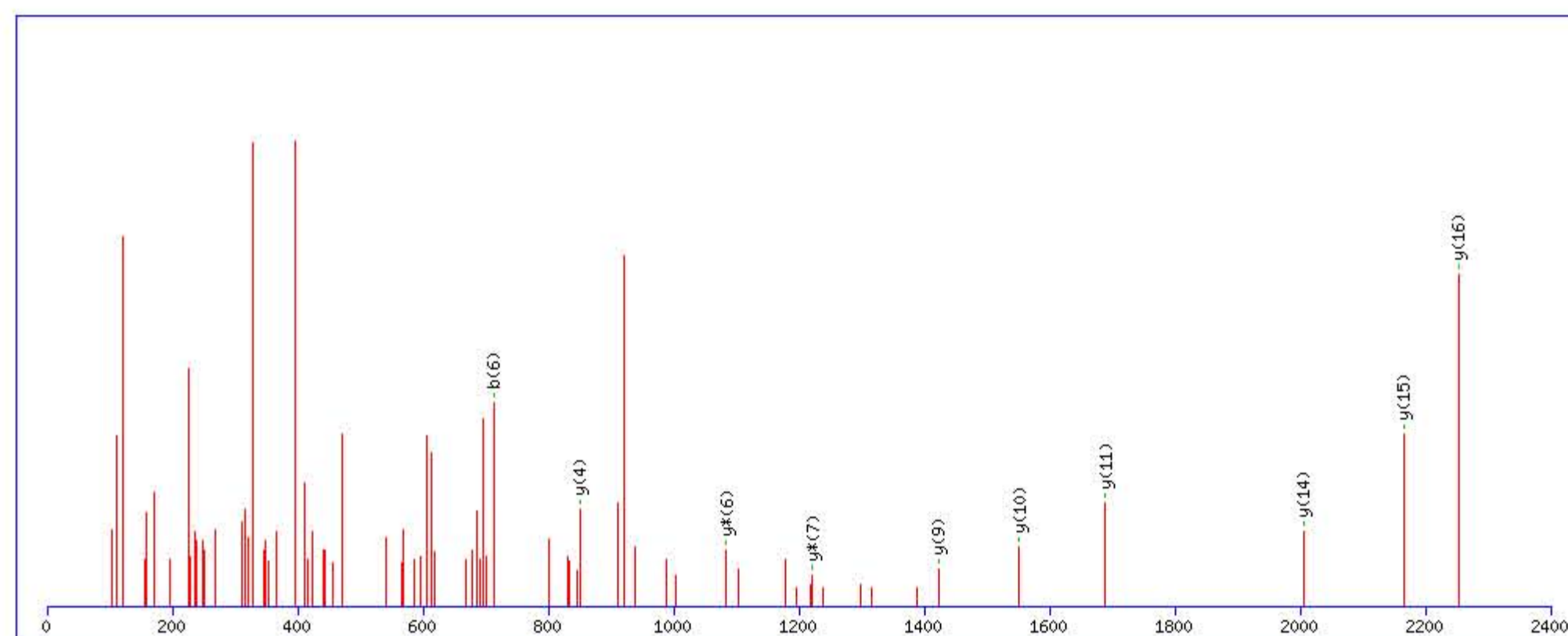
Title: Locus:1.1.1.1518.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3111.426590

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

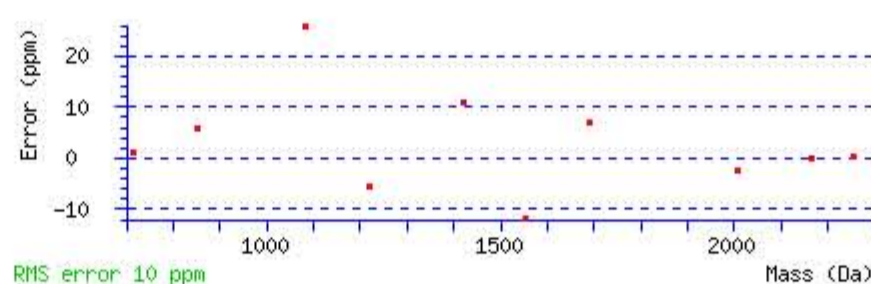
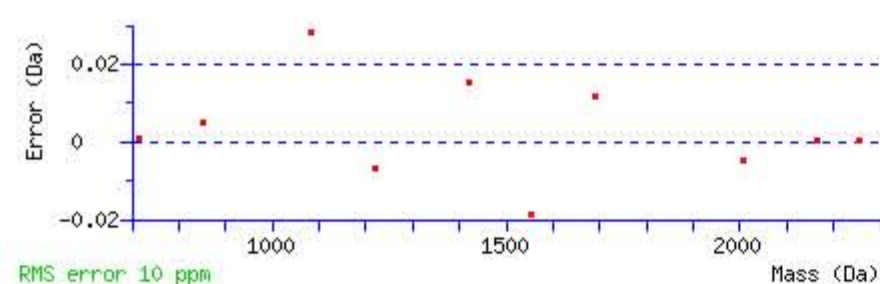
Variable modifications:

Q22 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.038

Matches : 10/244 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	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 **WQQGNVFSCSVMEALHNHYTQK**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.7	3111.426590	0.007330	WQQGNVFSCSVMEALHNHYTQK

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 33089: 1471.788588 from(736.901570,2+) rtinseconds(2245) index(70233)

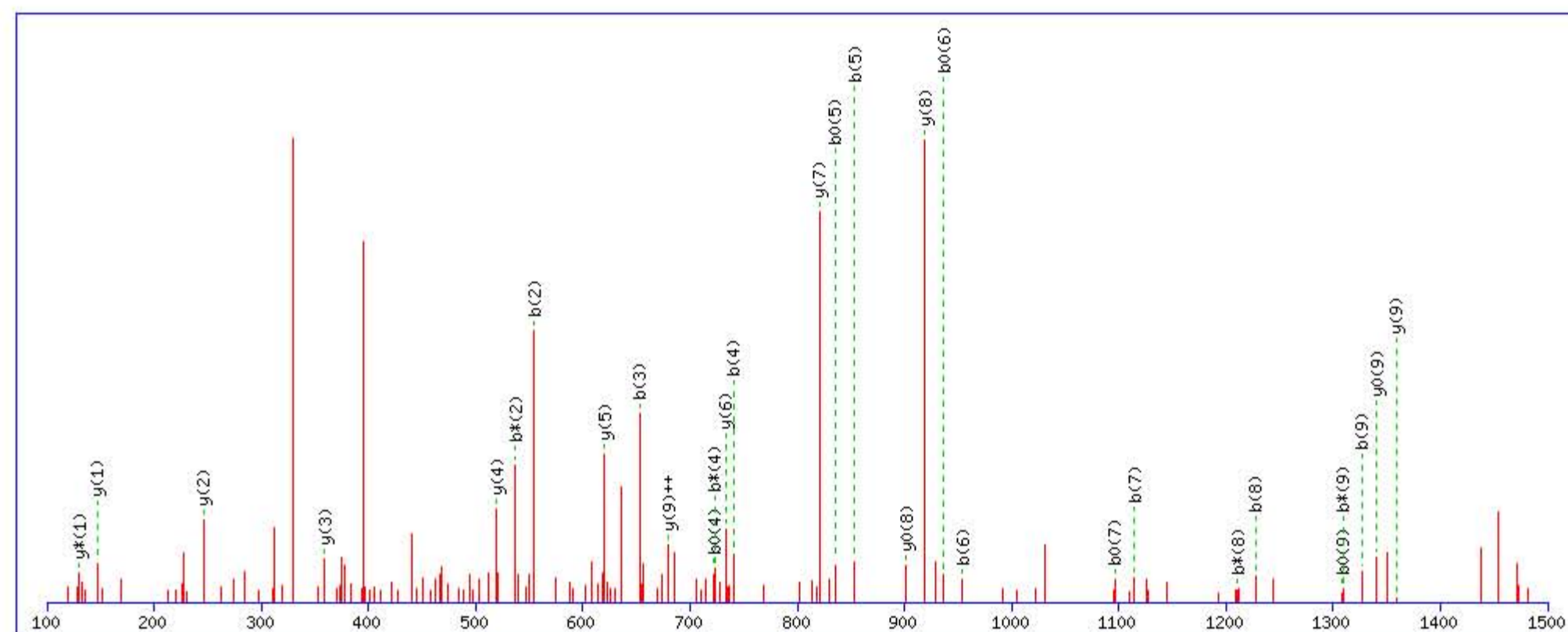
Title: Locus:1.1.1.1719.17 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1471.789093

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

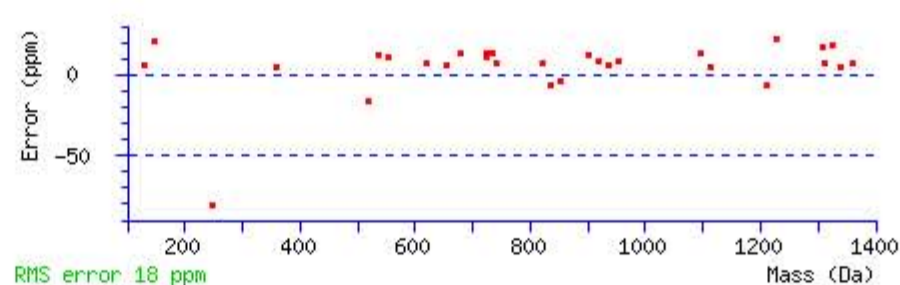
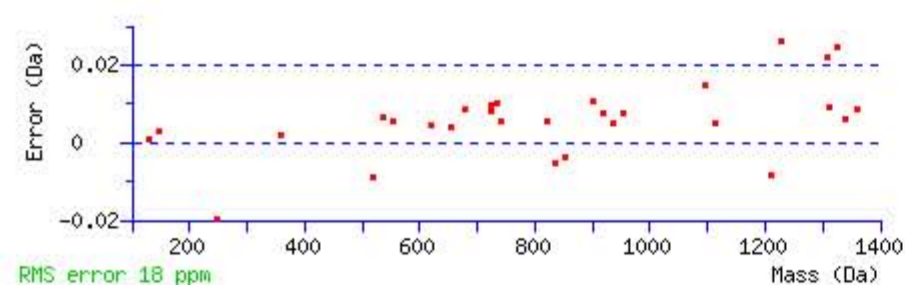
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 44 Expect: 0.00031

Matches : 30/94 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	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
43.5	1471.789093	-0.000505	NQVSLTCLVK
5.8	1471.806793	-0.018205	AAALLAKQAEMEVK
4.4	1471.797592	-0.009004	KYFWDR AFLVK
4.0	1471.803467	-0.014879	EKQG PLLDLFGQK
2.4	1471.799438	-0.010850	EVELDRLRDTVK
1.9	1471.792908	-0.004320	NITINCVKGINAR
1.9	1471.777847	0.010741	QLDMELVSVK
1.3	1471.792221	-0.003633	NESI IPLSPFEVK

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 37103: 1596.828222 from(533.283350,3+) rtinseconds(1978) index(68636)

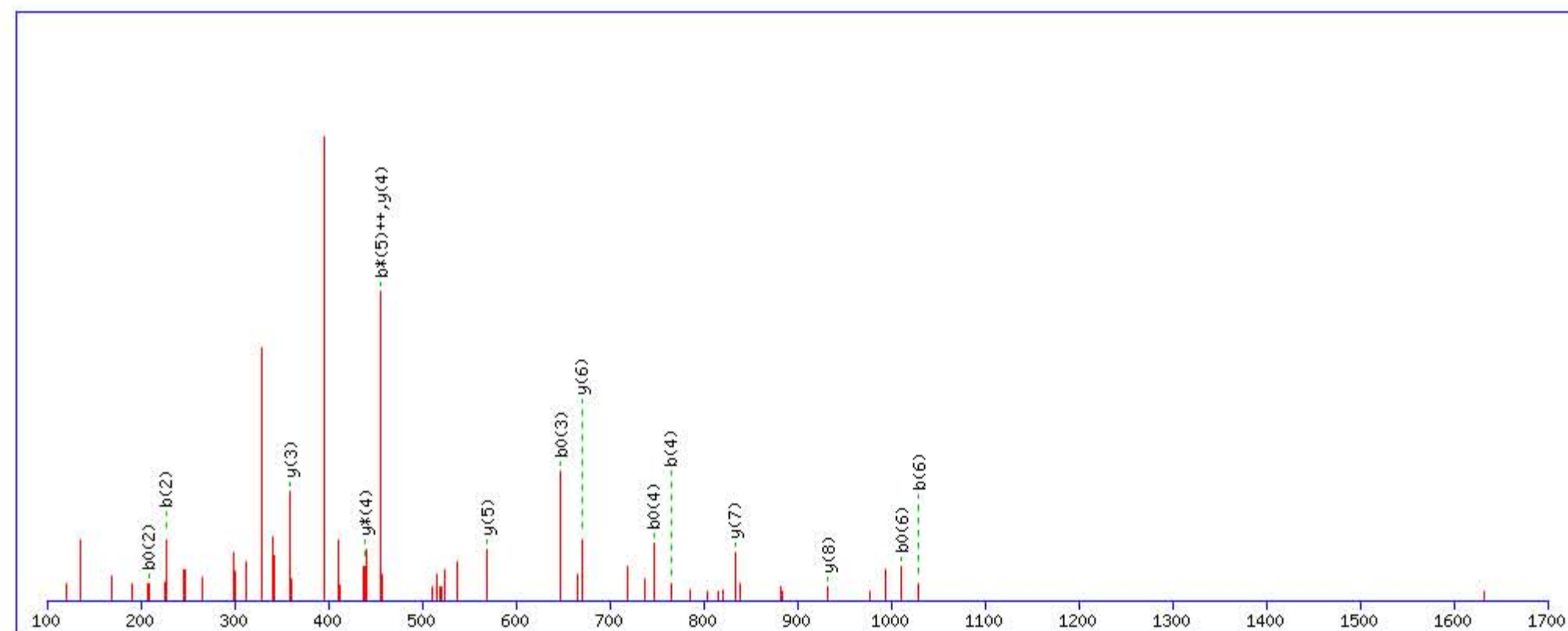
Title: Locus:1.1.1.1626.17 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf.5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1596.833389

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

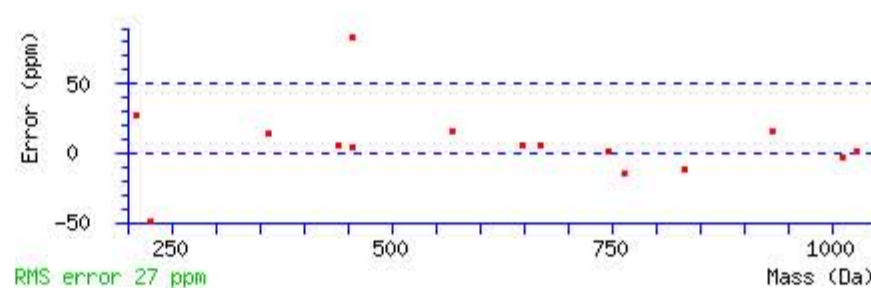
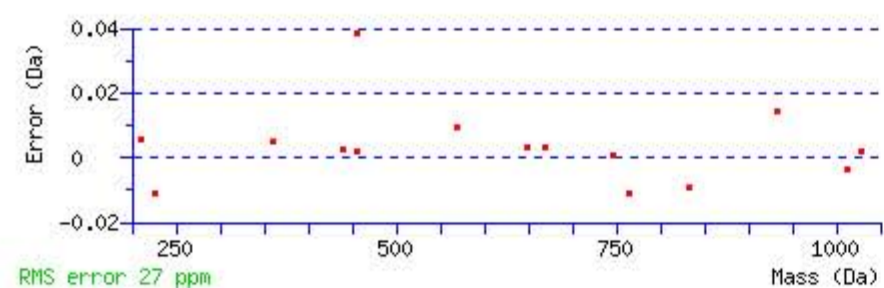
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.058

Matches : 15/114 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	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	$M_r(\text{calc})$:	Delta	Sequence
26.7	1596.833389	-0.005167	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 50831: 2186.084112 from(729.701980,3+) rtinseconds(1774) index(67349)

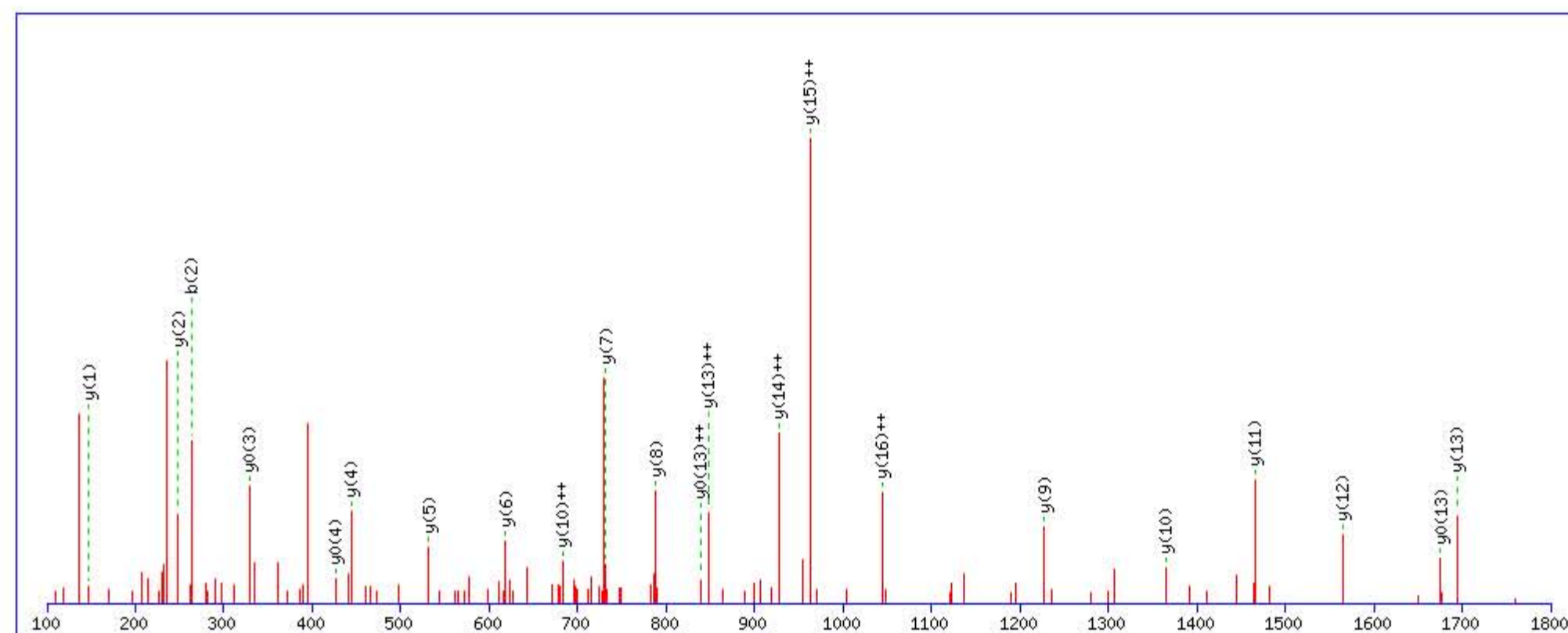
Title: Locus:1.1.1.1555.12 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2186.086411

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

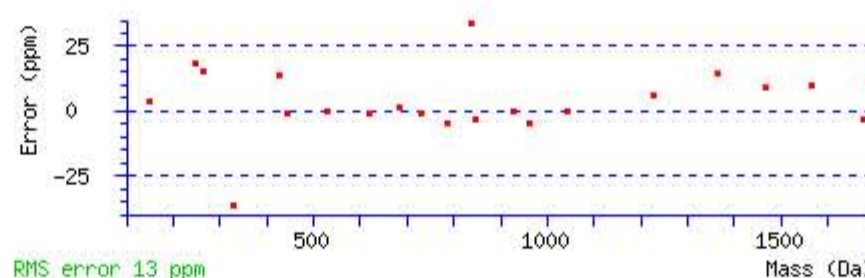
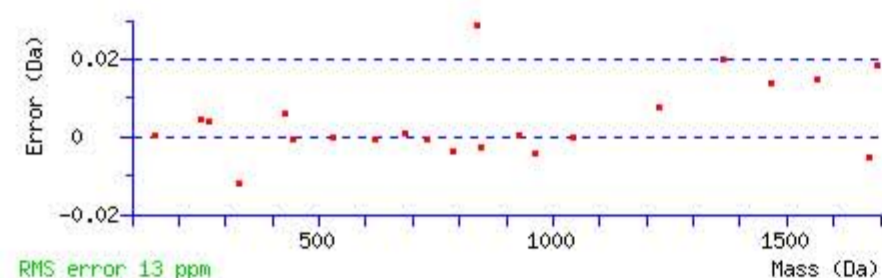
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 65 Expect: 8.3e-006

Matches : 22/166 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	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
65.2	2186.086411	-0.002299	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 52106: 2256.193482 from(753.071770,3+) rtinseconds(2679) index(72593)

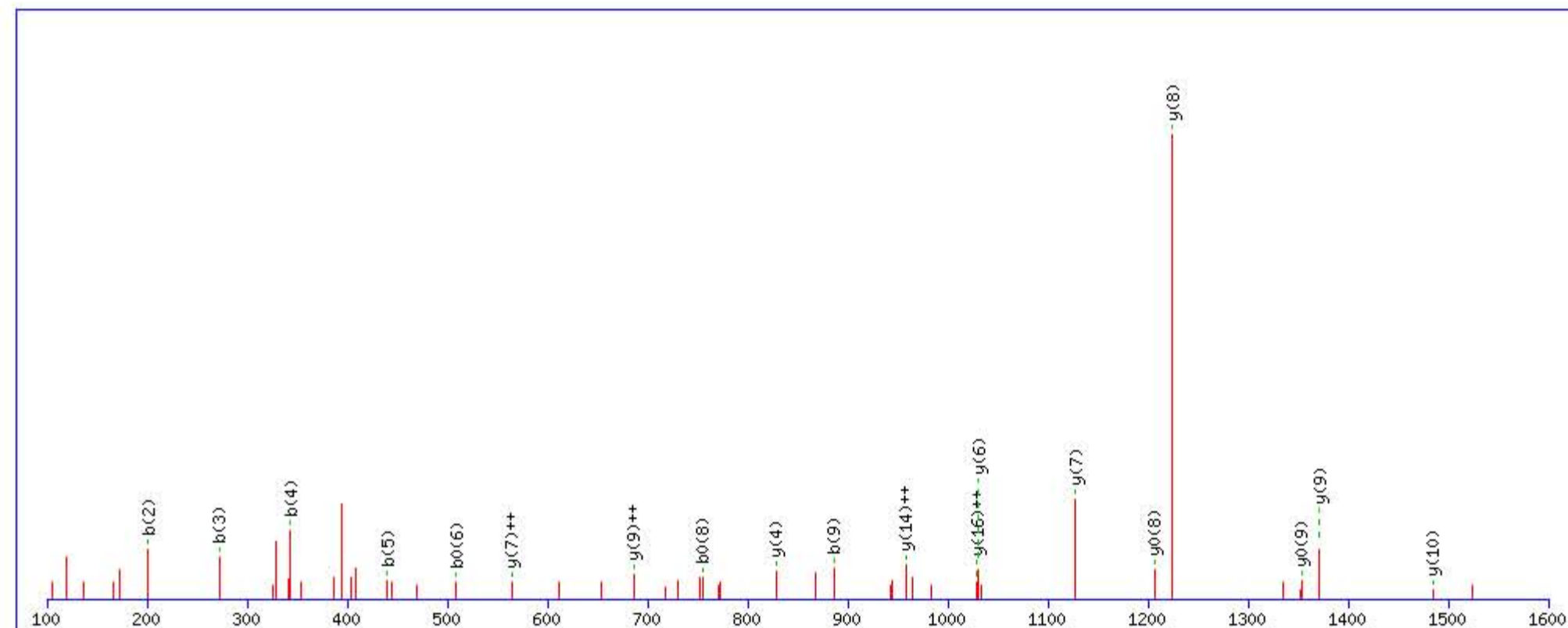
Title: Locus:1.1.1.1870.13 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2256.186432

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

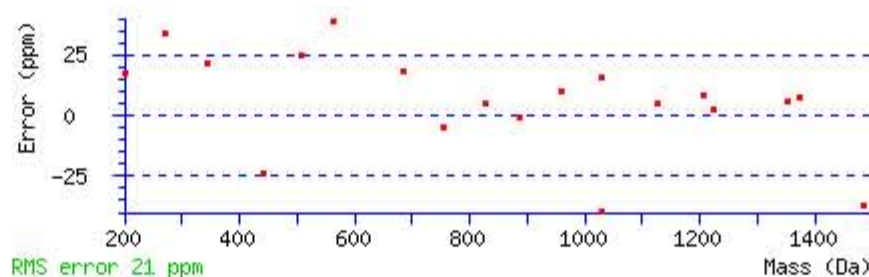
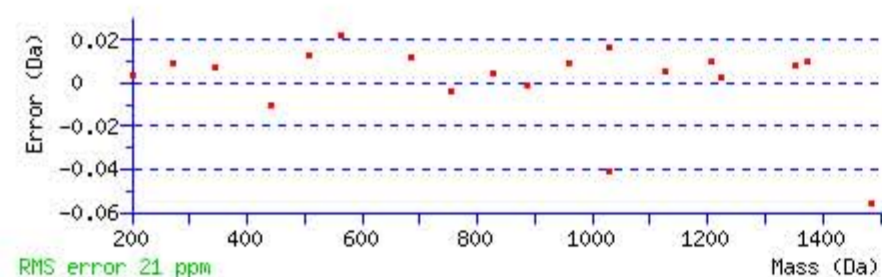
Variable modifications:

Q16 : Biotin:Thermo-21345 (Q)

Ions Score: 47 Expect: 7.5e-005

Matches : 19/168 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							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
47.4	2256.186432	0.007050	TVAAPSVFIFPPSDEQLK
3.5	2256.171860	0.021622	QVVCDLGNPMKAGTQLLAGLR

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

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **LICQATGFSPR**

Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

Match to Query 35292: 1559.799568 from(780.907060,2+) rtinseconds(1978) index(36286)

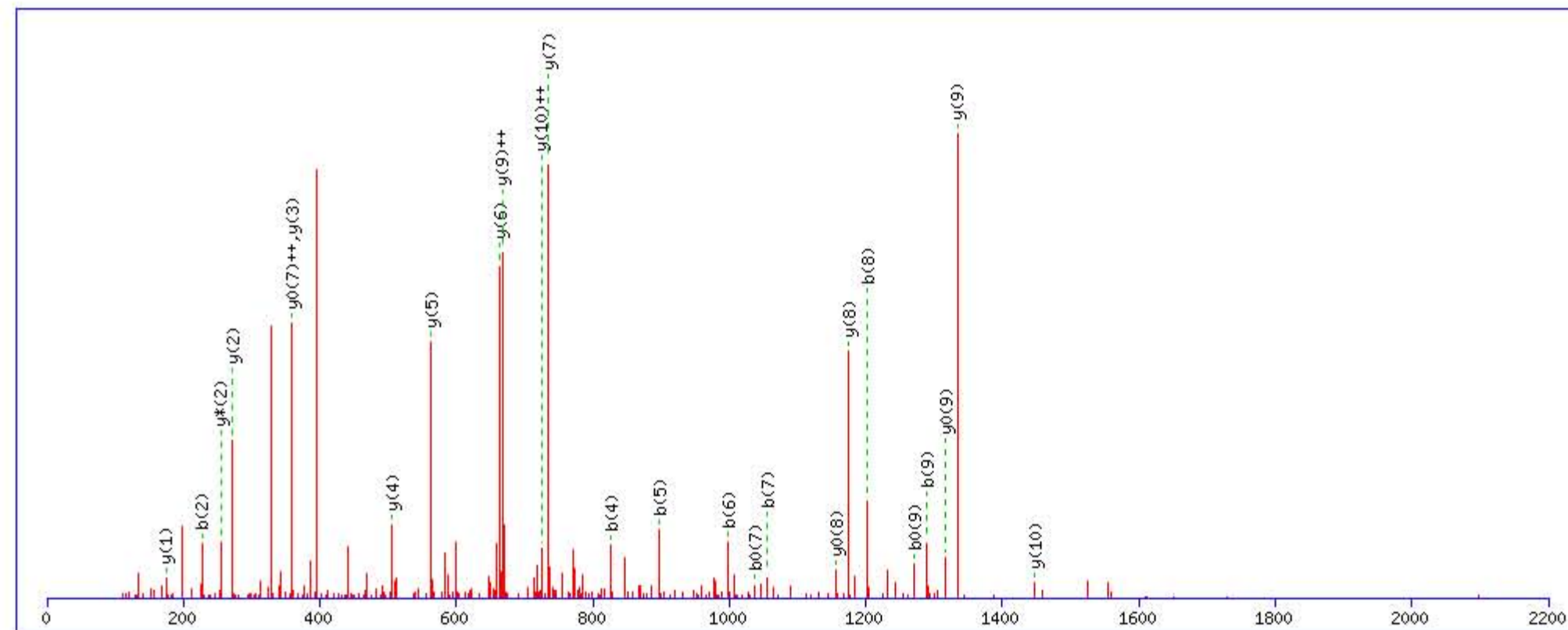
Title: Locus:1.1.1.3108.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1559.795242

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

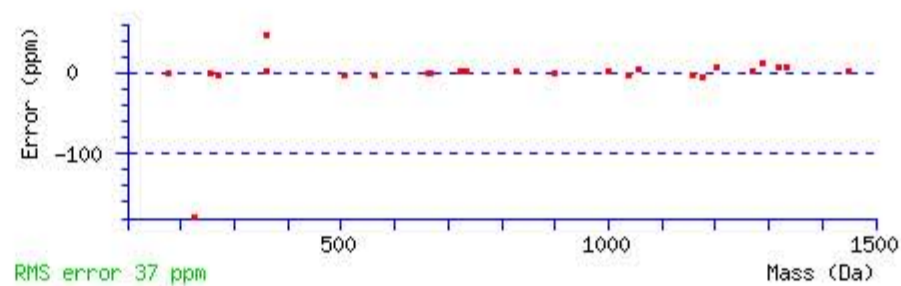
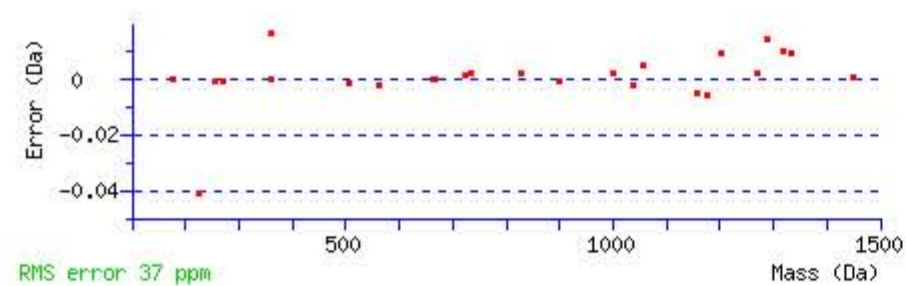
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 6.5e-006

Matches : 25/100 fragment ions using 44 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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
66.3	1559.795242	0.004326	LICQATGFSPR
13.0	1559.808960	-0.009392	LDRLSGLADQMVAR
8.8	1559.820190	-0.020622	MTRSATQAAKQVPR
4.7	1559.808975	-0.009407	LLDRDACDTRVK
1.6	1559.787827	0.011741	SLHPAMPLPAADGAGPR

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 36571: 1587.868092 from(530.296640,3+) rtinseconds(2041) index(36644)

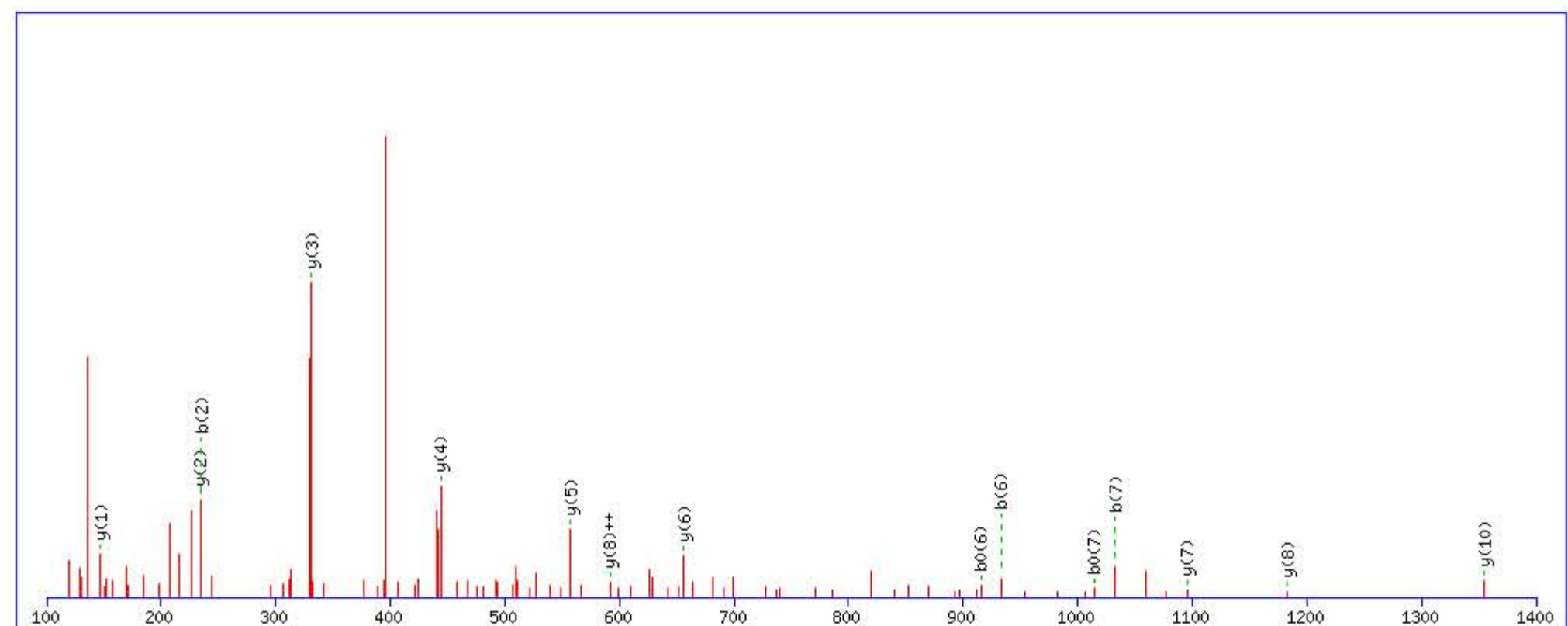
Title: Locus:1.1.1.3130.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1587.869431

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

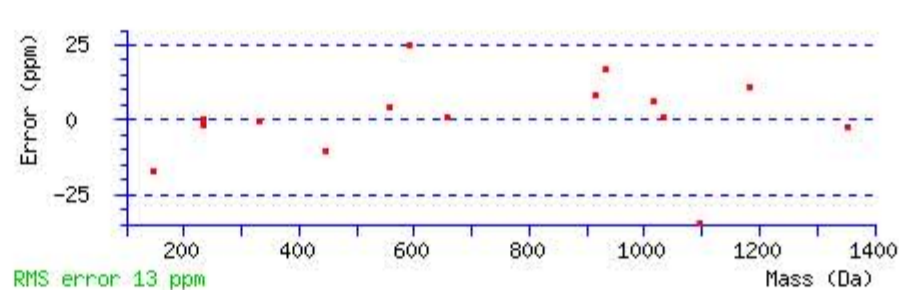
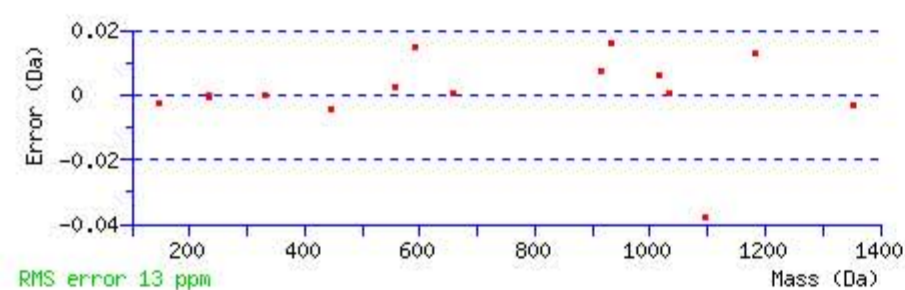
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 47 Expect: 0.00011

Matches : 15/114 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							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
47.1	1587.869431	-0.001339	YAATSQVLLPSK
4.4	1587.890533	-0.022441	EPTTKAEMLKIIISK
4.4	1587.862045	0.006047	VTGQNQEQLLLAK
4.1	1587.865402	0.002690	ENGLRDILAVLTMK
3.2	1587.891220	-0.023128	TIQTIVFLYSLYK
2.0	1587.854187	0.013905	VSPLQKSEVEMVK
1.4	1587.862045	0.006047	DGASLSPATLFIQIR
0.4	1587.858002	0.010090	LSQEQTLQALRSSK

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **LICQATGFSPR**

Found in **IGHM_HUMAN**, Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

Match to Query 35292: 1559.799568 from(780.907060,2+) rtinseconds(1978) index(36286)

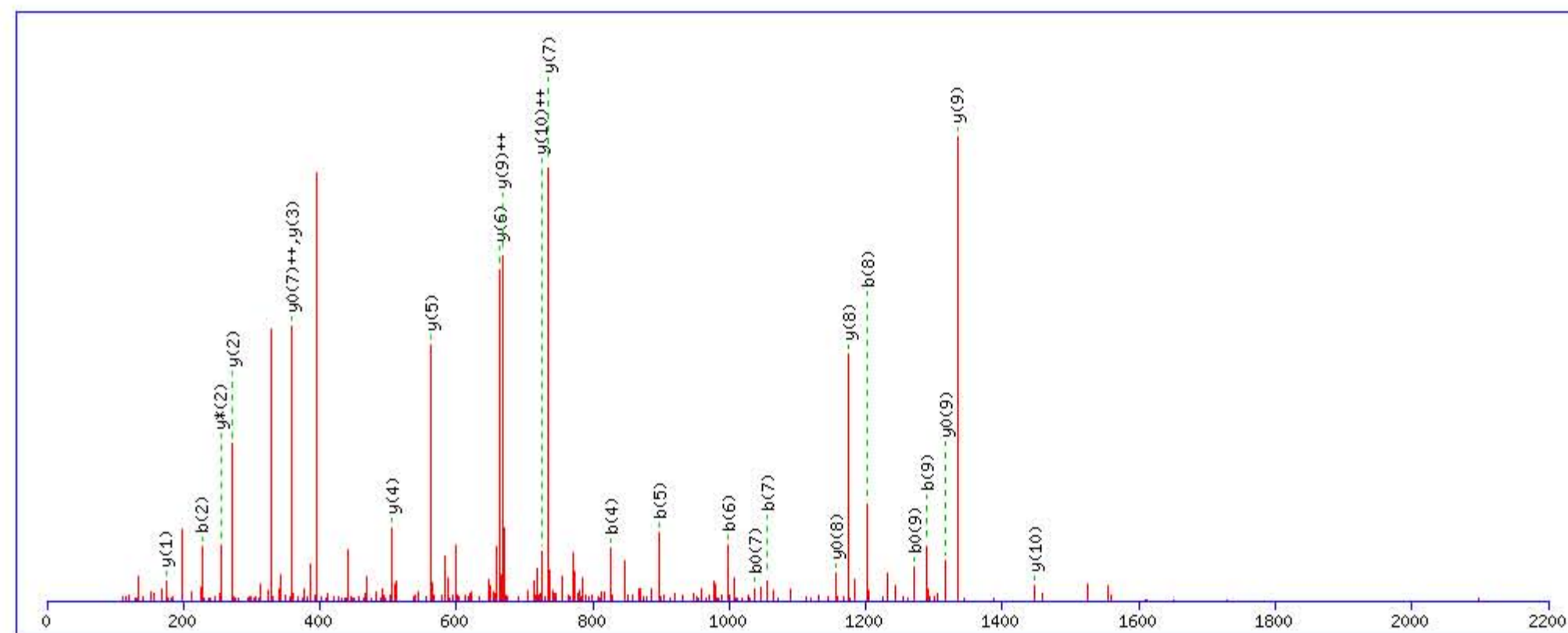
Title: Locus:1.1.1.3108.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1559.795242

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

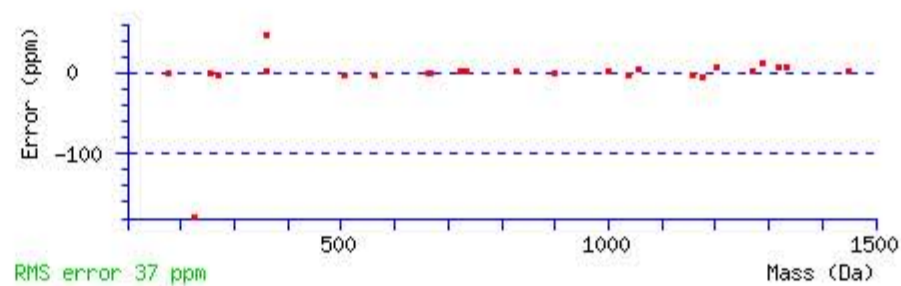
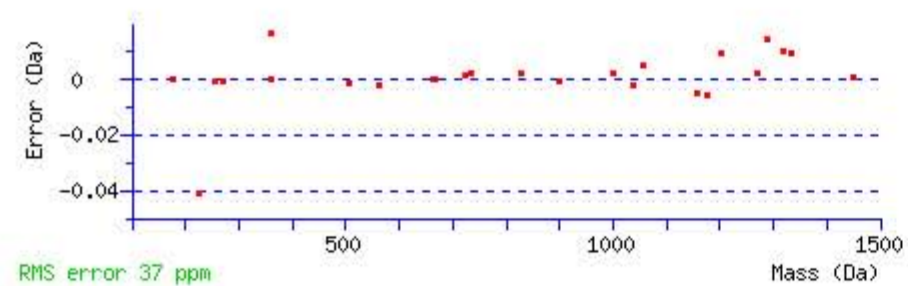
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 6.5e-006

Matches : 25/100 fragment ions using 44 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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
66.3	1559.795242	0.004326	LICQATGFSPR
13.0	1559.808960	-0.009392	LDRLSGLADQMVAR
8.8	1559.820190	-0.020622	MTRSATQAAKQVPR
4.7	1559.808975	-0.009407	LLDRDACDTRVK
1.6	1559.787827	0.011741	SLHPAMLPAADGAGPR

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

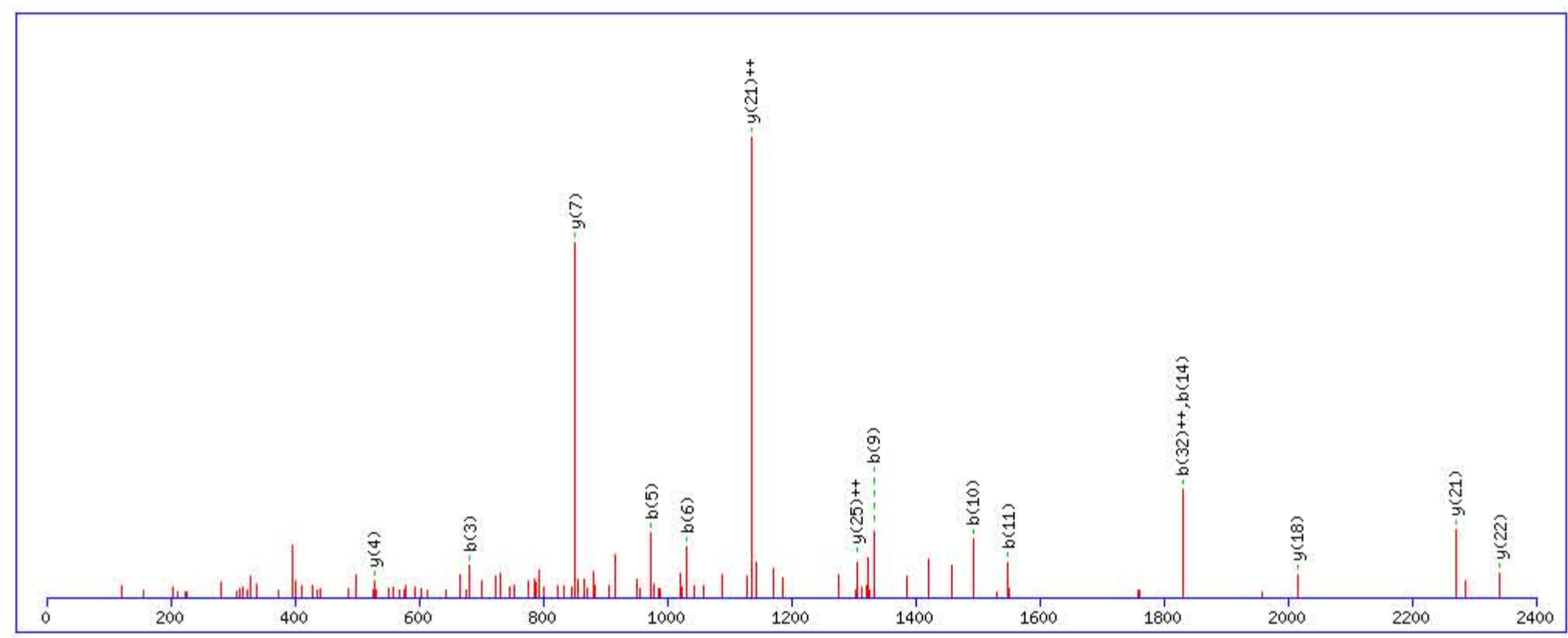
MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **LEQYEGPGFCGPLAPGTGGPFTTCHAHVPPESFFK**
 Found in **FCGBP_HUMAN**, IgGfC-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

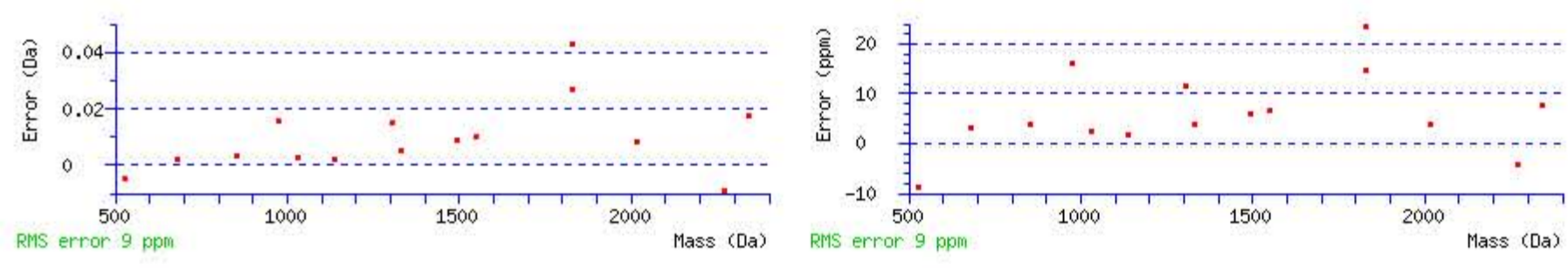
Match to Query 71377: 4099.942456 from(1025.992890,4+) rtinseconds(2485) index(39361)
 Title: Locus:1.1.1.3284.26 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 4099.905991
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q3 : Biotin:Thermo-21345 (Q)
 Ions Score: 45 Expect: 0.00063
 Matches : 15/396 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					L							35
2	243.133933	122.070605			225.123368	113.065322	E	3987.829155	1994.418215	3970.802606	1985.904941	3969.818590	1985.412933	34
3	682.359259	341.683268	665.332710	333.169993	664.348694	332.677985	Q	3858.786562	1929.896919	3841.760013	1921.383644	3840.775997	1920.891636	33
4	845.422588	423.214932	828.396039	414.701658	827.412023	414.209650	Y	3419.561236	1710.284256	3402.534687	1701.770981	3401.550671	1701.278973	32
5	974.465181	487.736229	957.438632	479.222954	956.454616	478.730946	E	3256.497907	1628.752591	3239.471358	1620.239317	3238.487342	1619.747309	31
6	1031.486645	516.246961	1014.460096	507.733686	1013.476080	507.241678	G	3127.455314	1564.231295	3110.428765	1555.718020	3109.444749	1555.226012	30
7	1128.539409	564.773343	1111.512860	556.260068	1110.528844	555.768060	P	3070.433850	1535.720563	3053.407301	1527.207288	3052.423285	1526.715280	29
8	1185.560873	593.284075	1168.534324	584.770800	1167.550308	584.278792	G	2973.381086	1487.194181	2956.354537	1478.680906	2955.370521	1478.188898	28
9	1332.629287	666.818282	1315.602738	658.305007	1314.618722	657.812999	F	2916.359622	1458.683449	2899.333073	1450.170174	2898.349057	1449.678166	27
10	1492.659936	746.833606	1475.633387	738.320332	1474.649371	737.828324	C	2769.291208	1385.149242	2752.264659	1376.635967	2751.280643	1376.143959	26
11	1549.681400	775.344338	1532.654851	766.831064	1531.670835	766.339056	G	2609.260559	1305.133917	2592.234010	1296.620643	2591.249994	1296.128635	25
12	1646.734164	823.870720	1629.707615	815.357446	1628.723599	814.865438	P	2552.239095	1276.623185	2535.212546	1268.109911	2534.228530	1267.617903	24
13	1759.818228	880.412752	1742.791679	871.899478	1741.807663	871.407470	L	2455.186331	1228.096803	2438.159782	1219.583529	2437.175766	1219.091521	23
14	1830.855342	915.931309	1813.828793	907.418035	1812.844777	906.926027	A	2342.102267	1171.554771	2325.075718	1163.041497	2324.091702	1162.549489	22
15	1927.908106	964.457691	1910.881557	955.944417	1909.897541	955.452409	P	2271.065153	1136.036214	2254.038604	1127.522940	2253.054588	1127.030932	21
16	1984.929570	992.968423	1967.903021	984.455149	1966.919005	983.963141	G	2174.012389	1087.509832	2156.985840	1078.996558	2156.001824	1078.504550	20
17	2085.977249	1043.492262	2068.950700	1034.978988	2067.966684	1034.486980	T	2116.990925	1058.999100	2099.964376	1050.485826	2098.980360	1049.993818	19
18	2142.998713	1072.002994	2125.972164	1063.489720	2124.988148	1062.997712	G	2015.943246	1008.475261	1998.916697	999.961986	1997.932681	999.469978	18
19	2200.020177	1100.513726	2182.993628	1092.000452	2182.009612	1091.508444	G	1958.921782	979.964529	1941.895233	971.451254	1940.911217	970.959246	17
20	2297.072941	1149.040108	2280.046392	1140.526834	2279.062376	1140.034826	P	1901.900318	951.453797	1884.873769	942.940522	1883.889753	942.448514	16
21	2444.141355	1222.574315	2427.114806	1214.061041	2426.130790	1213.569033	F	1804.847554	902.927415	1787.821005	894.414140	1786.836989	893.922132	15
22	2545.189034	1273.098155	2528.162485	1264.584880	2527.178469	1264.092872	T	1657.779140	829.393208	1640.752591	820.879933	1639.768575	820.387925	14
23	2646.236713	1323.621994	2629.210164	1315.108720	2628.226148	1314.616712	T	1556.731461	778.869368	1539.704912	770.356094	1538.720896	769.864086	13
24	2806.267362	1403.637319	2789.240813	1395.124044	2788.256797	1394.632036	C	1455.683782	728.345529	1438.657233	719.832254	1437.673217	719.340246	12
25	2943.326274	1472.166775	2926.299725	1463.653500	2925.315709	1463.161492	H	1295.653133	648.330205	1278.626584	639.816930	1277.642568	639.324922	11
26	3014.363388	1507.685332	2997.336839	1499.172057	2996.352823	1498.680049	A	1158.594221	579.800749	1141.567672	571.287474	1140.583656	570.795466	10
27	3151.422300	1576.214788	3134.395751	1567.701513	3133.411735	1567.209505	H	1087.557107	544.282191	1070.530558	535.768917	1069.546542	535.276909	9
28	3250.490714	1625.748995	3233.464165	1617.235720	3232.480149	1616.743712	V	950.498195	475.752735	933.471646	467.239461	932.487630	466.747453	8
29	3347.543478	1674.275377	3330.516929	1665.762102	3329.532913	1665.270094	P	851.429781	426.218529	834.403232	417.705254	833.419216	417.213246	7
30	3444.596242	1722.801759	3427.569693	1714.288484	3426.585677	1713.796476	P	754.377017	377.692147	737.350468	369.178872	736.366452	368.686864	6
31	3573.638835	1787.323055	3556.612286	1778.809781	3555.628270	1778.317773	E	657.324253	329.165765	640.297704	320.652490	639.313688	320.160482	5
32	3660.670863	1830.839069	3643.644314	1822.325795	3642.660298	1821.833787	S	528.281660	264.644468	511.255111	256.131193	510.271095	255.639185	4
33	3807.739277	1904.373276	3790.712728	1895.860002	3789.728712	1895.367994	F	441.249632	221.128454	424.223083	212.615179			3
34	3954.807691	1977.907483	3937.781142	1969.394209	3936.797126	1968.902201	F	294.181218	147.594247	277.154669	139.080972			2
35							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **LEQYEGPGFCGPLAPGTGGPFTTCHAHVPPESFFK**
 (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	4099.905991	0.036465	LEQYEGPGFCGPLAPGTGGPFTTCHAHVPPESFFK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GAQTLVVPNC DHR**

Found in **IBP6_HUMAN**, Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1

Match to Query 43499: 1840.872012 from(614.631280,3+) rtinseconds(1751) index(67201)

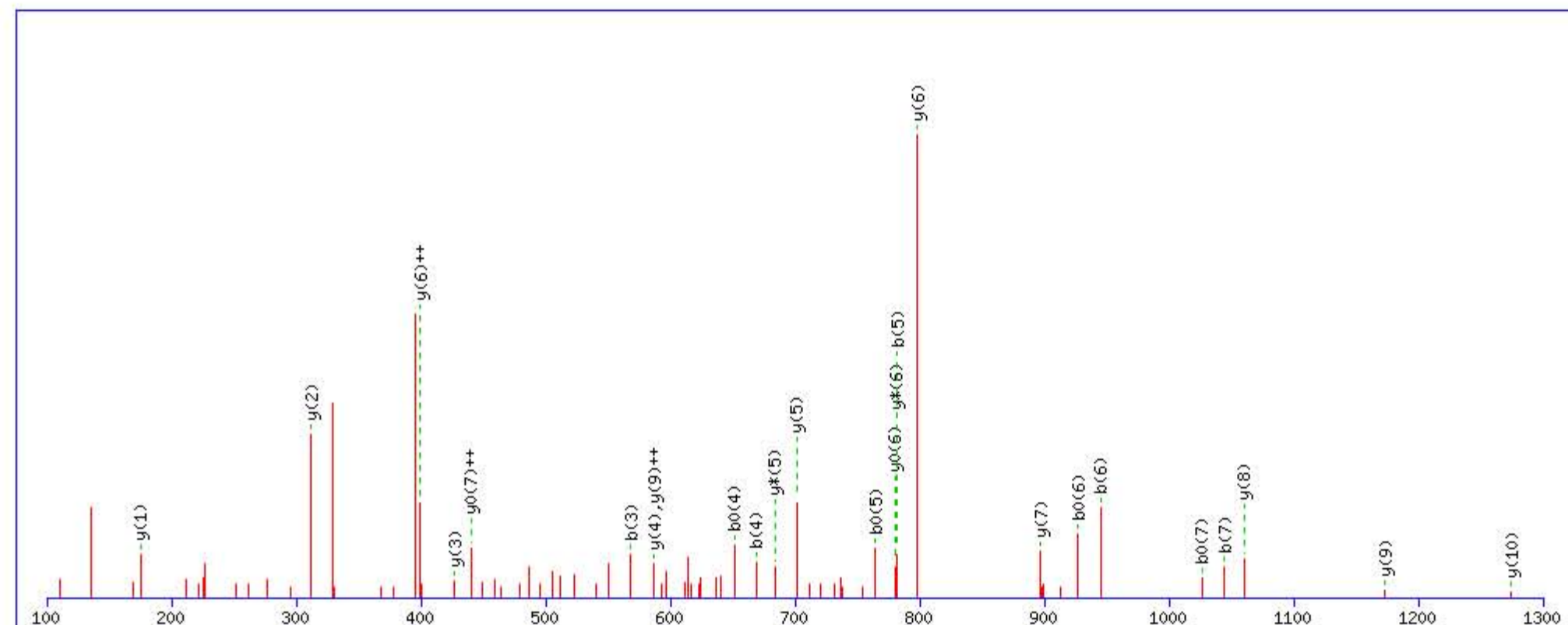
Title: Locus:1.1.1.1547.18 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1840.871262

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

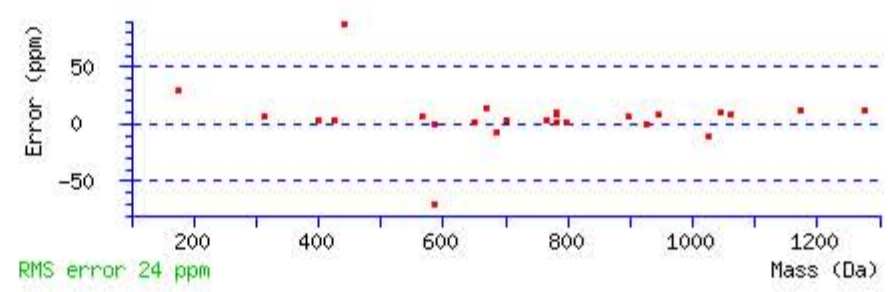
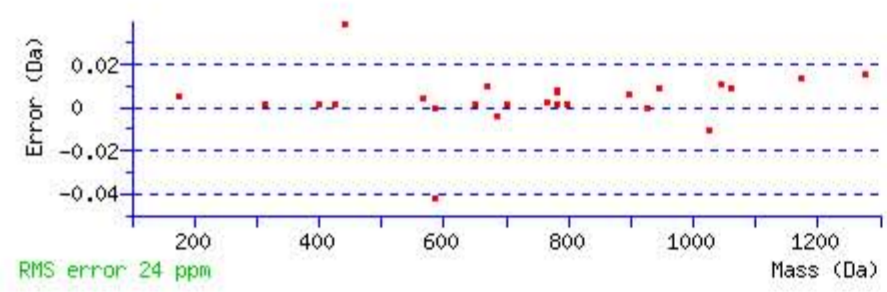
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 58 Expect: 2.5e-005

Matches : 25/130 fragment ions using 45 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							13
2	129.065854	65.036565					A	1784.857073	892.932175	1767.830524	884.418900	1766.846508	883.926892	12
3	568.291180	284.649228	551.264631	276.135954			Q	1713.819959	857.413618	1696.793410	848.900343	1695.809394	848.408335	11
4	669.338859	335.173068	652.312310	326.659793	651.328294	326.167785	T	1274.594633	637.800955	1257.568084	629.287680	1256.584068	628.795672	10
5	782.422923	391.715100	765.396374	383.201825	764.412358	382.709817	L	1173.546954	587.277115	1156.520405	578.763841	1155.536389	578.271833	9
6	945.486252	473.246764	928.459703	464.733490	927.475687	464.241482	Y	1060.462890	530.735083	1043.436341	522.221809	1042.452325	521.729801	8
7	1044.554666	522.780971	1027.528117	514.267697	1026.544101	513.775689	V	897.399561	449.203419	880.373012	440.690144	879.388996	440.198136	7
8	1141.607430	571.307353	1124.580881	562.794079	1123.596865	562.302071	P	798.331147	399.669212	781.304598	391.155937	780.320582	390.663929	6
9	1255.650357	628.328817	1238.623808	619.815542	1237.639792	619.323534	N	701.278383	351.142830	684.251834	342.629555	683.267818	342.137547	5
10	1415.681006	708.344141	1398.654457	699.830867	1397.670441	699.338859	C	587.235456	294.121366	570.208907	285.608092	569.224891	285.116084	4
11	1530.707949	765.857613	1513.681400	757.344338	1512.697384	756.852330	D	427.204807	214.106041	410.178258	205.592767	409.194242	205.100759	3
12	1667.766861	834.387069	1650.740312	825.873794	1649.756296	825.381786	H	312.177864	156.592570	295.151315	148.079295			2
13							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [GAQTLVVPNC DHR](#)

(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	1840.871262	0.000750	GAQTLVVPNC DHR
8.9	1840.887650	-0.015638	AALSASEGEEVPQDK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **HLDSVLQQLQTEVYR**

Found in **IBP6_HUMAN**, Insulin-like growth factor-binding protein 6 OS=Homo sapiens GN=IGFBP6 PE=1 SV=1

Match to Query 49817: 2139.118542 from(714.046790,3+) rtinseconds(2577) index(71950)

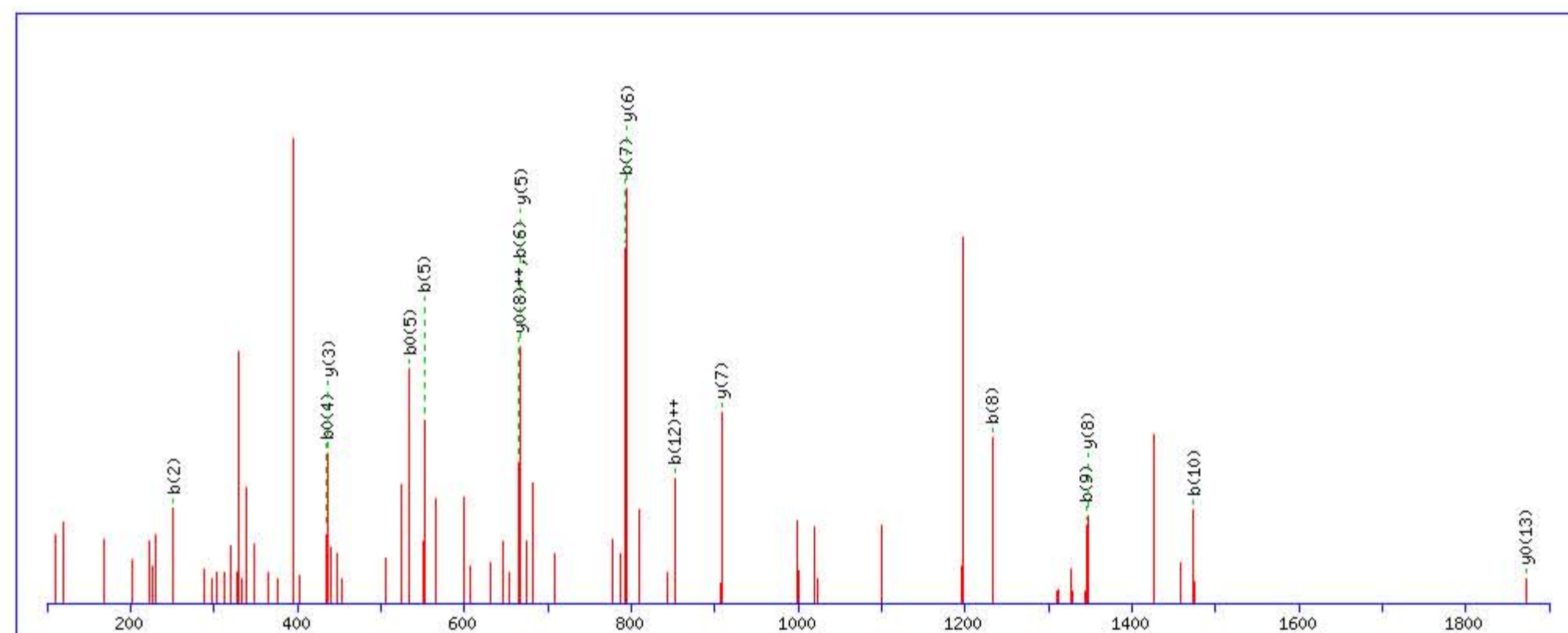
Title: Locus:1.1.1.1835.5 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2139.114655

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

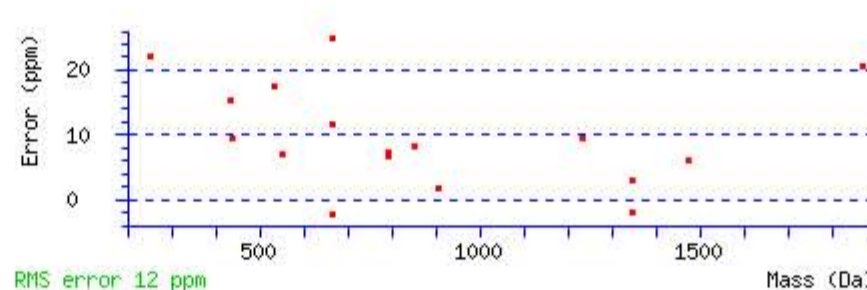
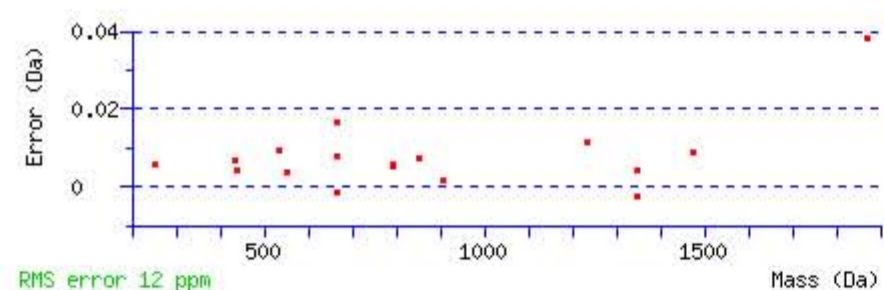
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.00091

Matches : 17/146 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	138.066188	69.536732					H							15
2	251.150252	126.078764					L	2003.063026	1002.035151	1986.036477	993.521877	1985.052461	993.029869	14
3	366.177195	183.592235			348.166630	174.586953	D	1889.978962	945.493119	1872.952413	936.979845	1871.968397	936.487836	13
4	453.209223	227.108250			435.198658	218.102967	S	1774.952019	887.979648	1757.925470	879.466373	1756.941454	878.974365	12
5	552.277637	276.642457			534.267072	267.637174	V	1687.919991	844.463634	1670.893442	835.950359	1669.909426	835.458351	11
6	665.361701	333.184489			647.351136	324.179206	L	1588.851577	794.929427	1571.825028	786.416152	1570.841012	785.924144	10
7	793.420279	397.213778	776.393730	388.700503	775.409714	388.208495	Q	1475.767513	738.387395	1458.740964	729.874120	1457.756948	729.382112	9
8	1232.645605	616.826440	1215.619056	608.313166	1214.635040	607.821158	Q	1347.708935	674.358105	1330.682386	665.844831	1329.698370	665.352823	8
9	1345.729669	673.368472	1328.703120	664.855198	1327.719104	664.363190	L	908.483609	454.745443	891.457060	446.232168	890.473044	445.740160	7
10	1473.788247	737.397761	1456.761698	728.884487	1455.777682	728.392479	Q	795.399545	398.203411	778.372996	389.690136	777.388980	389.198128	6
11	1574.835926	787.921601	1557.809377	779.408326	1556.825361	778.916318	T	667.340967	334.174122	650.314418	325.660847	649.330402	325.168839	5
12	1703.878519	852.442897	1686.851970	843.929623	1685.867954	843.437615	E	566.293288	283.650282	549.266739	275.137008	548.282723	274.645000	4
13	1802.946933	901.977104	1785.920384	893.463830	1784.936368	892.971822	V	437.250695	219.128986	420.224146	210.615711			3
14	1966.010262	983.508769	1948.983713	974.995494	1947.999697	974.503486	Y	338.182281	169.594779	321.155732	161.081504			2
15							R	175.118952	88.063114	158.092403	79.549840			1



NCBI BLAST search of **HLDSVLQQLQTEVYR**

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

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.7	2139.114655	0.003887	HLDSVLQQLQTEVYR
24.4	2139.114655	0.003887	HLDSVLQQLQTEVYR
13.9	2139.114655	0.003887	HLDSVLQQLQTEVYR
0.2	2139.122025	-0.003483	FNVETMAQLLNIPPNK

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **LAELPADALGPLQR**

Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

Match to Query 42262: 1773.994828 from(888.004690,2+) rtinseconds(2455) index(39149)

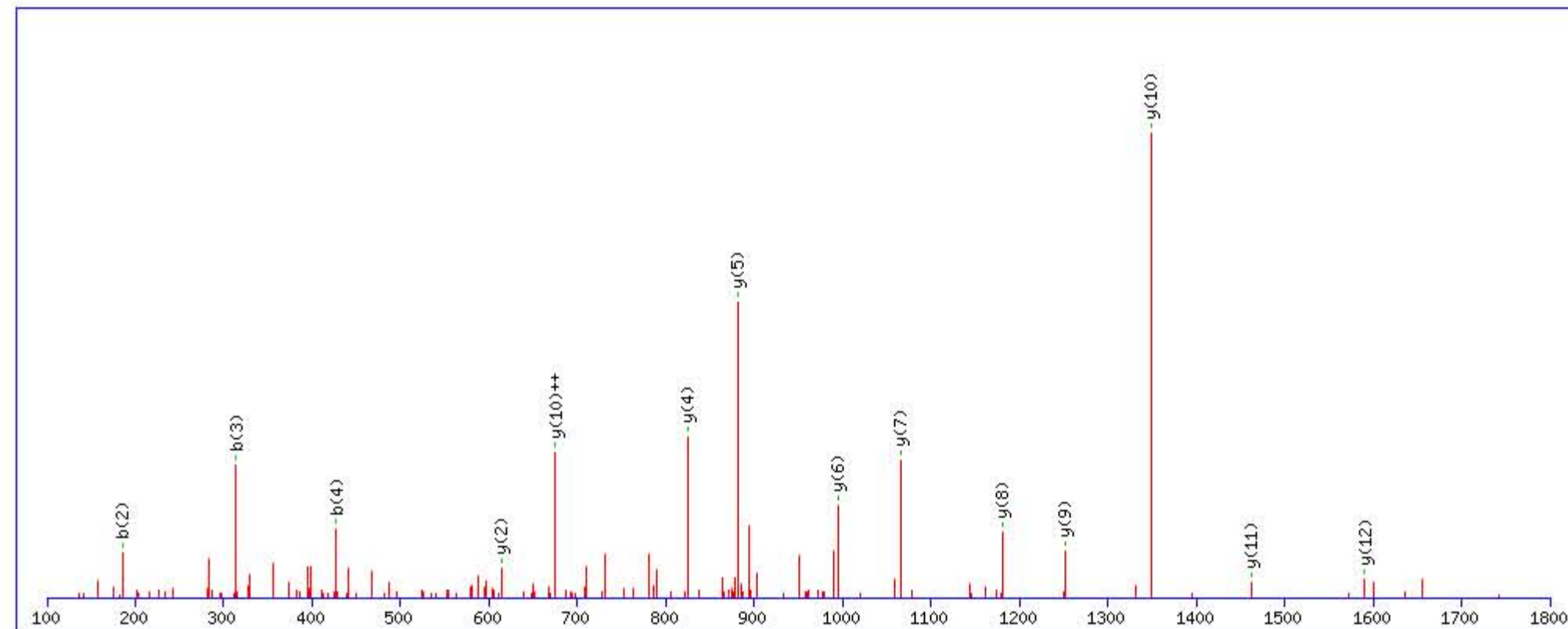
Title: Locus:1.1.1.3274.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1773.981094

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

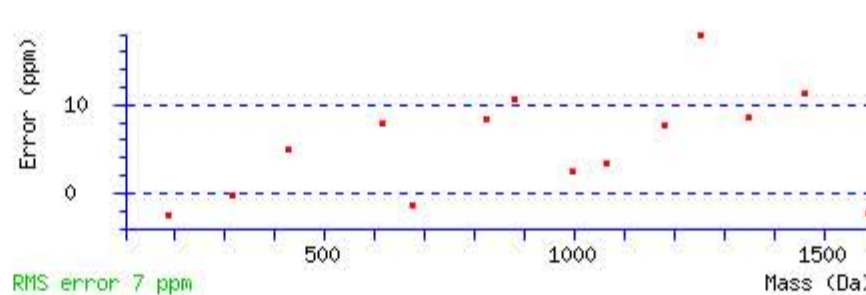
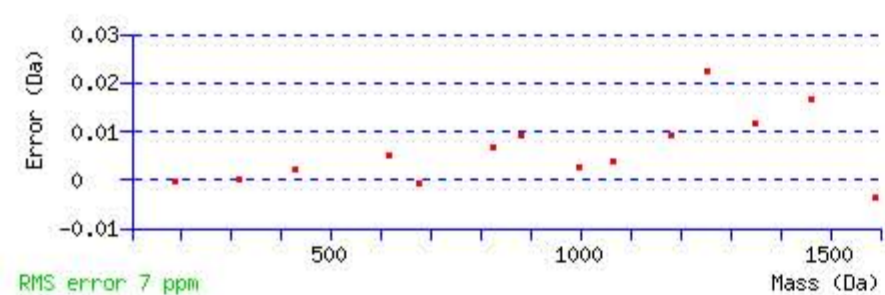
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 88 Expect: 1.8e-008

Matches : 14/114 fragment ions using 17 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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
88.4	1773.981094	0.013734	LAELPADALGPLQR

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

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SFEGLGQLEVLTLTDHNLQEQVK**

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 59504: 2807.470812 from(936.830880,3+) rtinseconds(2708) index(40870)

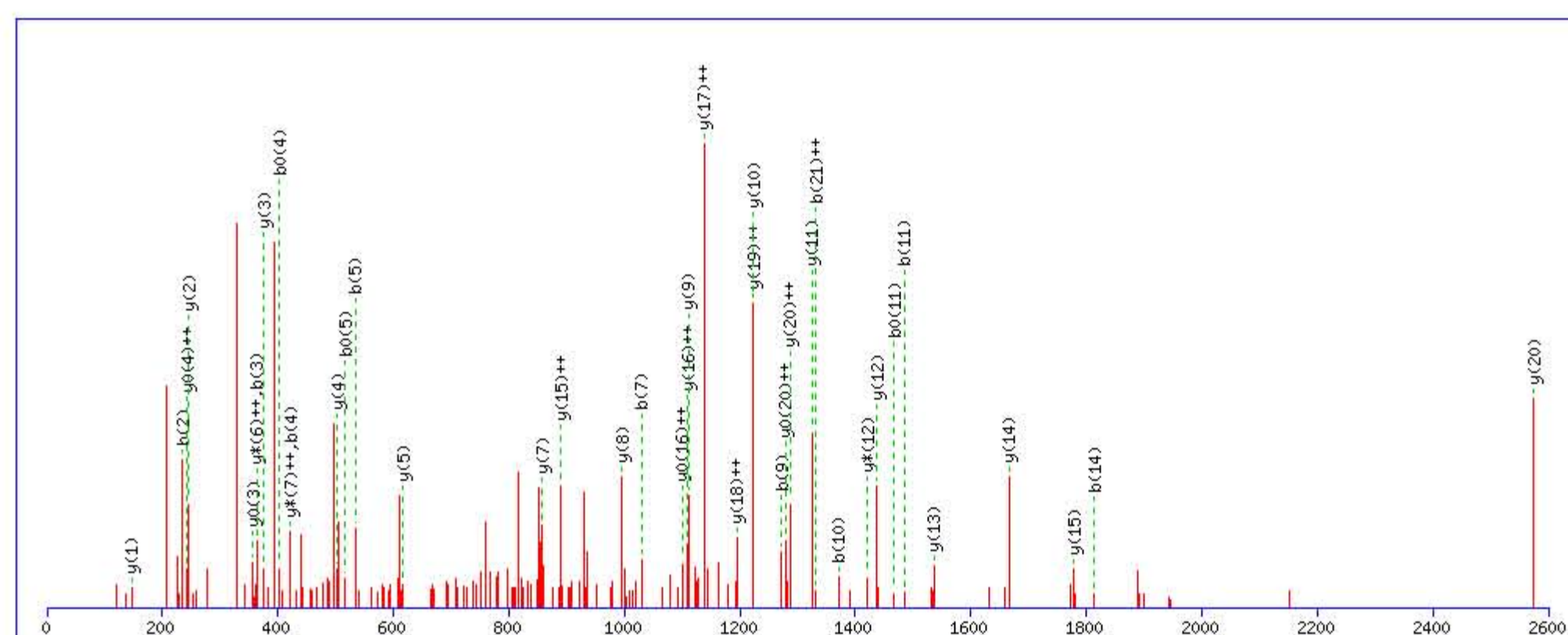
Title: Locus:1.1.1.3361.22 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2807.452759

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

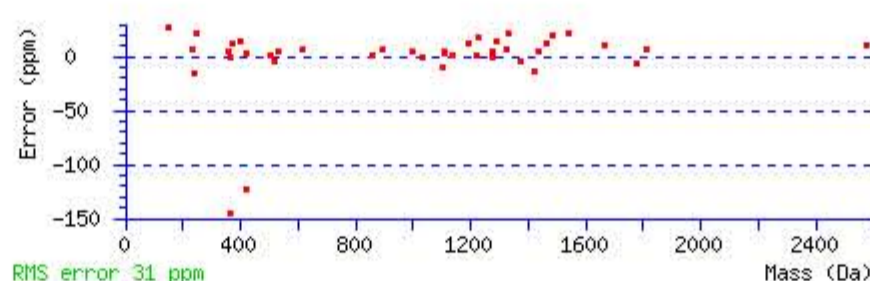
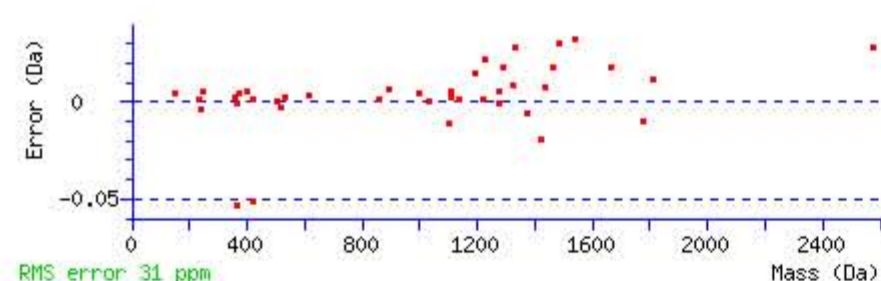
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 58 Expect: 3.8e-005

Matches : 41/236 fragment ions using 100 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 **SFEGLGQLEVLTLTDHNLQEQVK**

(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	2807.452759	0.018053	SFEGLGQLEVLTLTDHNLQEQVK
9.4	2807.452759	0.018053	SFEGLGQLEVLTLTDHNLQEQVK
0.3	2807.452759	0.018053	SFEGLGQLEVLTLTDHNLQEQVK

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

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 22876: 1183.664928 from(592.839740,2+) rtinseconds(1773) index(51327)

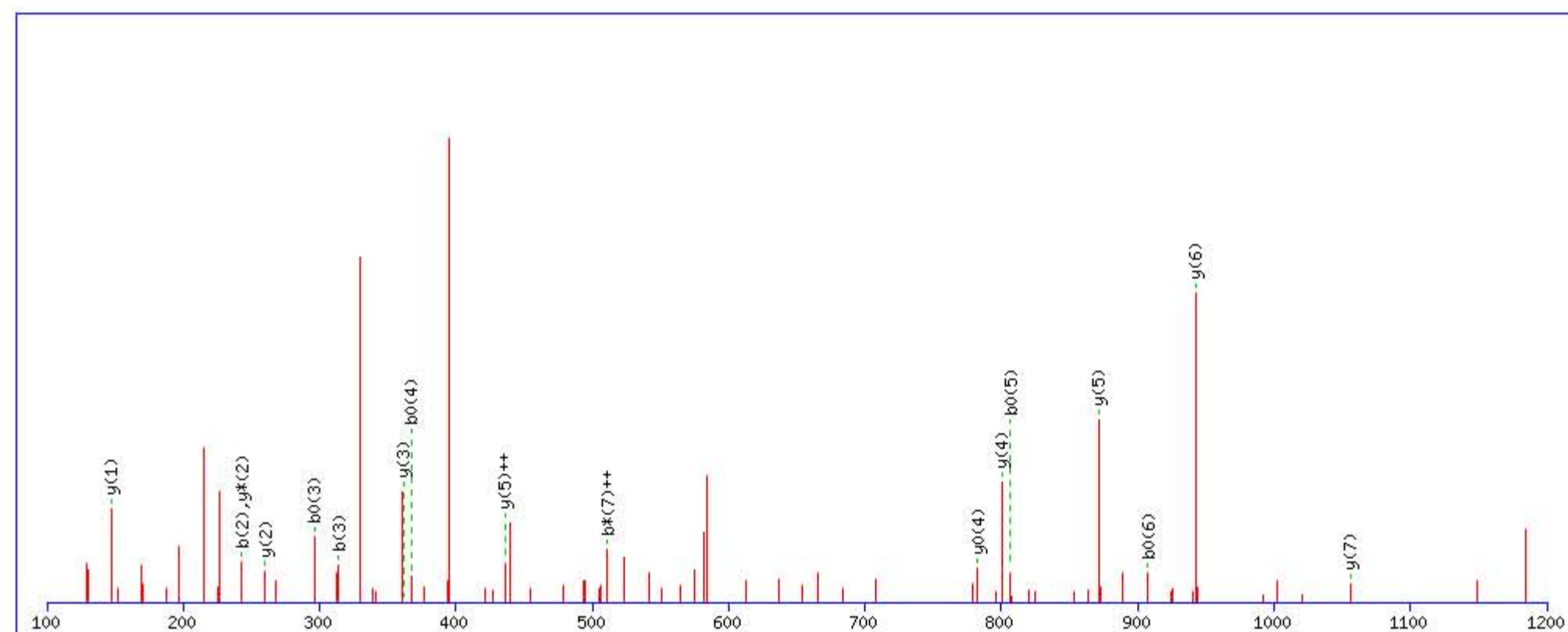
Title: Locus:1.1.1.1233.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1183.663452

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

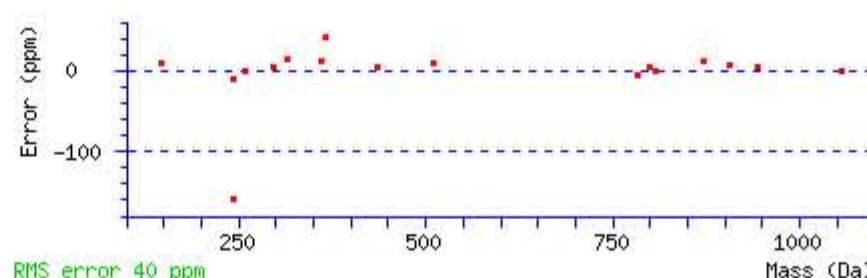
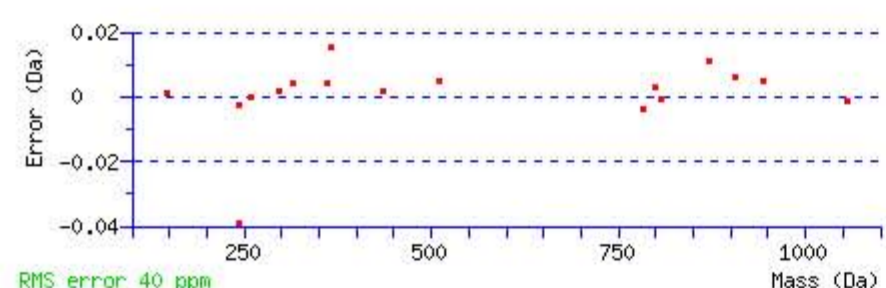
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 38 Expect: 0.0035

Matches : 17/72 fragment ions using 38 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							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
37.9	1183.663452	0.001476	ELAAQTIK
31.4	1183.663452	0.001476	ELAAQTIK
7.8	1183.667282	-0.002354	ELAERQGLLR
6.1	1183.663452	0.001476	LEQAATLK
3.8	1183.667282	-0.002354	QLLRALLEGR
3.7	1183.656937	0.007991	MRPQTLK
3.3	1183.663467	0.001461	TQLSPSIK
3.2	1183.681198	-0.016270	LEALLEAAGIGK
2.2	1183.667297	-0.002369	EPTGRVEIRK
2.2	1183.649551	0.015377	KVCGHKQSLK

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **LDAQASFLPK**

Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

Match to Query 30132: 1399.762468 from(700.888510,2+) rtinseconds(2232) index(54445)

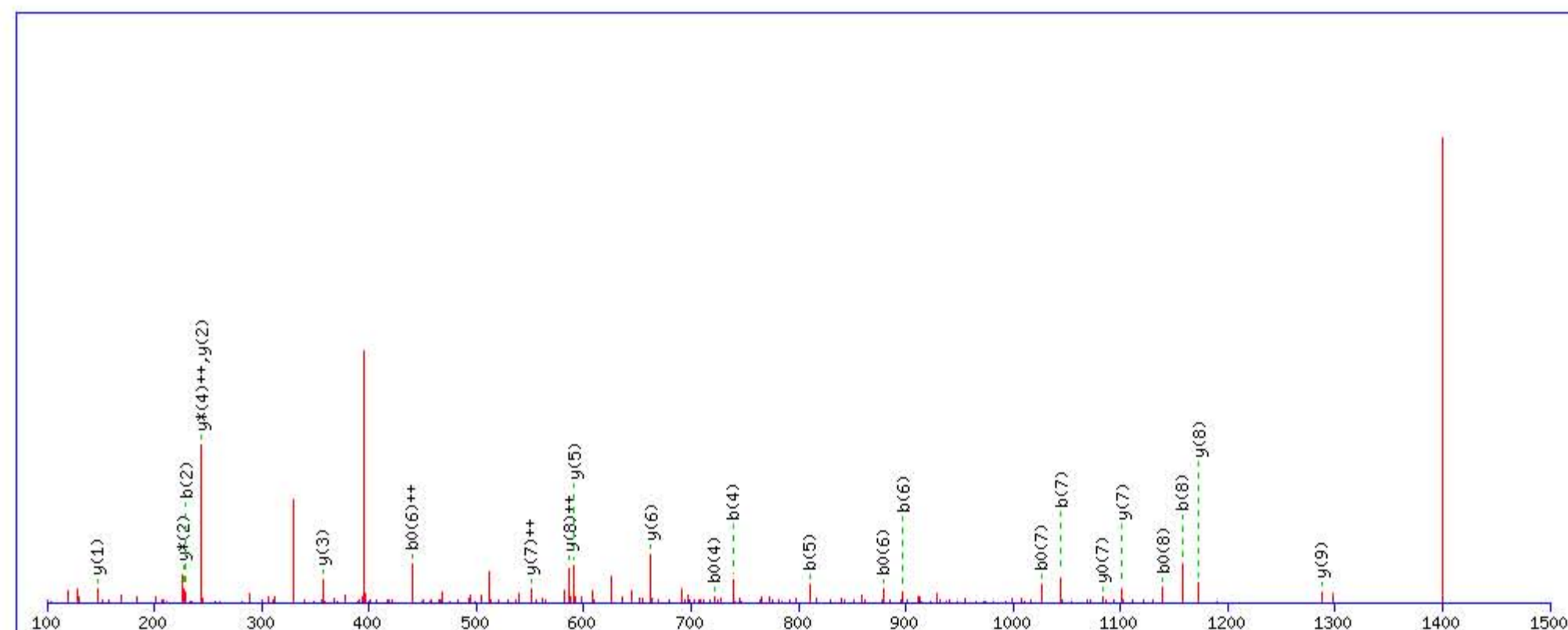
Title: Locus:1.1.1.1392.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1399.753342

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

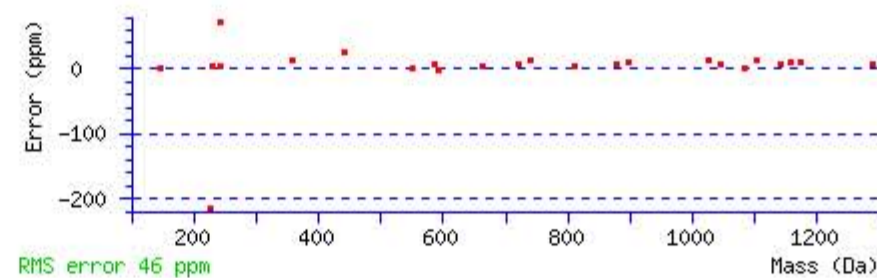
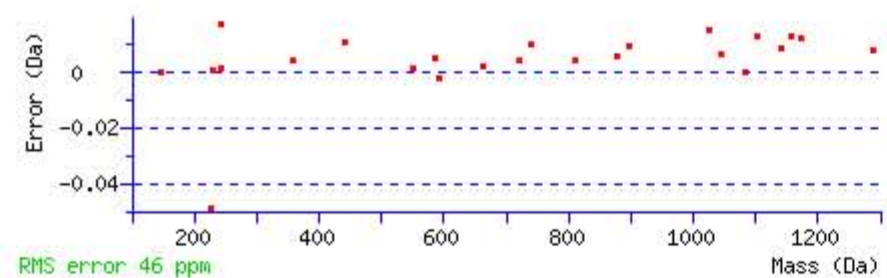
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.00047

Matches : 24/92 fragment ions using 46 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							10
2	229.118283	115.062779			211.107718	106.057497	D	1287.676571	644.341924	1270.650022	635.828649	1269.666006	635.336641	9
3	300.155397	150.581336			282.144832	141.576054	A	1172.649628	586.828452	1155.623079	578.315178	1154.639063	577.823169	8
4	739.380723	370.194000	722.354174	361.680725	721.370158	361.188717	Q	1101.612514	551.309895	1084.585965	542.796621	1083.601949	542.304612	7
5	810.417837	405.712557	793.391288	397.199282	792.407272	396.707274	A	662.387188	331.697232	645.360639	323.183957	644.376623	322.691949	6
6	897.449865	449.228570	880.423316	440.715296	879.439300	440.223288	S	591.350074	296.178675	574.323525	287.665400	573.339509	287.173392	5
7	1044.518279	522.762777	1027.491730	514.249503	1026.507714	513.757495	F	504.318046	252.662661	487.291497	244.149386			4
8	1157.602343	579.304809	1140.575794	570.791535	1139.591778	570.299527	L	357.249632	179.128454	340.223083	170.615179			3
9	1254.655107	627.831191	1237.628558	619.317917	1236.644542	618.825909	P	244.165568	122.586422	227.139019	114.073148			2
10							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **LDAQASFLPK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.2	1399.753342	0.009126	LDAQASFLPK
7.3	1399.745972	0.016496	IDAATGIPVTTWR
4.8	1399.771103	-0.008635	QKEPSVLFEVPK
3.7	1399.755814	0.006654	KTELGPLKEEEK
0.7	1399.772430	-0.009962	QHAFKQAFKPK

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 53224: 2314.183812 from(772.401880,3+) rtinseconds(2531) index(56101)

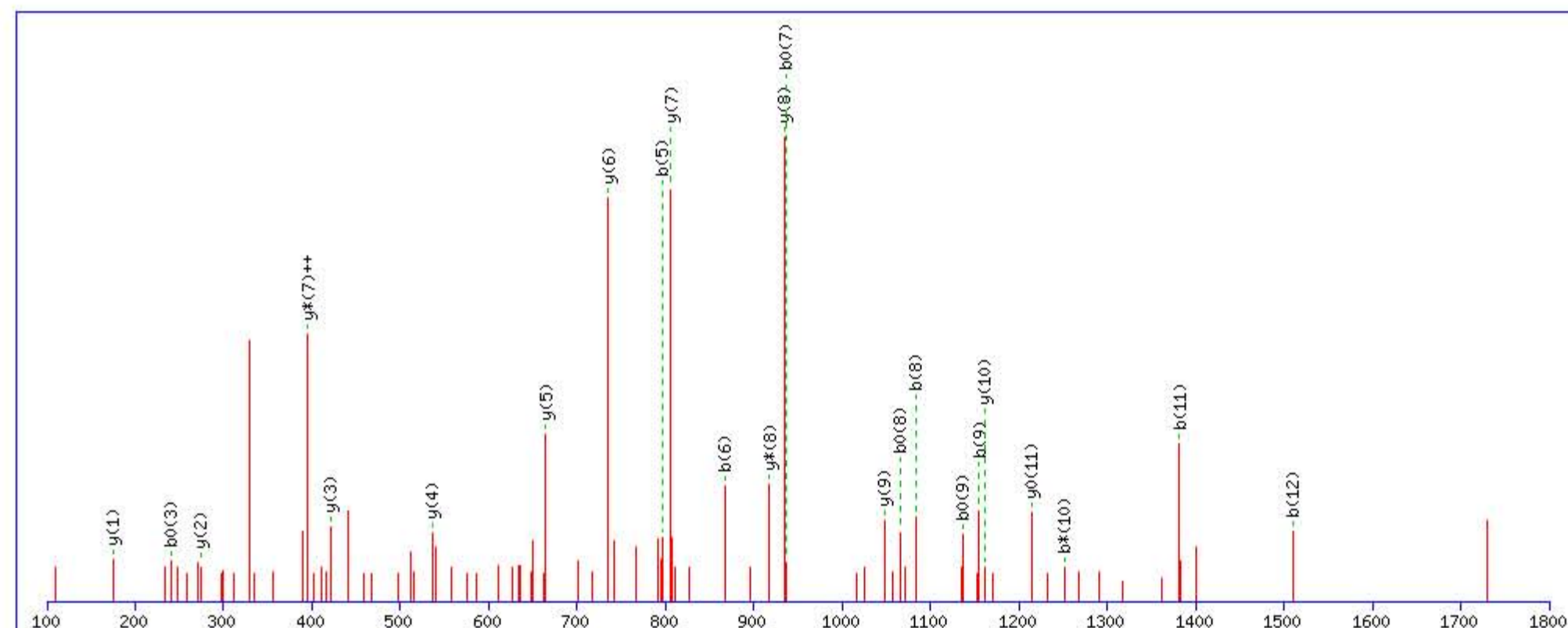
Title: Locus:1.1.1.1496.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 2314.173950

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

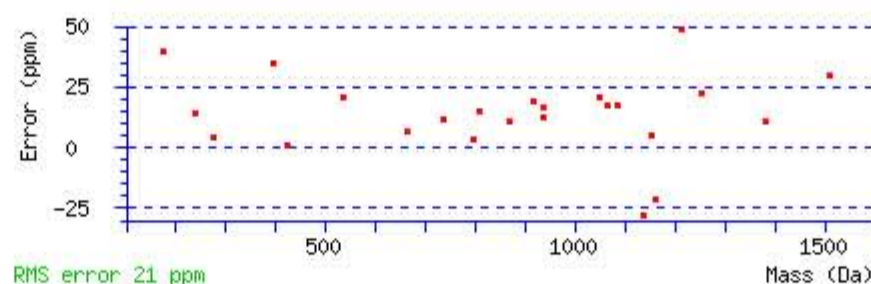
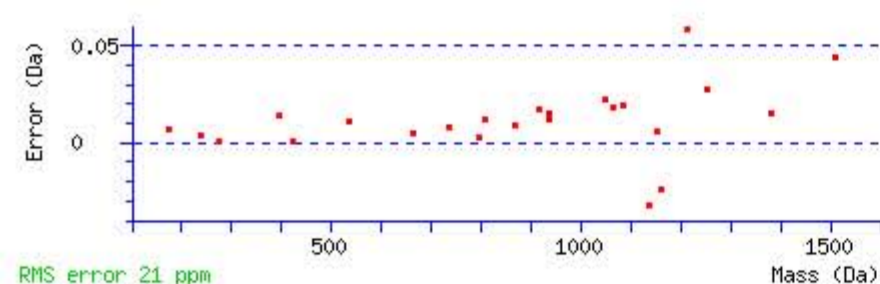
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 59 Expect: 3.8e-006

Matches : 24/200 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							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	796.438572	398.722924	779.412023	390.209650	778.428007	389.717642	Q	1958.975273	979.991274	1941.948724	971.478000	1940.964708	970.985992	15
6	867.475686	434.241481	850.449137	425.728207	849.465121	425.236199	A	1519.749947	760.378611	1502.723398	751.865337	1501.739382	751.373329	14
7	954.507714	477.757495	937.481165	469.244220	936.497149	468.752212	S	1448.712833	724.860054	1431.686284	716.346780	1430.702268	715.854772	13
8	1083.550307	542.278792	1066.523758	533.765517	1065.539742	533.273509	E	1361.680805	681.344040	1344.654256	672.830766	1343.670240	672.338758	12
9	1154.587421	577.797349	1137.560872	569.284074	1136.576856	568.792066	A	1232.638212	616.822744	1215.611663	608.309469	1214.627647	607.817461	11
10	1268.630348	634.818812	1251.603799	626.305538	1250.619783	625.813529	N	1161.601098	581.304187	1144.574549	572.790912	1143.590533	572.298904	10
11	1381.714412	691.360844	1364.687863	682.847569	1363.703847	682.355561	L	1047.558171	524.282723	1030.531622	515.769449	1029.547606	515.277441	9
12	1509.772990	755.390133	1492.746441	746.876858	1491.762425	746.384850	Q	934.474107	467.740692	917.447558	459.227417	916.463542	458.735409	8
13	1580.810104	790.908690	1563.783555	782.395415	1562.799539	781.903407	A	806.415529	403.711403	789.388980	395.198128	788.404964	394.706120	7
14	1651.847218	826.427247	1634.820669	817.913972	1633.836653	817.421964	A	735.378415	368.192846	718.351866	359.679571	717.367850	359.187563	6
15	1779.905796	890.456536	1762.879247	881.943261	1761.895231	881.451253	Q	664.341301	332.674289	647.314752	324.161014	646.330736	323.669006	5
16	1894.932739	947.970007	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	$M_r(\text{calc})$:	Delta	Sequence
59.0	2314.173950	0.009862	GSLVQASEANLQAAQDFVR
12.4	2314.173950	0.009862	GSLVQASEANLQAAQDFVR
1.1	2314.170776	0.013036	MADLRQLVTEHAQMMQRIK

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 53225: 2314.193412 from(772.405080,3+) rtinseconds(2577) index(56391)

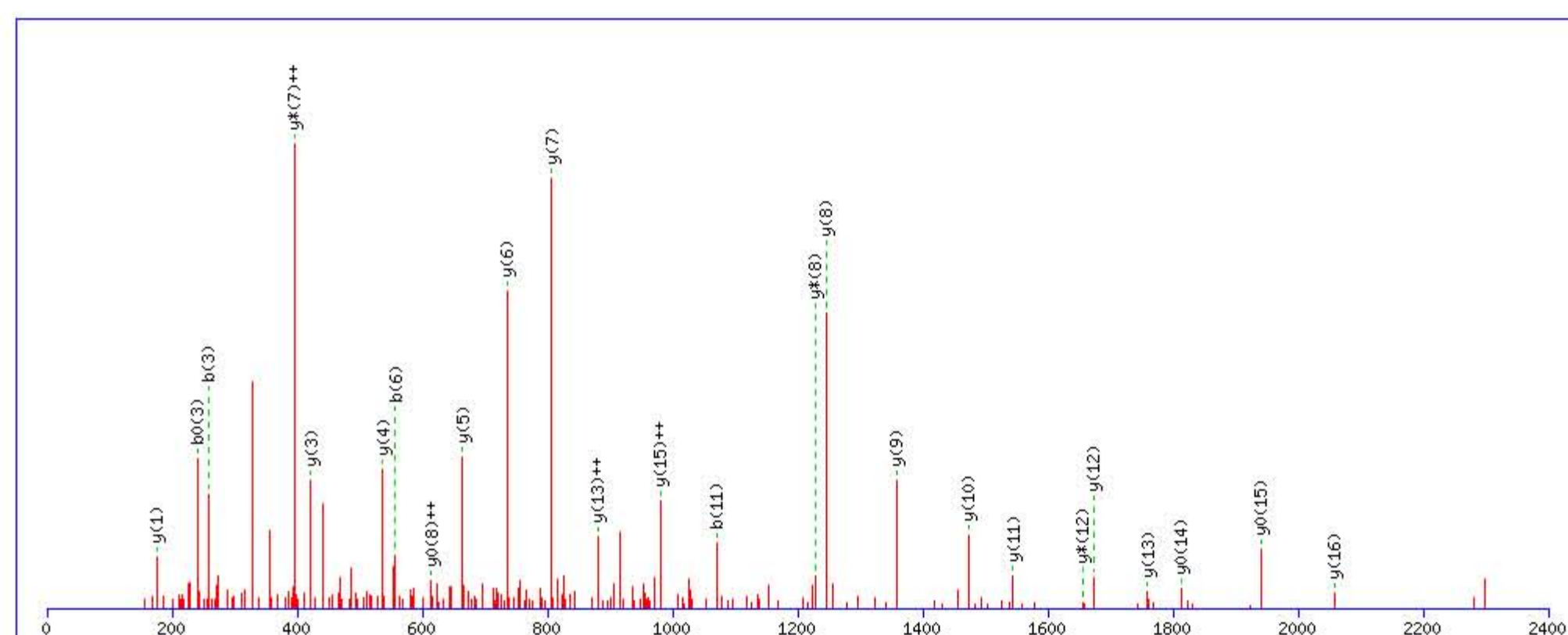
Title: Locus:1.1.1.1512.8 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2314.173950

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

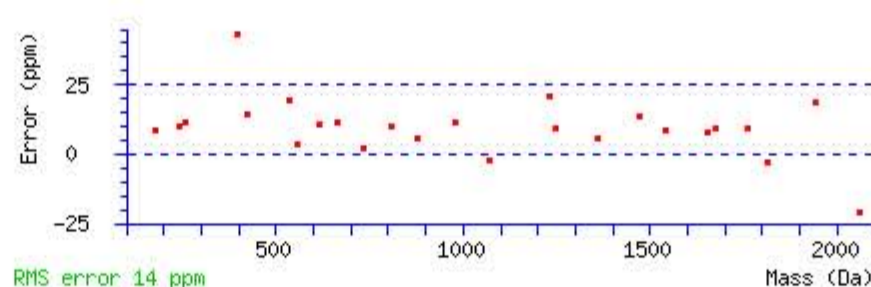
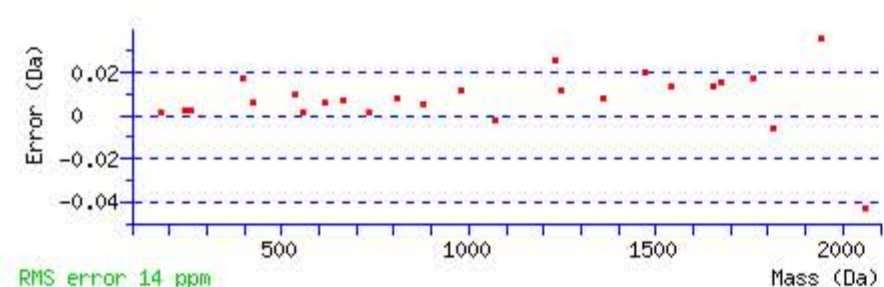
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 99 Expect: 3.9e-009

Matches : 25/200 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							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
98.5	2314.173950	0.019462	GSLVQASEANLQAAQDFVR
58.6	2314.173950	0.019462	GSLVQASEANLQAAQDFVR
17.5	2314.173950	0.019462	GSLVQASEANLQAAQDFVR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **FAHYVVTSQVVNTANEAR**

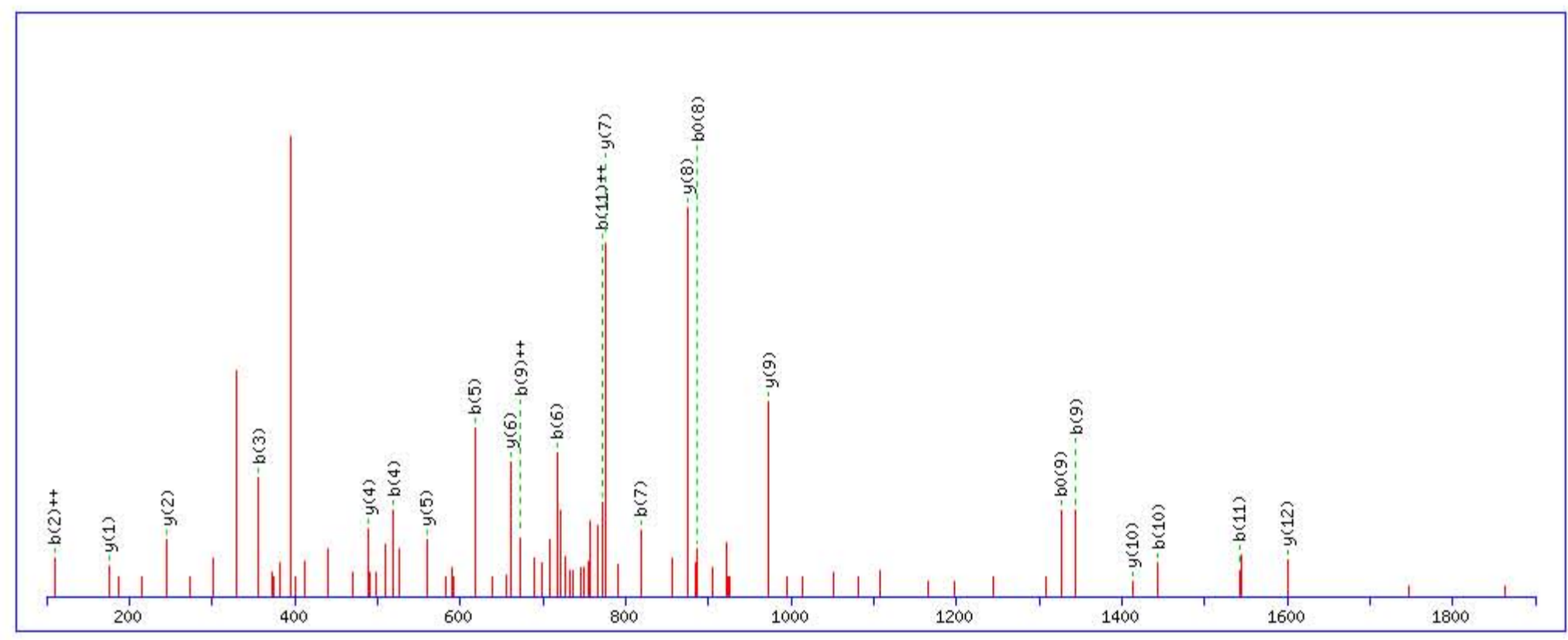
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

Match to Query 53259: 2316.178602 from(773.066810,3+) rtinseconds(1985) index(52769)
 Title: Locus:1.1.1.1306.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

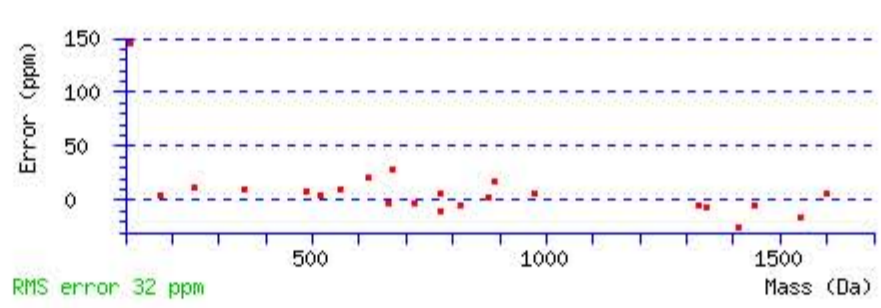
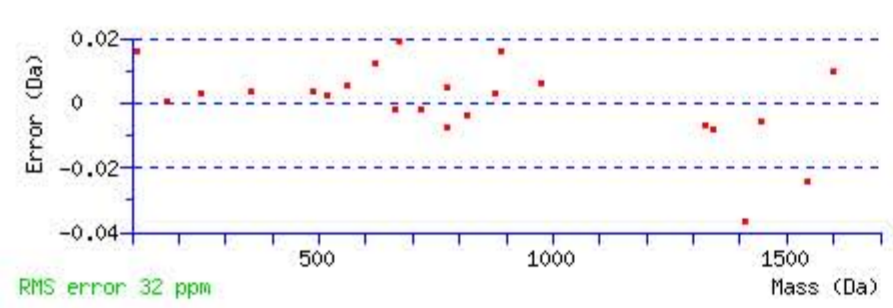
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2316.168488
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q9 : Biotin:Thermo-21345 (Q)
 Ions Score: 64 Expect: 1.1e-005
 Matches : 23/172 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	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
63.6	2316.168488	0.010114	FAHYVVTSQVVNTANEAR

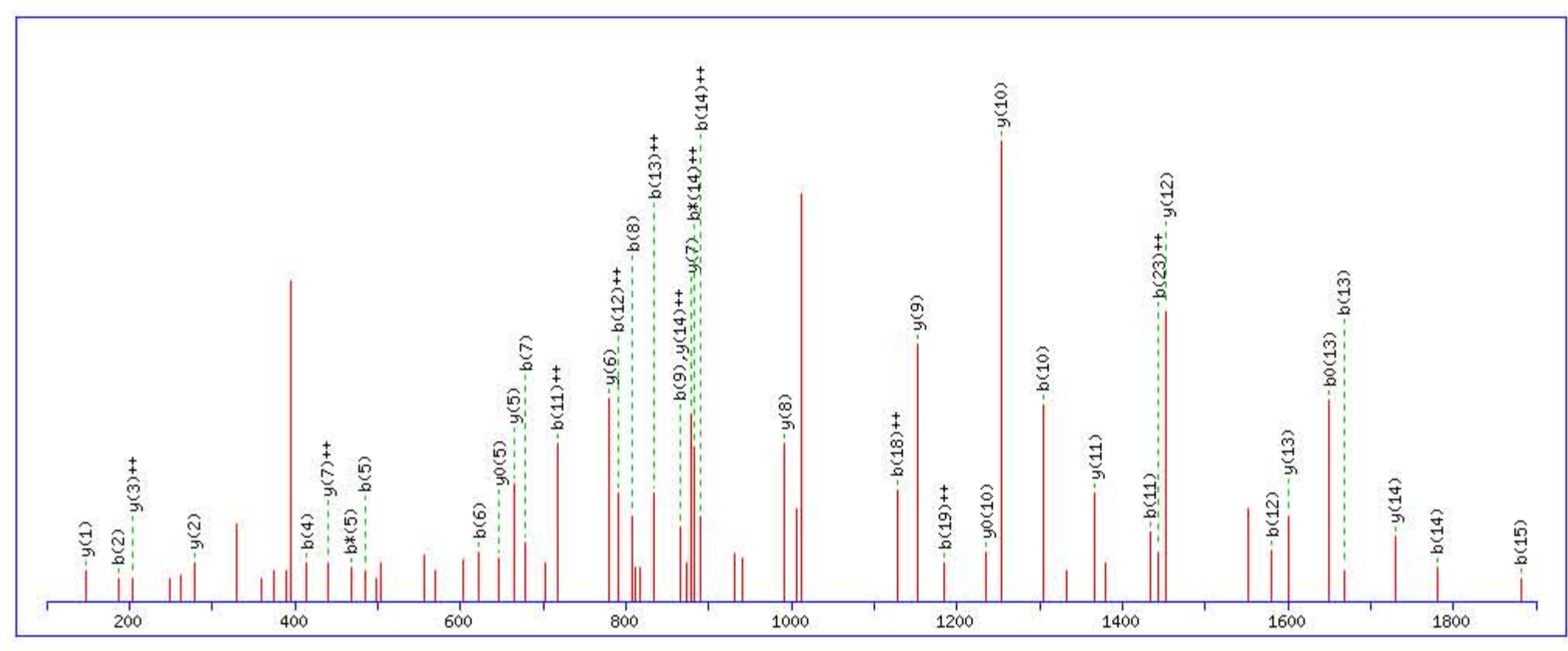
MASCOT Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADVQAHGEGQEF SITCLVDEEEMK**
 Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

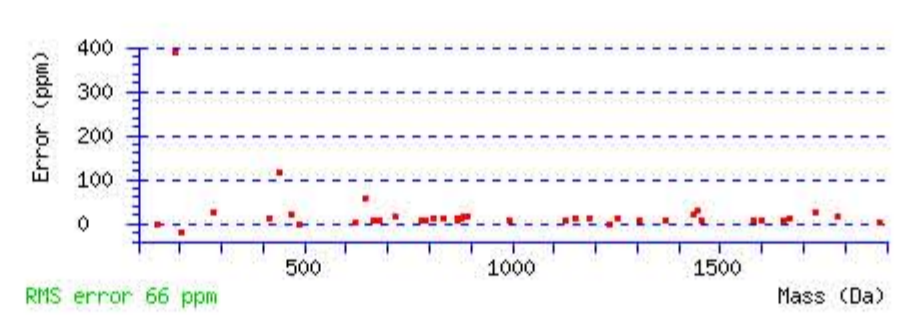
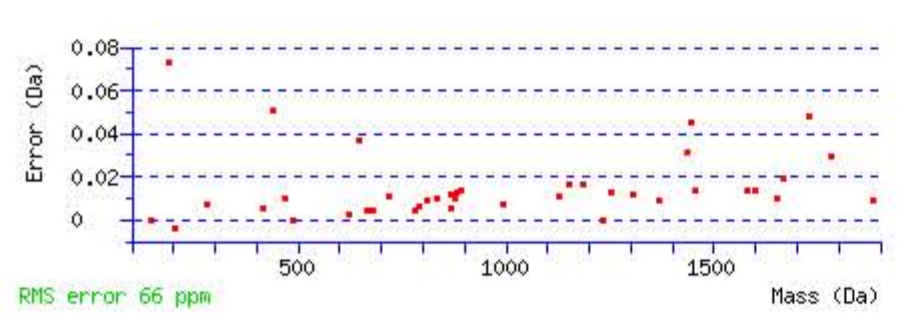
Match to Query 61928: 3032.393802 from(1011.805210,3+) rtinseconds(2544) index(56211)
 Title: Locus:1.1.1.1500.26 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3032.356552
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q10 : Biotin:Thermo-21345 (Q)
 Ions Score: 103 Expect: 6e-010
 Matches : 40/264 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							24
2	187.071333	94.039304			169.060768	85.034022	D	2962.326724	1481.667000	2945.300175	1473.153725	2944.316159	1472.661717	23
3	286.139747	143.573512			268.129182	134.568229	V	2847.299781	1424.153528	2830.273232	1415.640254	2829.289216	1415.148246	22
4	414.198325	207.602801	397.171776	199.089526	396.187760	198.597518	Q	2748.231367	1374.619321	2731.204818	1366.106047	2730.220802	1365.614039	21
5	485.235439	243.121357	468.208890	234.608083	467.224874	234.116075	A	2620.172789	1310.590032	2603.146240	1302.076758	2602.162224	1301.584750	20
6	622.294351	311.650814	605.267802	303.137539	604.283786	302.645531	H	2549.135675	1275.071475	2532.109126	1266.558201	2531.125110	1266.066193	19
7	679.315815	340.161546	662.289266	331.648271	661.305250	331.156263	G	2412.076763	1206.542019	2395.050214	1198.028745	2394.066198	1197.536737	18
8	808.358408	404.682842	791.331859	396.169568	790.347843	395.677560	E	2355.055299	1178.031287	2338.028750	1169.518013	2337.044734	1169.026005	17
9	865.379872	433.193574	848.353323	424.680300	847.369307	424.188292	G	2226.012706	1113.509991	2208.986157	1104.996716	2208.002141	1104.504708	16
10	1304.605198	652.806237	1287.578649	644.292963	1286.594633	643.800954	Q	2168.991242	1084.999259	2151.964693	1076.485984	2150.980677	1075.993976	15
11	1433.647791	717.327534	1416.621242	708.814259	1415.637226	708.322251	E	1729.765916	865.386596	1712.739367	856.873322	1711.755351	856.381314	14
12	1580.716205	790.861741	1563.689656	782.348466	1562.705640	781.856458	F	1600.723323	800.865300	1583.696774	792.352025	1582.712758	791.860017	13
13	1667.748233	834.377755	1650.721684	825.864480	1649.737668	825.372472	S	1453.654909	727.331093	1436.628360	718.817818	1435.644344	718.325810	12
14	1780.832297	890.919787	1763.805748	882.406512	1762.821732	881.914504	I	1366.622881	683.815079	1349.596332	675.301804	1348.612316	674.809796	11
15	1881.879976	941.443626	1864.853427	932.930352	1863.869411	932.438344	T	1253.538817	627.273047	1236.512268	618.759772	1235.528252	618.267764	10
16	2041.910625	1021.458951	2024.884076	1012.945676	2023.900060	1012.453668	C	1152.491138	576.749207	1135.464589	568.235933	1134.480573	567.743925	9
17	2154.994689	1078.000983	2137.968140	1069.487708	2136.984124	1068.995700	L	992.460489	496.733883	975.433940	488.220608	974.449924	487.728600	8
18	2254.063103	1127.535189	2237.036554	1119.021915	2236.052538	1118.529907	V	879.376425	440.191851	862.349876	431.678576	861.365860	431.186568	7
19	2369.090046	1185.048661	2352.063497	1176.535386	2351.079481	1176.043378	D	780.308011	390.657644	763.281462	382.144369	762.297446	381.652361	6
20	2498.132639	1249.569957	2481.106090	1241.056683	2480.122074	1240.564675	E	665.281068	333.144172	648.254519	324.630898	647.270503	324.138890	5
21	2627.175232	1314.091254	2610.148683	1305.577979	2609.164667	1305.085971	E	536.238475	268.622876	519.211926	260.109601	518.227910	259.617593	4
22	2756.217825	1378.612551	2739.191276	1370.099276	2738.207260	1369.607268	E	407.195882	204.101579	390.169333	195.588305	389.185317	195.096297	3
23	2887.258310	1444.132793	2870.231761	1435.619518	2869.247745	1435.127511	M	278.153289	139.580282	261.126740	131.067008			2
24							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **ADVQAHGEGQEF SITCLVDEEEMK**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
103.3	3032.356552	0.037250	ADVQAHGEGQEF SITCLVDEEEMK
80.9	3032.356552	0.037250	ADVQAHGEGQEF SITCLVDEEEMK

MASCOT Search Results

Peptide View

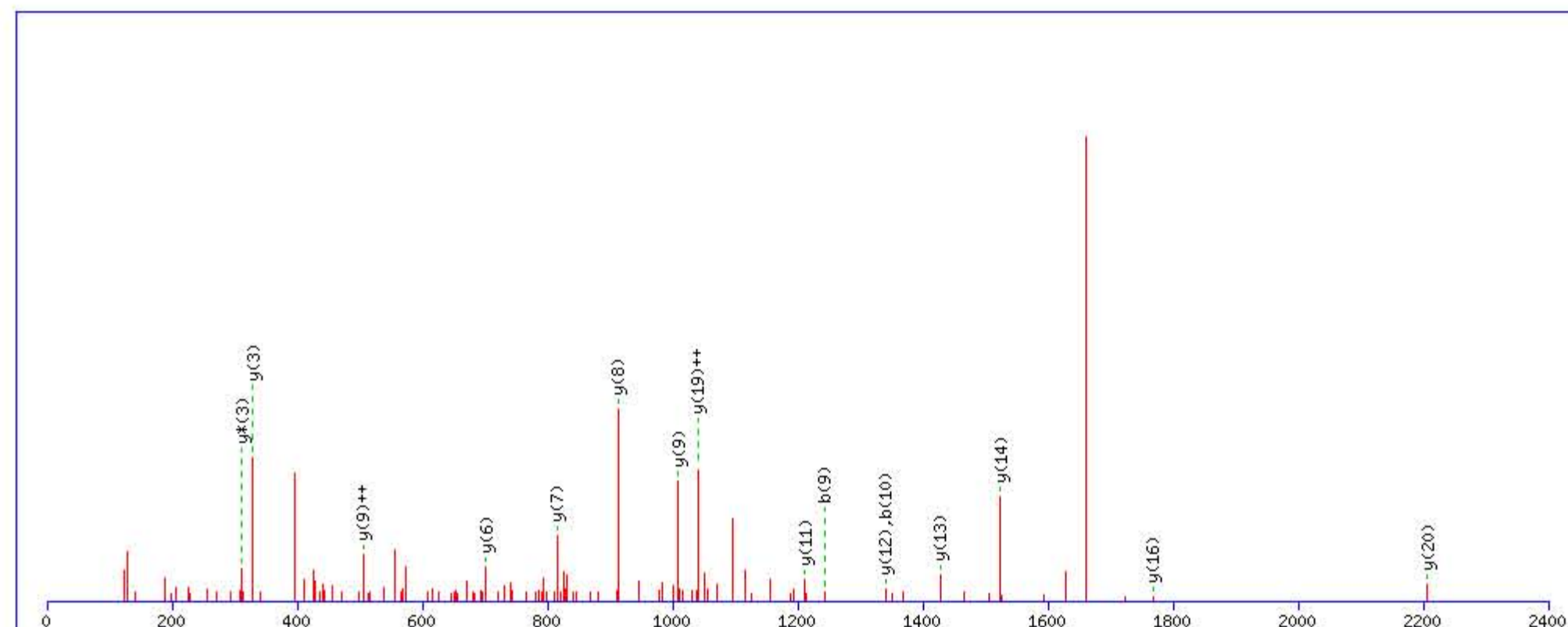
MS/MS Fragmentation of **GMADQDGLKPTIDKPSEDSPPLEMLGPR**
 Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

Match to Query 65781: 3320.644416 from(831.168380,4+) rtinseconds(2193) index(54171)
 Title: Locus:1.1.1.1378.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

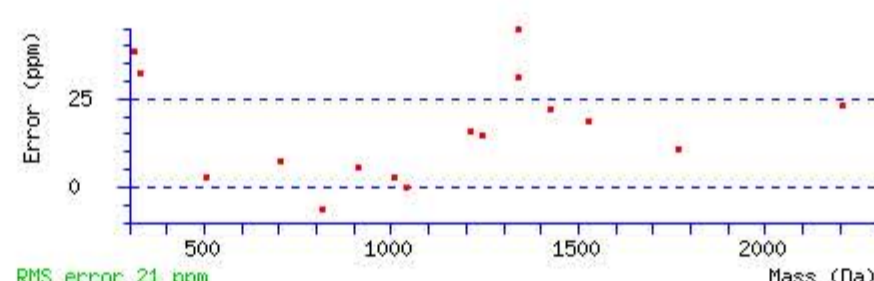
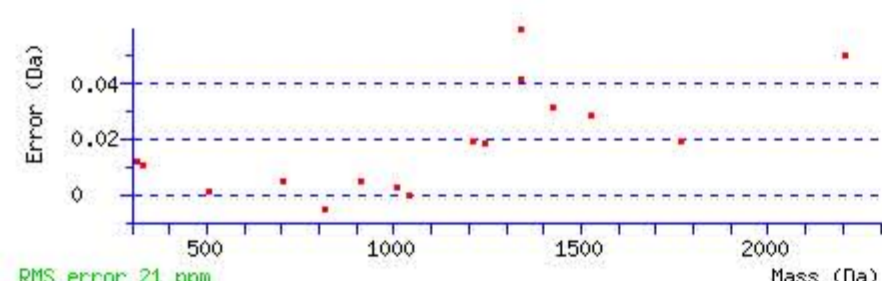
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3320.609070
 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
 Q5 : Biotin:Thermo-21345 (Q)
 Ions Score: 92 Expect: 3.9e-009
 Matches : 16/452 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							28
2	205.064140	103.035708					M	3264.594900	1632.801088	3247.568351	1624.287813	3246.584335	1623.795805	27
3	276.101254	138.554265					A	3117.559500	1559.283388	3100.532951	1550.770113	3099.548935	1550.278105	26
4	391.128197	196.067737			373.117632	187.062454	D	3046.522386	1523.764831	3029.495837	1515.251556	3028.511821	1514.759548	25
5	830.353523	415.680400	813.326974	407.167125	812.342958	406.675117	Q	2931.495443	1466.251359	2914.468894	1457.738085	2913.484878	1457.246077	24
6	945.380466	473.193871	928.353917	464.680597	927.369901	464.188589	D	2492.270117	1246.638696	2475.243568	1238.125422	2474.259552	1237.633414	23
7	1002.401930	501.704603	985.375381	493.191329	984.391365	492.699321	G	2377.243174	1189.125225	2360.216625	1180.611950	2359.232609	1180.119942	22
8	1115.485994	558.246635	1098.459445	549.733361	1097.475429	549.241353	L	2320.221710	1160.614493	2303.195161	1152.101218	2302.211145	1151.609210	21
9	1243.580957	622.294117	1226.554408	613.780842	1225.570392	613.288834	K	2207.137646	1104.072461	2190.111097	1095.559186	2189.127081	1095.067178	20
10	1340.633721	670.820499	1323.607172	662.307224	1322.623156	661.815216	P	2079.042683	1040.024980	2062.016134	1031.511705	2061.032118	1031.019697	19
11	1441.681400	721.344338	1424.654851	712.831064	1423.670835	712.339056	T	1981.989919	991.498598	1964.963370	982.985323	1963.979354	982.493315	18
12	1554.765464	777.886370	1537.738915	769.373096	1536.754899	768.881088	I	1880.942240	940.974758	1863.915691	932.461484	1862.931675	931.969476	17
13	1669.792407	835.399842	1652.765858	826.886567	1651.781842	826.394559	D	1767.858176	884.432726	1750.831627	875.919452	1749.847611	875.427444	16
14	1797.887370	899.447323	1780.860821	890.934049	1779.876805	890.442041	K	1652.831233	826.919255	1635.804684	818.405980	1634.820668	817.913972	15
15	1894.940134	947.973705	1877.913585	939.460431	1876.929569	938.968423	P	1524.736270	762.871773	1507.709721	754.358499	1506.725705	753.866491	14
16	1981.972162	991.489719	1964.945613	982.976445	1963.961597	982.484437	S	1427.683506	714.345391	1410.656957	705.832117	1409.672941	705.340109	13
17	2111.014755	1056.011016	2093.988206	1047.497741	2093.004190	1047.005733	E	1340.651478	670.829377	1323.624929	662.316103	1322.640913	661.824095	12
18	2226.041698	1113.524487	2209.015149	1105.011212	2208.031133	1104.519204	D	1211.608885	606.308081	1194.582336	597.794806	1193.598320	597.302798	11
19	2313.073726	1157.040501	2296.047177	1148.527226	2295.063161	1148.035218	S	1096.581942	548.794609	1079.555393	540.281335	1078.571377	539.789327	10
20	2410.126490	1205.566883	2393.099941	1197.053608	2392.115925	1196.561600	P	1009.549914	505.278595	992.523365	496.765321	991.539349	496.273313	9
21	2507.179254	1254.093265	2490.152705	1245.579990	2489.168689	1245.087983	P	912.497150	456.752213	895.470601	448.238939	894.486585	447.746931	8
22	2620.263318	1310.635297	2603.236769	1302.122023	2602.252753	1301.630015	L	815.444386	408.225831	798.417837	399.712557	797.433821	399.220549	7
23	2749.305911	1375.156594	2732.279362	1366.643319	2731.295346	1366.151311	E	702.360322	351.683799	685.333773	343.170525	684.349757	342.678517	6
24	2880.346396	1440.676836	2863.319847	1432.163562	2862.335831	1431.671554	M	573.317729	287.162503	556.291180	278.649228			5
25	2993.430460	1497.218868	2976.403911	1488.705594	2975.419895	1488.213586	L	442.277244	221.642260	425.250695	213.128986			4
26	3050.451924	1525.729600	3033.425375	1517.216326	3032.441359	1516.724318	G	329.193180	165.100228	312.166631	156.586953			3
27	3147.504688	1574.255982	3130.478139	1565.742708	3129.494123	1565.250700	P	272.171716	136.589496	255.145167	128.076221			2
28							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **GMADQDGLKPTIDKPSEDSPPLEMLGPR**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
91.5	3320.609070	0.035346	GMADQDGLKPTIDKPSEDSPPLEMLGPR
1.8	3320.689682	-0.045266	LLSQLPEVHEPPQEKQEPPCSQSPKK
0.9	3320.645462	-0.001046	QDIGDILHQIMTITDQSLDEAQAQ
0.2	3320.689682	-0.045266	LLSQLPEVHEPPQEKQEPPCSQSPKK
0.2	3320.689682	-0.045266	LLSQLPEVHEPPQEKQEPPCSQSPKK

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 17358: 1042.548268 from(522.281410,2+) rtinseconds(1332) index(48430)

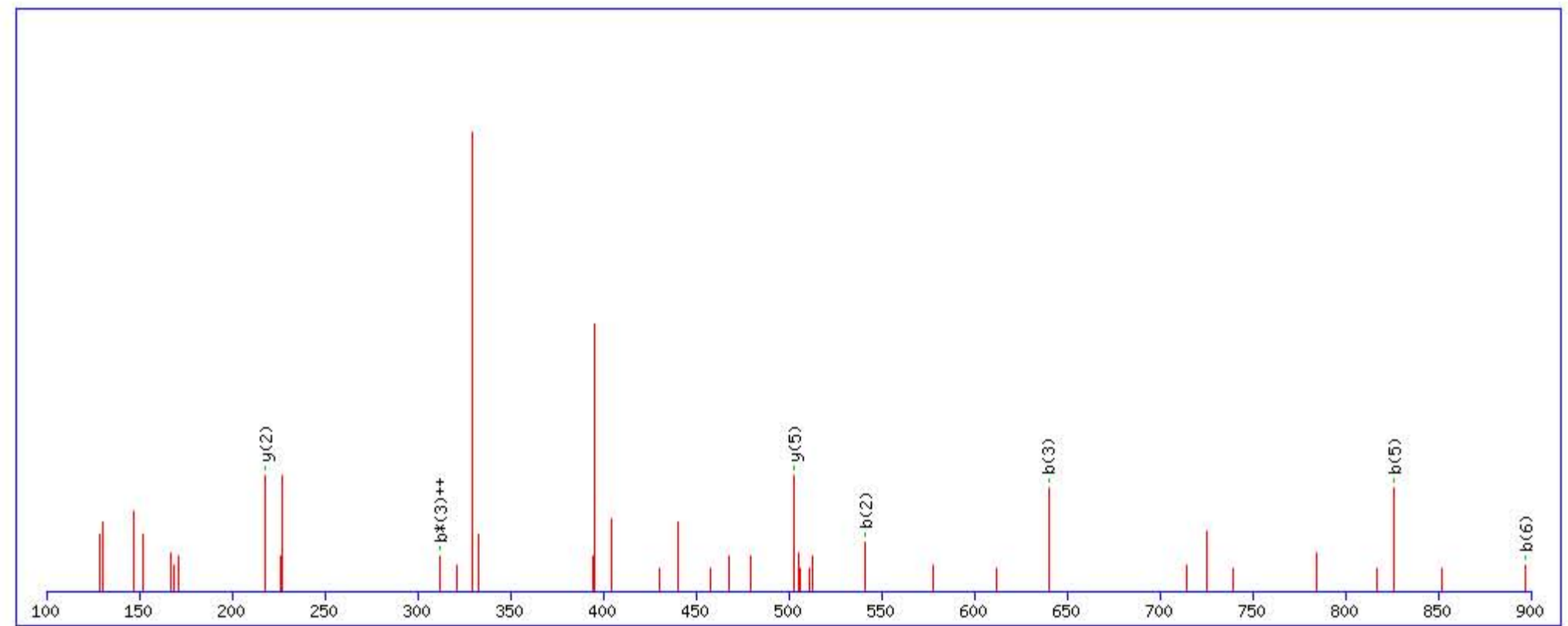
Title: Locus:1.1.1.1079.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1042.548111

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

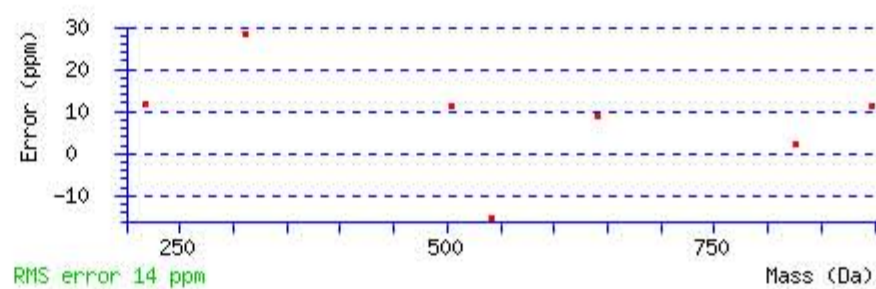
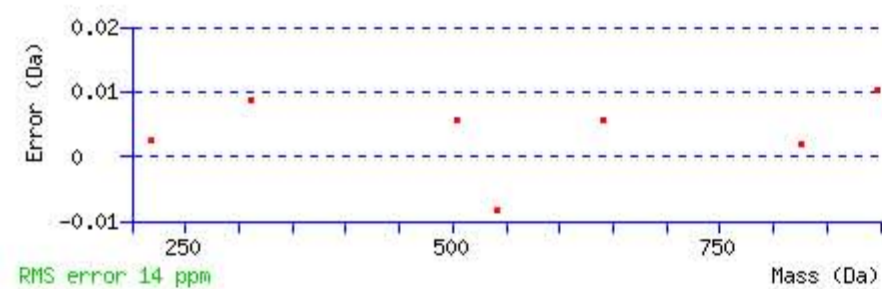
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.027

Matches : 7/66 fragment ions using 8 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
30.0	1042.548111	0.000157	TQVADAK
12.4	1042.548096	0.000172	SLQADAK
11.7	1042.540726	0.007542	KPVSEVGDGR
10.0	1042.540680	0.007588	EAEKRPADK
8.7	1042.540695	0.007573	GREPEASGLK
8.4	1042.540680	0.007588	SLENPAERK
7.5	1042.548080	0.000188	EKEQAK
7.0	1042.548096	0.000172	QTENLK
6.3	1042.554611	-0.006343	EPSEIVELK
6.1	1042.548096	0.000172	QEAGLSK

{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALYAQAR**

Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

Match to Query 18789: 1102.595728 from(552.305140,2+) rtinseconds(1681) index(50706)

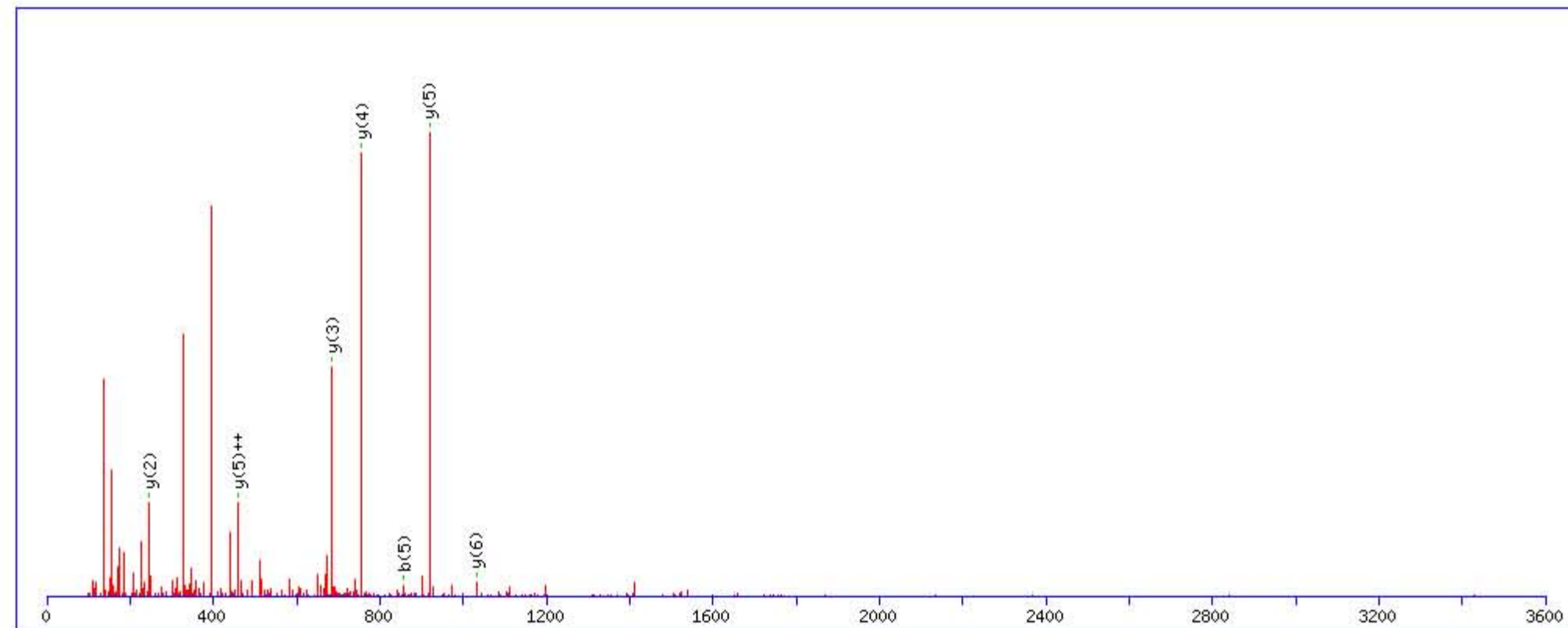
Title: Locus:1.1.1.1201.3 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1102.595703

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

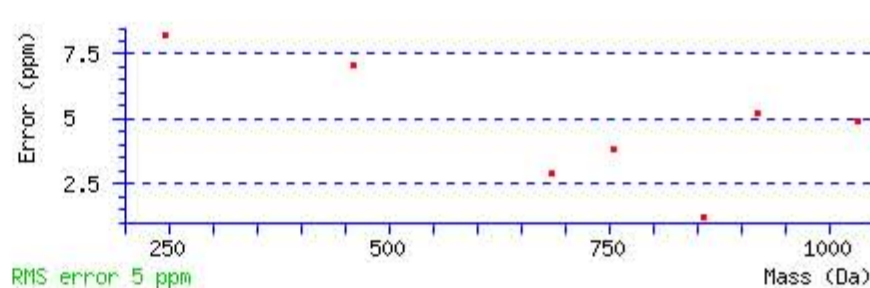
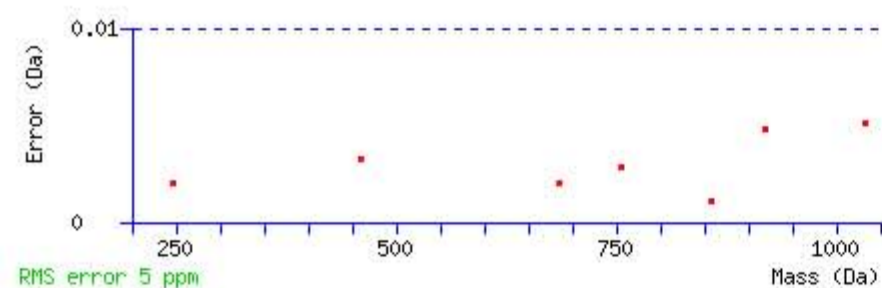
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 38 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
37.5	1102.595703	0.000025	ALYAQAR
10.5	1102.602234	-0.006506	AIELGYNPVK
3.6	1102.580460	0.015268	AMVENVTLAR
1.6	1102.584305	0.011423	QSSQRGLTAR
0.9	1102.598221	-0.002493	DDLKATLTAR
0.7	1102.588333	0.007395	SPYGLTPRGR
0.3	1102.591660	0.004068	KMREELAAR

Mascot: <http://www.matrixscience.com/>

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQSTITSR**

Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

Match to Query 23336: 1201.649588 from(601.832070,2+) rtinseconds(1533) index(49759)

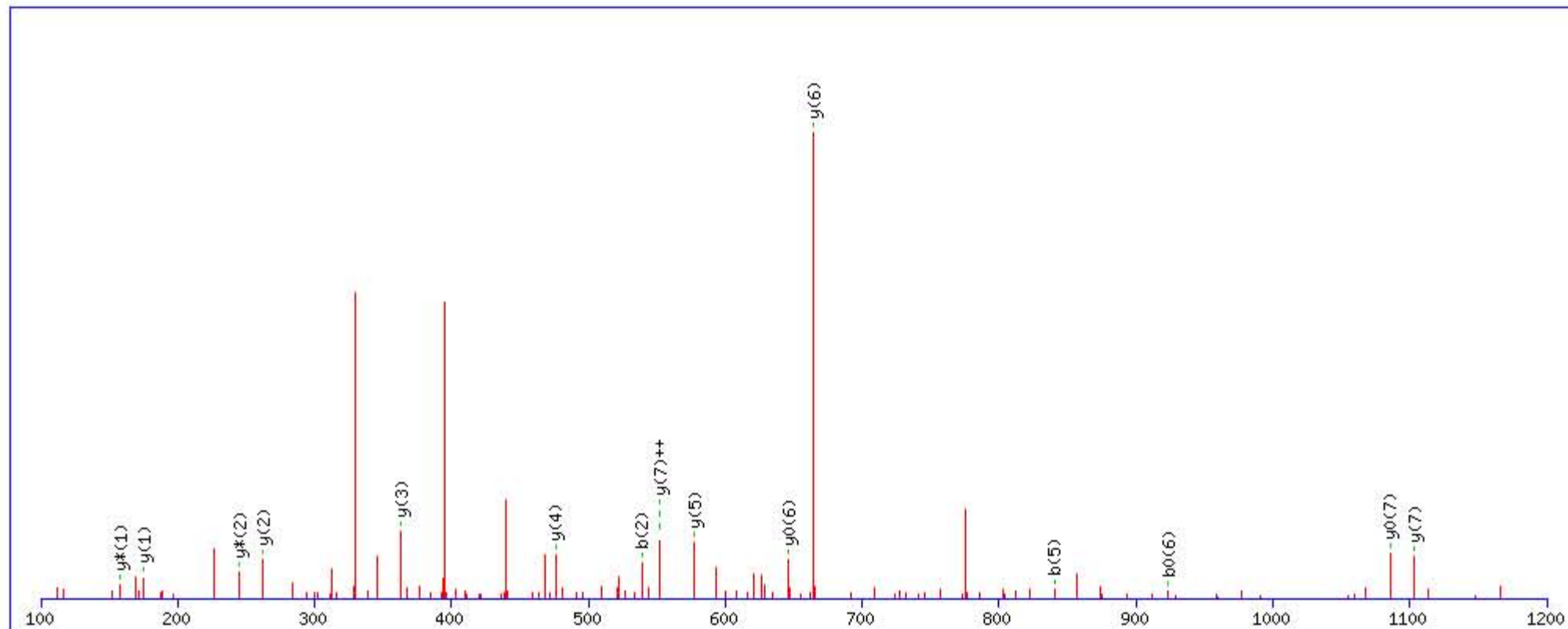
Title: Locus:1.1.1.1149.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1201.648895

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

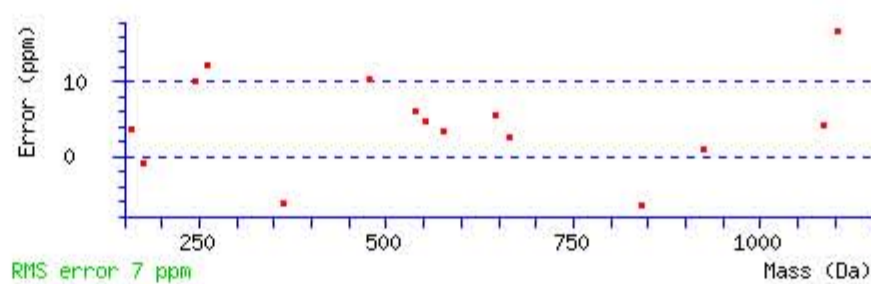
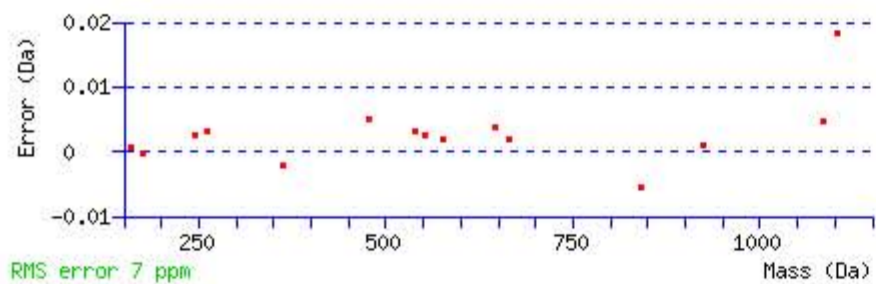
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.00042

Matches : 15/76 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	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
36.9	1201.648895	0.000693	VQSTITSR
0.9	1201.638992	0.010596	VQPPSHAR
0.3	1201.638992	0.010596	VQGREFR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **MATMIQSK**

Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

Match to Query 26547: 1320.664428 from(661.339490,2+) rtinseconds(1776) index(51353)

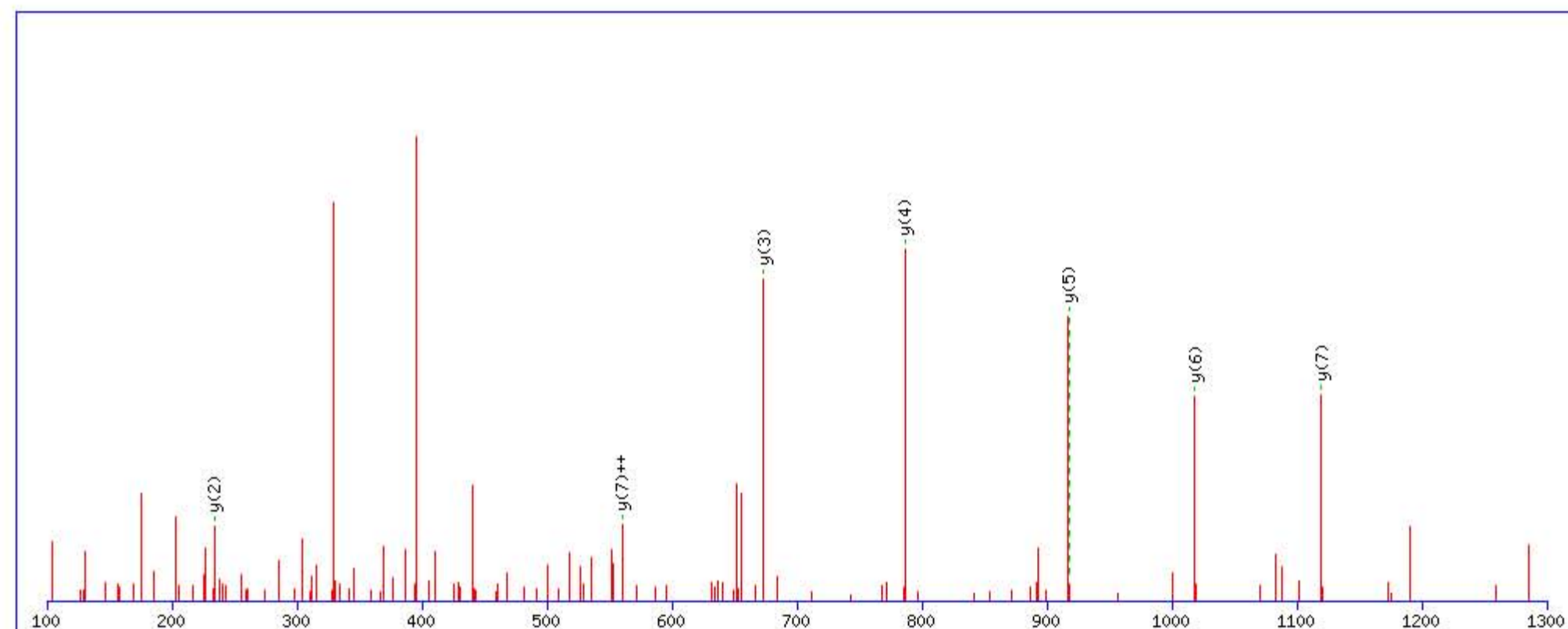
Title: Locus:1.1.1.1234.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1320.660370

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

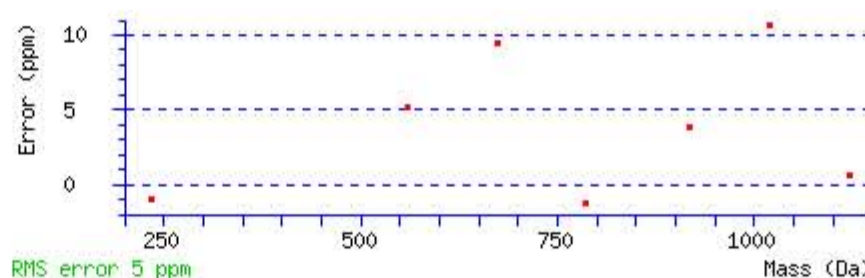
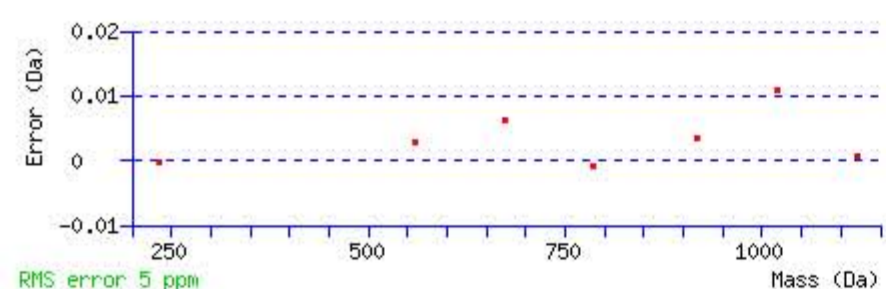
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.00075

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	132.047761	66.527518					M							9
2	203.084875	102.046075					A	1190.627179	595.817228	1173.600630	587.303953	1172.616614	586.811945	8
3	304.132554	152.569915			286.121989	143.564632	T	1119.590065	560.298671	1102.563516	551.785396	1101.579500	551.293388	7
4	405.180233	203.093754			387.169668	194.088472	T	1018.542386	509.774831	1001.515837	501.261557	1000.531821	500.769549	6
5	536.220718	268.613997			518.210153	259.608715	M	917.494707	459.250992	900.468158	450.737717	899.484142	450.245709	5
6	649.304782	325.156029			631.294217	316.150747	I	786.454222	393.730749	769.427673	385.217475	768.443657	384.725467	4
7	1088.530108	544.768692	1071.503559	536.255418	1070.519543	535.763410	Q	673.370158	337.188717	656.343609	328.675443	655.359593	328.183435	3
8	1175.562136	588.284706	1158.535587	579.771432	1157.551571	579.279424	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 **MATMIQSK**

(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	1320.660370	0.004058	MATMIQSK
6.0	1320.677292	-0.012864	LATTTTDTSSVPK
4.6	1320.670715	-0.006287	IAPKASMAGASSSK
2.7	1320.675461	-0.011033	RMRLVVDGMGR
1.8	1320.682816	-0.018388	RMKPLMDRDK
0.9	1320.674759	-0.010331	QSTEFASK
0.4	1320.678574	-0.014146	SFRAAAETLER

Mascot: <http://www.matrixscience.com/>

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 35026: 1548.764742 from(517.262190,3+) rtinseconds(1441) index(49103)

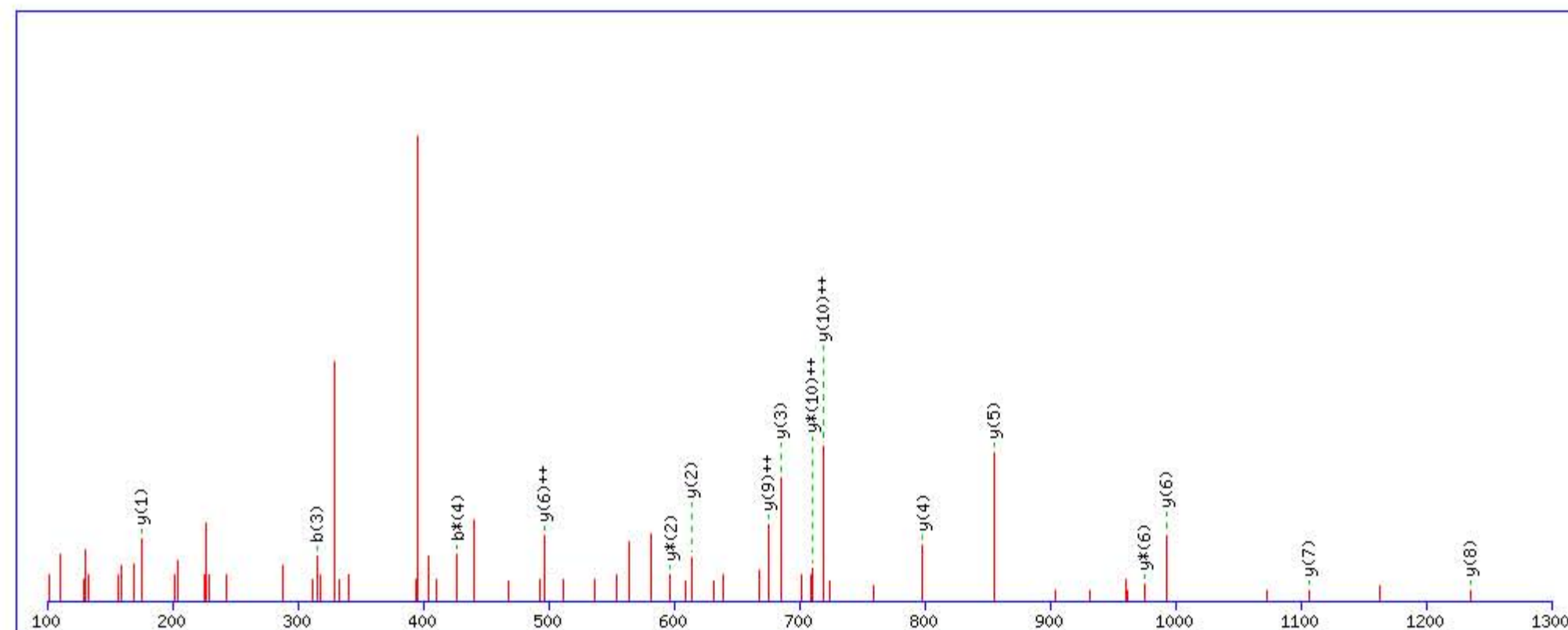
Title: Locus:1.1.1.1117.14 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1548.783066

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

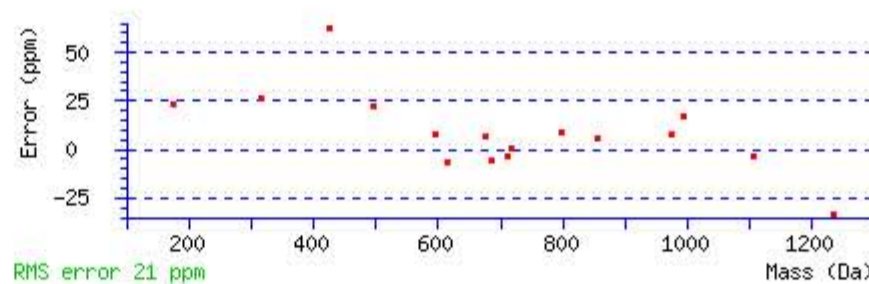
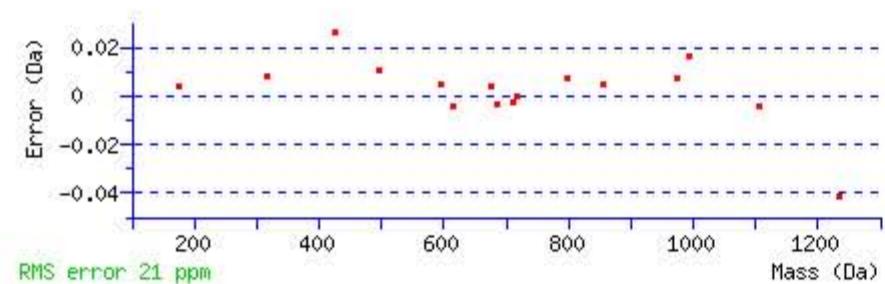
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 44 Expect: 0.00012

Matches : 16/100 fragment ions using 29 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							11
2	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
43.6	1548.783066	-0.018324	LSNENHGIAQR
1.7	1548.786438	-0.021696	MMQAQEAVSRVKR
1.7	1548.786438	-0.021696	MMQAQEAVSRVKR

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 39357: 1647.871848 from(824.943200,2+) rtinseconds(2394) index(55338)

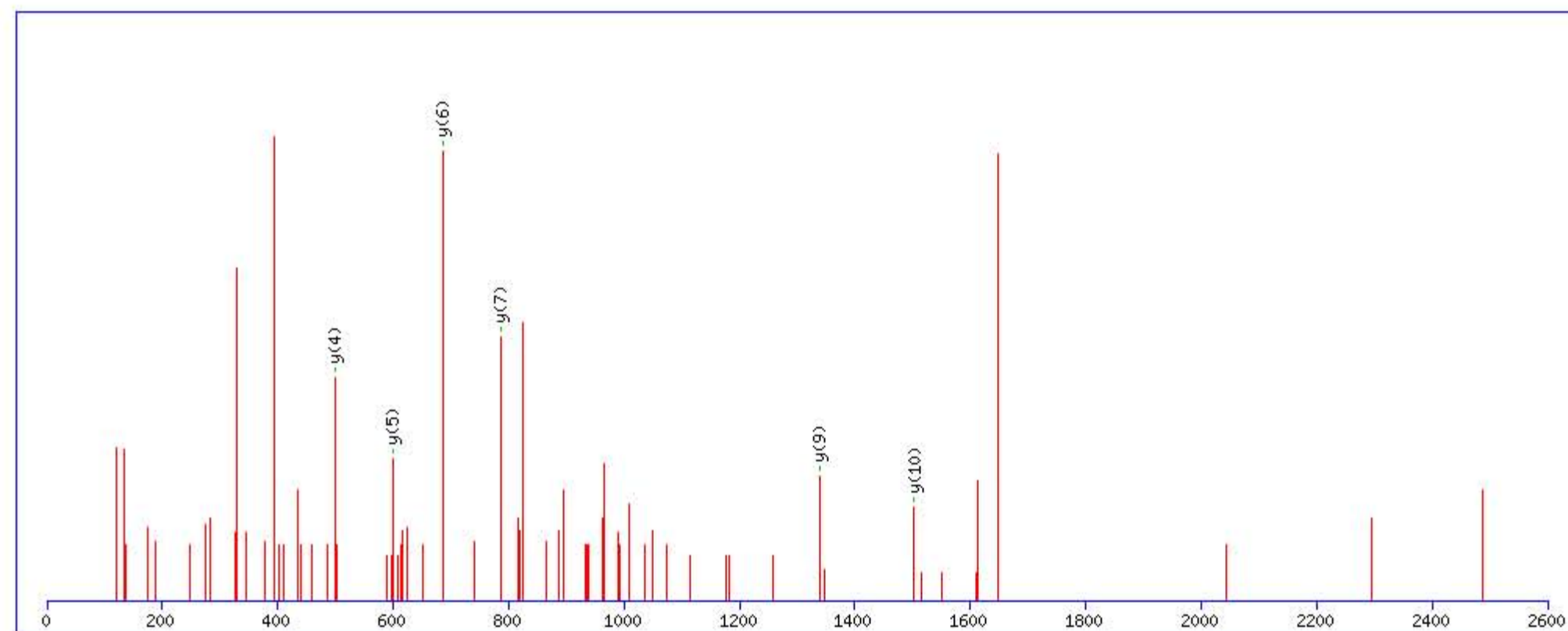
Title: Locus:1.1.1.1448.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1647.880676

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

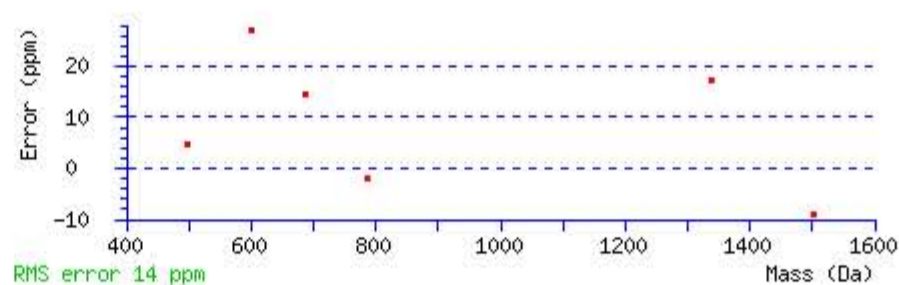
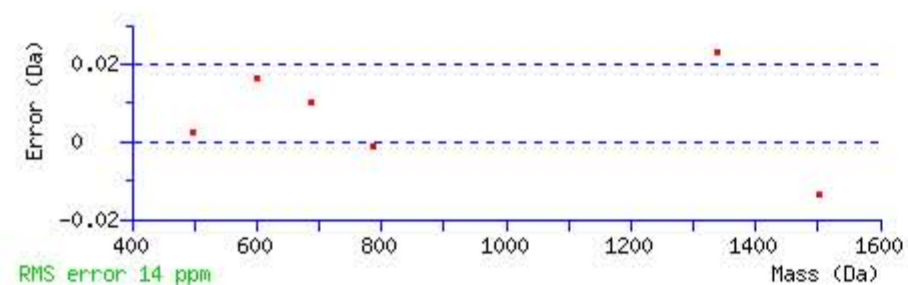
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 26 Expect: 0.066

Matches : 6/98 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	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
25.9	1647.880676	-0.008828	FYNQVSTPLLR

Mascot: <http://www.matrixscience.com/>

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 39662: 1663.830888 from(832.922720,2+) rtinseconds(1688) index(50741)

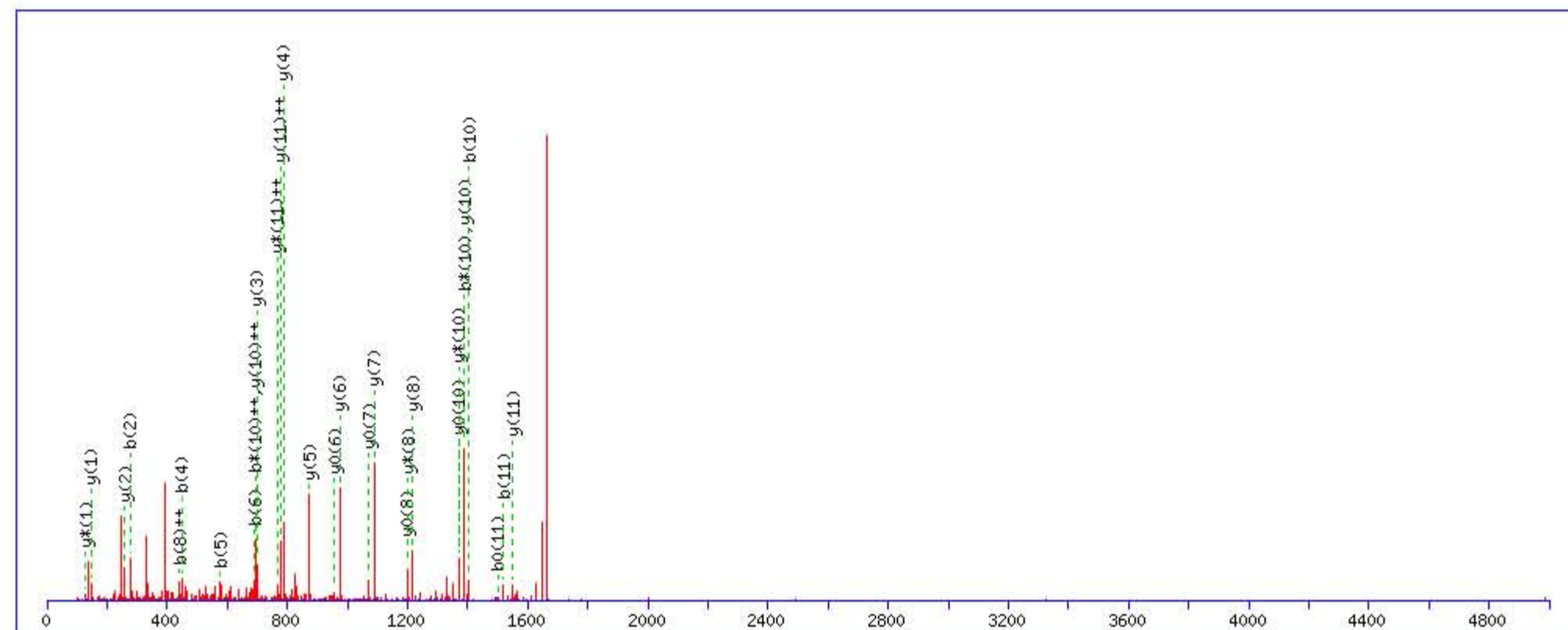
Title: Locus:1.1.1.1203.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1663.823944

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

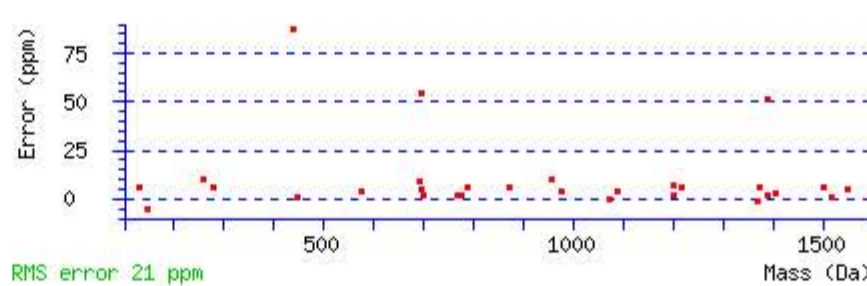
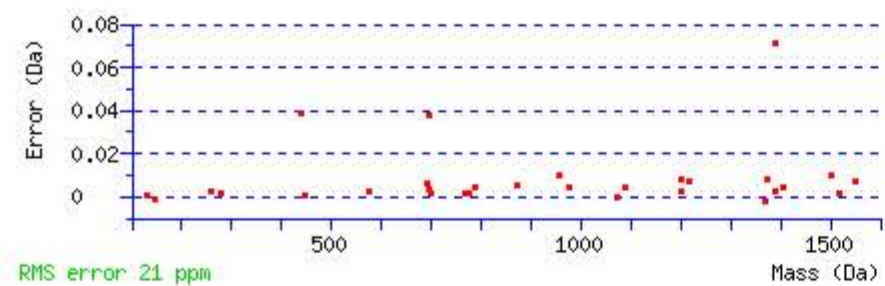
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 67 Expect: 9e-007

Matches : 30/110 fragment ions using 48 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					I							12
2	277.154669	139.080973					Y	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
67.2	1663.823944	0.006944	IYGNQDTSSQLK
13.6	1663.823944	0.006944	IYGNQDTSSQLK
2.6	1663.827957	0.002931	EEAFLHVAVDMYLK
2.4	1663.831345	-0.000457	QLTDCISEFLK
2.1	1663.845078	-0.014190	LMSGVENSQKVDISTK
1.6	1663.806183	0.024705	DLSMFSQNMTHIK

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 42336: 1778.961732 from(593.994520,3+) rtinseconds(1556) index(49906)

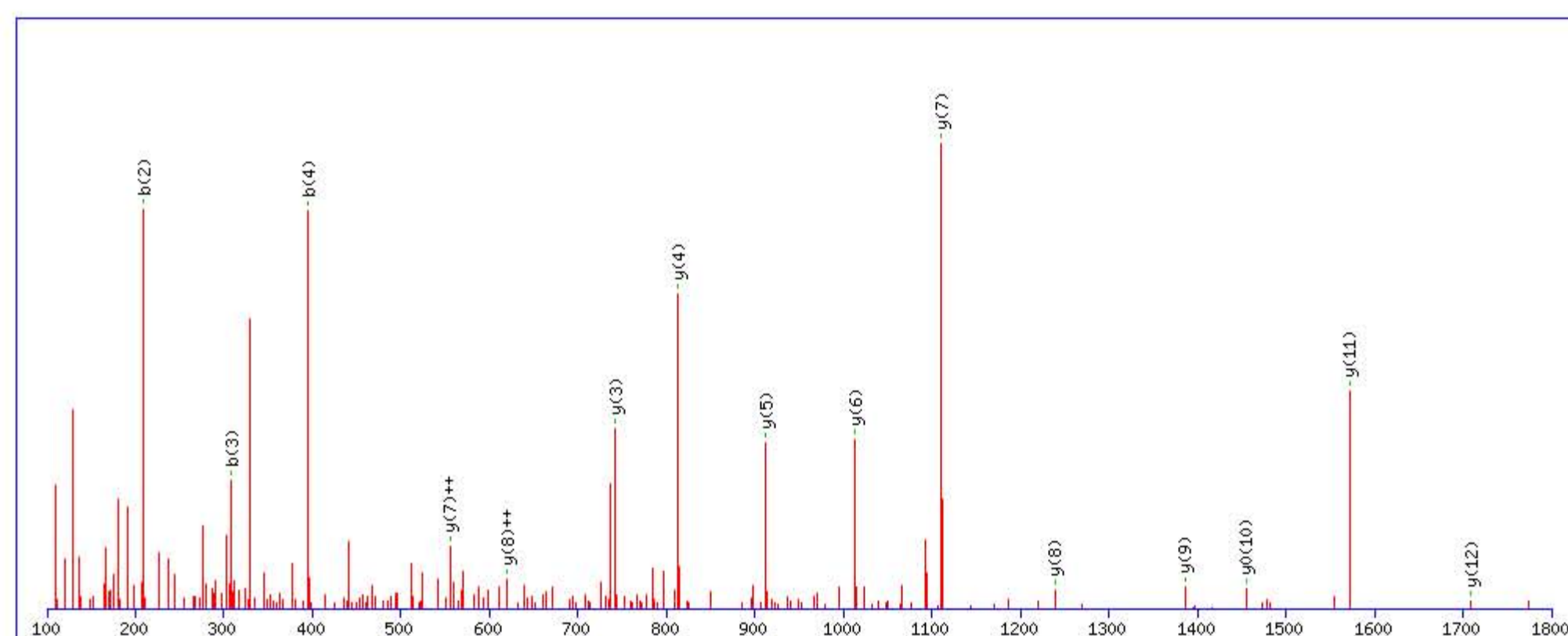
Title: Locus:1.1.1.1157.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1778.961395

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

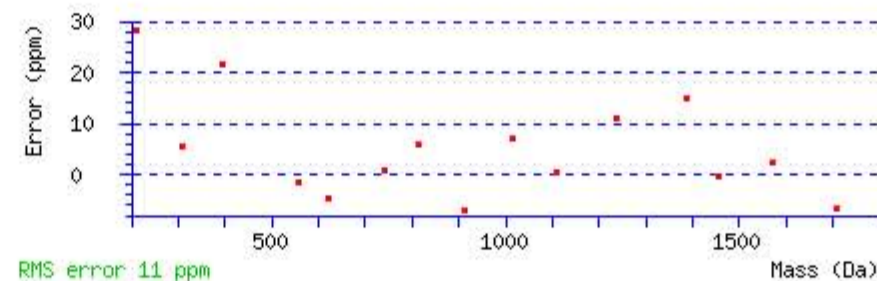
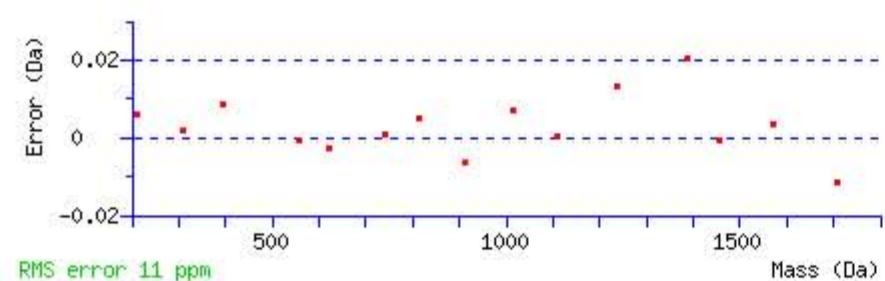
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 82 Expect: 1.3e-007

Matches : 15/118 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	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
81.7	1778.961395	0.000337	AHVSFKPTVAQQR
81.7	1778.961395	0.000337	AHVSFKPTVAQQR

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **IYGNQDTSSQLK**

Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

Match to Query 46034: 1974.996942 from(659.339590,3+) rtinseconds(2030) index(53152)

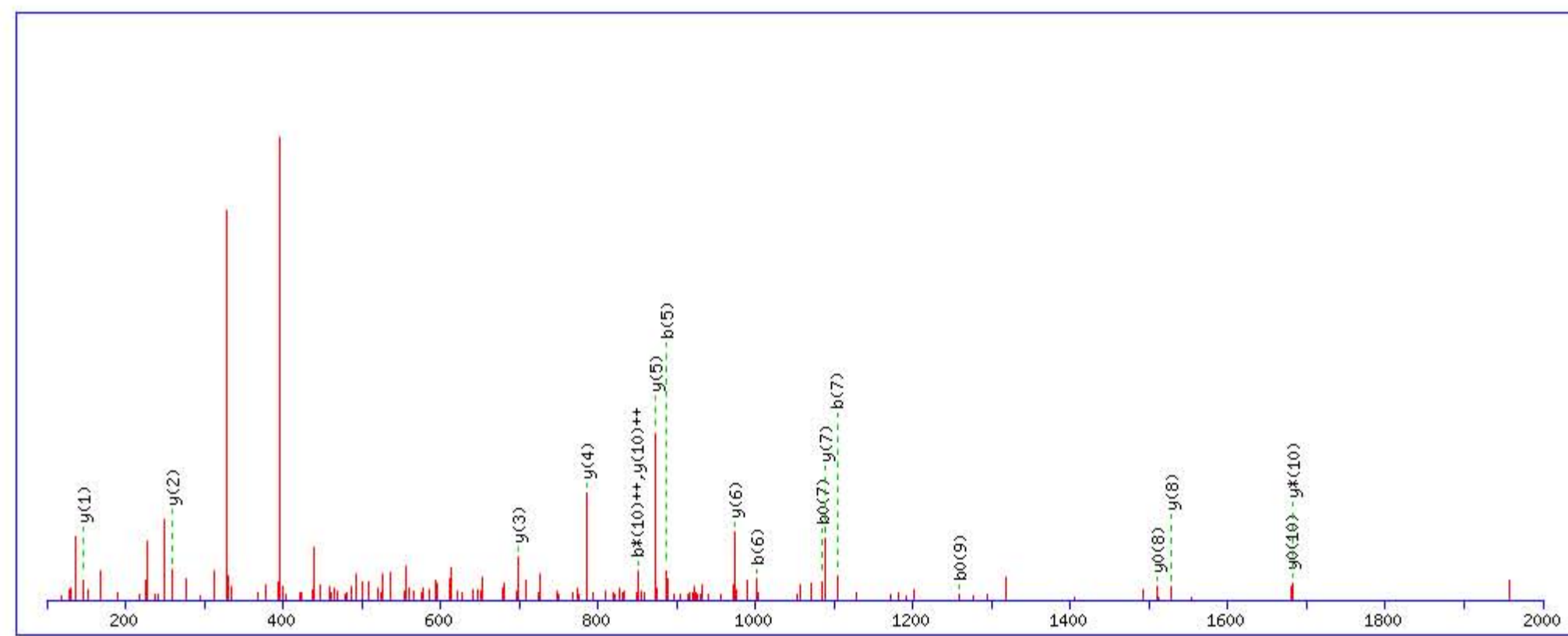
Title: Locus:1.1.1.1322.2 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1974.990692

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

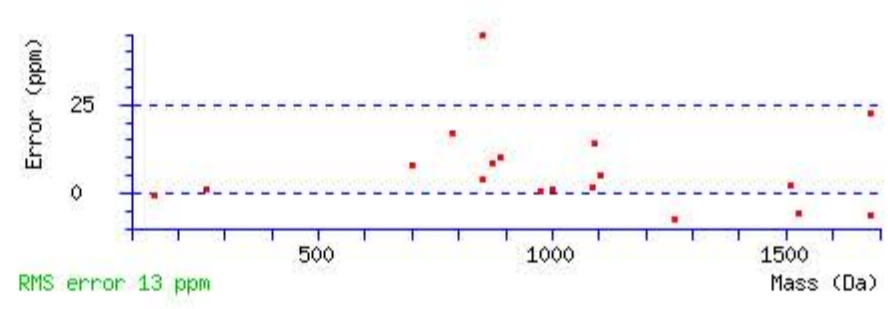
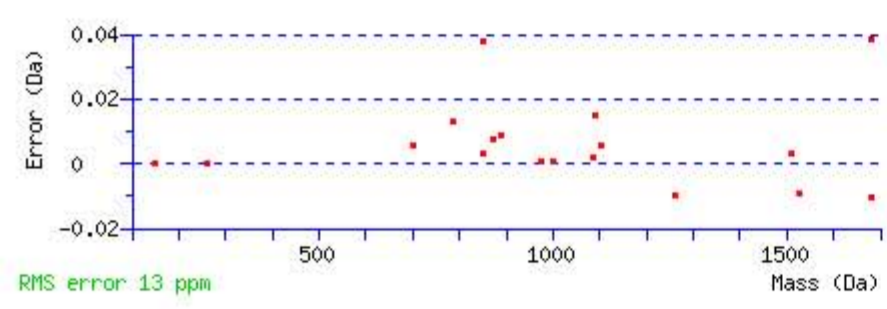
Q5 : Biotin:Thermo-21345 (Q)

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.0047

Matches : 18/110 fragment ions using 46 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					I							12
2	277.154669	139.080973					Y	1862.913918	931.960597	1845.887369	923.447323	1844.903353	922.955315	11
3	334.176133	167.591704					G	1699.850589	850.428933	1682.824040	841.915658	1681.840024	841.423650	10
4	448.219060	224.613168	431.192511	216.099894			N	1642.829125	821.918201	1625.802576	813.404926	1624.818560	812.912918	9
5	887.444386	444.225831	870.417837	435.712557			Q	1528.786198	764.896737	1511.759649	756.383463	1510.775633	755.891455	8
6	1002.471329	501.739303	985.444780	493.226028	984.460764	492.734020	D	1089.560872	545.284074	1072.534323	536.770800	1071.550307	536.278792	7
7	1103.519008	552.263142	1086.492459	543.749868	1085.508443	543.257860	T	974.533929	487.770603	957.507380	479.257328	956.523364	478.765320	6
8	1190.551036	595.779156	1173.524487	587.265882	1172.540471	586.773874	S	873.486250	437.246763	856.459701	428.733489	855.475685	428.241481	5
9	1277.583064	639.295170	1260.556515	630.781896	1259.572499	630.289888	S	786.454222	393.730749	769.427673	385.217475	768.443657	384.725467	4
10	1716.808390	858.907833	1699.781841	850.394559	1698.797825	849.902551	Q	699.422194	350.214735	682.395645	341.701461			3
11	1829.892454	915.449865	1812.865905	906.936591	1811.881889	906.444583	L	260.196868	130.602072	243.170319	122.088797			2
12							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [IYGNQDTSSQLK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.9	1974.990692	0.006250	IYGNQDTSSQLK
2.1	1975.019684	-0.022742	SMTQTHNGKLYKIVDPK

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 49079: 2090.132296 from(523.540350,4+) rtinseconds(1799) index(51516)

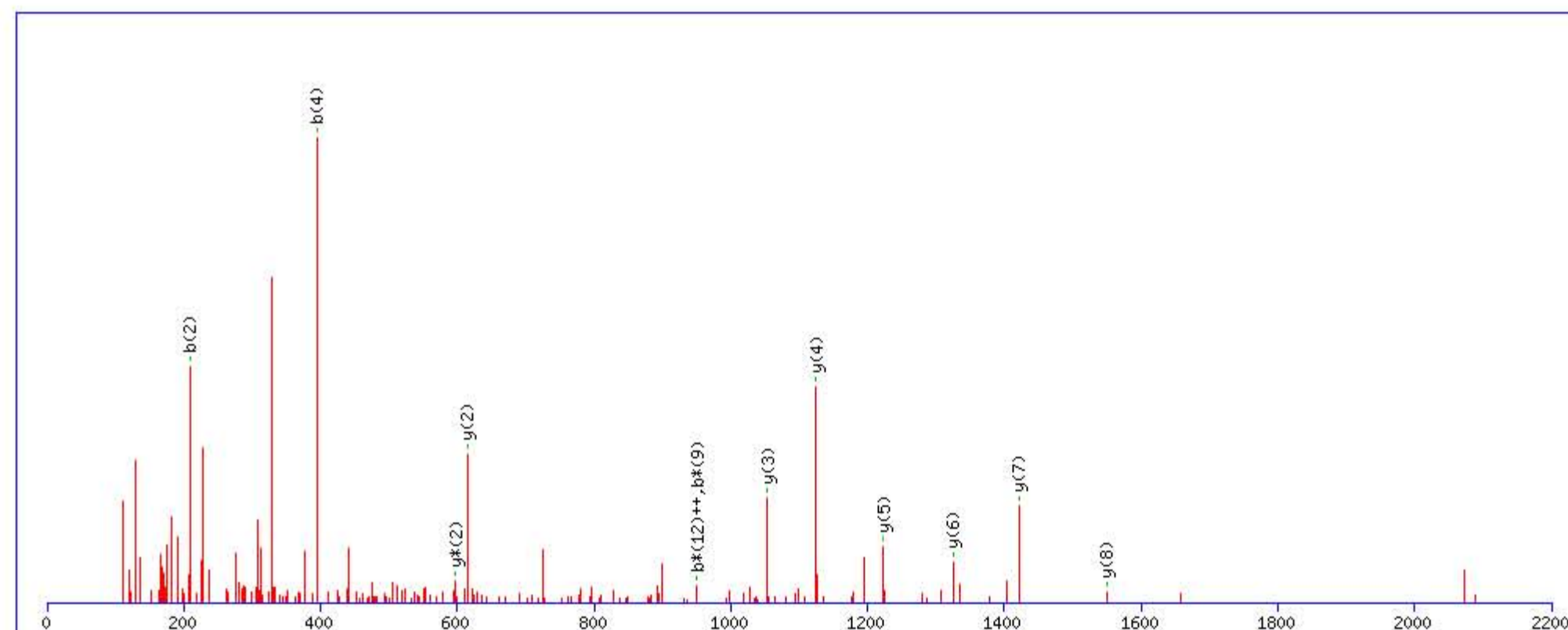
Title: Locus:1.1.1.1242.4 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2090.128143

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

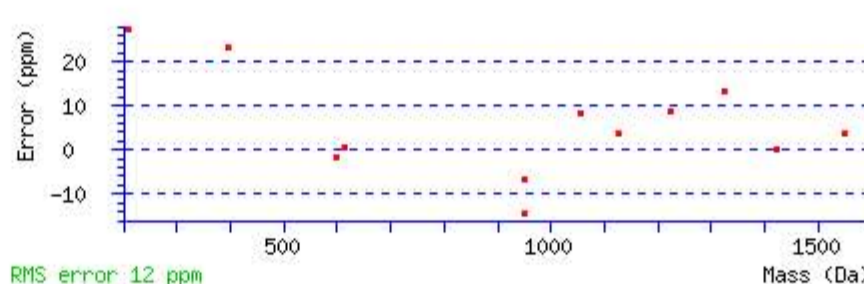
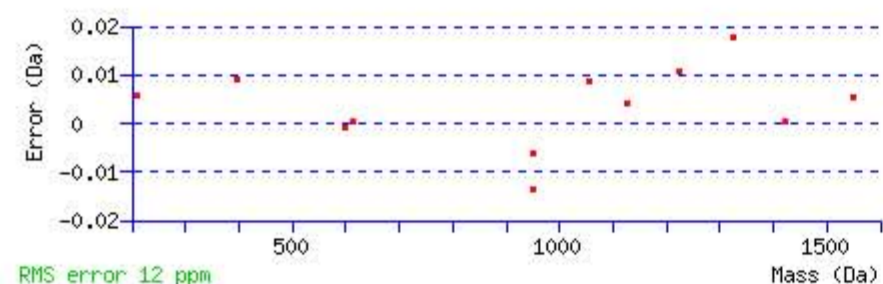
Q11 : Biotin:Thermo-21345 (Q)

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 43 Expect: 0.00097

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
43.0	2090.128143	0.004153	AHVSFKPTVAQQR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **AEDHFSVIDFNQIR**

Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

Match to Query 49452: 2115.032982 from(706.018270,3+) rtinseconds(2301) index(54854)

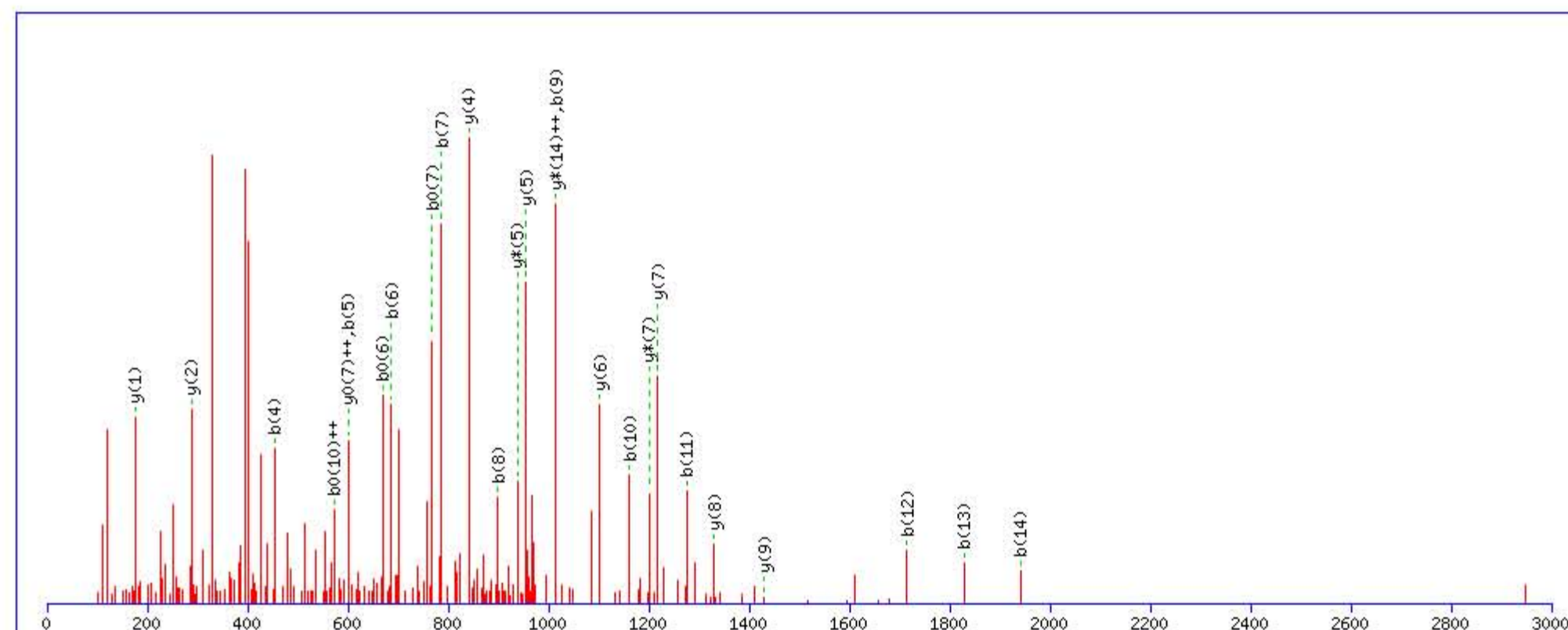
Title: Locus:1.1.1.1416.8 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2115.020752

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

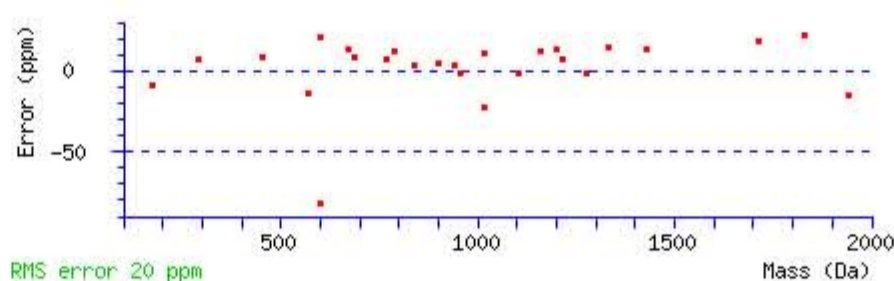
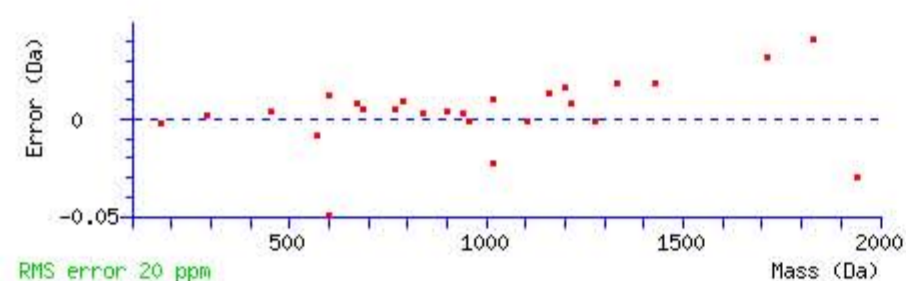
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 78 Expect: 1.7e-007

Matches : 26/134 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	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 **AEDHFSVIDFNQIR**

(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	2115.020752	0.012230	AEDHFSVIDFNQIR
5.5	2115.033981	-0.000999	ESADRQVLMQEEIK
1.2	2115.008850	0.024132	LTSDAEKESVMMFGRNLR

Mascot: <http://www.matrixscience.com/>

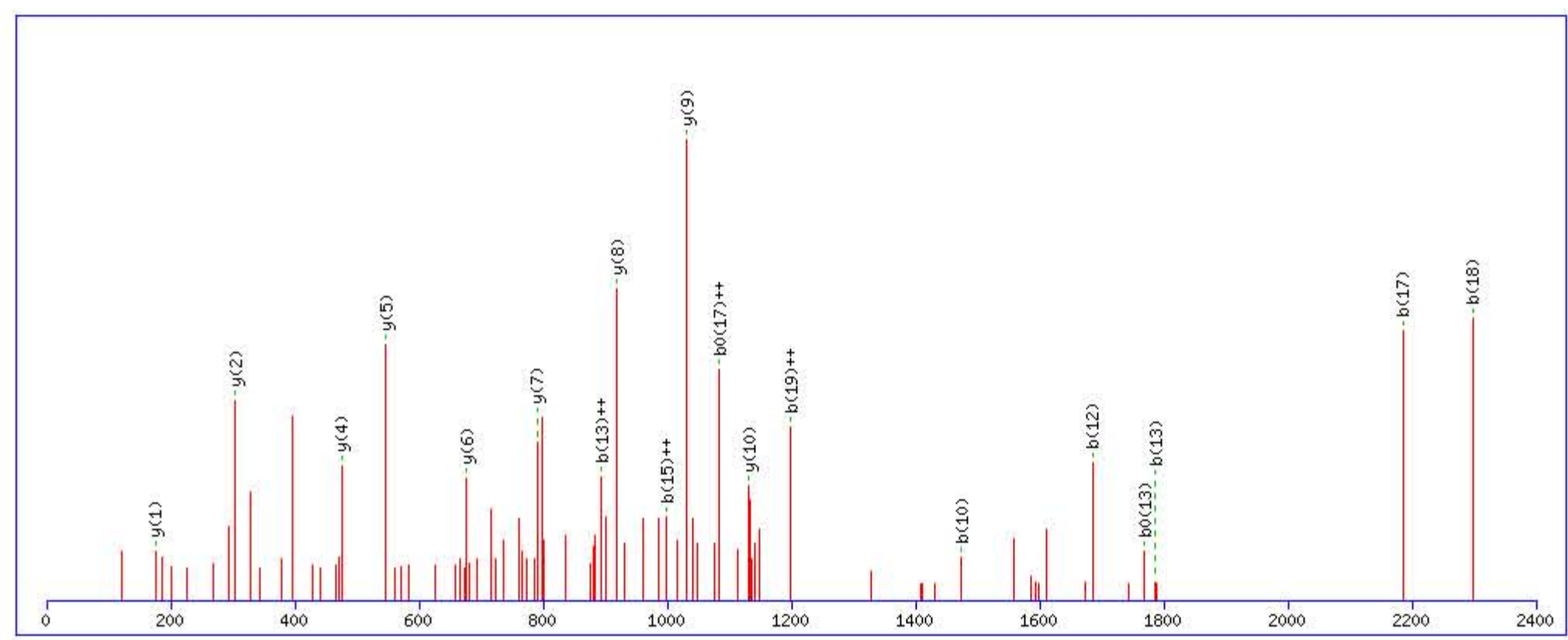
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SILQMSLDHHIVTPLTSLVIENEAGDER**
 Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

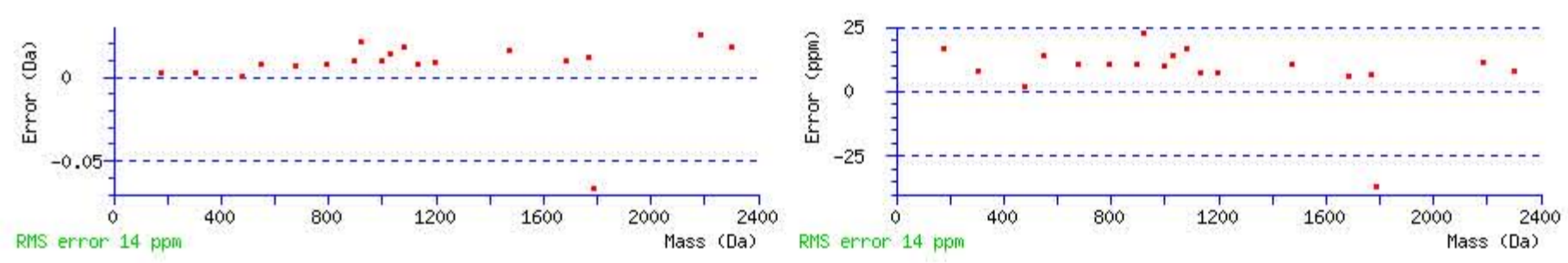
Match to Query 66512: 3427.779056 from(857.952040,4+) rtinseconds(2760) index(57514)
 Title: Locus:1.1.1.1575.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3427.747940
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q4 : Biotin:Thermo-21345 (Q)
 Ions Score: 45 Expect: 0.00073
 Matches : 19/316 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	88.039304	44.523290			70.028739	35.518008	S							28
2	201.123368	101.065322			183.112803	92.060039	I	3341.723211	1671.365243	3324.696662	1662.851969	3323.712646	1662.359961	27
3	314.207432	157.607354			296.196867	148.602071	L	3228.639147	1614.823211	3211.612598	1606.309937	3210.628582	1605.817929	26
4	753.432758	377.220017	736.406209	368.706743	735.422193	368.214735	Q	3115.555083	1558.281179	3098.528534	1549.767905	3097.544518	1549.275897	25
5	884.473243	442.740260	867.446694	434.226985	866.462678	433.734977	M	2676.329757	1338.668516	2659.303208	1330.155242	2658.319192	1329.663234	24
6	971.505271	486.256274	954.478722	477.742999	953.494706	477.250991	S	2545.289272	1273.148274	2528.262723	1264.634999	2527.278707	1264.142991	23
7	1084.589335	542.798305	1067.562786	534.285031	1066.578770	533.793023	L	2458.257244	1229.632260	2441.230695	1221.118985	2440.246679	1220.626977	22
8	1199.616278	600.311777	1182.589729	591.798503	1181.605713	591.306494	D	2345.173180	1173.090228	2328.146631	1164.576953	2327.162615	1164.084945	21
9	1336.675190	668.841233	1319.648641	660.327959	1318.664625	659.835950	H	2230.146237	1115.576756	2213.119688	1107.063482	2212.135672	1106.571474	20
10	1473.734102	737.370689	1456.707553	728.857415	1455.723537	728.365406	H	2093.087325	1047.047300	2076.060776	1038.534026	2075.076760	1038.042018	19
11	1586.818166	793.912721	1569.791617	785.399446	1568.807601	784.907438	I	1956.028413	978.517845	1939.001864	970.004570	1938.017848	969.512562	18
12	1685.886580	843.446928	1668.860031	834.933653	1667.876015	834.441645	V	1842.944349	921.975813	1825.917800	913.462538	1824.933784	912.970530	17
13	1786.934259	893.970767	1769.907710	885.457493	1768.923694	884.965485	T	1743.875935	872.441606	1726.849386	863.928331	1725.865370	863.436323	16
14	1883.987023	942.497149	1866.960474	933.983875	1865.976458	933.491867	P	1642.828256	821.917766	1625.801707	813.404492	1624.817691	812.912484	15
15	1997.071087	999.039181	1980.044538	990.525907	1979.060522	990.033899	L	1545.775492	773.391384	1528.748943	764.878110	1527.764927	764.386102	14
16	2098.118766	1049.563021	2081.092217	1041.049746	2080.108201	1040.557738	T	1432.691428	716.849352	1415.664879	708.336078	1414.680863	707.844070	13
17	2185.150794	1093.079035	2168.124245	1084.565760	2167.140229	1084.073752	S	1331.643749	666.325513	1314.617200	657.812238	1313.633184	657.320230	12
18	2298.234858	1149.621067	2281.208309	1141.107792	2280.224293	1140.615784	L	1244.611721	622.809499	1227.585172	614.296224	1226.601156	613.804216	11
19	2397.303272	1199.155274	2380.276723	1190.641999	2379.292707	1190.149991	V	1131.527657	566.267467	1114.501108	557.754192	1113.517092	557.262184	10
20	2510.387336	1255.697306	2493.360787	1247.184031	2492.376771	1246.692023	I	1032.459243	516.733260	1015.432694	508.219985	1014.448678	507.727977	9
21	2639.429929	1320.218602	2622.403380	1311.705328	2621.419364	1311.213320	E	919.375179	460.191228	902.348630	451.677953	901.364614	451.185945	8
22	2753.472856	1377.240066	2736.446307	1368.726791	2735.462291	1368.234783	N	790.332586	395.669931	773.306037	387.156657	772.322021	386.664649	7
23	2882.515449	1441.761362	2865.488900	1433.248088	2864.504884	1432.756080	E	676.289659	338.648468	659.263110	330.135193	658.279094	329.643185	6
24	2953.552563	1477.279920	2936.526014	1468.766645	2935.541998	1468.274637	A	547.247066	274.127171	530.220517	265.613897	529.236501	265.121889	5
25	3010.574027	1505.790652	2993.547478	1497.277377	2992.563462	1496.785369	G	476.209952	238.608614	459.183403	230.095339	458.199387	229.603331	4
26	3125.600970	1563.304123	3108.574421	1554.790848	3107.590405	1554.298840	D	419.188488	210.097882	402.161939	201.584607	401.177923	201.092599	3
27	3254.643563	1627.825420	3237.617014	1619.312145	3236.632998	1618.820137	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
28							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **SILQMSLDHHIVTPLTSLVIENEAGDER**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.1	3427.747940	0.031116	SILQMSLDHHIVTPLTSLVIENEAGDER

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **NVQFNYPHTSVTDVTDQNNFHNHYFGGSEIVVAGK**

Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

Match to Query 69824: 3993.948016 from(999.494280,4+) rtinseconds(2411) index(55456)

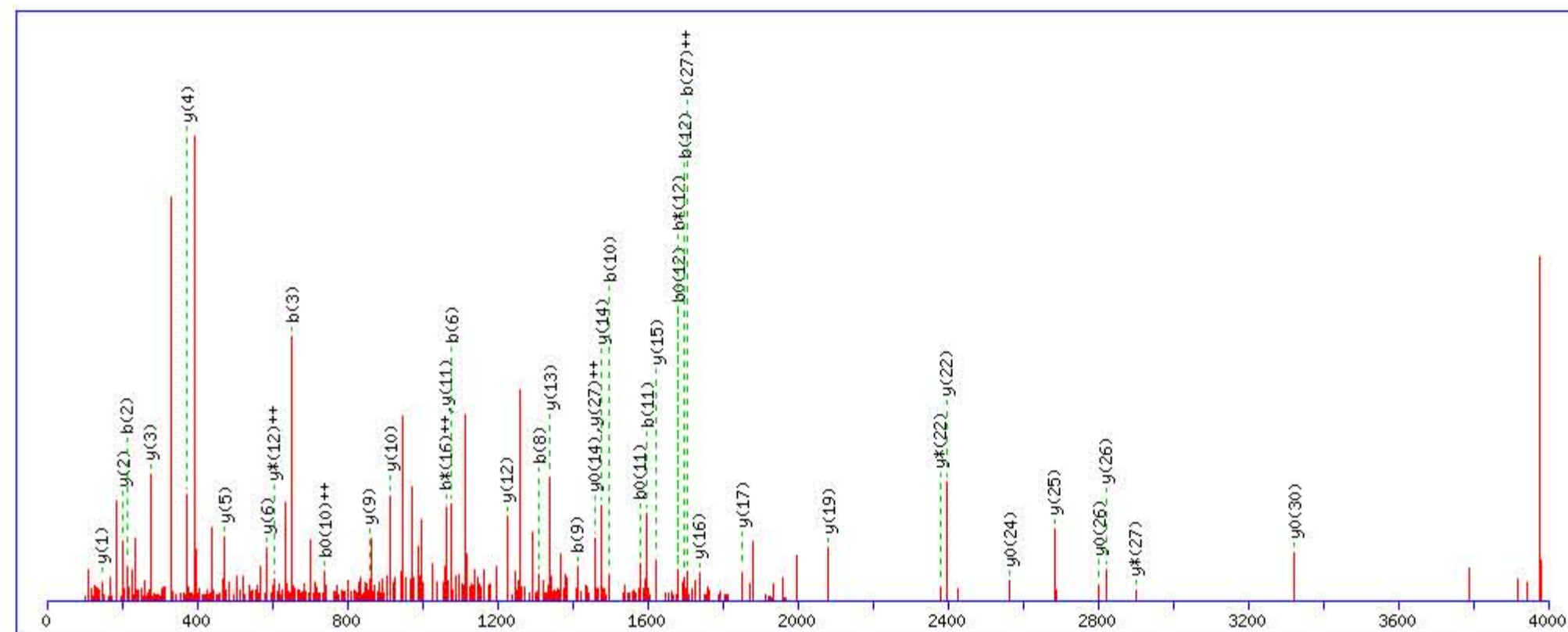
Title: Locus:1.1.1.1454.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3993.910858

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

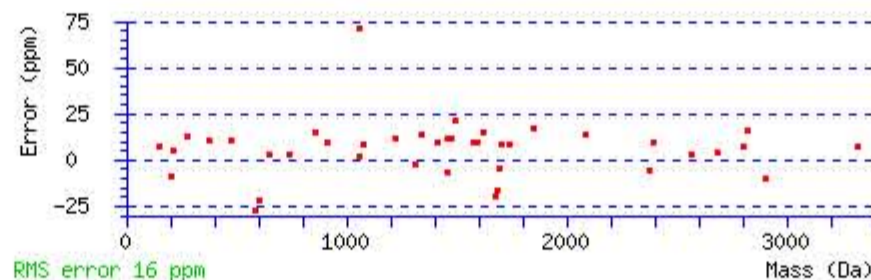
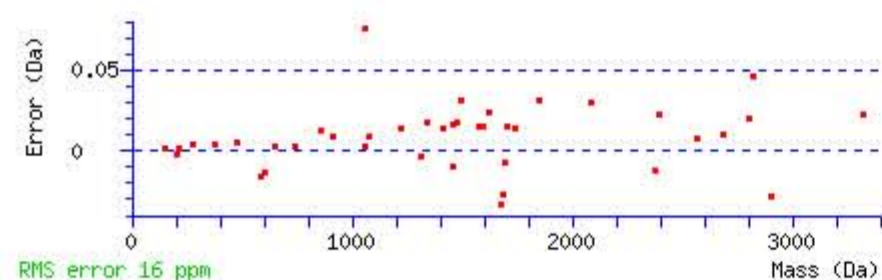
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 82 Expect: 1.4e-007

Matches : 41/356 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	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 **NVQFNYPHTSVTDVTDQNNFHNHYFGGSEIVVAGK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.2	3993.910858	0.037158	NVQFNYPHTSVTDVTDQNNFHNHYFGGSEIVVAGK
26.1	3993.910858	0.037158	NVQFNYPHTSVTDVTDQNNFHNHYFGGSEIVVAGK

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 42894: 1808.937672 from(603.986500,3+) rtinseconds(1608) index(50300)

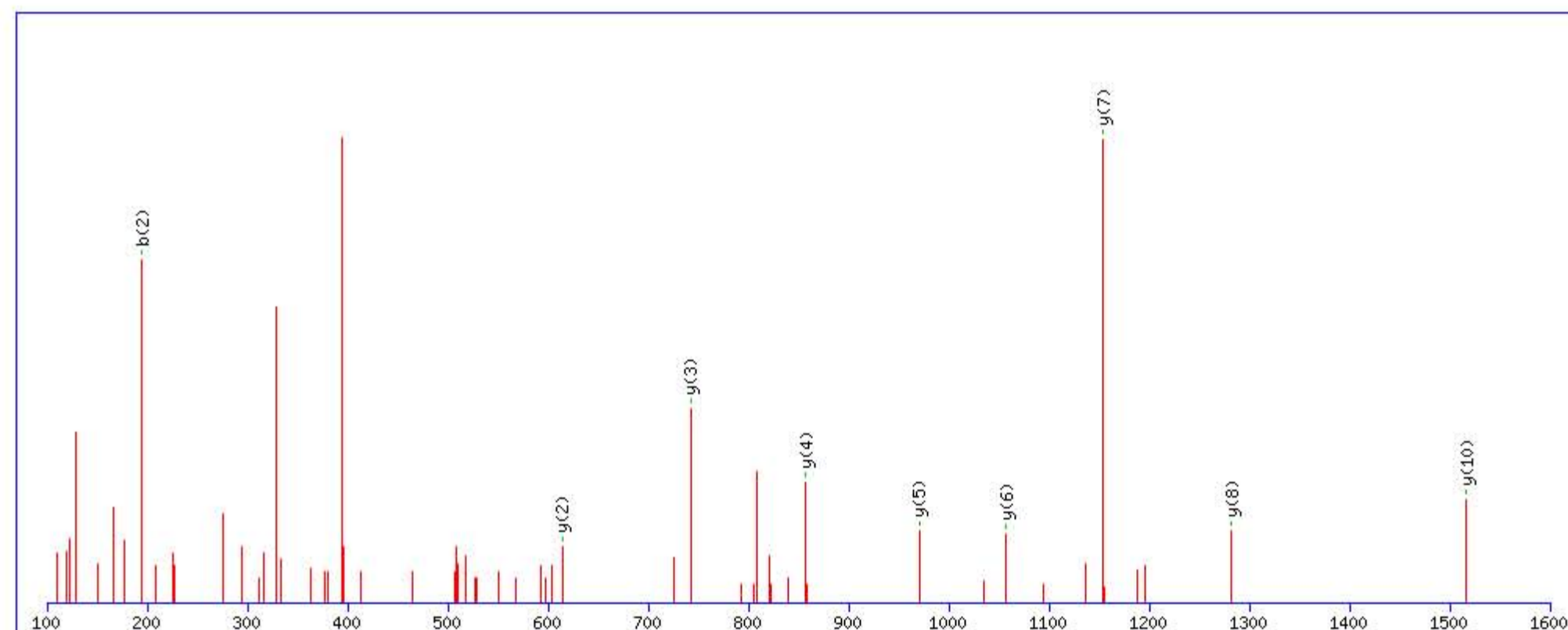
Title: Locus:1.1.1.1175.14 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1808.935577

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

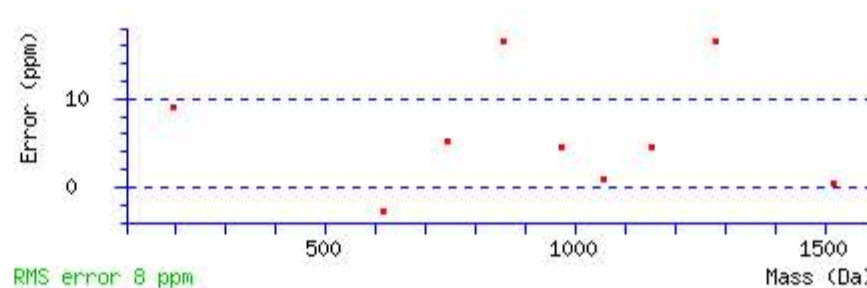
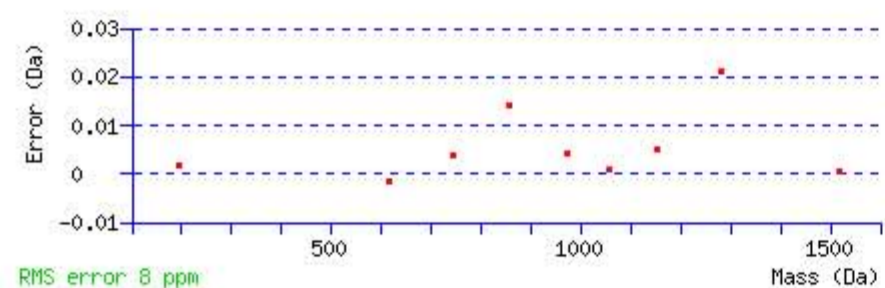
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 60 Expect: 2.9e-005

Matches : 9/122 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	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	$M_r(\text{calc})$:	Delta	Sequence
59.5	1808.935577	0.002095	GHVSFKPSLDQQR
45.3	1808.935577	0.002095	GHVSFKPSLDQQR

Mascot: <http://www.matrixscience.com/>

MASCOT SCIENCE 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 45313: 1937.031456 from(485.265140,4+) rtinseconds(1532) index(49755)

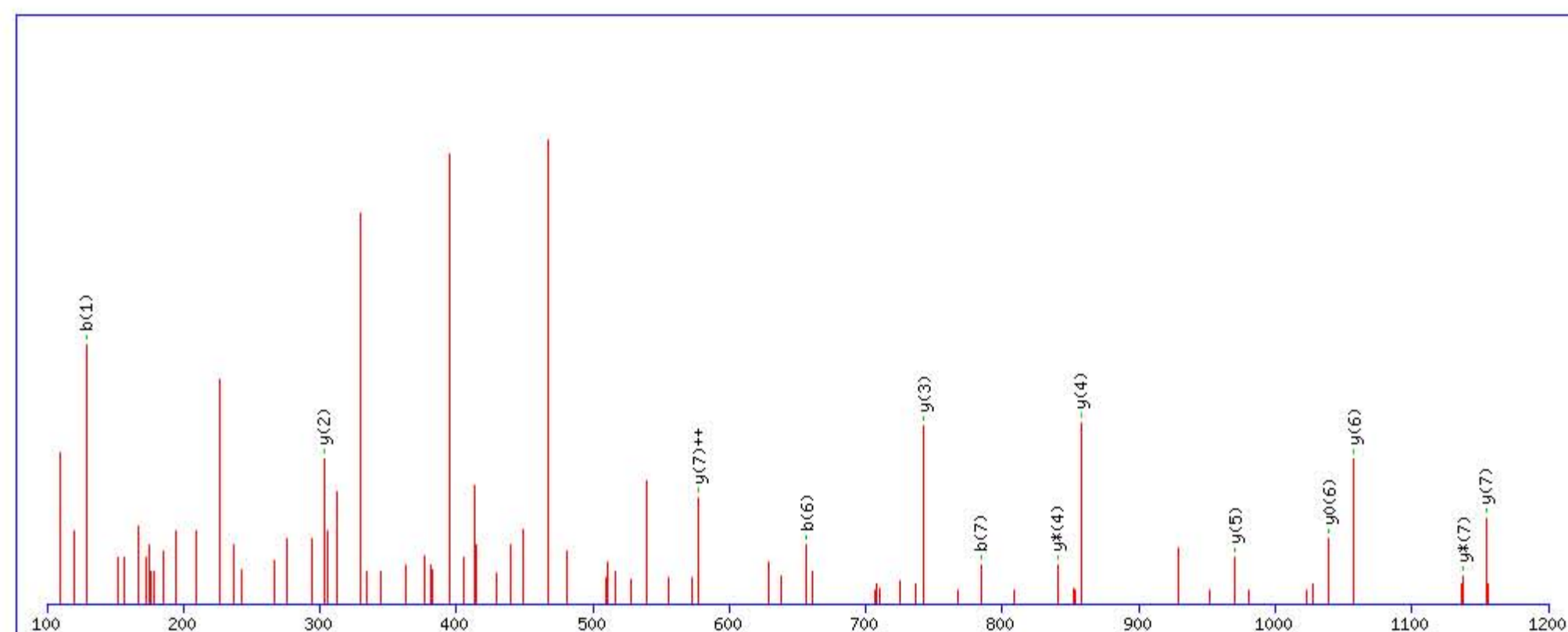
Title: Locus:1.1.1.1149.5 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1937.030533

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

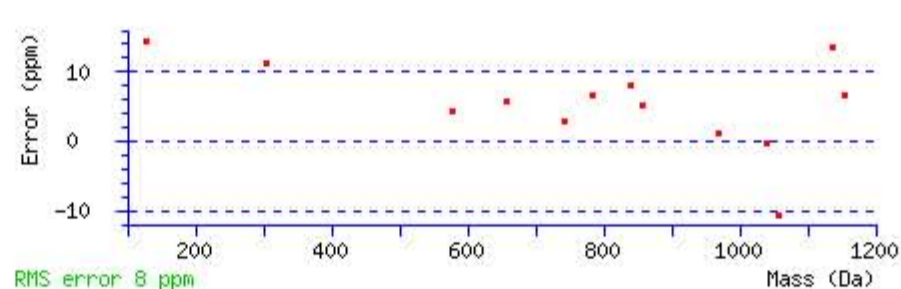
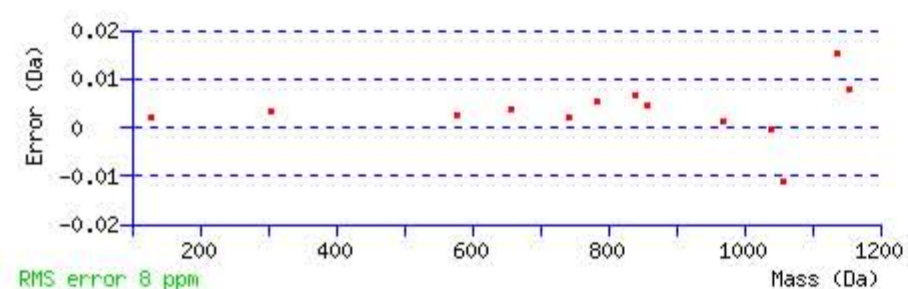
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.048

Matches : 13/142 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	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
26.9	1937.030533	0.000923	KGHVSFKPSLDQQR
19.1	1937.030533	0.000923	KGHVSFKPSLDQQR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **EHLVQATPENLQEAR**

Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

Match to Query 48259: 2045.046702 from(682.689510,3+) rtinseconds(1777) index(51354)

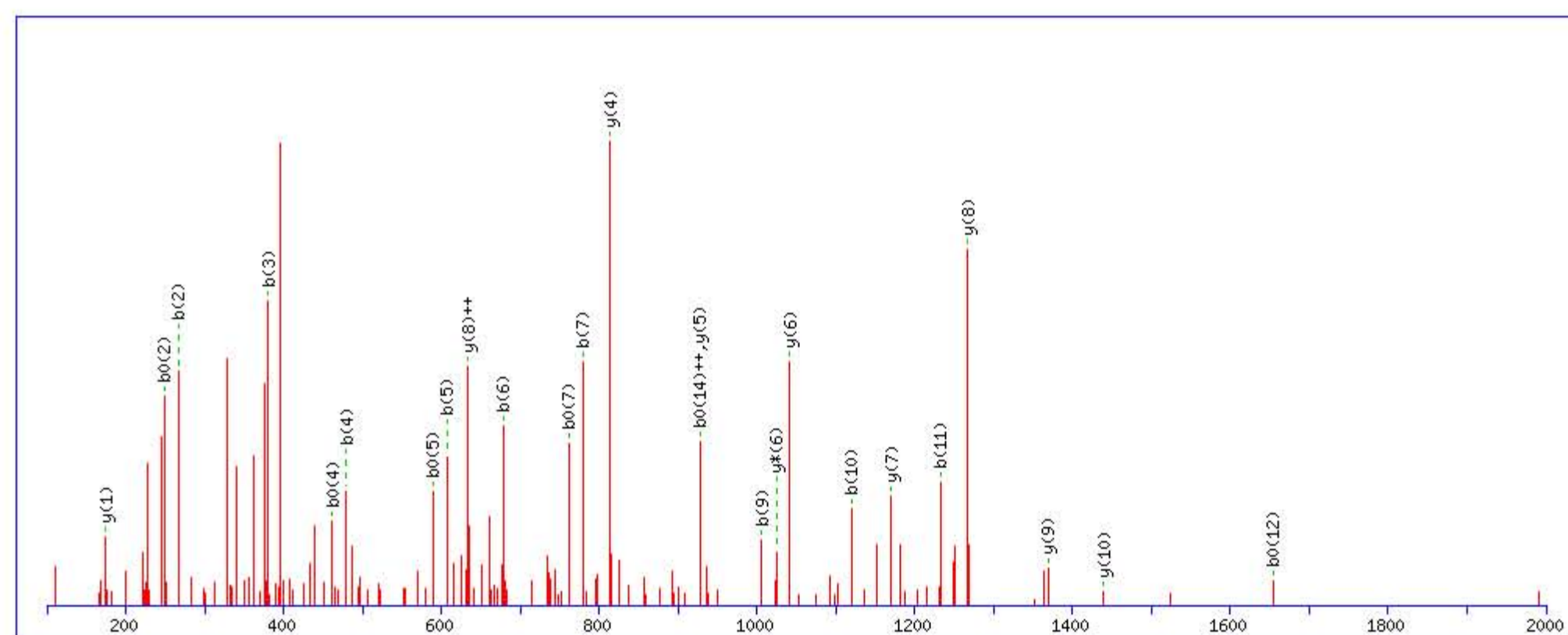
Title: Locus:1.1.1.1234.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2045.036377

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

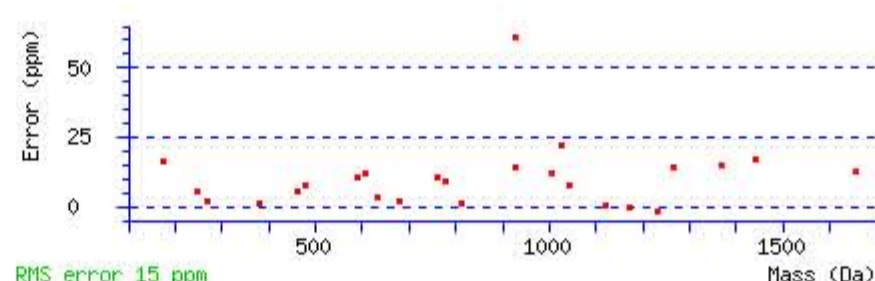
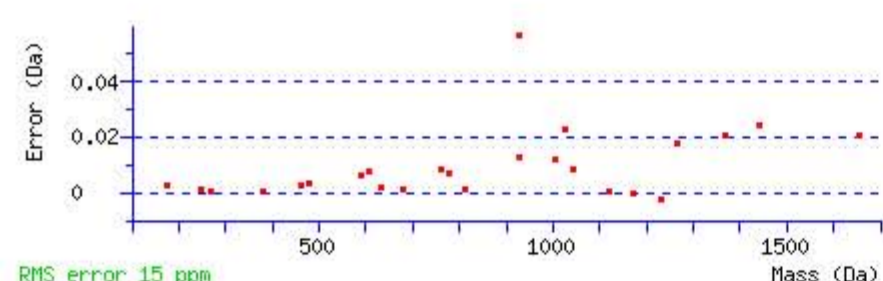
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 73 Expect: 3.9e-007

Matches : 25/156 fragment ions using 30 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							15
2	267.108781	134.058028			249.098216	125.052746	H	1917.001094	959.004185	1899.974545	950.490911	1898.990529	949.998903	14
3	380.192845	190.600060			362.182280	181.594778	L	1779.942182	890.474729	1762.915633	881.961455	1761.931617	881.469447	13
4	479.261259	240.134267			461.250694	231.128985	V	1666.858118	833.932697	1649.831569	825.419423	1648.847553	824.927415	12
5	607.319837	304.163557	590.293288	295.650282	589.309272	295.158274	Q	1567.789704	784.398490	1550.763155	775.885216	1549.779139	775.393208	11
6	678.356951	339.682114	661.330402	331.168839	660.346386	330.676831	A	1439.731126	720.369201	1422.704577	711.855927	1421.720561	711.363919	10
7	779.404630	390.205953	762.378081	381.692679	761.394065	381.200671	T	1368.694012	684.850644	1351.667463	676.337370	1350.683447	675.845362	9
8	876.457394	438.732335	859.430845	430.219061	858.446829	429.727053	P	1267.646333	634.326805	1250.619784	625.813530	1249.635768	625.321522	8
9	1005.499987	503.253632	988.473438	494.740357	987.489422	494.248349	E	1170.593569	585.800423	1153.567020	577.287148	1152.583004	576.795140	7
10	1119.542914	560.275095	1102.516365	551.761821	1101.532349	551.269813	N	1041.550976	521.279126	1024.524427	512.765852	1023.540411	512.273844	6
11	1232.626978	616.817127	1215.600429	608.303853	1214.616413	607.811845	L	927.508049	464.257663	910.481500	455.744388	909.497484	455.252380	5
12	1671.852304	836.429790	1654.825755	827.916516	1653.841739	827.424508	Q	814.423985	407.715631	797.397436	399.202356	796.413420	398.710348	4
13	1800.894897	900.951087	1783.868348	892.437812	1782.884332	891.945804	E	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
14	1871.932011	936.469644	1854.905462	927.956369	1853.921446	927.464361	A	246.156066	123.581671	229.129517	115.068396			2
15							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **EHLVQATPENLQEAR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.4	2045.036377	0.010325	EHLVQATPENLQEAR
4.9	2045.022446	0.024256	EHNENMLRNILPSHVAR
2.8	2045.051193	-0.004491	VVGGYLLMLAYACVTMLR

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 37884: 1617.820728 from(809.917640,2+) rtinseconds(1559) index(18889)

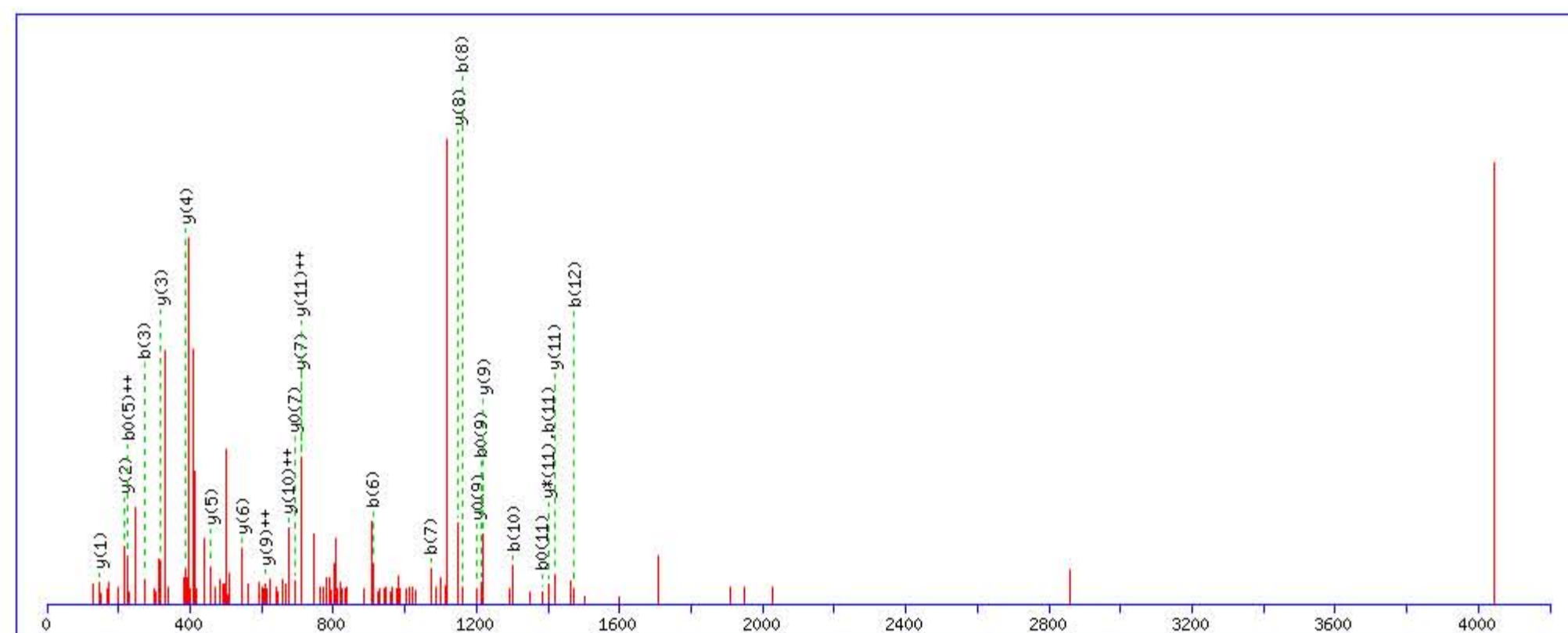
Title: Locus:1.1.1.545.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1617.818436

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

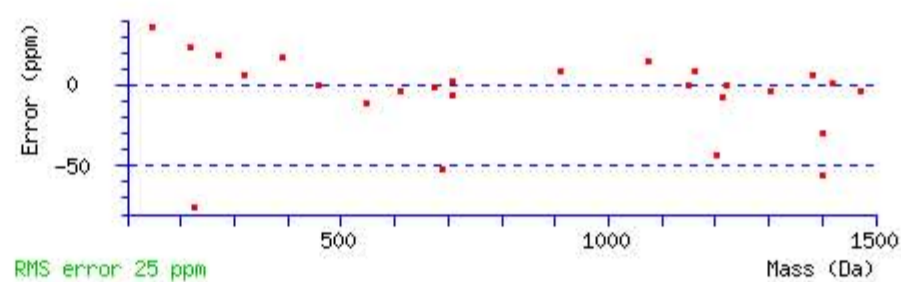
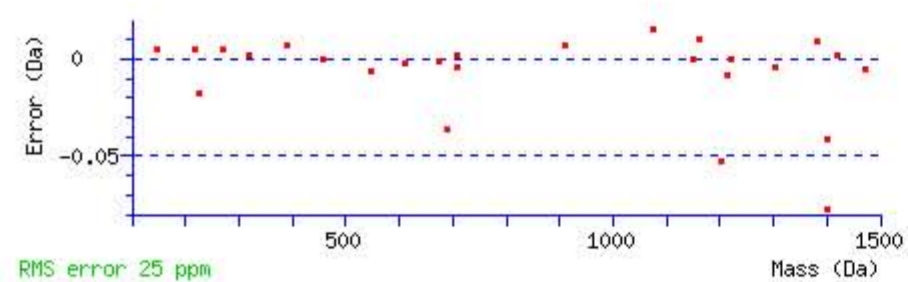
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 44 Expect: 0.00011

Matches : 26/126 fragment ions using 65 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	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



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
44.0	1617.818436	0.002292	AEAQAQYSAAVAK
41.2	1617.818436	0.002292	AEAQAQYSAAVAK
1.7	1617.800690	0.020038	EAAQAIFPSMAR
1.0	1617.829681	-0.008953	NDVMIRKEAYVHK

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 56565: 2494.251096 from(624.570050,4+) rtinseconds(2148) index(22577)

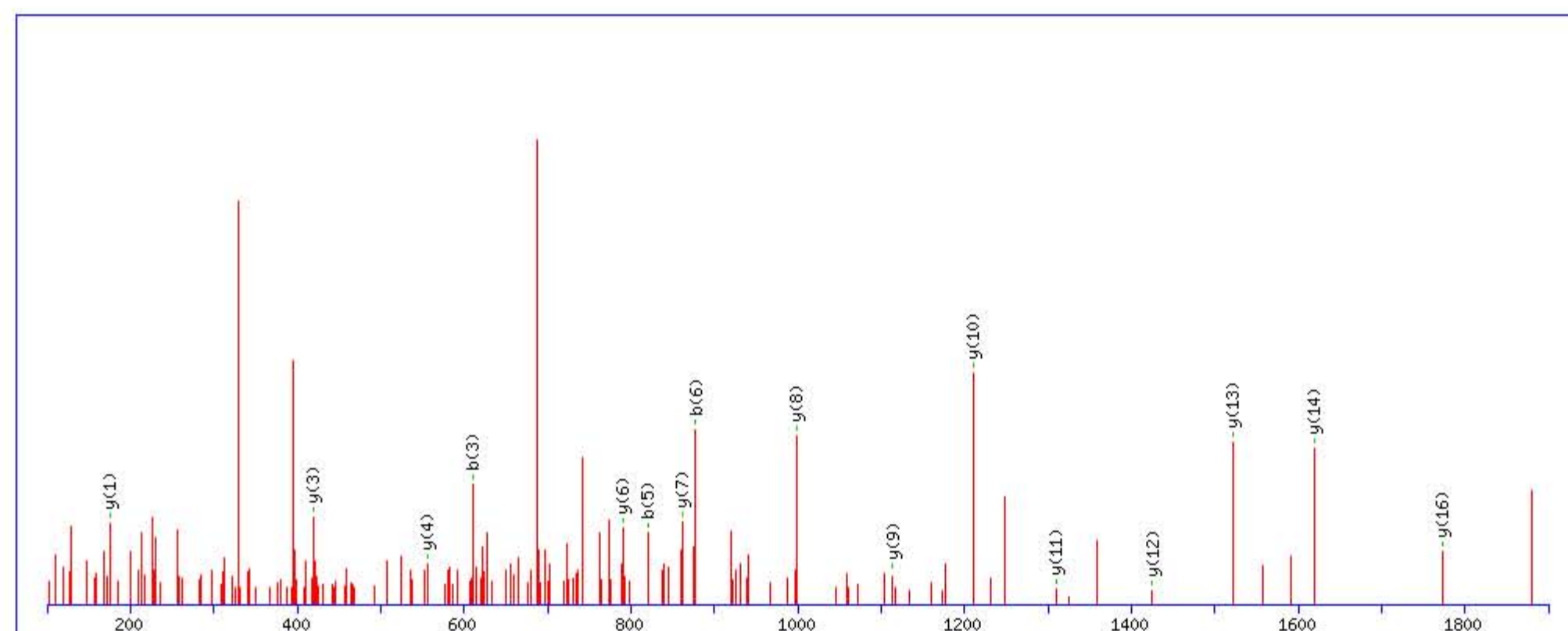
Title: Locus:1.1.1.750.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2494.257980

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

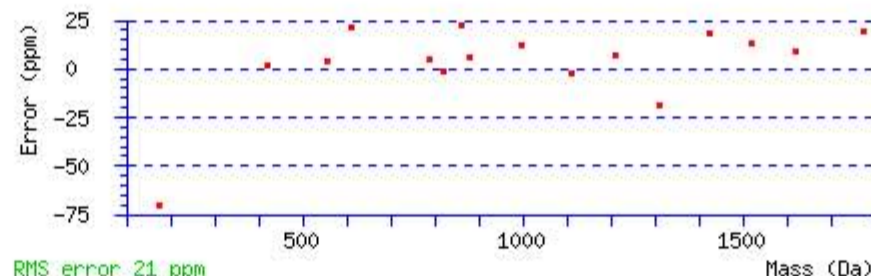
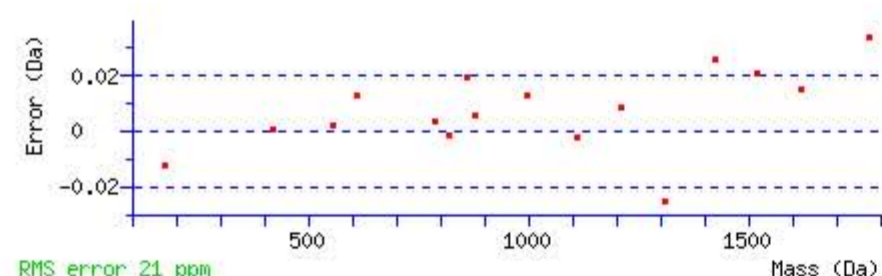
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 7.2e-006

Matches : 16/196 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
56.6	2494.257980	-0.006884	QLGLPGPPDVPDHAAYHPFR
1.8	2494.256424	-0.005328	SPHRESLPGLSSTATPGNPALYSR

Mascot: <http://www.matrixscience.com/>

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 29572: 1386.624508 from(694.319530,2+) rtinseconds(1360) index(32269)

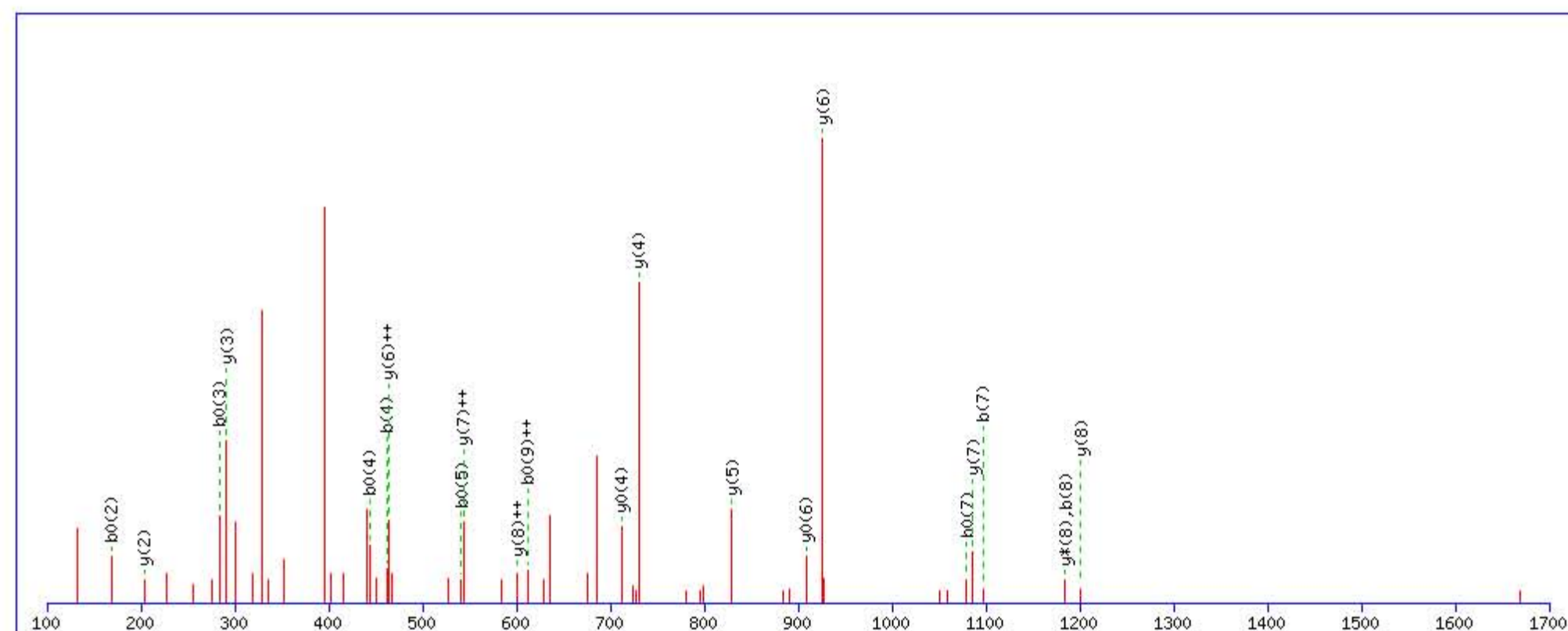
Title: Locus:1.1.1.2892.26 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1386.627182

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

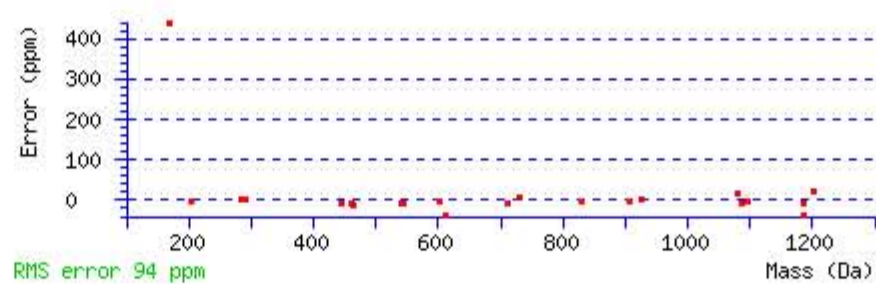
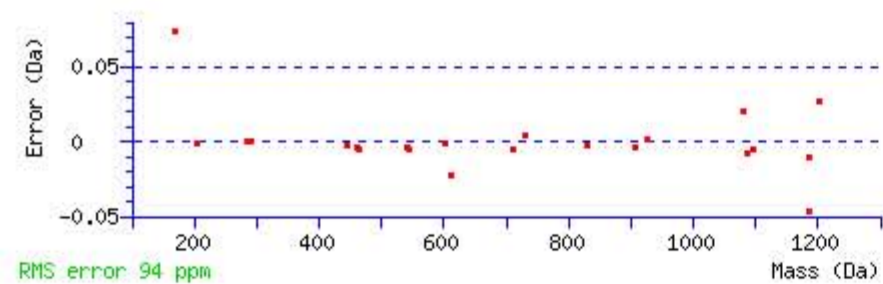
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.00067

Matches : 22/92 fragment ions using 38 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							10
2	187.071333	94.039305			169.060768	85.034022	G	1258.591856	629.799566	1241.565307	621.286292	1240.581291	620.794284	9
3	302.098276	151.552776			284.087711	142.547494	D	1201.570392	601.288834	1184.543843	592.775560	1183.559827	592.283552	8
4	462.128925	231.568101			444.118360	222.562818	C	1086.543449	543.775363	1069.516900	535.262088	1068.532884	534.770080	7
5	559.181689	280.094483			541.171124	271.089200	P	926.512800	463.760038	909.486251	455.246764	908.502235	454.754756	6
6	658.250103	329.628690			640.239538	320.623407	V	829.460036	415.233656	812.433487	406.720382	811.449471	406.228374	5
7	1097.475429	549.241353	1080.448880	540.728078	1079.464864	540.236070	Q	730.391622	365.699449	713.365073	357.186175	712.381057	356.694167	4
8	1184.507457	592.757367	1167.480908	584.244092	1166.496892	583.752084	S	291.166296	146.086786	274.139747	137.573512	273.155731	137.081504	3
9	1241.528921	621.268099	1224.502372	612.754824	1223.518356	612.262816	G	204.134268	102.570772	187.107719	94.057497			2
10							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **EGDCPVQSGK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.0	1386.627182	-0.002674	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 32165: 1439.620668 from(720.817610,2+) rtinseconds(1778) index(34934)

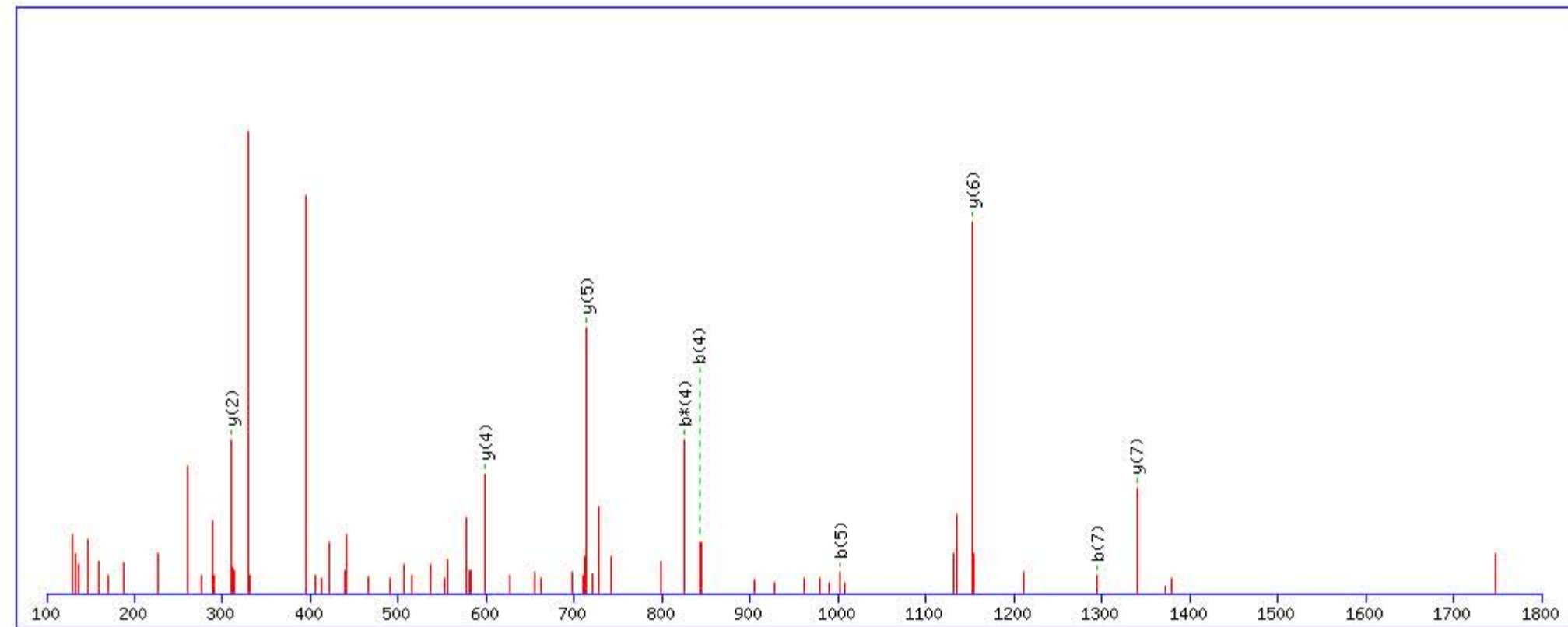
Title: Locus:1.1.1.3038.24 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1439.621353

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

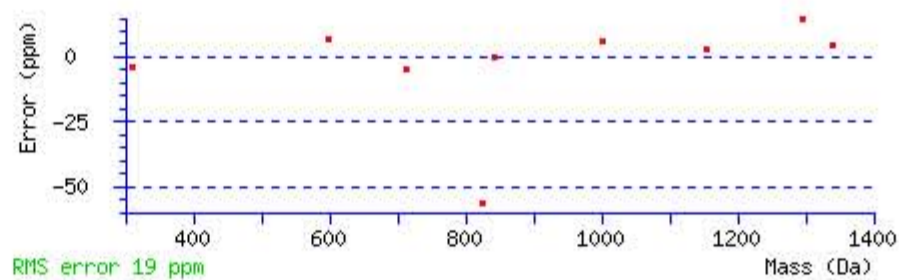
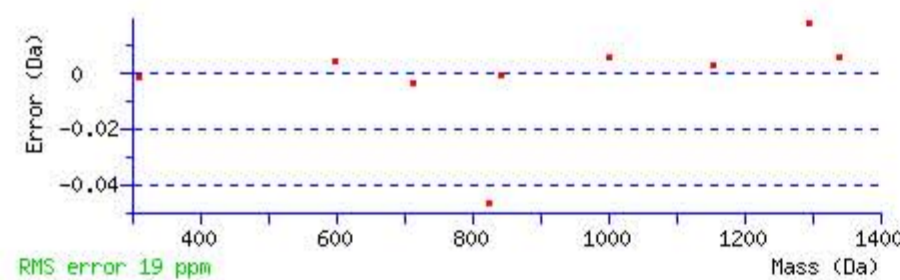
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.00073

Matches : 9/76 fragment ions using 12 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	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
37.3	1439.621353	-0.000685	TWQDCEYK
0.8	1439.602036	0.018632	EQMEEEQKAMR
0.3	1439.635056	-0.014388	MRAEDGENYDIK

Mascot: <http://www.matrixscience.com/>

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 39291: 1644.825528 from(823.420040,2+) rtinseconds(1826) index(35184)

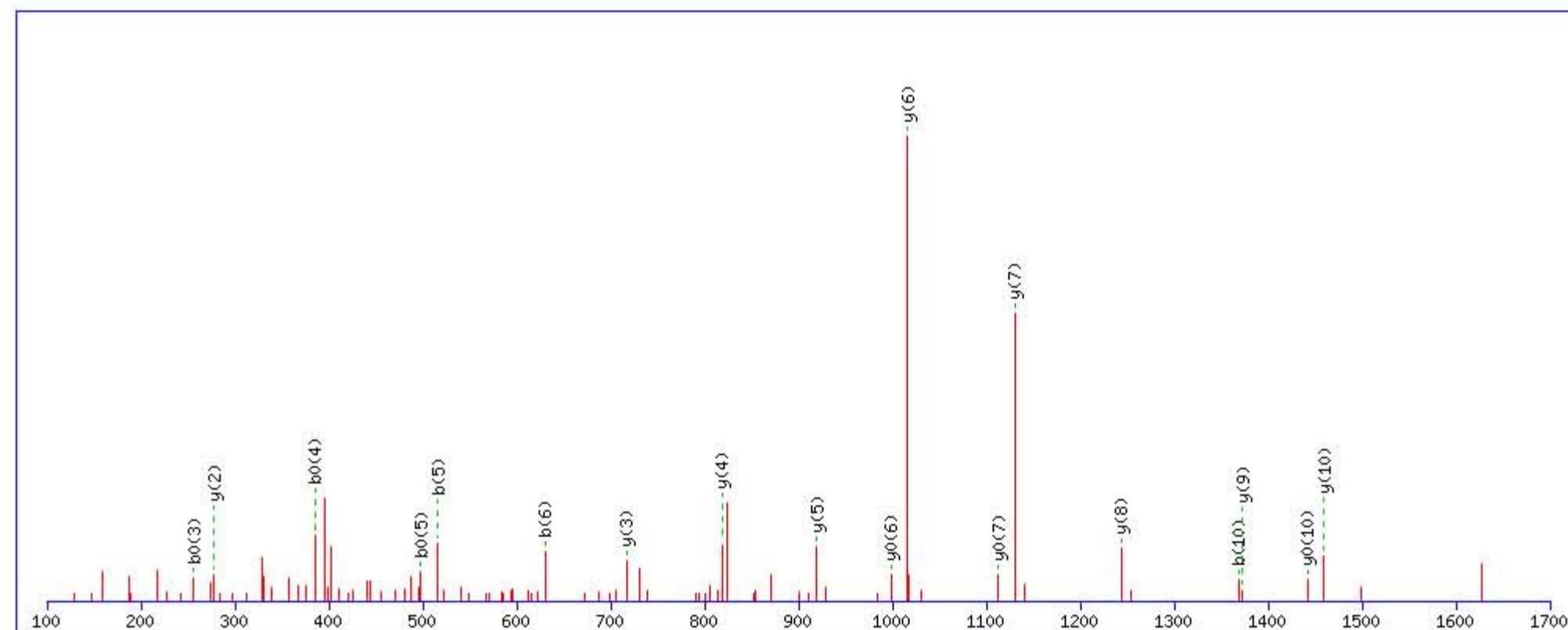
Title: Locus:1.1.1.3055.14 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1644.821503

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

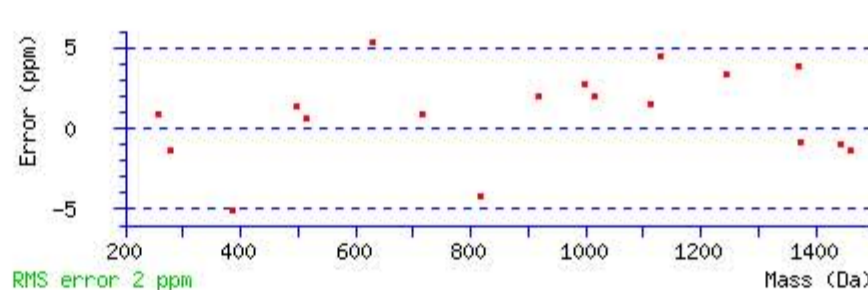
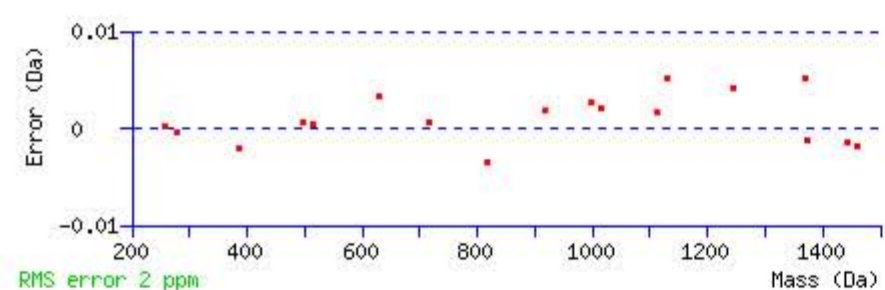
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 65 Expect: 2.3e-006

Matches : 18/116 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	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
65.1	1644.821503	0.004025	SVSEINPTTQMK
4.7	1644.840607	-0.015079	ESGRQFCIAVTHLK
3.4	1644.814133	0.011395	VTDQGSPPMSATAIVR
1.3	1644.803757	0.021771	TISTMKVMQFQGMK
0.5	1644.826889	-0.001361	VPHFCDIRPVMK

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **YNSQNQSNNQFVLYR**

Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

Match to Query 50804: 2185.047408 from(1093.530980,2+) rtinseconds(2026) index(21850)

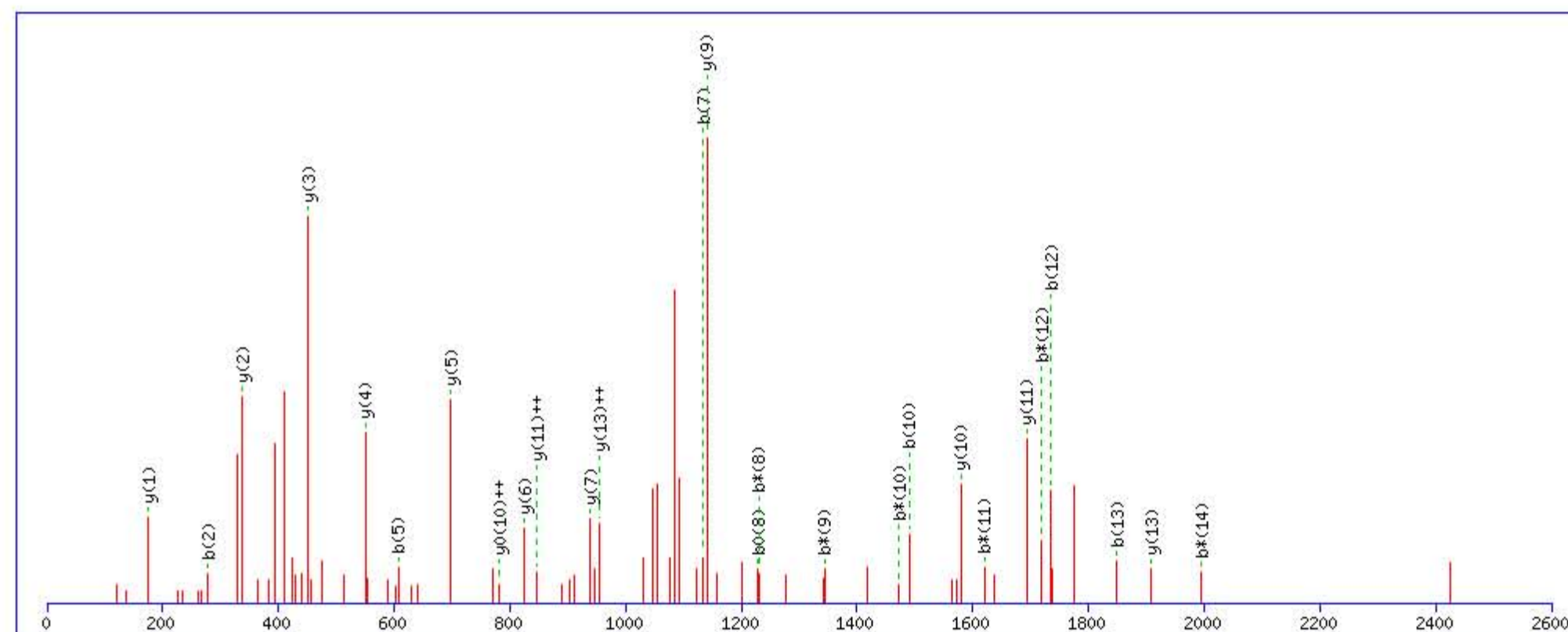
Title: Locus:1.1.1.707.24 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2185.037445

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

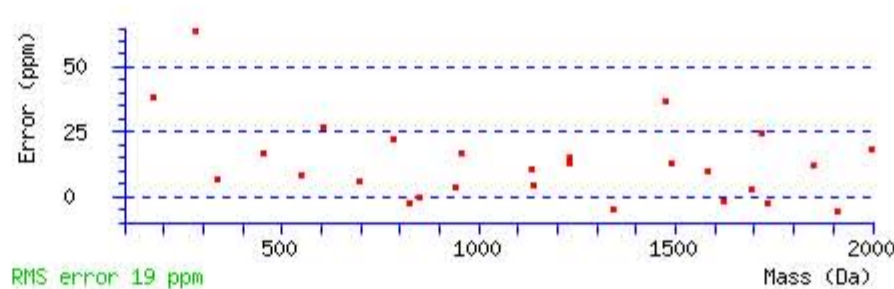
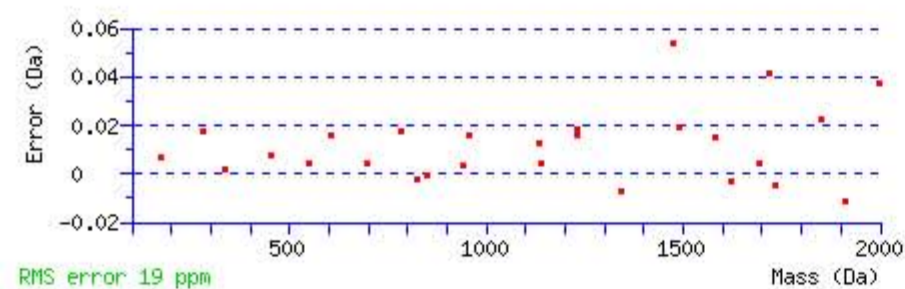
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 84 Expect: 1.7e-008

Matches : 27/146 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							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	1046.472391	523.739834	1029.445842	515.226559	1028.461826	514.734551	Q	1579.804959	790.406118	1562.778410	781.892843	1561.794394	781.400835	10
7	1133.504419	567.255848	1116.477870	558.742573	1115.493854	558.250565	S	1140.579633	570.793455	1123.553084	562.280180	1122.569068	561.788172	9
8	1247.547346	624.277311	1230.520797	615.764037	1229.536781	615.272029	N	1053.547605	527.277441	1036.521056	518.764166			8
9	1361.590273	681.298775	1344.563724	672.785500	1343.579708	672.293492	N	939.504678	470.255977	922.478129	461.742703			7
10	1489.648851	745.328064	1472.622302	736.814789	1471.638286	736.322781	Q	825.461751	413.234514	808.435202	404.721239			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
83.8	2185.037445	0.009963	YNSQNQSNNQFVLYR
50.8	2185.037445	0.009963	YNSQNQSNNQFVLYR
39.6	2185.037445	0.009963	YNSQNQSNNQFVLYR
0.9	2185.040604	0.006804	ERAAAAAAAAQMHAKNGGSSSR
0.1	2185.047348	0.000060	HLSSLTDNEQADIFER

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **YNSQNQSNNQFVLYR**

Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

Match to Query 50808: 2185.051028 from(1093.532790,2+) rtinseconds(2123) index(22434)

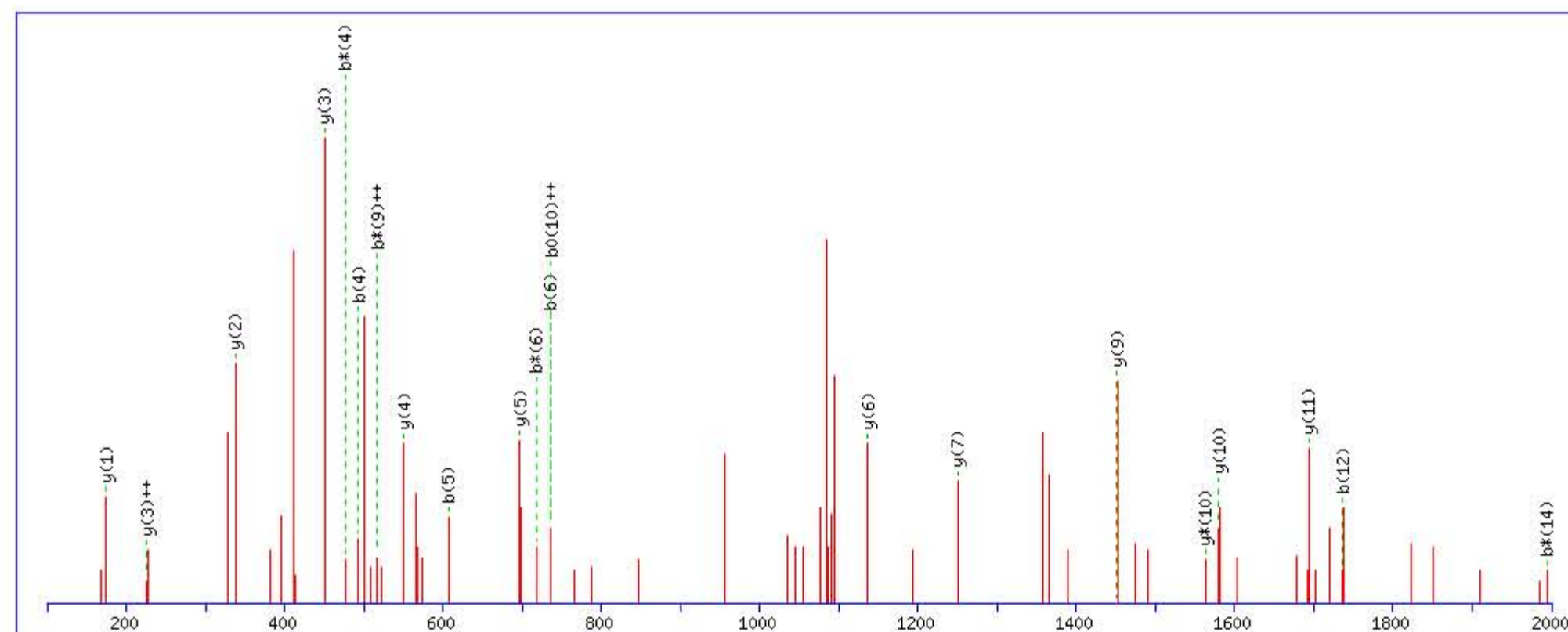
Title: Locus:1.1.1.741.22 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2185.037445

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

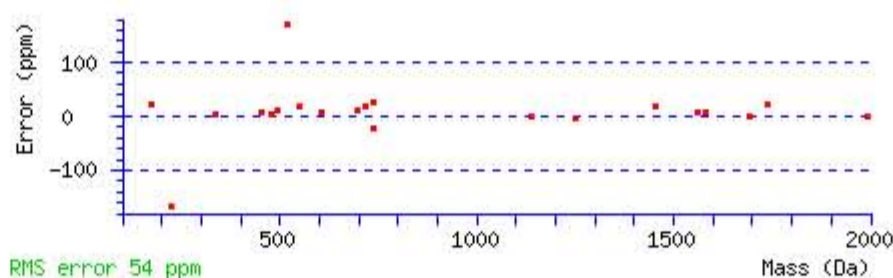
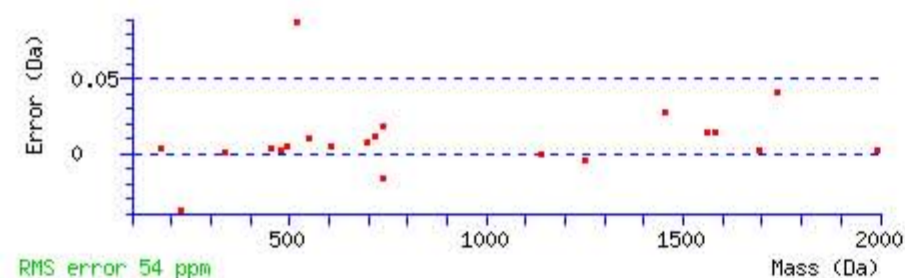
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.036

Matches : 21/146 fragment ions using 69 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	164.070605	82.538940					Y							15
2	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
27.4	2185.037445	0.013583	YNSQNQSNNQFVLYR
7.9	2185.037445	0.013583	YNSQNQSNNQFVLYR
2.1	2185.037445	0.013583	YNSQNQSNNQFVLYR

MASCOT Search Results

Peptide View

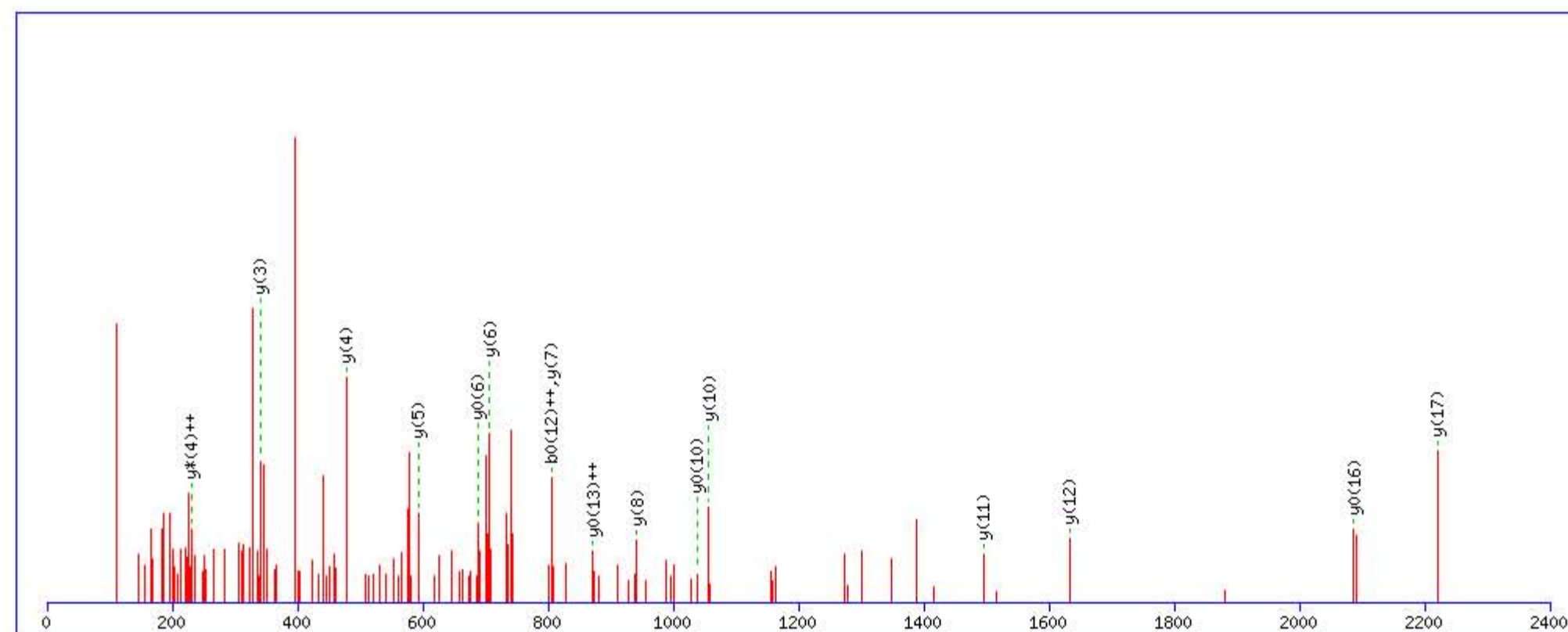
MS/MS Fragmentation of **LDDDLHQGGHVLDPHGK**
 Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

Match to Query 53579: 2332.097296 from(584.031600,4+) rtinseconds(1493) index(33236)
 Title: Locus:1.1.1.2939.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

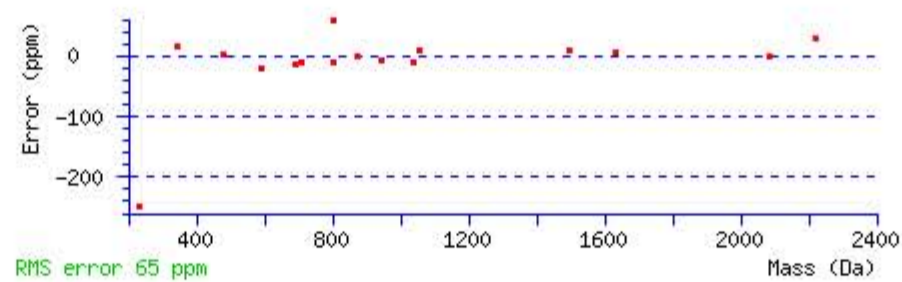
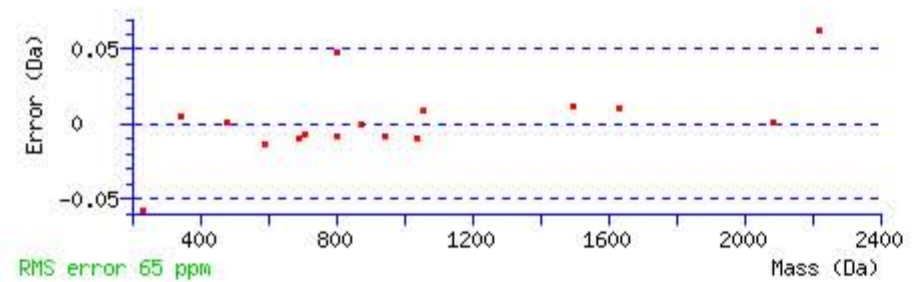
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2332.101883
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q8 : Biotin:Thermo-21345 (Q)
 Ions Score: 32 Expect: 0.01
 Matches : 16/180 fragment ions using 46 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					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 **LDDDLHQGGHVLDPHGK**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

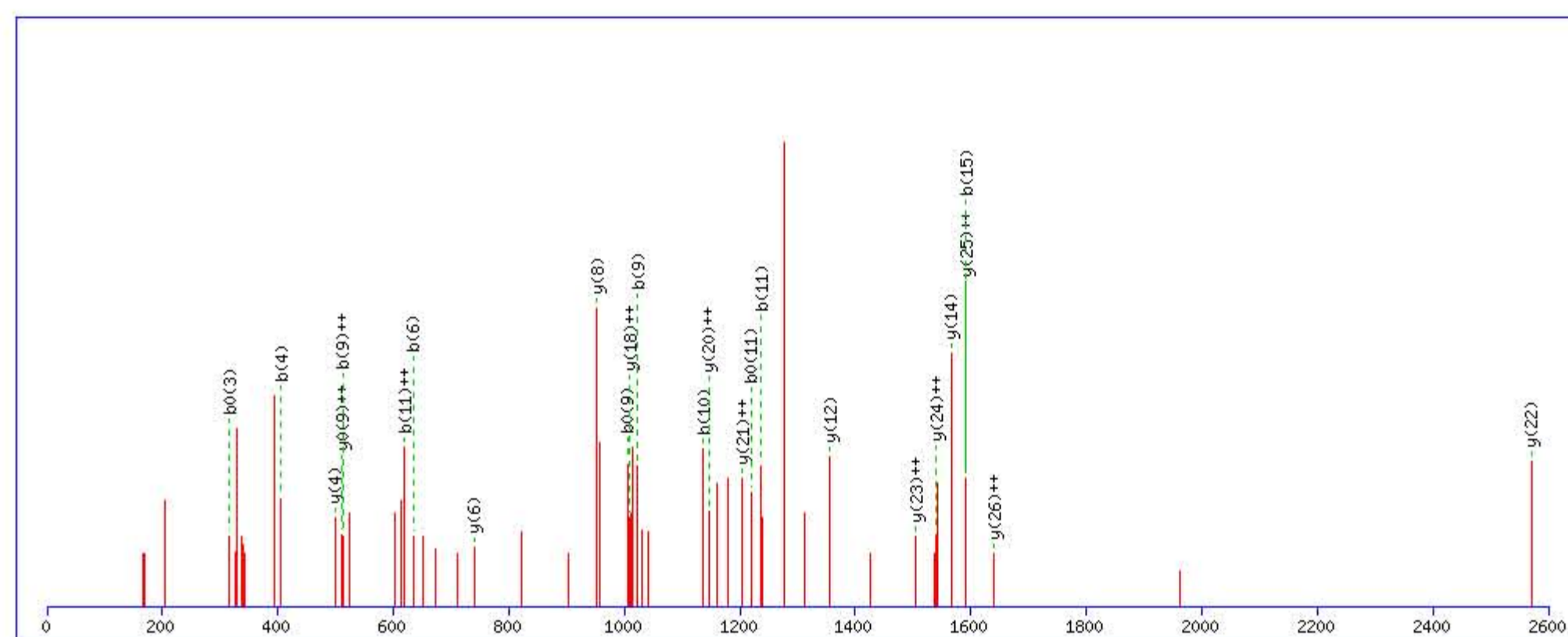
Score	Mr(calc):	Delta	Sequence
32.5	2332.101883	-0.004587	LDDDLHQGGHVLDPHGK

Peptide View

MS/MS Fragmentation of **FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR**
 Found in **KNG1_HUMAN**, Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

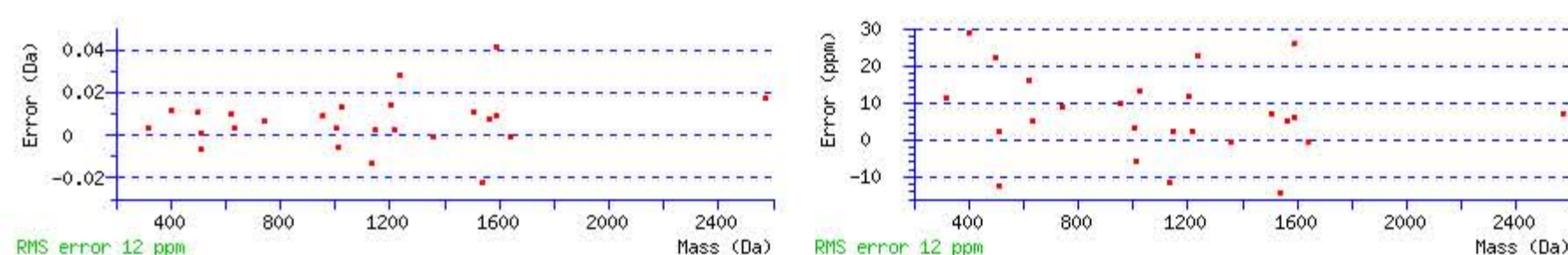
Match to Query 75585: 5066.501220 from(1014.307520,5+) rtinseconds(2667) index(25496)
 Title: Locus:1.1.1.930.23 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 5066.465057
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q21 : Biotin:Thermo-21345 (Q)
 Ions Score: 31 Expect: 0.017
 Matches : 25/484 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							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
30.5	5066.465057	0.036163	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
8.1	5066.465057	0.036163	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
1.6	5066.465057	0.036163	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR
1.3	5066.465057	0.036163	FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **NIPTVNENLENYYLEVNQLEK**

Found in **LUM_HUMAN**, Lumican OS=Homo sapiens GN=LUM PE=1 SV=2

Match to Query 60037: 2846.446572 from(949.822800,3+) rtinseconds(2710) index(57093)

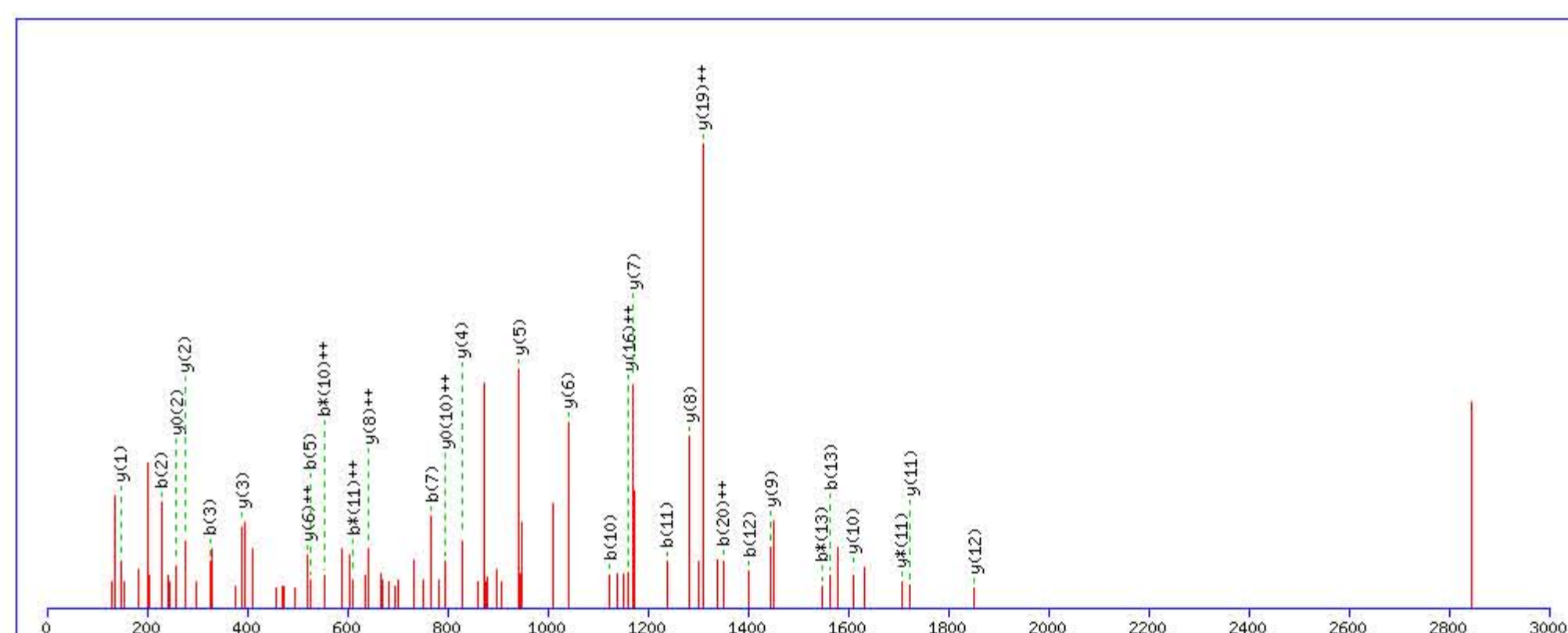
Title: Locus:1.1.1.1558.23 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2846.415985

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

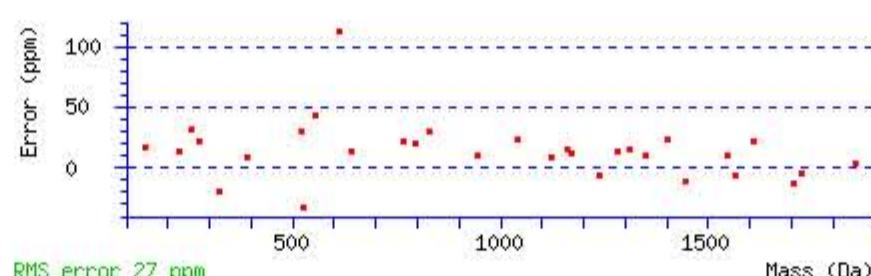
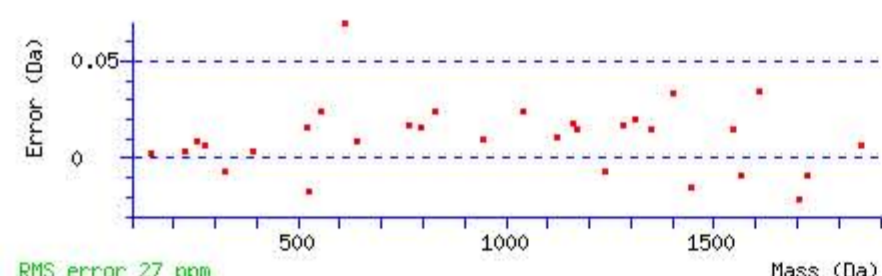
Variable modifications:

Q18 : Biotin:Thermo-21345 (Q)

Ions Score: 59 Expect: 3.1e-006

Matches : 31/232 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	115.050203	58.028740	98.023654	49.515465			N							21
2	228.134267	114.570771	211.107718	106.057497			I	2733.380395	1367.193835	2716.353846	1358.680561	2715.369830	1358.188553	20
3	325.187031	163.097153	308.160482	154.583879			P	2620.296331	1310.651803	2603.269782	1302.138529	2602.285766	1301.646521	19
4	426.234710	213.620993	409.208161	205.107719	408.224145	204.615711	T	2523.243567	1262.125421	2506.217018	1253.612147	2505.233002	1253.120139	18
5	525.303124	263.155200	508.276575	254.641926	507.292559	254.149918	V	2422.195888	1211.601582	2405.169339	1203.088307	2404.185323	1202.596299	17
6	639.346051	320.176664	622.319502	311.663389	621.335486	311.171381	N	2323.127474	1162.067375	2306.100925	1153.554100	2305.116909	1153.062092	16
7	768.388644	384.697960	751.362095	376.184686	750.378079	375.692678	E	2209.084547	1105.045911	2192.057998	1096.532637	2191.073982	1096.040629	15
8	882.431571	441.719424	865.405022	433.206149	864.421006	432.714141	N	2080.041954	1040.524615	2063.015405	1032.011340	2062.031389	1031.519332	14
9	995.515635	498.261456	978.489086	489.748181	977.505070	489.256173	L	1965.999027	983.503152	1948.972478	974.989877	1947.988462	974.497869	13
10	1124.558228	562.782752	1107.531679	554.269478	1106.547663	553.777470	E	1852.914963	926.961120	1835.888414	918.447845	1834.904398	917.955837	12
11	1238.601155	619.804216	1221.574606	611.290941	1220.590590	610.798933	N	1723.872370	862.439823	1706.845821	853.926549	1705.861805	853.434541	11
12	1401.664484	701.335880	1384.637935	692.822606	1383.653919	692.330598	Y	1609.829443	805.418360	1592.802894	796.905085	1591.818878	796.413077	10
13	1564.727813	782.867545	1547.701264	774.354270	1546.717248	773.862262	Y	1446.766114	723.886695	1429.739565	715.373421	1428.755549	714.881413	9
14	1677.811877	839.409577	1660.785328	830.896302	1659.801312	830.404294	L	1283.702785	642.355031	1266.676236	633.841756	1265.692220	633.349748	8
15	1806.854470	903.930873	1789.827921	895.417599	1788.843905	894.925591	E	1170.618721	585.812999	1153.592172	577.299724	1152.608156	576.807716	7
16	1905.922884	953.465080	1888.896335	944.951806	1887.912319	944.459798	V	1041.576128	521.291702	1024.549579	512.778428	1023.565563	512.286420	6
17	2019.965811	1010.486544	2002.939262	1001.973269	2001.955246	1001.481261	N	942.507714	471.757495	925.481165	463.244221	924.497149	462.752213	5
18	2459.191137	1230.099206	2442.164588	1221.585932	2441.180572	1221.093924	Q	828.464787	414.736032	811.438238	406.222757	810.454222	405.730749	4
19	2572.275201	1286.641238	2555.248652	1278.127964	2554.264636	1277.635956	L	389.239461	195.123369	372.212912	186.610094	371.228896	186.118086	3
20	2701.317794	1351.162535	2684.291245	1342.649260	2683.307229	1342.157252	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
21							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [NIPTVNENLENYYLEVNQLEK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.9	2846.415985	0.030587	NIPTVNENLENYYLEVNQLEK
0.2	2846.417358	0.029214	NLLALDKDSFSDPYAHICFLHRSK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VECSDNLFTQR**

Found in **MASP1_HUMAN**, Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3

Match to Query 40024: 1678.784532 from(560.602120,3+) rtinseconds(2136) index(53793)

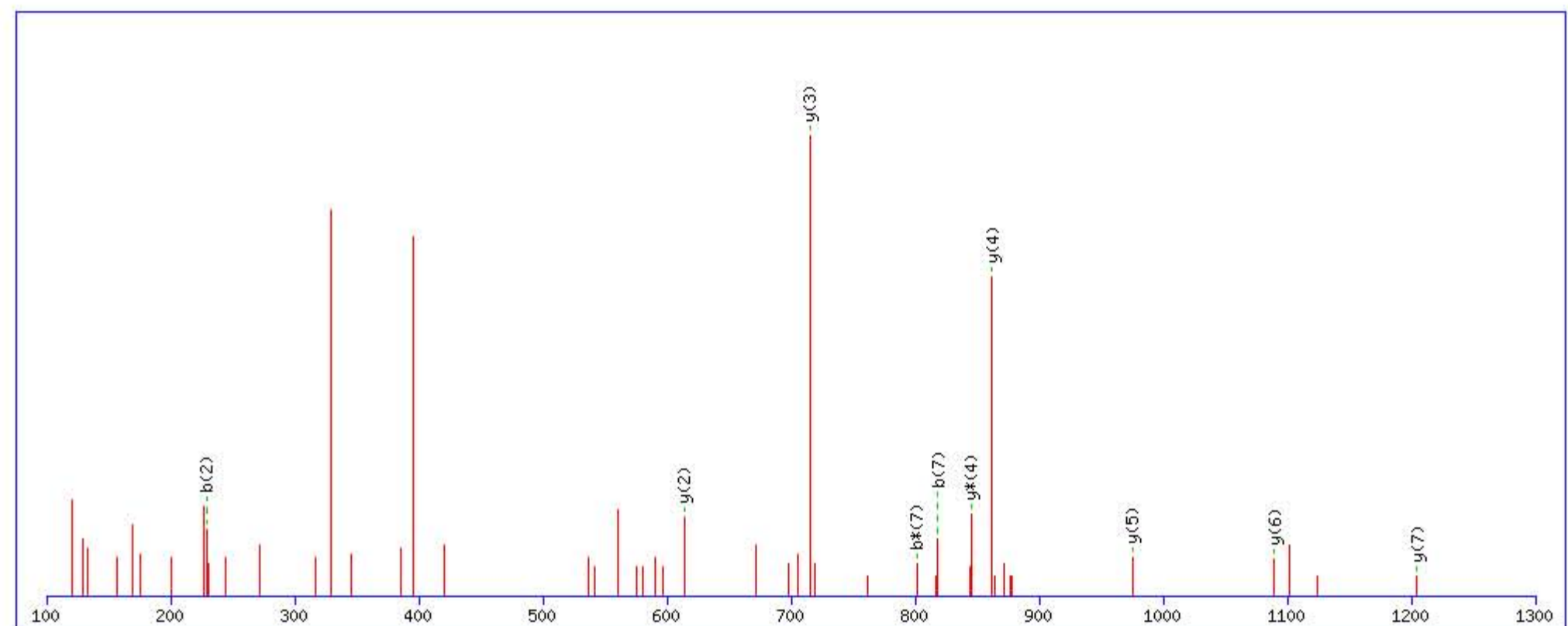
Title: Locus:1.1.1.1359.2 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1678.780716

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

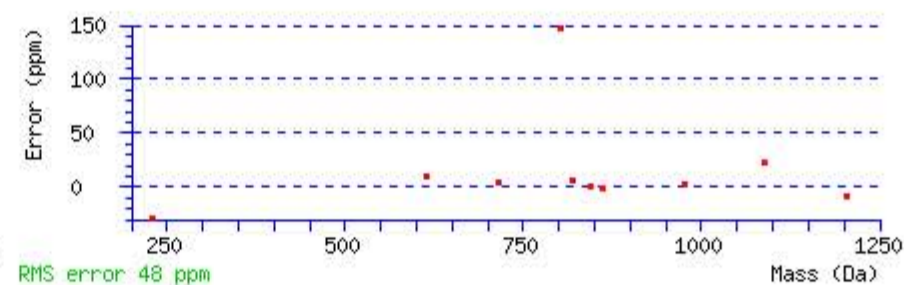
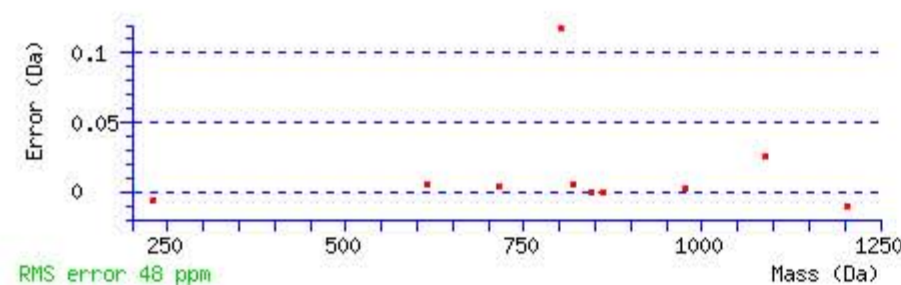
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 29 Expect: 0.019

Matches : 10/104 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							11
2	229.118283	115.062780			211.107718	106.057497	E	1580.719575	790.863426	1563.693026	782.350151	1562.709010	781.858143	10
3	389.148932	195.078104			371.138367	186.072822	C	1451.676982	726.342129	1434.650433	717.828855	1433.666417	717.336847	9
4	476.180960	238.594118			458.170395	229.588835	S	1291.646333	646.326805	1274.619784	637.813530	1273.635768	637.321522	8
5	591.207903	296.107590			573.197338	287.102307	D	1204.614305	602.810791	1187.587756	594.297516	1186.603740	593.805508	7
6	705.250830	353.129053	688.224281	344.615778	687.240265	344.123770	N	1089.587362	545.297319	1072.560813	536.784045	1071.576797	536.292037	6
7	818.334894	409.671085	801.308345	401.157810	800.324329	400.665802	L	975.544435	488.275856	958.517886	479.762581	957.533870	479.270573	5
8	965.403308	483.205292	948.376759	474.692017	947.392743	474.200009	F	862.460371	431.733824	845.433822	423.220549	844.449806	422.728541	4
9	1066.450987	533.729131	1049.424438	525.215857	1048.440422	524.723849	T	715.391957	358.199617	698.365408	349.686342	697.381392	349.194334	3
10	1505.676313	753.341795	1488.649764	744.828520	1487.665748	744.336512	Q	614.344278	307.675777	597.317729	299.162503			2
11							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [VECSDNLFTQR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
28.8	1678.780716	0.003816	VECSDNLFTQR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **FPETLMEIEIPIVDHSTCQK**

Found in **MASP1_HUMAN**, Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3

Match to Query 58324: 2697.347022 from(900.122950,3+) rtinseconds(2789) index(57762)

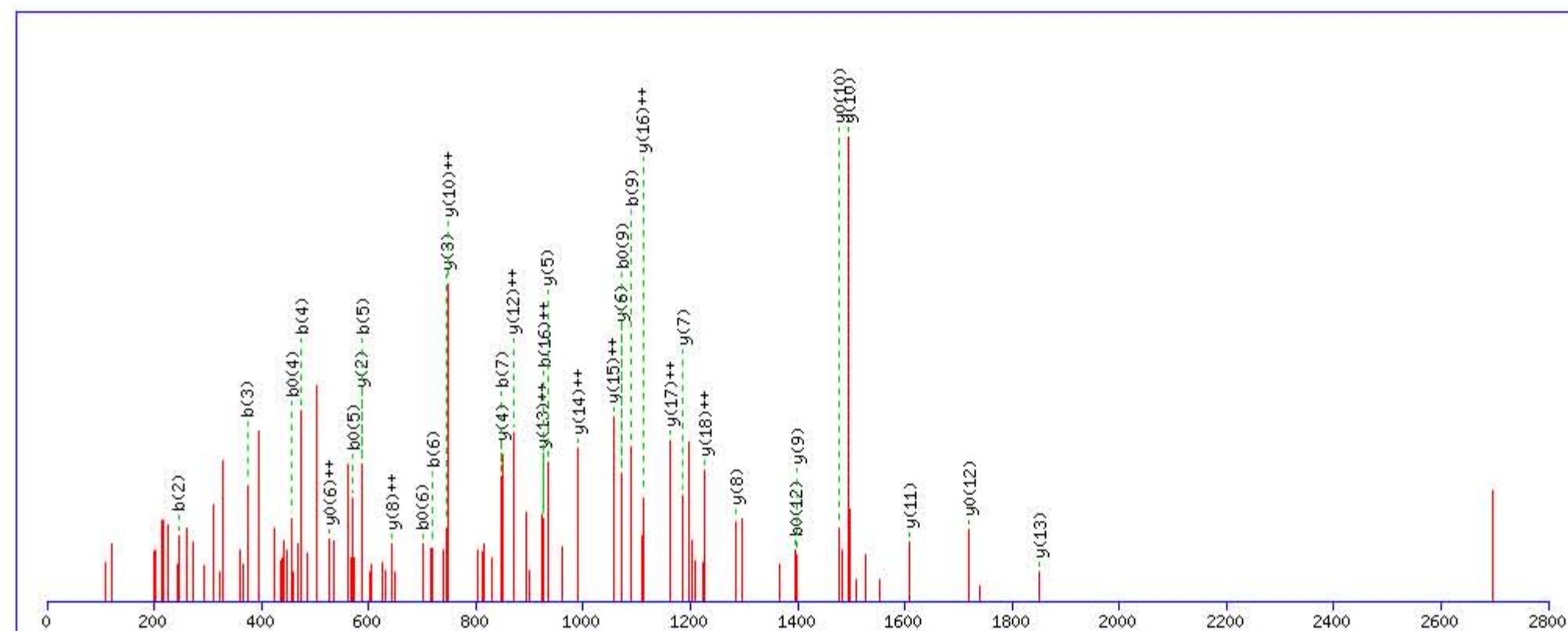
Title: Locus:1.1.1.1585.17 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2697.321609

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

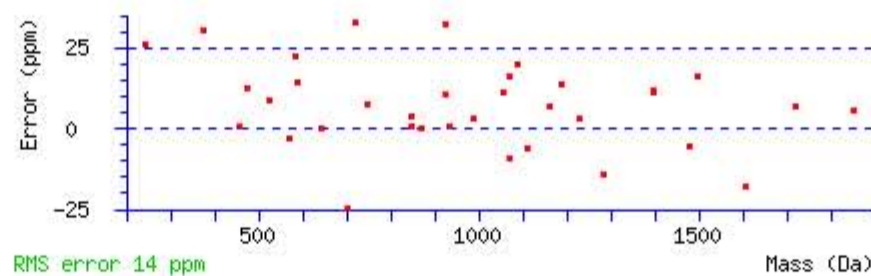
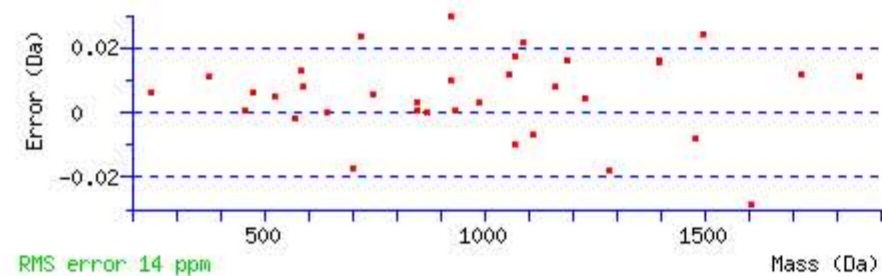
Variable modifications:

Q19 : Biotin:Thermo-21345 (Q)

Ions Score: 60 Expect: 2.7e-006

Matches : 36/182 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	148.075690	74.541483					F							20
2	245.128454	123.067865					P	2551.260482	1276.133879	2534.233933	1267.620604	2533.249917	1267.128596	19
3	374.171047	187.589161			356.160482	178.583879	E	2454.207718	1227.607497	2437.181169	1219.094222	2436.197153	1218.602214	18
4	475.218726	238.113001			457.208161	229.107719	T	2325.165125	1163.086200	2308.138576	1154.572926	2307.154560	1154.080918	17
5	588.302790	294.655033			570.292225	285.649751	L	2224.117446	1112.562361	2207.090897	1104.049086	2206.106881	1103.557078	16
6	719.343275	360.175276			701.332710	351.169993	M	2111.033382	1056.020329	2094.006833	1047.507054	2093.022817	1047.015046	15
7	848.385868	424.696572			830.375303	415.691290	E	1979.992897	990.500087	1962.966348	981.986812	1961.982332	981.494804	14
8	961.469932	481.238604			943.459367	472.233322	I	1850.950304	925.978790	1833.923755	917.465516	1832.939739	916.973508	13
9	1090.512525	545.759901			1072.501960	536.754618	E	1737.866240	869.436758	1720.839691	860.923484	1719.855675	860.431476	12
10	1203.596589	602.301933			1185.586024	593.296650	I	1608.823647	804.915462	1591.797098	796.402187	1590.813082	795.910179	11
11	1300.649353	650.828315			1282.638788	641.823032	P	1495.739583	748.373430	1478.713034	739.860155	1477.729018	739.368147	10
12	1413.733417	707.370346			1395.722852	698.365064	I	1398.686819	699.847048	1381.660270	691.333773	1380.676254	690.841765	9
13	1512.801831	756.904554			1494.791266	747.899271	V	1285.602755	643.305016	1268.576206	634.791741	1267.592190	634.299733	8
14	1627.828774	814.418025			1609.818209	805.412743	D	1186.534341	593.770809	1169.507792	585.257534	1168.523776	584.765526	7
15	1764.887686	882.947481			1746.877121	873.942199	H	1071.507398	536.257337	1054.480849	527.744063	1053.496833	527.252055	6
16	1851.919714	926.463495			1833.909149	917.458213	S	934.448486	467.727881	917.421937	459.214607	916.437921	458.722599	5
17	1952.967393	976.987335			1934.956828	967.982052	T	847.416458	424.211867	830.389909	415.698593	829.405893	415.206585	4
18	2112.998042	1057.002659			2094.987477	1047.997376	C	746.368779	373.688028	729.342230	365.174753			3
19	2552.223368	1276.615322	2535.196819	1268.102047	2534.212803	1267.610039	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 [FPETLMEIEIPIVDHSTCQK](#)

(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	2697.321609	0.025413	FPETLMEIEIPIVDHSTCQK
0.3	2697.379593	-0.032571	LVVLF SQMRLANFQTDSQESI QK

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **APEPISTQSHSVLILFHSDNSGENR**

Found in **MASPI_HUMAN**, Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASPI PE=1 SV=3

Match to Query 62047: 3045.518216 from(762.386830,4+) rtinseconds(2270) index(54676)

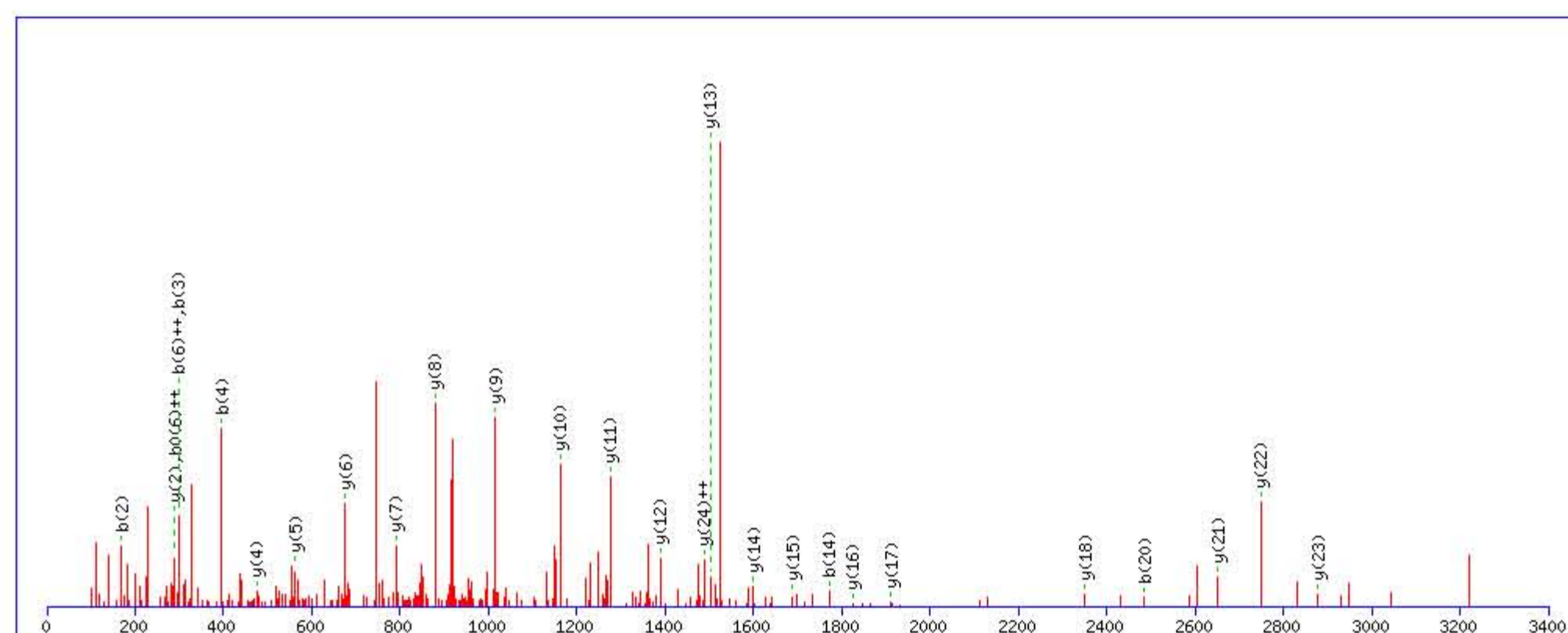
Title: Locus:1.1.1.1405.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3045.497803

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

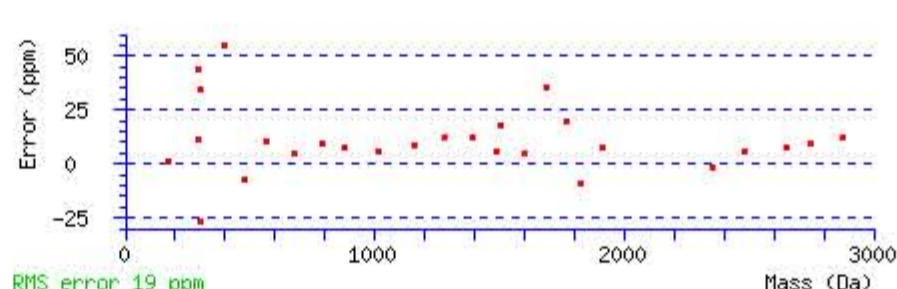
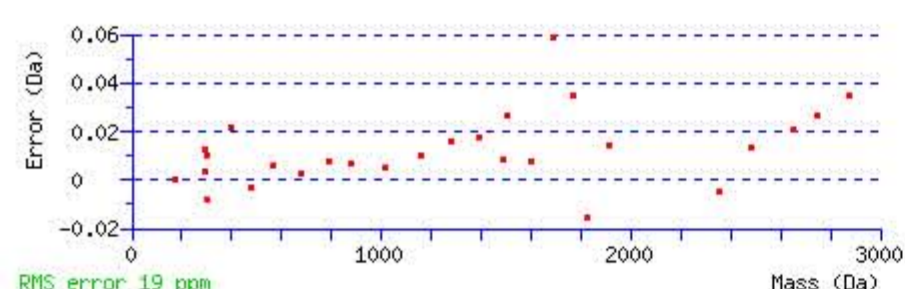
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 93 Expect: 1.3e-008

Matches : 27/266 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	72.044390	36.525833					A							25
2	169.097154	85.052215					P	2975.467980	1488.237628	2958.441431	1479.724353	2957.457415	1479.232345	24
3	298.139747	149.573512			280.129182	140.568229	E	2878.415216	1439.711246	2861.388667	1431.197971	2860.404651	1430.705963	23
4	395.192511	198.099894			377.181946	189.094611	P	2749.372623	1375.189949	2732.346074	1366.676675	2731.362058	1366.184667	22
5	508.276575	254.641926			490.266010	245.636643	I	2652.319859	1326.663567	2635.293310	1318.150293	2634.309294	1317.658285	21
6	595.308603	298.157940			577.298038	289.152657	S	2539.235795	1270.121535	2522.209246	1261.608261	2521.225230	1261.116253	20
7	696.356282	348.681779			678.345717	339.676497	T	2452.203767	1226.605521	2435.177218	1218.092247	2434.193202	1217.600239	19
8	1135.581608	568.294442	1118.555059	559.781168	1117.571043	559.289160	Q	2351.156088	1176.081682	2334.129539	1167.568407	2333.145523	1167.076399	18
9	1222.613636	611.810456	1205.587087	603.297182	1204.603071	602.805174	S	1911.930762	956.469019	1894.904213	947.955745	1893.920197	947.463737	17
10	1359.672548	680.339912	1342.645999	671.826638	1341.661983	671.334630	H	1824.898734	912.953005	1807.872185	904.439731	1806.888169	903.947723	16
11	1446.704576	723.855926	1429.678027	715.342652	1428.694011	714.850644	S	1687.839822	844.423549	1670.813273	835.910275	1669.829257	835.418267	15
12	1545.772990	773.390133	1528.746441	764.876859	1527.762425	764.384851	V	1600.807794	800.907535	1583.781245	792.394261	1582.797229	791.902253	14
13	1658.857054	829.932165	1641.830505	821.418891	1640.846489	820.926883	L	1501.739380	751.373328	1484.712831	742.860054	1483.728815	742.368045	13
14	1771.941118	886.474197	1754.914569	877.960923	1753.930553	877.468915	I	1388.655316	694.831296	1371.628767	686.318022	1370.644751	685.826014	12
15	1885.025182	943.016229	1867.998633	934.502955	1867.014617	934.010947	L	1275.571252	638.289264	1258.544703	629.775990	1257.560687	629.283982	11
16	2032.093596	1016.550436	2015.067047	1008.037162	2014.083031	1007.545154	F	1162.487188	581.747232	1145.460639	573.233958	1144.476623	572.741950	10
17	2169.152508	1085.079892	2152.125959	1076.566617	2151.141943	1076.074610	H	1015.418774	508.213025	998.392225	499.699751	997.408209	499.207743	9
18	2256.184536	1128.595906	2239.157987	1120.082631	2238.173971	1119.590624	S	878.359862	439.683569	861.333313	431.170295	860.349297	430.678287	8
19	2371.211479	1186.109377	2354.184930	1177.596103	2353.200914	1177.104095	D	791.327834	396.167555	774.301285	387.654280	773.317269	387.162272	7
20	2485.254406	1243.130841	2468.227857	1234.617566	2467.243841	1234.125558	N	676.300891	338.654084	659.274342	330.140809	658.290326	329.648801	6
21	2572.286434	1286.646855	2555.259885	1278.133580	2554.275869	1277.641572	S	562.257964	281.632620	545.231415	273.119346	544.247399	272.627338	5
22	2629.307898	1315.157587	2612.281349	1306.644312	2611.297333	1306.152304	G	475.225936	238.116606	458.199387	229.603331	457.215371	229.111323	4
23	2758.350491	1379.678884	2741.323942	1371.165609	2740.339926	1370.673601	E	418.204472	209.605874	401.177923	201.092600	400.193907	200.600592	3
24	2872.393418	1436.700347	2855.366869	1428.187072	2854.382853	1427.695064	N	289.161879	145.084577	272.135330	136.571303			2
25							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [APEPISTQSHSVLILFHSDNSGENR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
93.3	3045.497803	0.020413	APEPISTQSHSVLILFHSDNSGENR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **VLSIAQAHSPAFSCEQVR**

Found in **CD14_HUMAN**, Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2

Match to Query 53176: 2310.166692 from(771.062840,3+) rtinseconds(1984) index(36314)

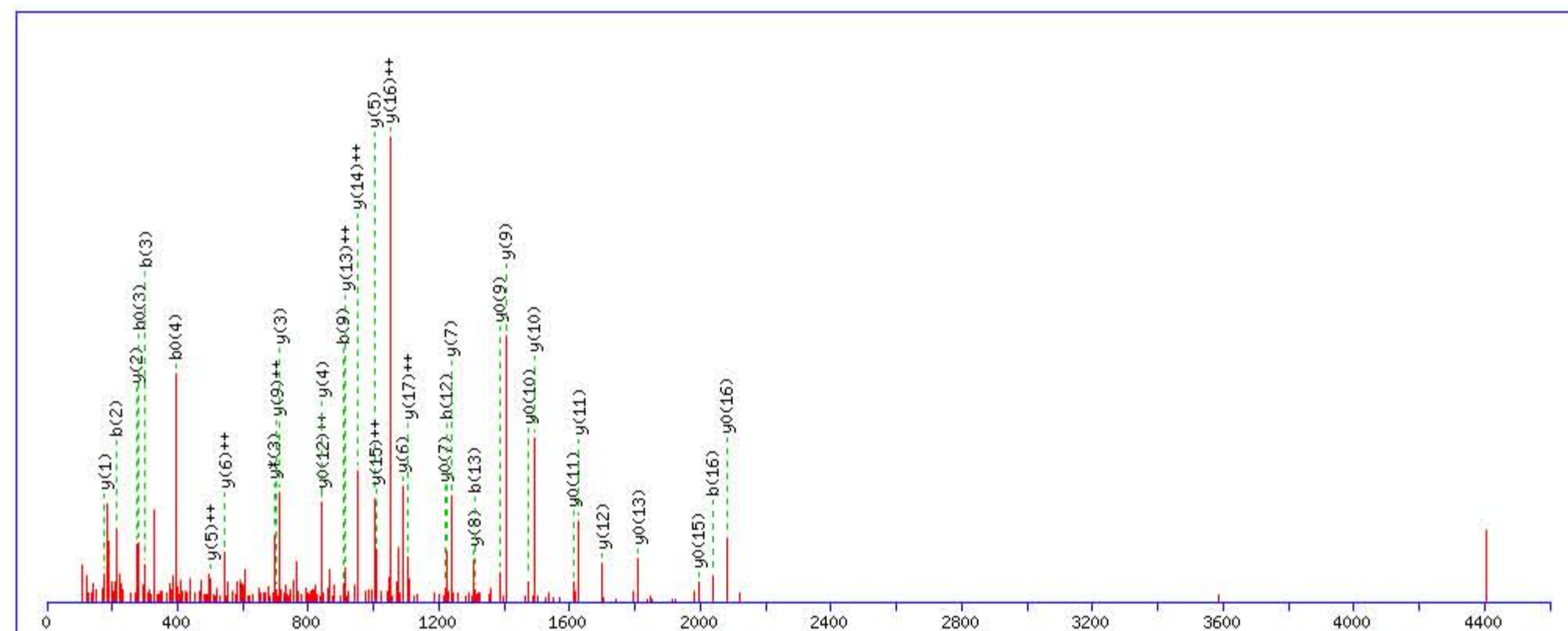
Title: Locus:1.1.1.3110.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2310.161285

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

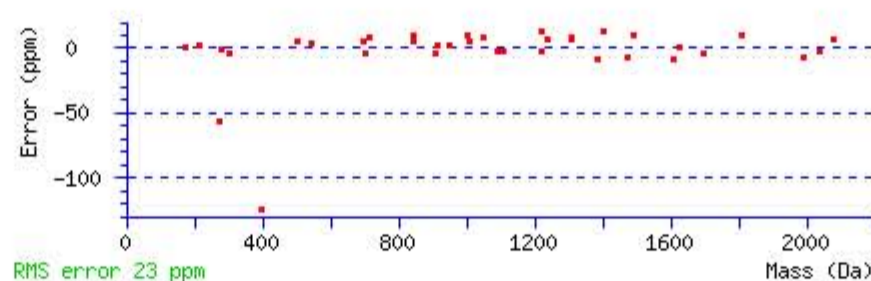
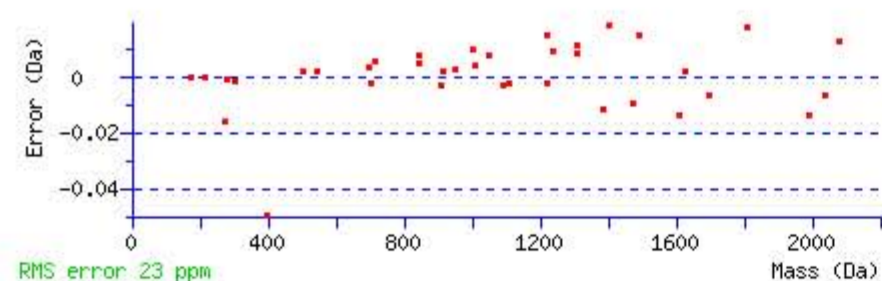
Variable modifications:

Q16 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 6.2e-005

Matches : 37/184 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							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
56.6	2310.161285	0.005407	VLSIAQAHSPAFSCEQVR
7.0	2310.161285	0.005407	VLSIAQAHSPAFSCEQVR

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIGLDQVAGMSETALPGAFK**

Found in **MYH9_HUMAN**, Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4

Match to Query 53495: 2328.229452 from(777.083760,3+) rtinseconds(2872) index(58462)

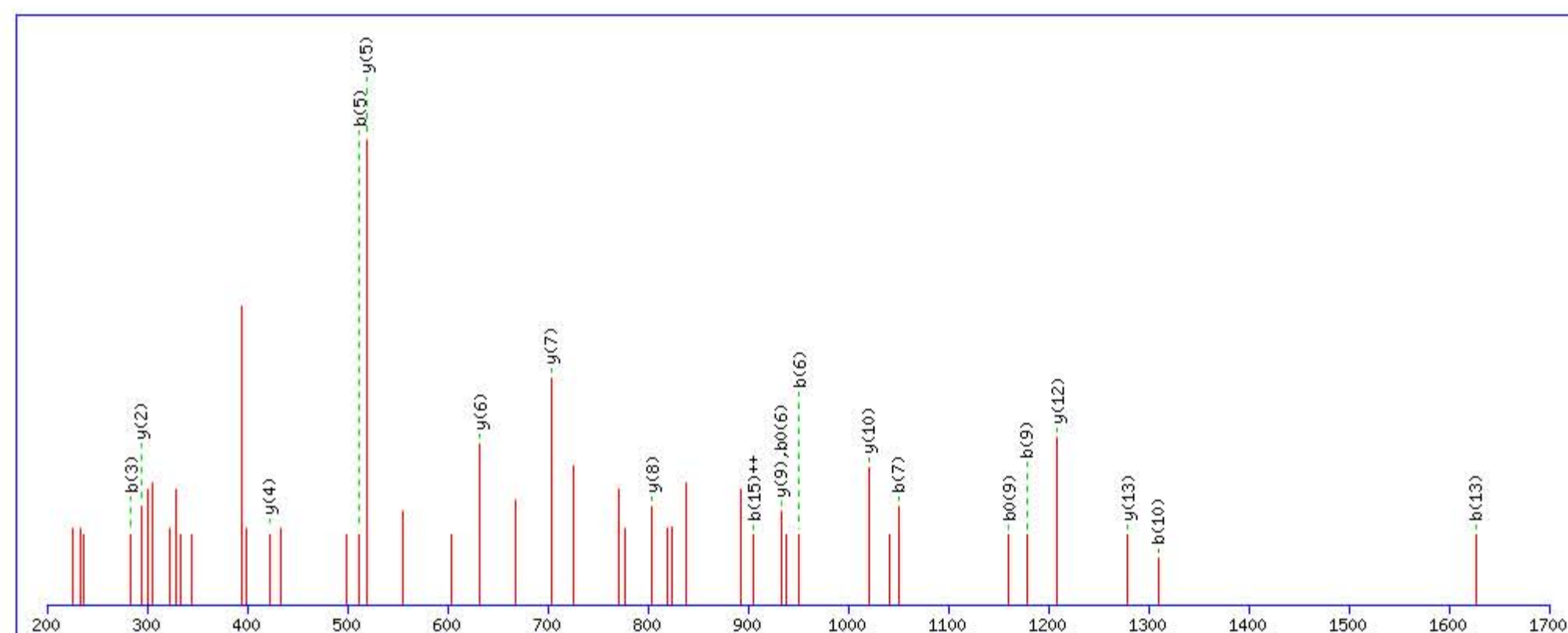
Title: Locus:1.1.1.1613.17 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2328.222153

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

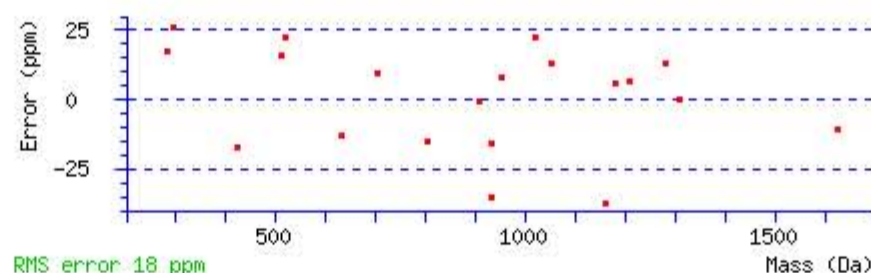
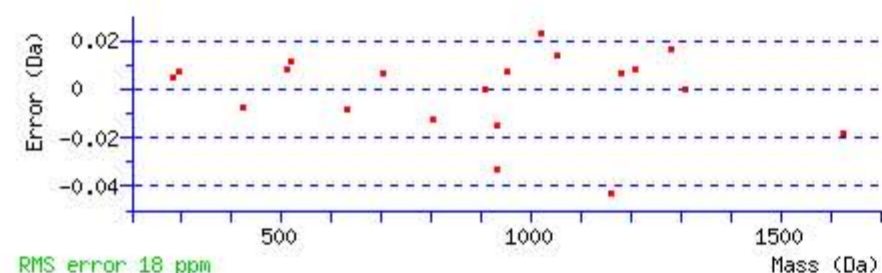
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 51 Expect: 0.00018

Matches : 20/196 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							20
2	227.175404	114.091340					I	2216.145376	1108.576326	2199.118827	1100.063051	2198.134811	1099.571043	19
3	284.196868	142.602072					G	2103.061312	1052.034294	2086.034763	1043.521019	2085.050747	1043.029011	18
4	397.280932	199.144104					L	2046.039848	1023.523562	2029.013299	1015.010288	2028.029283	1014.518279	17
5	512.307875	256.657576			494.297310	247.652293	D	1932.955784	966.981530	1915.929235	958.468255	1914.945219	957.976247	16
6	951.533201	476.270239	934.506652	467.756964	933.522636	467.264956	Q	1817.928841	909.468058	1800.902292	900.954784	1799.918276	900.462776	15
7	1050.601615	525.804446	1033.575066	517.291171	1032.591050	516.799163	V	1378.703515	689.855395	1361.676966	681.342121	1360.692950	680.850113	14
8	1121.638729	561.323003	1104.612180	552.809728	1103.628164	552.317720	A	1279.635101	640.321188	1262.608552	631.807914	1261.624536	631.315906	13
9	1178.660193	589.833734	1161.633644	581.320460	1160.649628	580.828452	G	1208.597987	604.802631	1191.571438	596.289357	1190.587422	595.797349	12
10	1309.700678	655.353977	1292.674129	646.840703	1291.690113	646.348694	M	1151.576523	576.291900	1134.549974	567.778625	1133.565958	567.286617	11
11	1396.732706	698.869991	1379.706157	690.356717	1378.722141	689.864709	S	1020.536038	510.771657	1003.509489	502.258382	1002.525473	501.766374	10
12	1525.775299	763.391288	1508.748750	754.878013	1507.764734	754.386005	E	933.504010	467.255643	916.477461	458.742368	915.493445	458.250360	9
13	1626.822978	813.915127	1609.796429	805.401853	1608.812413	804.909845	T	804.461417	402.734346	787.434868	394.221072	786.450852	393.729064	8
14	1697.860092	849.433684	1680.833543	840.920410	1679.849527	840.428402	A	703.413738	352.210507	686.387189	343.697232			7
15	1810.944156	905.975716	1793.917607	897.462442	1792.933591	896.970434	L	632.376624	316.691950	615.350075	308.178675			6
16	1907.996920	954.502098	1890.970371	945.988824	1889.986355	945.496816	P	519.292560	260.149918	502.266011	251.636643			5
17	1965.018384	983.012830	1947.991835	974.499556	1947.007819	974.007547	G	422.239796	211.623536	405.213247	203.110261			4
18	2036.055498	1018.531387	2019.028949	1010.018113	2018.044933	1009.526105	A	365.218332	183.112804	348.191783	174.599529			3
19	2183.123912	1092.065594	2166.097363	1083.552319	2165.113347	1083.060311	F	294.181218	147.594247	277.154669	139.080972			2
20							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **IIGLDQVAGMSETALPGAFK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.2	2328.222153	0.007299	IIGLDQVAGMSETALPGAFK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SPEQLR**

Found in **GNPTG_HUMAN**, N-acetylglucosamine-1-phosphotransferase subunit gamma OS=Homo sapiens GN=GNPTG PE=1 SV=1

Match to Query 17290: 1039.544788 from(520.779670,2+) rtinseconds(1465) index(33054)

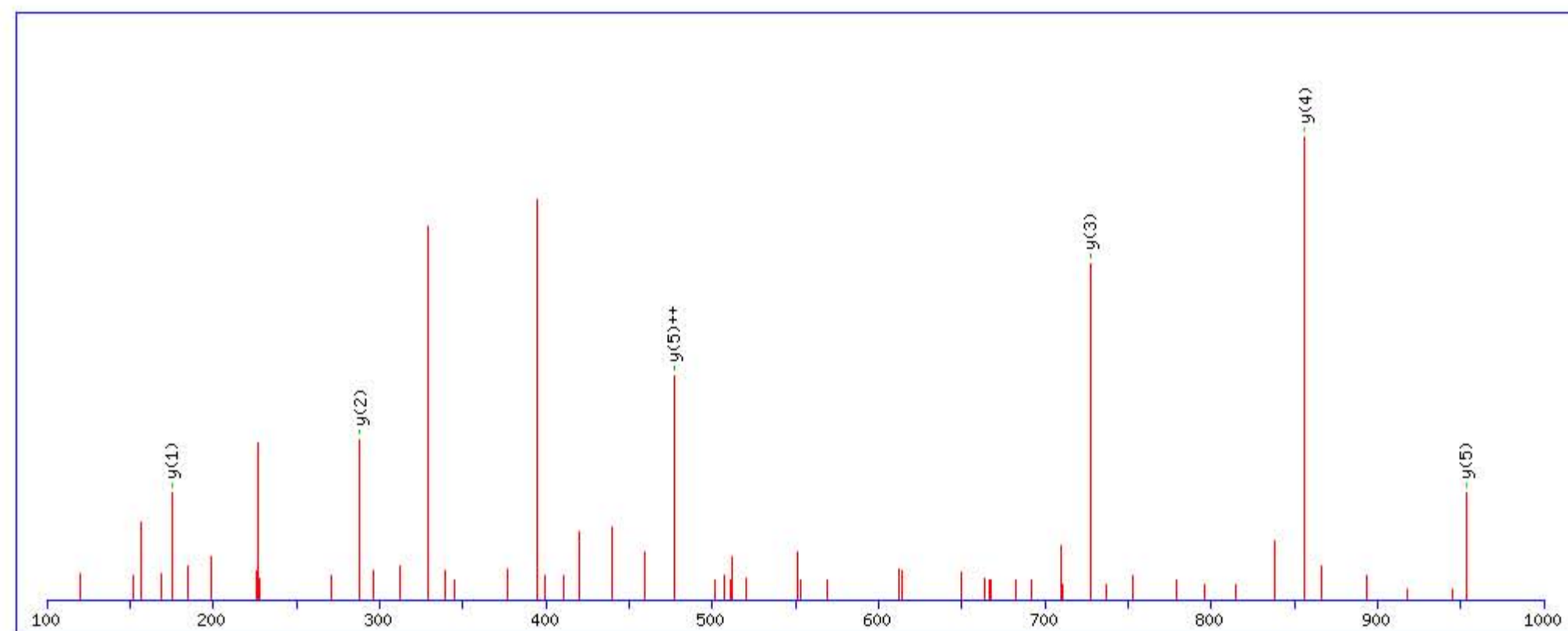
Title: Locus:1.1.1.2929.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1039.548431

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

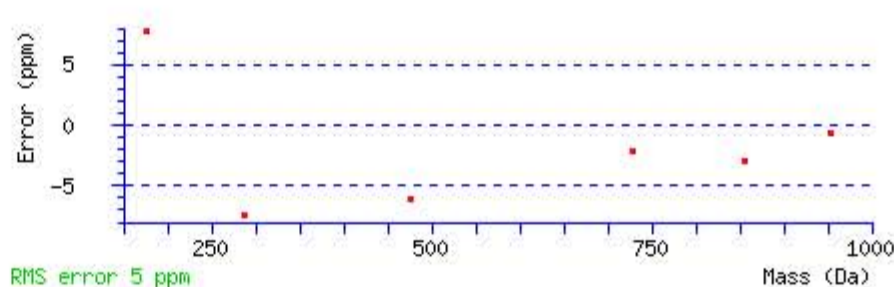
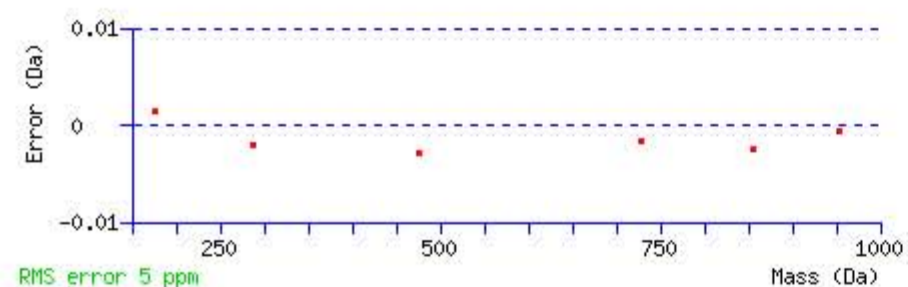
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.0035

Matches : 6/48 fragment ions using 9 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							6
2	185.092068	93.049672			167.081503	84.044389	P	953.523699	477.265488	936.497150	468.752213	935.513134	468.260205	5
3	314.134661	157.570968			296.124096	148.565686	E	856.470935	428.739106	839.444386	420.225831	838.460370	419.733823	4
4	753.359987	377.183632	736.333438	368.670357	735.349422	368.178349	Q	727.428342	364.217809	710.401793	355.704535			3
5	866.444051	433.725664	849.417502	425.212389	848.433486	424.720381	L	288.203016	144.605146	271.176467	136.091872			2
6							R	175.118952	88.063114	158.092403	79.549840			1



NCBI BLAST search of **SPEQLR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.8	1039.548431	-0.003643	SPEQLR
23.0	1039.548431	-0.003643	SPEIQR
22.6	1039.541031	0.003757	ALESNHILR
9.5	1039.533813	0.010975	EALFYELR
3.8	1039.541046	0.003742	ALQSGPPQSR
3.5	1039.556290	-0.011502	FPERAPAPR
1.9	1039.529831	0.014957	TTFVSKDSR
0.8	1039.548447	-0.003659	MATATPVPPR
0.2	1039.541046	0.003742	NLPADGQGLR
0.0	1039.552261	-0.007473	LRSDEKHR

Mascot: <http://www.matrixscience.com/>

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGEQCVHTASGPR**

Found in **NOTC2_HUMAN**, Neurogenic locus notch homolog protein 2 OS=Homo sapiens GN=NOTCH2 PE=1 SV=3

Match to Query 41213: 1736.838496 from(435.216900,4+) rtinseconds(1070) index(30850)

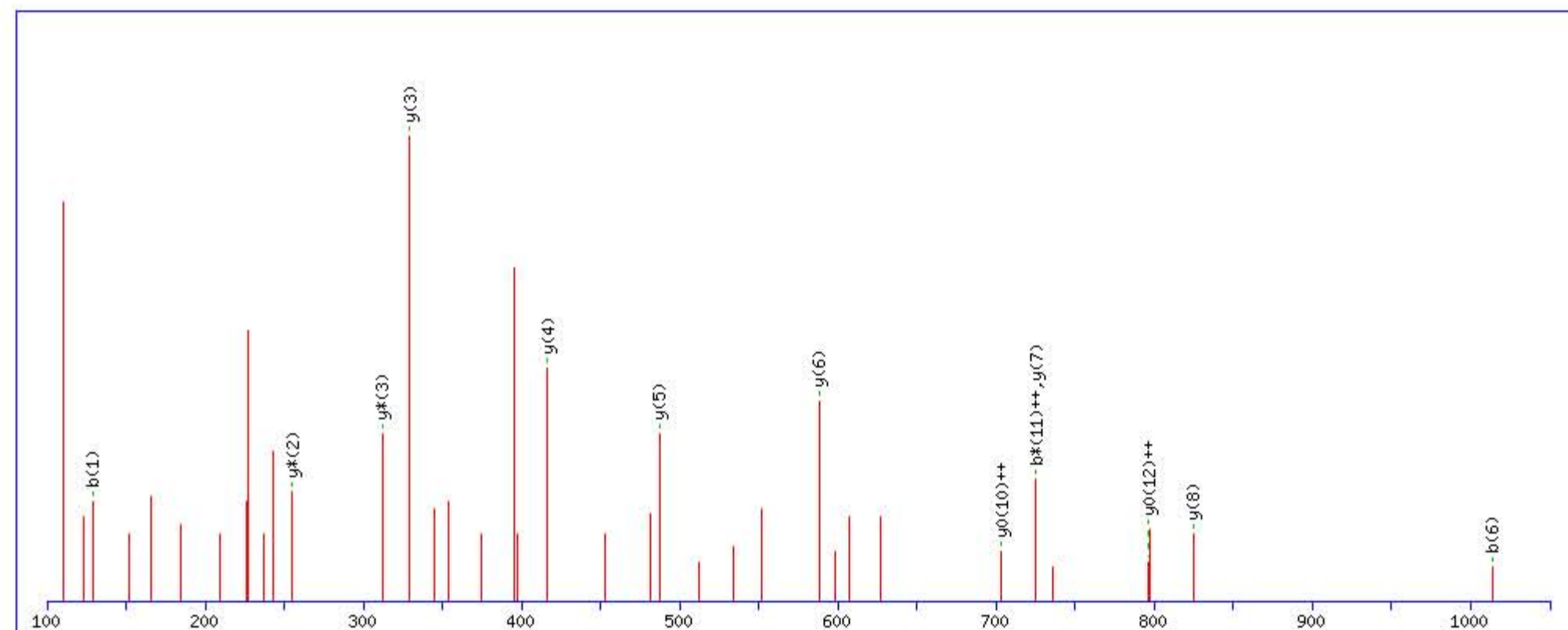
Title: Locus:1.1.1.2792.2 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1736.845047

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

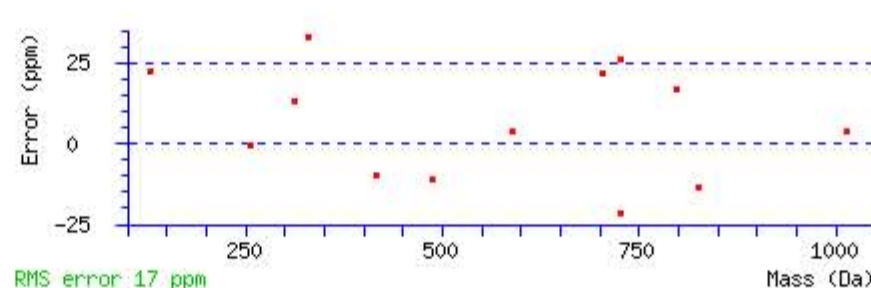
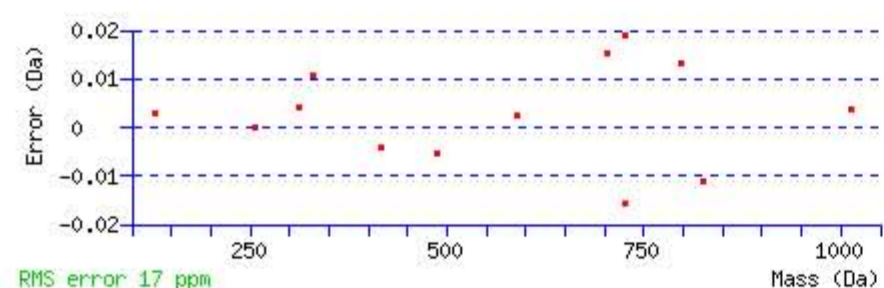
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.018

Matches : 13/134 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	129.102239	65.054757	112.075690	56.541483			K							13
2	186.123703	93.565489	169.097154	85.052215			G	1609.757359	805.382318	1592.730810	796.869043	1591.746794	796.377035	12
3	315.166296	158.086786	298.139747	149.573512	297.155731	149.081504	E	1552.735895	776.871586	1535.709346	768.358311	1534.725330	767.866303	11
4	754.391622	377.699449	737.365073	369.186175	736.381057	368.694167	Q	1423.693302	712.350289	1406.666753	703.837015	1405.682737	703.345007	10
5	914.422271	457.714774	897.395722	449.201499	896.411706	448.709491	C	984.467976	492.737626	967.441427	484.224352	966.457411	483.732344	9
6	1013.490685	507.248981	996.464136	498.735706	995.480120	498.243698	V	824.437327	412.722302	807.410778	404.209027	806.426762	403.717019	8
7	1150.549597	575.778437	1133.523048	567.265162	1132.539032	566.773154	H	725.368913	363.188095	708.342364	354.674820	707.358348	354.182812	7
8	1251.597276	626.302276	1234.570727	617.789002	1233.586711	617.296994	T	588.310001	294.658639	571.283452	286.145364	570.299436	285.653356	6
9	1322.634390	661.820833	1305.607841	653.307559	1304.623825	652.815551	A	487.262322	244.134799	470.235773	235.621524	469.251757	235.129516	5
10	1409.666418	705.336847	1392.639869	696.823573	1391.655853	696.331565	S	416.225208	208.616242	399.198659	200.102967	398.214643	199.610959	4
11	1466.687882	733.847579	1449.661333	725.334305	1448.677317	724.842297	G	329.193180	165.100228	312.166631	156.586953			3
12	1563.740646	782.373961	1546.714097	773.860687	1545.730081	773.368679	P	272.171716	136.589496	255.145167	128.076221			2
13							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **KGEQCVHTASGPR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.2	1736.845047	-0.006551	KGEQCVHTASGPR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **RPYQEGTPCSQCPSGYHCK**

Found in **PII6_HUMAN**, Peptidase inhibitor 16 OS=Homo sapiens GN=PI16 PE=1 SV=1

Match to Query 57801: 2622.117336 from(656.536610,4+) rtinseconds(1287) index(31822)

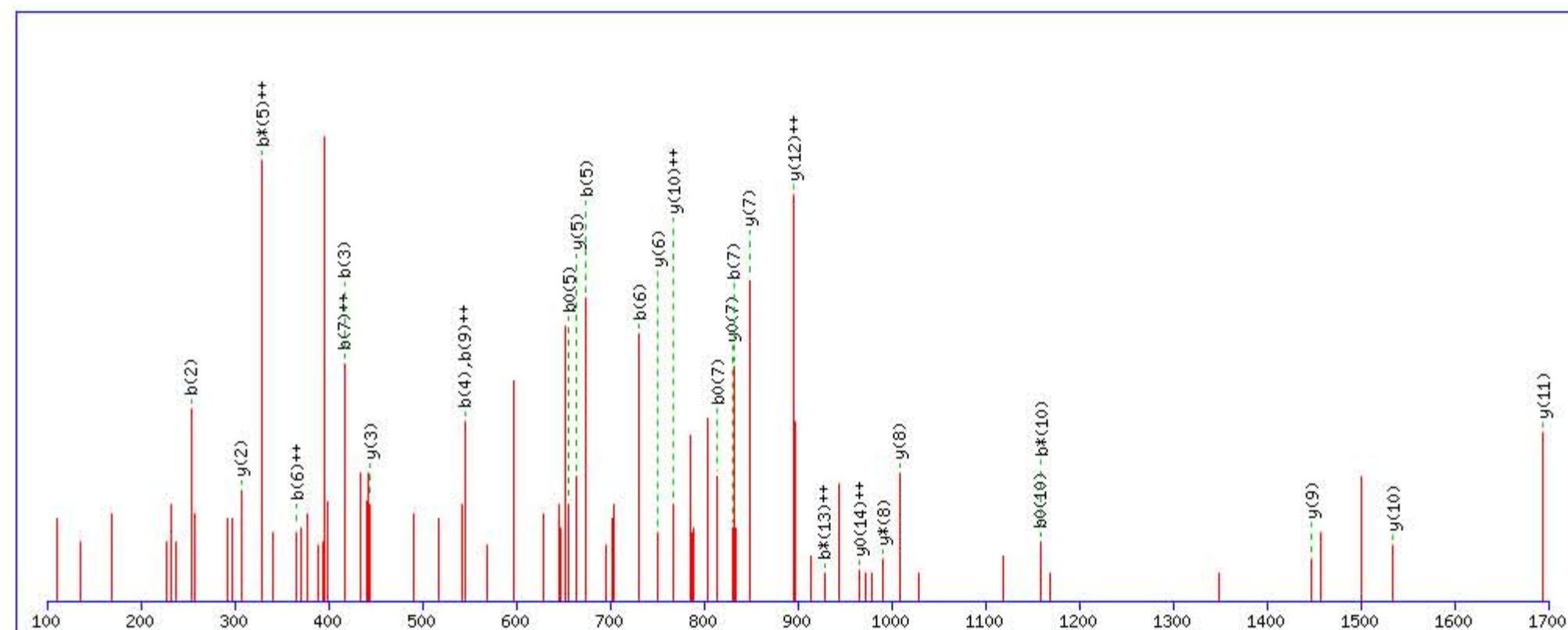
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2622.123611

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

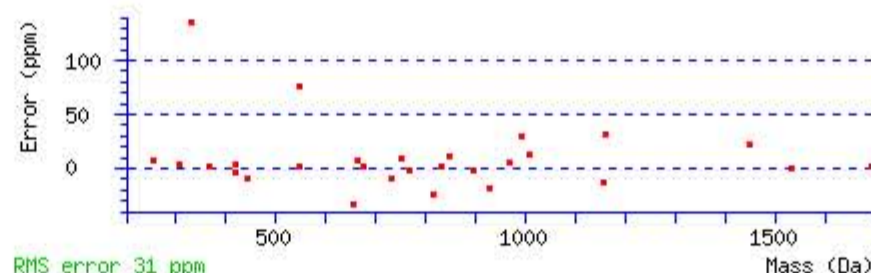
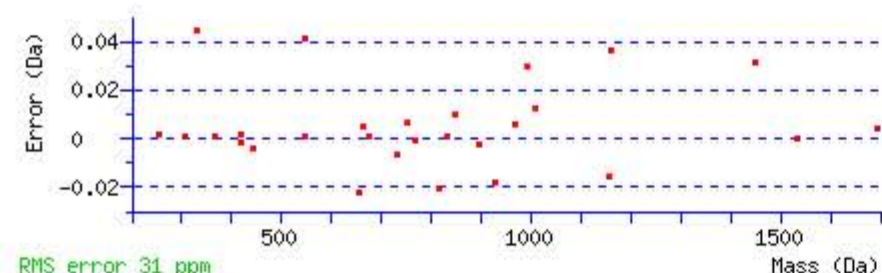
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 36 Expect: 0.00074

Matches : 29/198 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	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
36.3	2622.123611	-0.006275	RPYQEGTPCSQCPSGYHCK

Mascot: <http://www.matrixscience.com/>

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 37370: 1606.840608 from(804.427580,2+) rtinseconds(2155) index(53932)

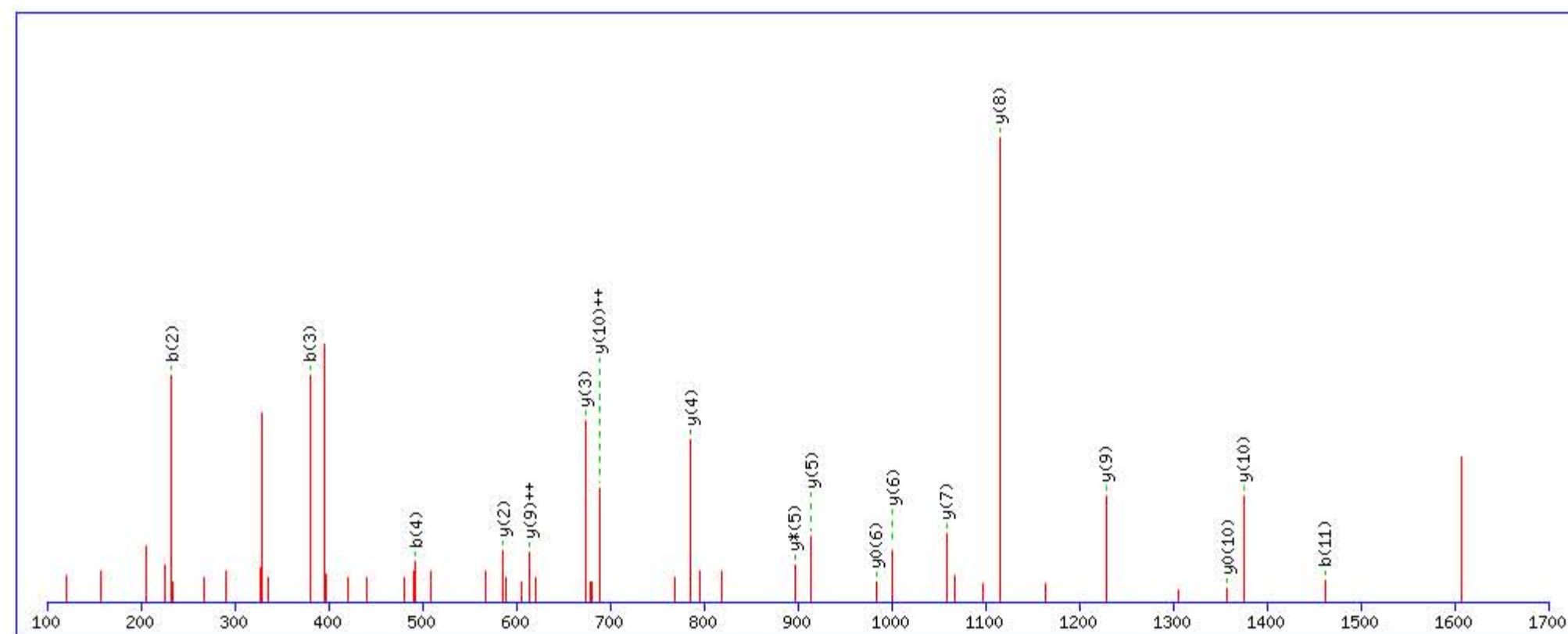
Title: Locus:1.1.1.1365.17 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1606.821121

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

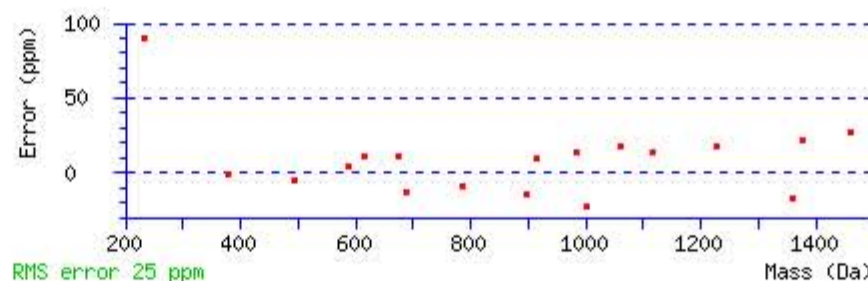
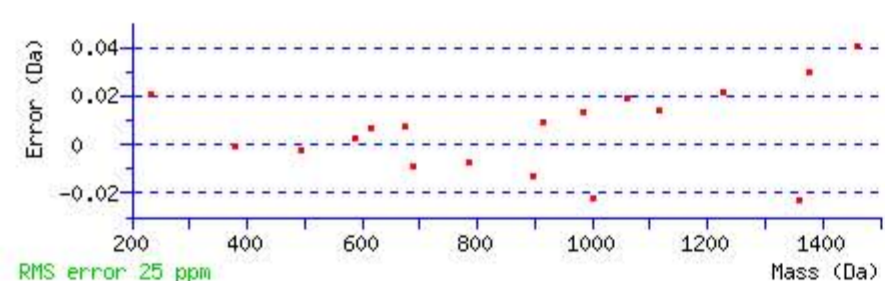
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 72 Expect: 2.6e-007

Matches : 18/114 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							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
71.8	1606.821121	0.019487	TMFIGGSQLSQK
35.5	1606.821121	0.019487	TMFIGGSQLSQK
1.5	1606.859970	-0.019362	TMLES LIADKSGSKK
1.2	1606.863998	-0.023390	SVLLMELEVNYGLK

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **QVLLVGAPTYDDVSK**

Found in **PHLD_HUMAN**, Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

Match to Query 44870: 1915.022688 from(958.518620,2+) rtinseconds(2300) index(38236)

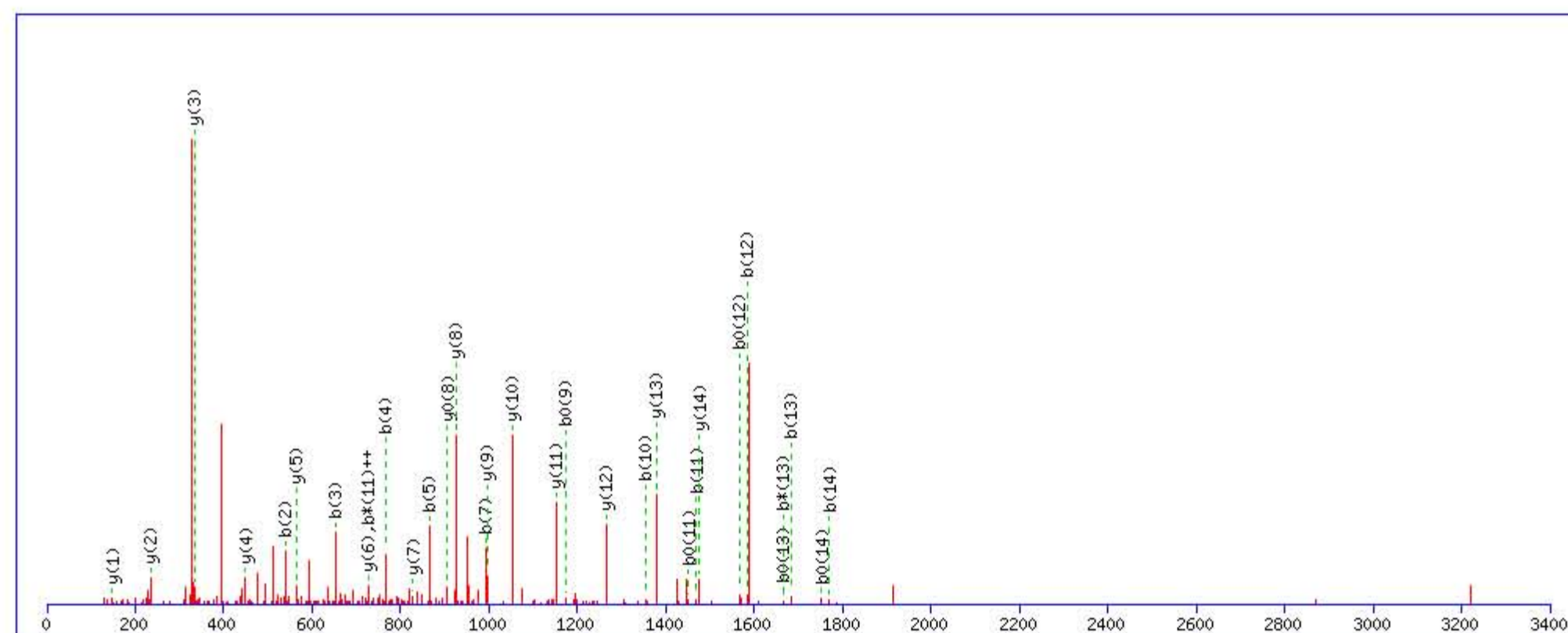
Title: Locus:1.1.1.3220.8 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1915.012497

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

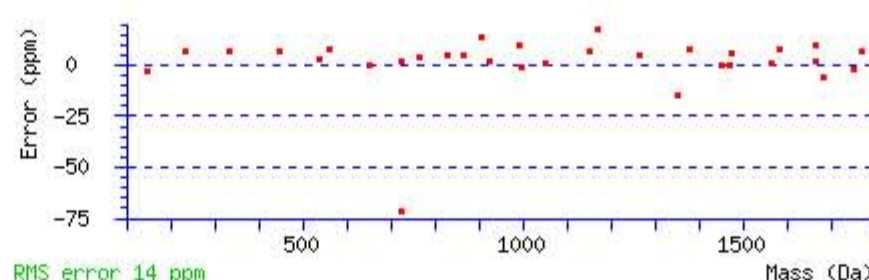
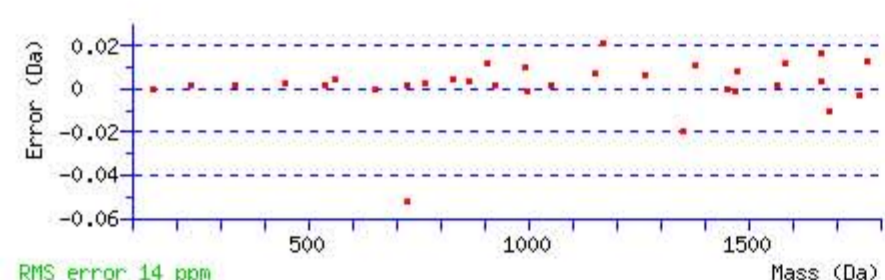
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 87 Expect: 5e-008

Matches : 32/150 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	440.232602	220.619939	423.206053	212.106664			Q							15
2	539.301016	270.154146	522.274467	261.640872			V	1476.794438	738.900857	1459.767889	730.387583	1458.783873	729.895575	14
3	652.385080	326.696178	635.358531	318.182904			L	1377.726024	689.366650	1360.699475	680.853376	1359.715459	680.361368	13
4	765.469144	383.238210	748.442595	374.724936			L	1264.641960	632.824618	1247.615411	624.311344	1246.631395	623.819336	12
5	864.537558	432.772417	847.511009	424.259143			V	1151.557896	576.282586	1134.531347	567.769312	1133.547331	567.277304	11
6	921.559022	461.283149	904.532473	452.769875			G	1052.489482	526.748379	1035.462933	518.235105	1034.478917	517.743097	10
7	992.596136	496.801706	975.569587	488.288432			A	995.468018	498.237647	978.441469	489.724373	977.457453	489.232365	9
8	1089.648900	545.328088	1072.622351	536.814814			P	924.430904	462.719090	907.404355	454.205816	906.420339	453.713808	8
9	1190.696579	595.851927	1173.670030	587.338653	1172.686014	586.846645	T	827.378140	414.192708	810.351591	405.679434	809.367575	405.187426	7
10	1353.759908	677.383592	1336.733359	668.870318	1335.749343	668.378310	Y	726.330461	363.668869	709.303912	355.155594	708.319896	354.663586	6
11	1468.786851	734.897064	1451.760302	726.383789	1450.776286	725.891781	D	563.267132	282.137204	546.240583	273.623930	545.256567	273.131922	5
12	1583.813794	792.410535	1566.787245	783.897261	1565.803229	783.405253	D	448.240189	224.623733	431.213640	216.110458	430.229624	215.618450	4
13	1682.882208	841.944742	1665.855659	833.431468	1664.871643	832.939460	V	333.213246	167.110261	316.186697	158.596987	315.202681	158.104979	3
14	1769.914236	885.460756	1752.887687	876.947482	1751.903671	876.455474	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
15							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **QVLLVGAPTYDDVSK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
86.6	1915.012497	0.010191	QVLLVGAPTYDDVSK
10.8	1915.027710	-0.005022	DYPIYLLKFKQLSK
9.6	1915.008438	0.014250	VIQKNQEETTSISK
6.3	1915.008438	0.014250	VIQKNQEETTSISK

Mascot: <http://www.matrixscience.com/>

MASCOT 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 29350: 1375.647068 from(688.830810,2+) rtinseconds(1373) index(32383)

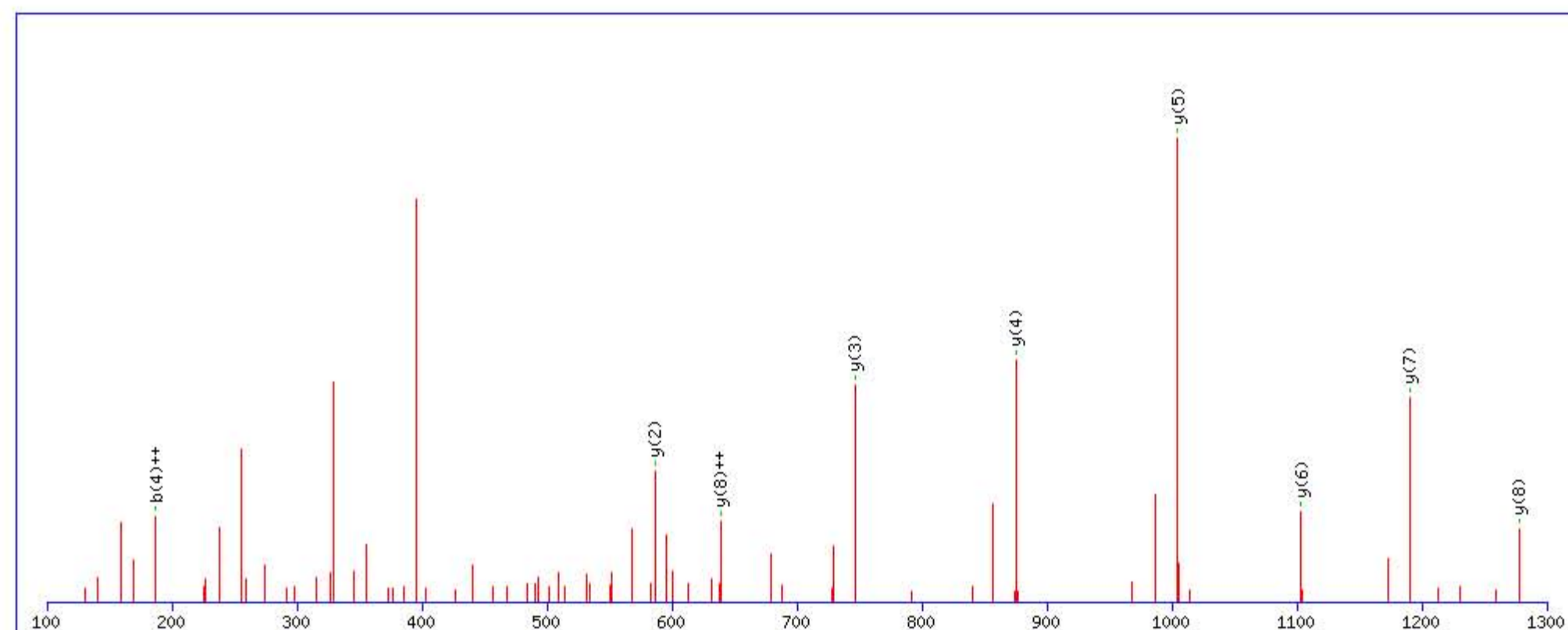
Title: Locus:1.1.1.2897.15 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1375.647568

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

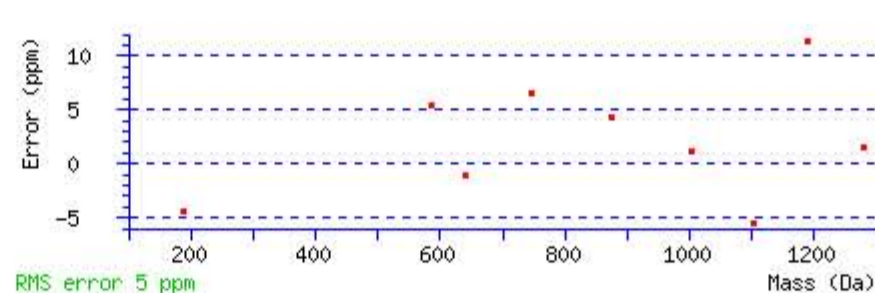
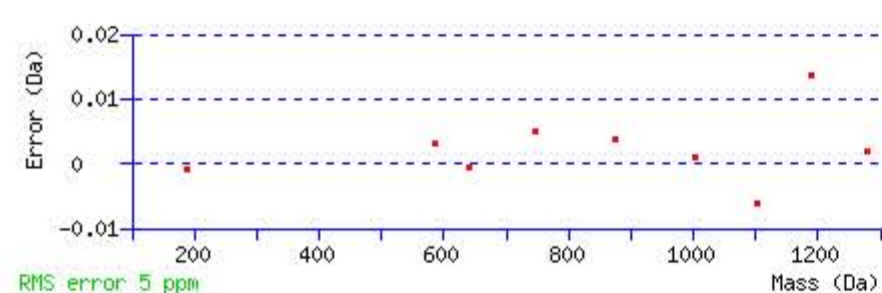
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 1.9e-005

Matches : 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	100.075690	50.541483					V							9
2	187.107718	94.057497			169.097153	85.052214	S	1277.586435	639.296856	1260.559886	630.783581	1259.575870	630.291573	8
3	274.139746	137.573511			256.129181	128.568229	S	1190.554407	595.780842	1173.527858	587.267567	1172.543842	586.775559	7
4	373.208160	187.107718			355.197595	178.102436	V	1103.522379	552.264828	1086.495830	543.751553	1085.511814	543.259545	6
5	502.250753	251.629015			484.240188	242.623732	E	1004.453965	502.730621	987.427416	494.217346	986.443400	493.725338	5
6	631.293346	316.150311			613.282781	307.145029	E	875.411372	438.209324	858.384823	429.696050	857.400807	429.204042	4
7	791.323995	396.165636			773.313430	387.160353	C	746.368779	373.688028	729.342230	365.174753			3
8	1230.549321	615.778299	1213.522772	607.265024	1212.538756	606.773016	Q	586.338130	293.672703	569.311581	285.159429			2
9							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **VSSVEECQK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.2	1375.647568	-0.000500	VSSVEECQK
6.8	1375.662827	-0.015759	GFSIPECQK

Mascot: <http://www.matrixscience.com/>

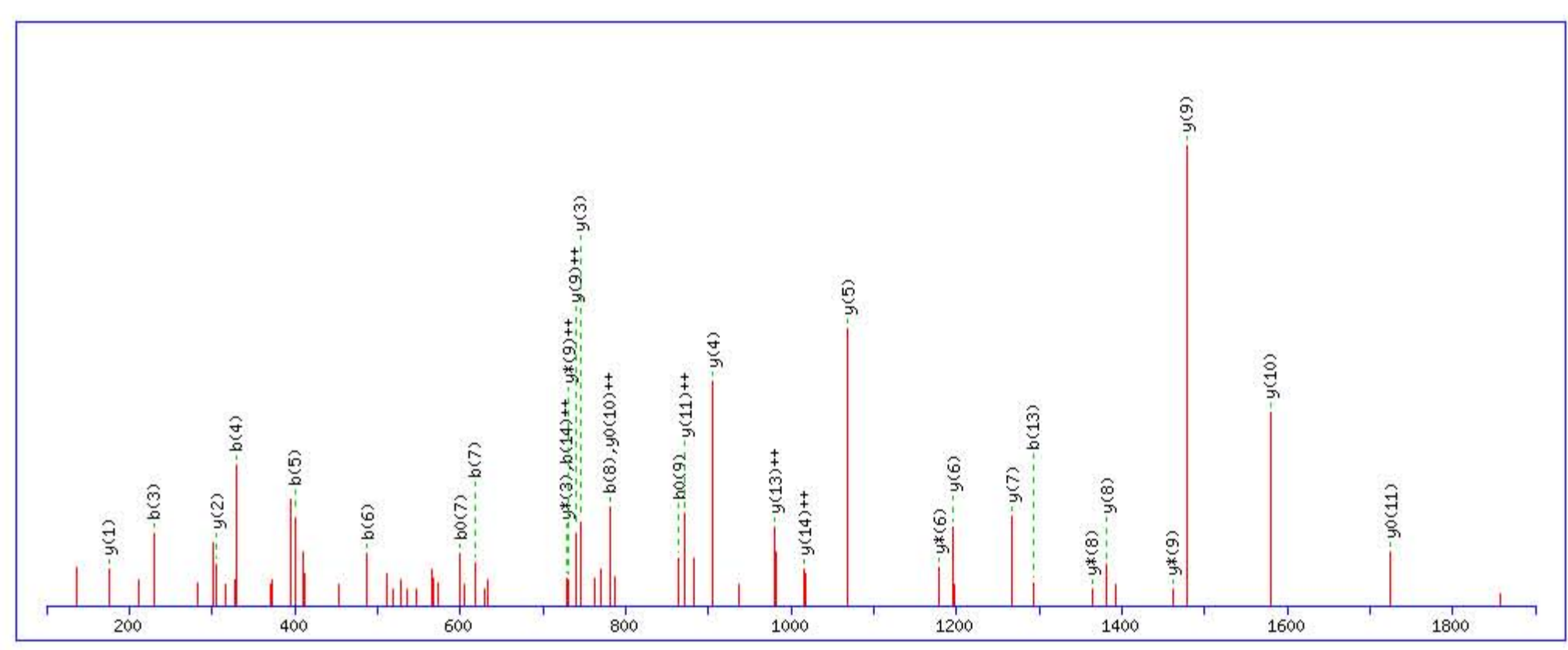
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GGDVASMYTPNAQYCQMR**
 Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

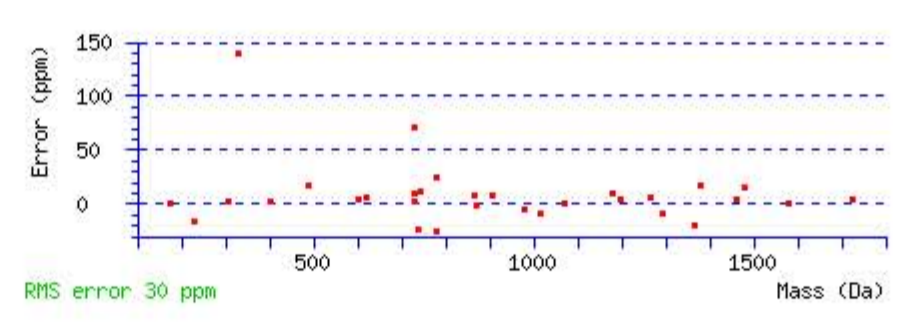
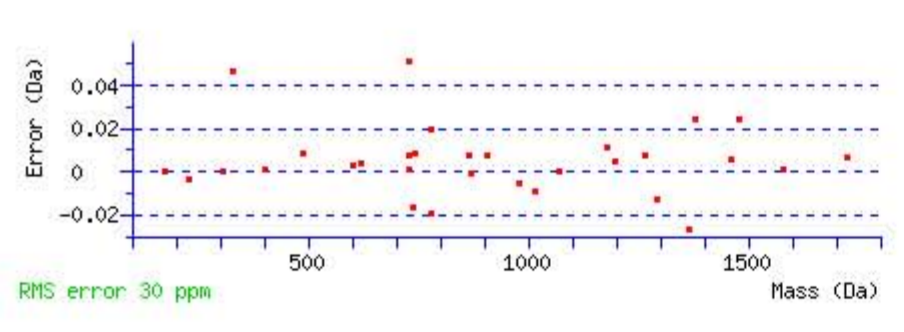
Match to Query 35770: 2359.026252 from(787.349360,3+) rtinseconds(2059) index(36777)
 Title: Locus:1.1.1.3136.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2359.021759
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q16 : Biotin:Thermo-21345 (Q)
 Ions Score: 82 Expect: 1e-007
 Matches : 31/162 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	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
81.6	2359.021759	0.004493	GGDVASMYTPNAQYCQMR
46.8	2359.021759	0.004493	GGDVASMYTPNAQYCQMR

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 39649: 1663.748856 from(416.944490,4+) rtinseconds(1122) index(63679)

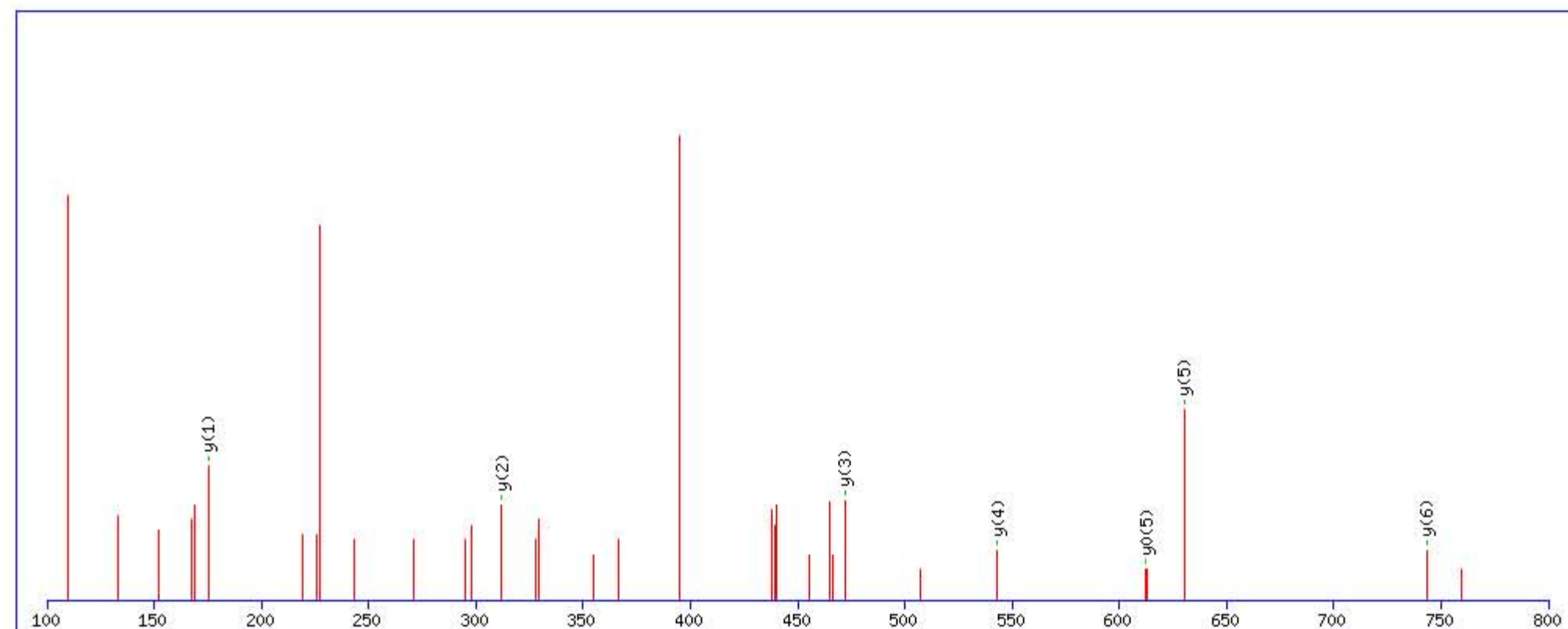
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Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1663.749374

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

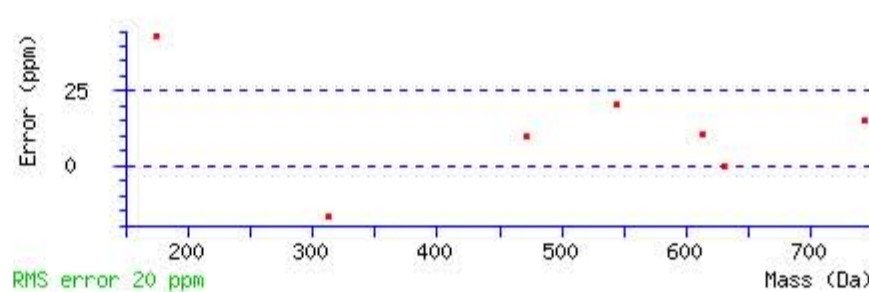
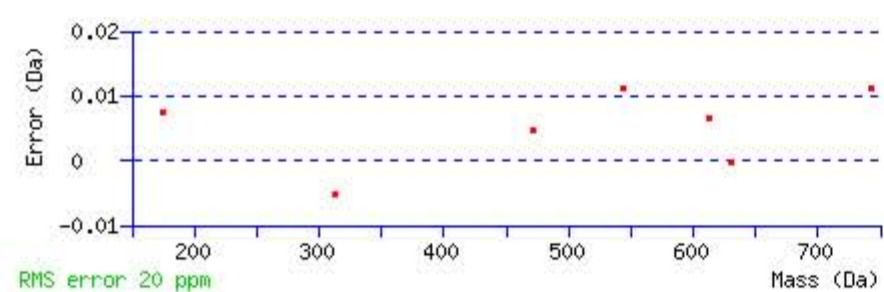
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 32 Expect: 0.004

Matches : 7/100 fragment ions using 13 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b*	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.065854	65.036565	112.039305	56.523291			Q							11
2	289.096503	145.051890	272.069954	136.538615			C	1536.698070	768.852673	1519.671521	760.339399	1518.687505	759.847391	10
3	346.117967	173.562622	329.091418	165.049347			G	1376.667421	688.837348	1359.640872	680.324074	1358.656856	679.832066	9
4	483.176879	242.092078	466.150330	233.578803			H	1319.645957	660.326617	1302.619408	651.813342	1301.635392	651.321334	8
5	922.402205	461.704741	905.375656	453.191466			Q	1182.587045	591.797161	1165.560496	583.283886	1164.576480	582.791878	7
6	1035.486269	518.246773	1018.459720	509.733498			I	743.361719	372.184498	726.335170	363.671223	725.351154	363.179215	6
7	1122.518297	561.762787	1105.491748	553.249512	1104.507732	552.757504	S	630.277655	315.642466	613.251106	307.129191	612.267090	306.637183	5
8	1193.555411	597.281344	1176.528862	588.768069	1175.544846	588.276061	A	543.245627	272.126452	526.219078	263.613177			4
9	1353.586060	677.296668	1336.559511	668.783394	1335.575495	668.291386	C	472.208513	236.607894	455.181964	228.094620			3
10	1490.644972	745.826124	1473.618423	737.312850	1472.634407	736.820842	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
32.0	1663.749374	-0.000518	QCGHQISACHR
32.0	1663.749374	-0.000518	QCGHQISACHR
6.5	1663.755905	-0.007049	FASCVDASGGLKCHR

Mascot: <http://www.matrixscience.com/>

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 43838: 1853.939532 from(618.987120,3+) rtinseconds(2151) index(69667)

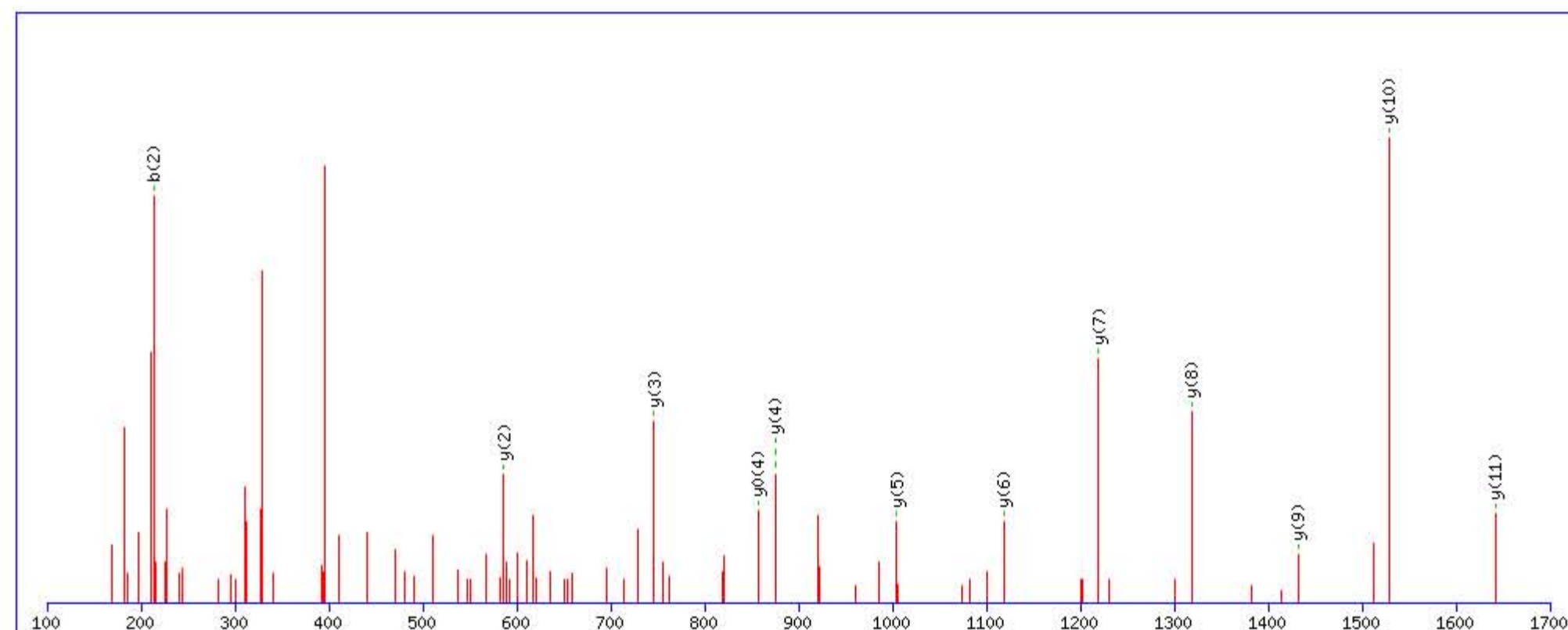
Title: Locus:1.1.1.1686.20 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1853.937927

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

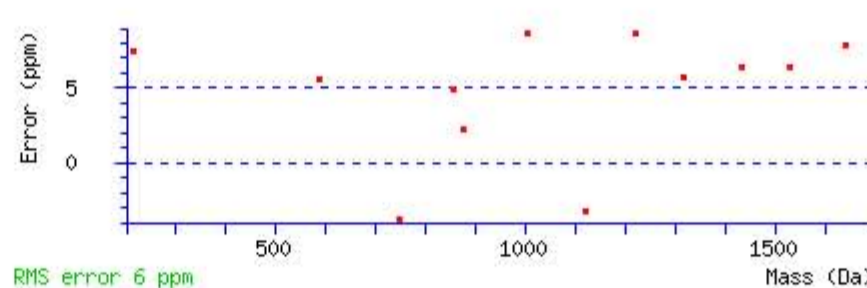
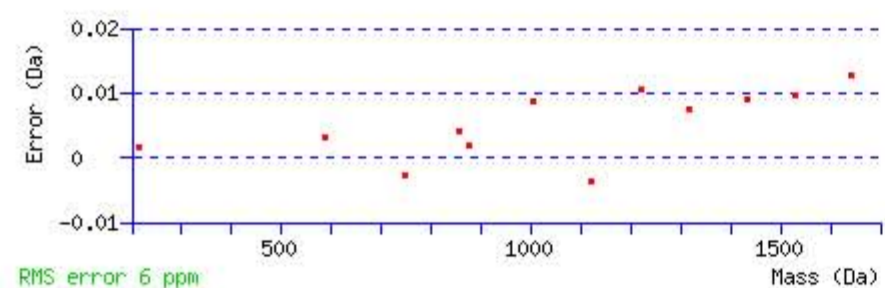
Variable modifications:

Q12 : Biotin:Thermo-21345 (Q)

Ions Score: 84 Expect: 3.8e-008

Matches : 12/124 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							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
84.0	1853.937927	0.001605	VNIPLVTNEECQK
4.9	1853.934341	0.005191	RGLSNPNELQAIDSNR

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 46028: 1974.911616 from(494.735180,4+) rtinseconds(1459) index(65560)

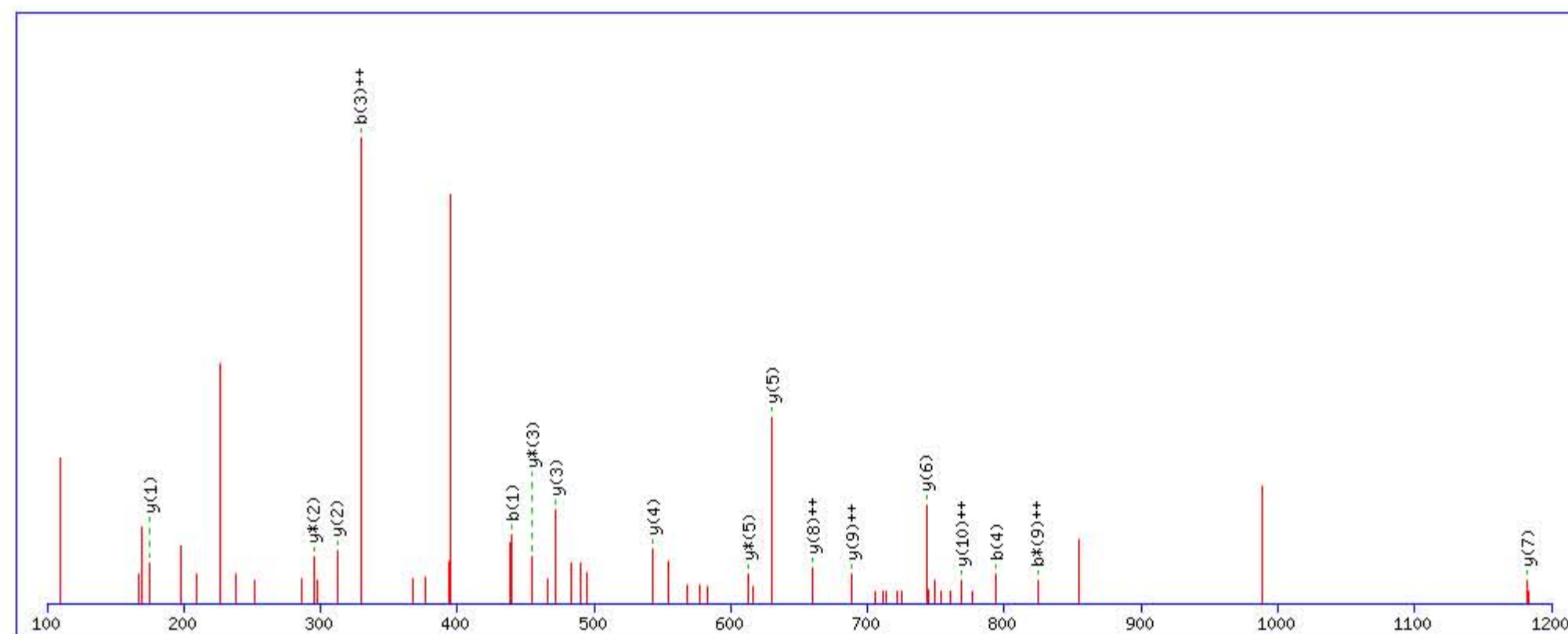
Title: Locus:1.1.1.1445.18 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1974.916122

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

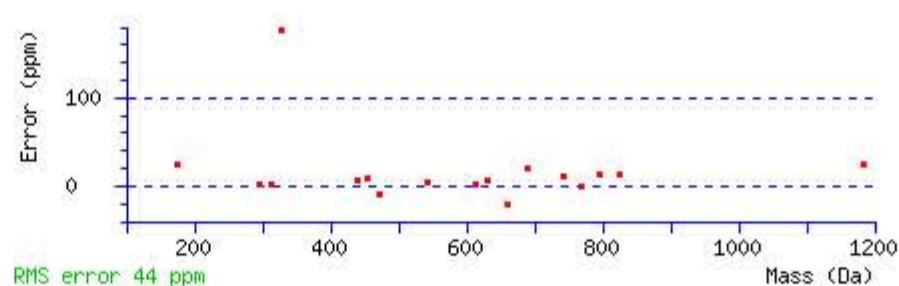
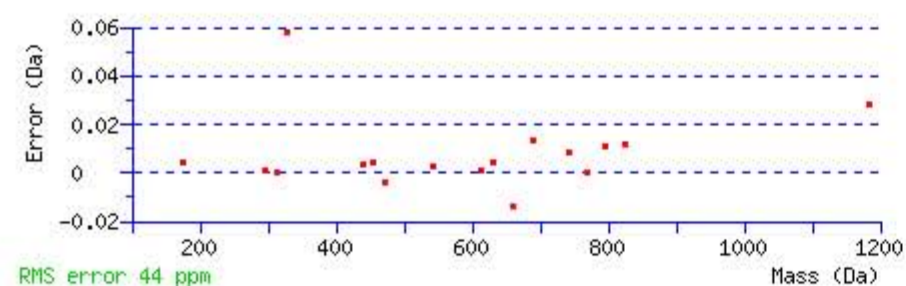
Q1 : Biotin:Thermo-21345 (Q)

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 34 Expect: 0.0054

Matches : 17/100 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	$M_r(\text{calc})$:	Delta	Sequence
33.8	1974.916122	-0.004506	QCGHQISACHR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **DFTCVHQALK**

Found in **IC1_HUMAN**, Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2

Match to Query 34641: 1528.765408 from(765.389980,2+) rtinseconds(1829) index(51724)

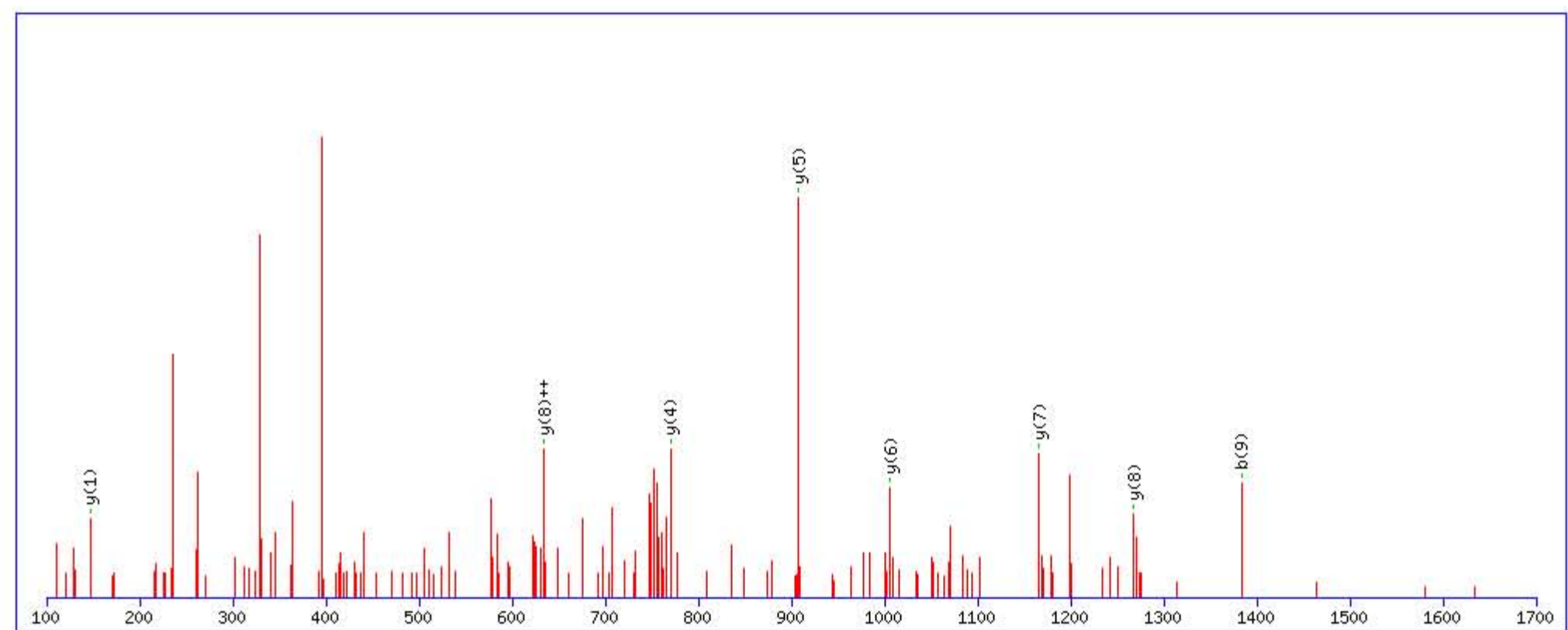
Title: Locus:1.1.1.1252.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1528.753052

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

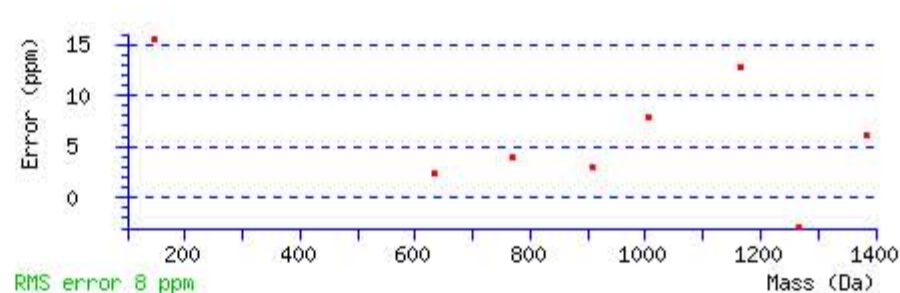
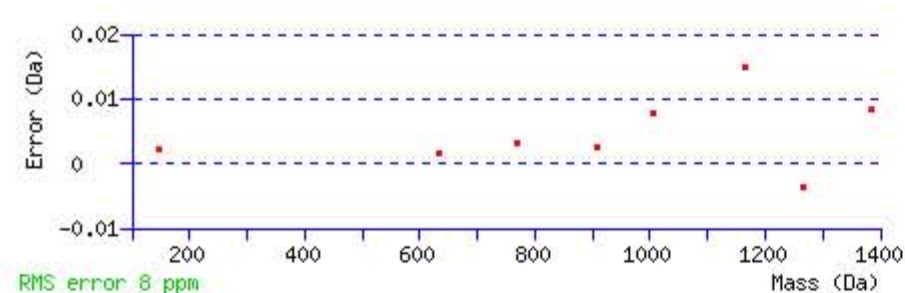
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.0028

Matches : 8/82 fragment ions using 14 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.034219	58.520748			98.023654	49.515465	D							10
2	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
33.4	1528.753052	0.012356	DFTCVHQALK
5.8	1528.755524	0.009884	MIQSDKGADPPDKK
4.9	1528.752121	0.013287	NRKEESYIFESK
3.3	1528.780685	-0.015277	EVLDQGTEISK
2.7	1528.744293	0.021115	KDYTSGAMLTGELK
0.9	1528.755524	0.009884	QQNEGDSIISK
0.4	1528.773254	-0.007846	ENLQLNQETEAIK
0.1	1528.782043	-0.016635	GPMGPKGGPGAPGAPGPK

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 44584: 1903.943502 from(635.655110,3+) rtinseconds(2437) index(39082)

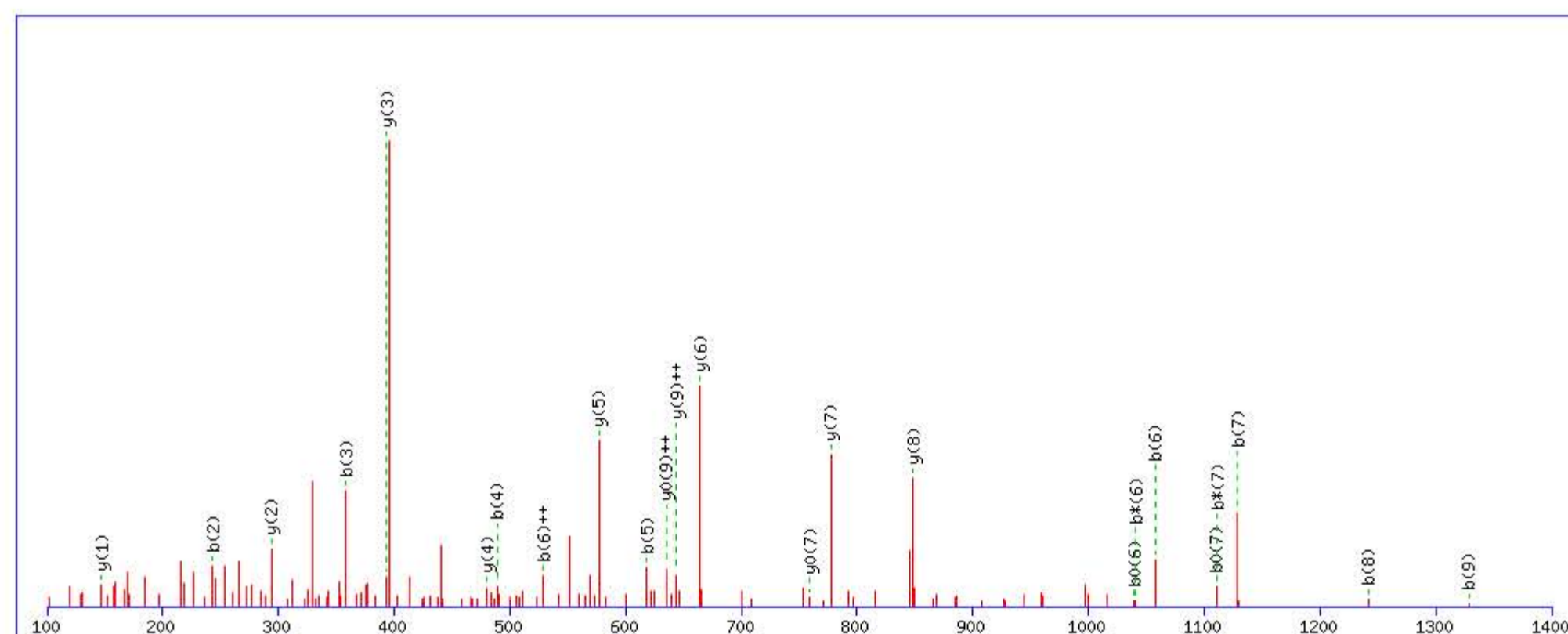
Title: Locus:1.1.1.3268.5 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1903.942337

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

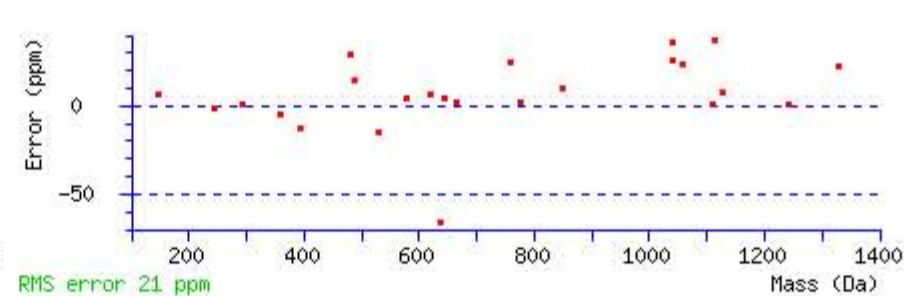
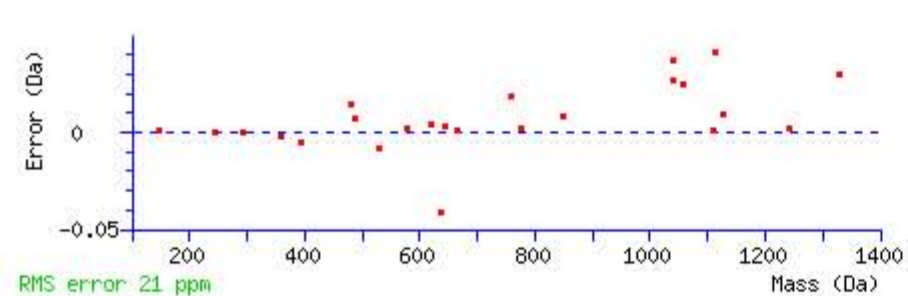
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 50 Expect: 0.00027

Matches : 24/138 fragment ions using 46 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					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
49.6	1903.942337	0.001165	LEDMEQALSPSVFK

Mascot: <http://www.matrixscience.com/>

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 49793: 2137.158028 from(1069.586290,2+) rtinseconds(2341) index(38460)

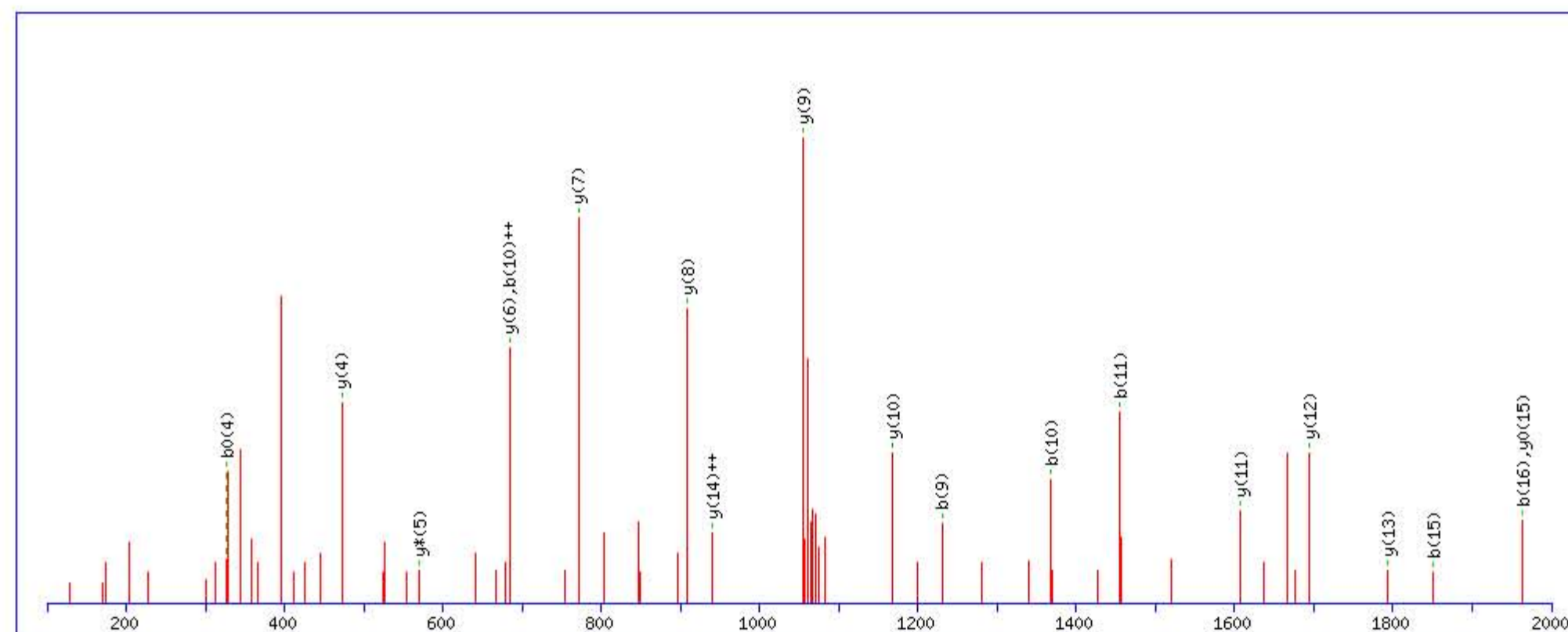
Title: Locus:1.1.1.3234.24 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2137.135406

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

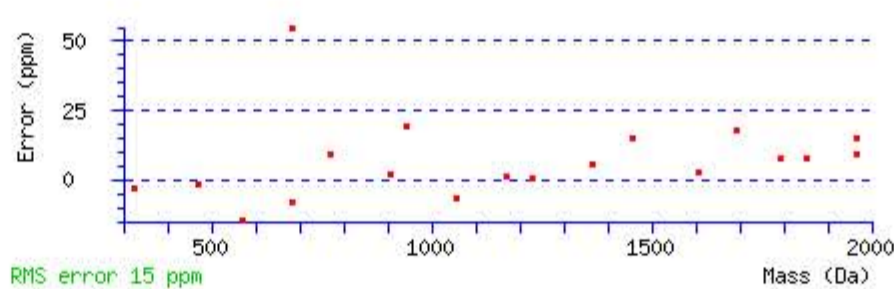
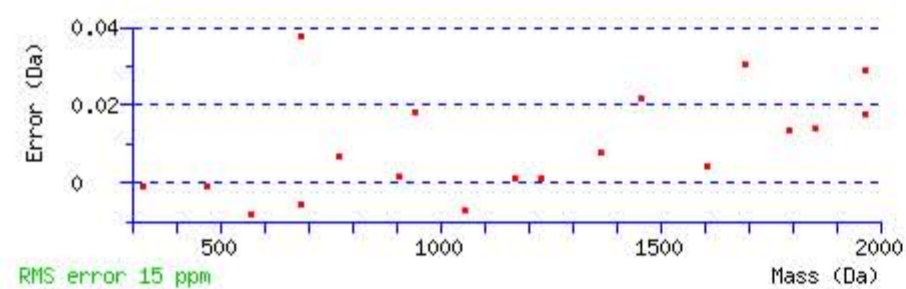
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 74 Expect: 1.4e-007

Matches : 19/168 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							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
74.4	2137.135406	0.022622	GVTSVSQIFHSPDLAIR
1.1	2137.185455	-0.027427	ISERTPSALAIENANVLAR
0.2	2137.178955	-0.020927	VAEAMRLAGPLARTVADLQR

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 32464: 1450.784868 from(726.399710,2+) rtinseconds(1964) index(5676)

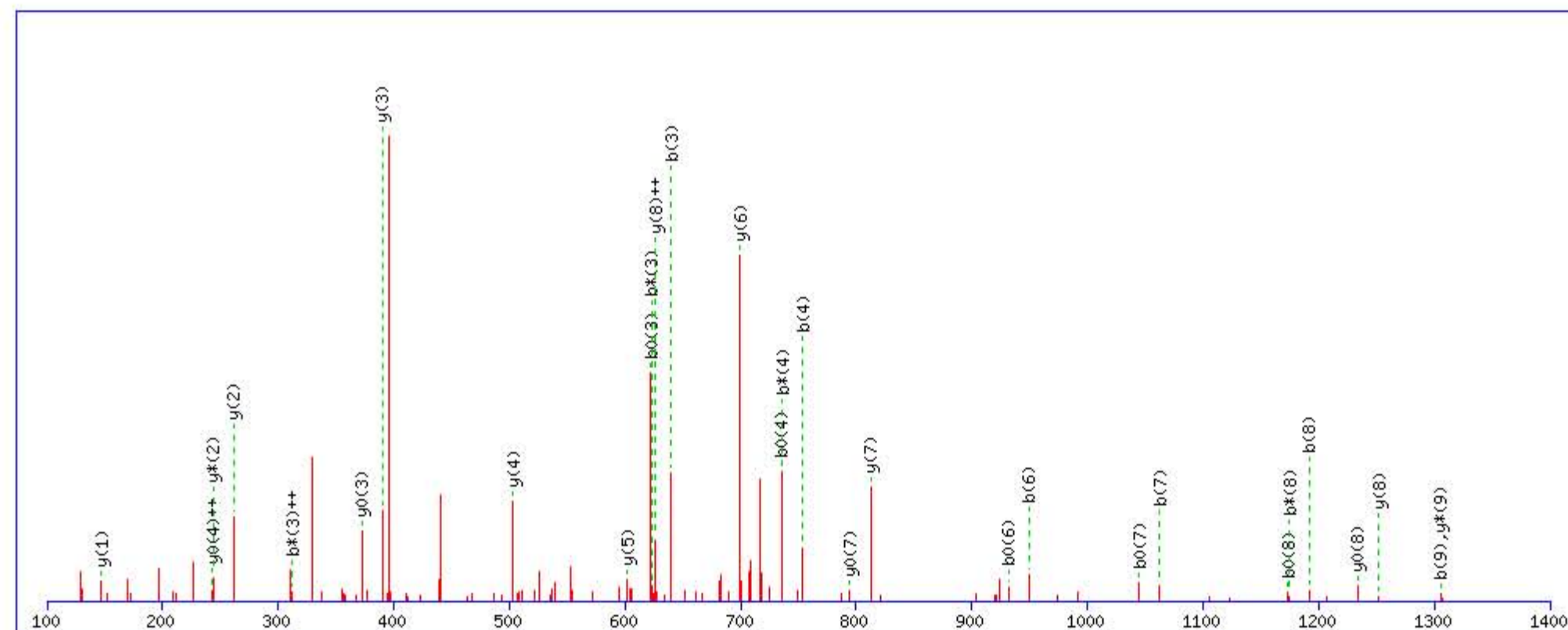
Title: Locus:1.1.1.1493.10 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1450.785355

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

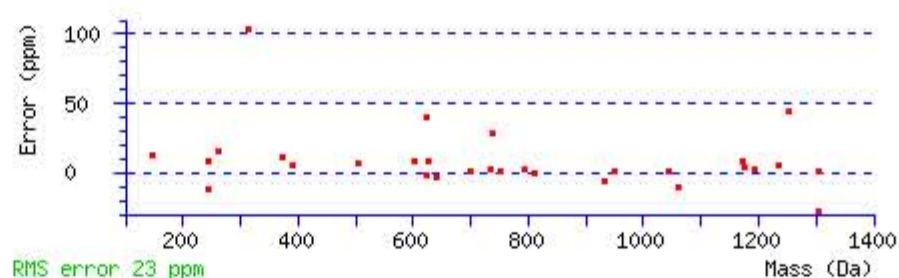
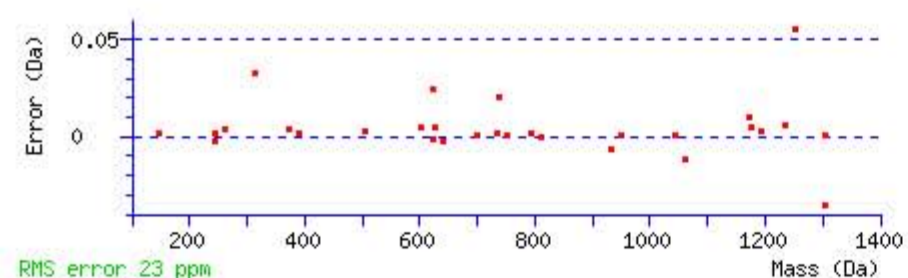
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 39 Expect: 0.00079

Matches : 30/100 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	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
38.6	1450.785355	-0.000487	EAQLPVIENK
5.3	1450.764236	0.020632	EIFHPEIQK
4.5	1450.790527	-0.005659	QNIWRHNRLSK
3.9	1450.764236	0.020632	AEPPTWAQLK
2.5	1450.796600	-0.011732	QISAVHKETK
0.9	1450.789429	-0.004561	VIAFGFMVPDVK
0.8	1450.775467	0.009401	QAPPTKWNK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **CQSWSSMTPHR**

Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 40196: 1686.740292 from(563.254040,3+) rtinseconds(1783) index(67397)

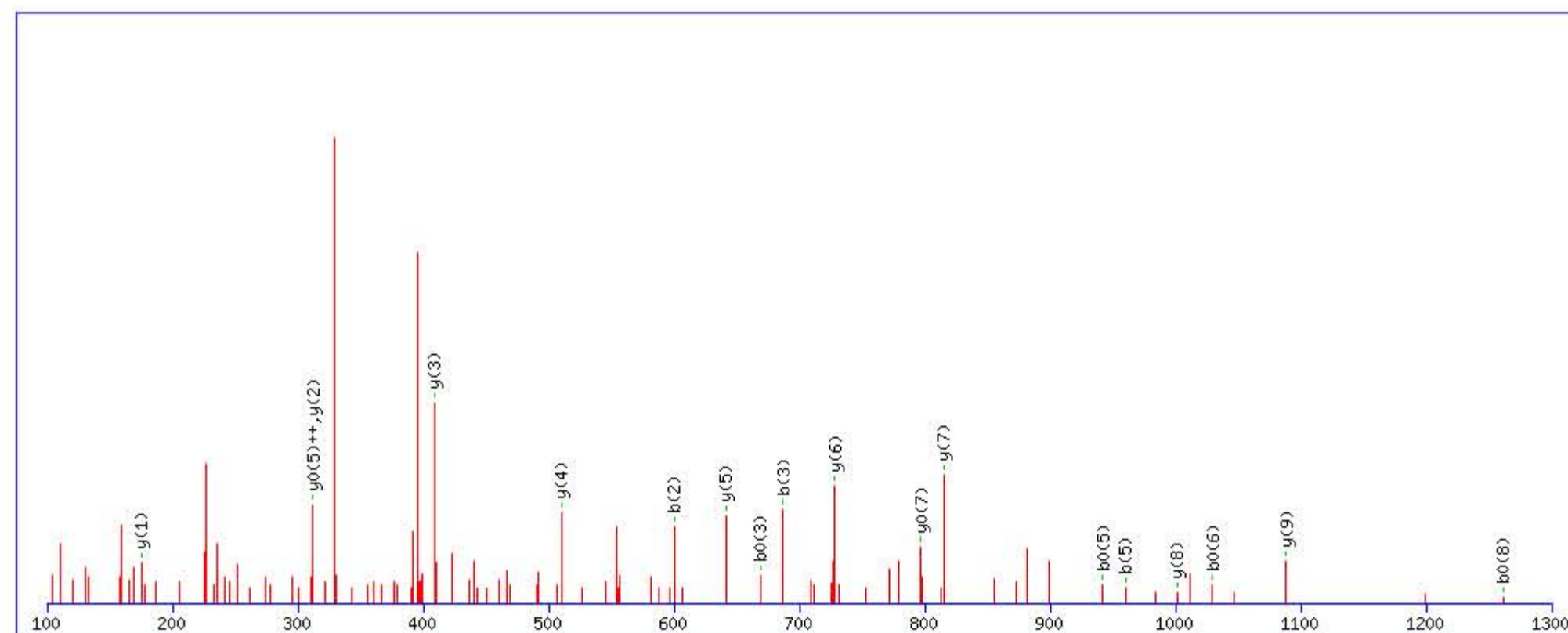
Title: Locus:1.1.1.1558.16 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1686.742889

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

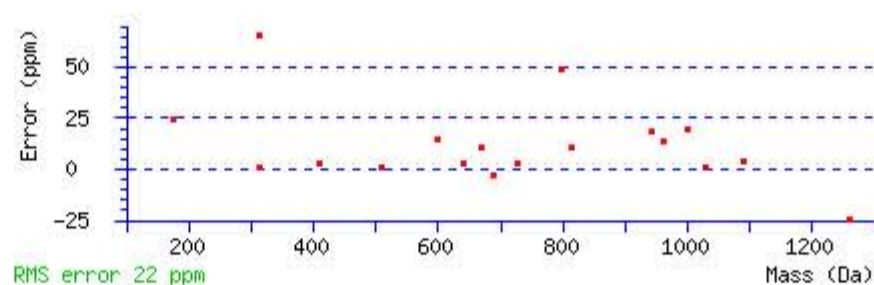
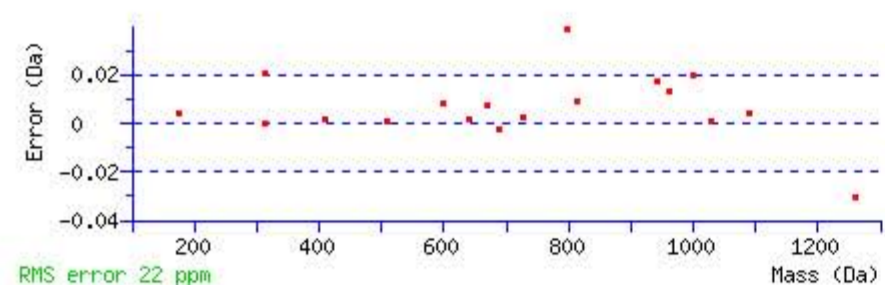
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 52 Expect: 4.1e-005

Matches : 18/108 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							11
2	600.263251	300.635264	583.236702	292.121989			Q	1527.719515	764.363396	1510.692966	755.850121	1509.708950	755.358113	10
3	687.295279	344.151278	670.268730	335.638003	669.284714	335.145995	S	1088.494189	544.750733	1071.467640	536.237458	1070.483624	535.745450	9
4	873.374592	437.190934	856.348043	428.677660	855.364027	428.185652	W	1001.462161	501.234719	984.435612	492.721444	983.451596	492.229436	8
5	960.406620	480.706948	943.380071	472.193674	942.396055	471.701666	S	815.382848	408.195062	798.356299	399.681787	797.372283	399.189779	7
6	1047.438648	524.222962	1030.412099	515.709688	1029.428083	515.217680	S	728.350820	364.679048	711.324271	356.165774	710.340255	355.673766	6
7	1178.479133	589.743205	1161.452584	581.229930	1160.468568	580.737922	M	641.318792	321.163034	624.292243	312.649760	623.308227	312.157752	5
8	1279.526812	640.267044	1262.500263	631.753770	1261.516247	631.261762	T	510.278307	255.642791	493.251758	247.129517	492.267742	246.637509	4
9	1376.579576	688.793426	1359.553027	680.280152	1358.569011	679.788144	P	409.230628	205.118952	392.204079	196.605677			3
10	1513.638488	757.322882	1496.611939	748.809608	1495.627923	748.317600	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 **CQSWSSMTPHR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
51.6	1686.742889	-0.002597	CQSWSSMTPHR
5.3	1686.759964	-0.019672	MAMAMSDSGASRLRR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **EQQCHEMAENR**

Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

Match to Query 40212: 1687.782908 from(844.898730,2+) rtinseconds(1812) index(67558)

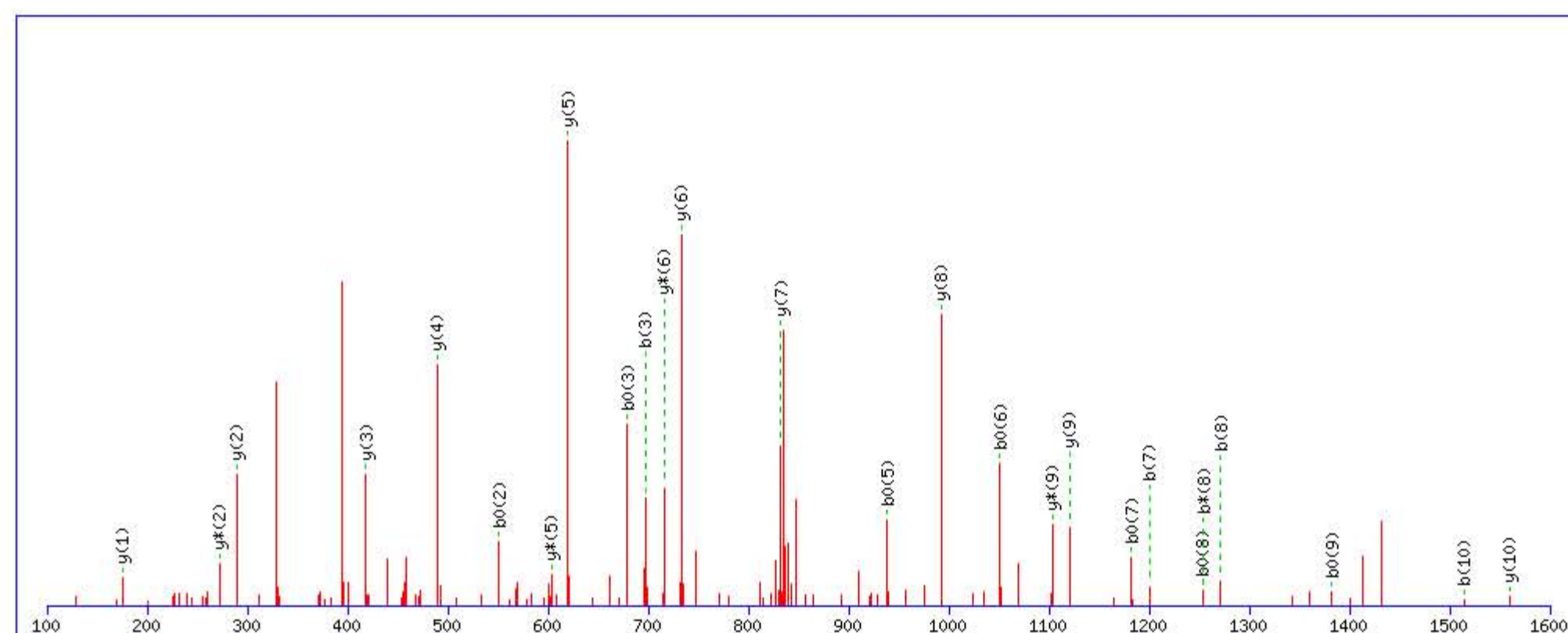
Title: Locus:1.1.1.1568.12 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1687.784393

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

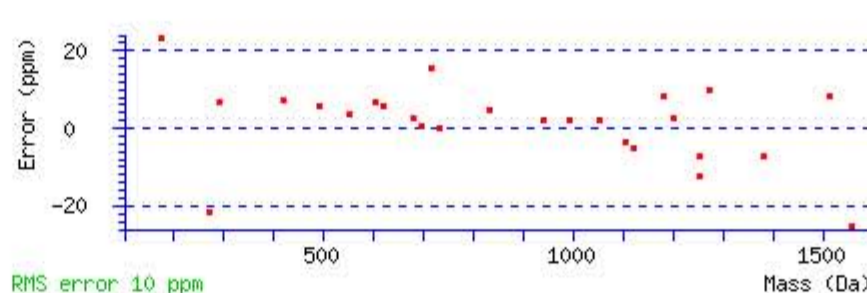
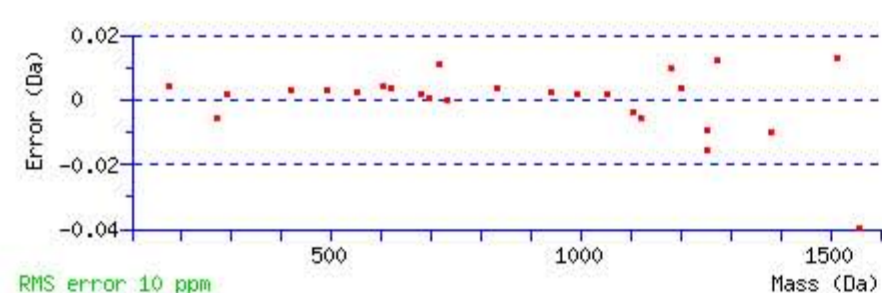
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 71 Expect: 1.1e-006

Matches : 26/114 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	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 [EQQCHEMAENR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.6	1687.784393	-0.001485	EQQCHEMAENR
68.7	1687.784393	-0.001485	EQQCHEMAENR
10.7	1687.781006	0.001902	ELMAWNQAENR
7.0	1687.758408	0.024500	ADGSCSTDFKTTRSR
4.1	1687.763275	0.019633	KMFQQTWMDNMGR
3.6	1687.773666	0.009242	TTGPPSGQMPDNPPHR
3.6	1687.776093	0.006815	QQEEAQAASAAASAESR
3.4	1687.791382	-0.008474	GAEDSLADQAANKWGR
2.2	1687.773193	0.009715	FGAVCTCMEKATGLK
2.2	1687.773636	0.009272	GSSLCSYYGRSAAGPR

MASCOT 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 42017: 1766.825622 from(589.949150,3+) rtinseconds(1498) index(18476)

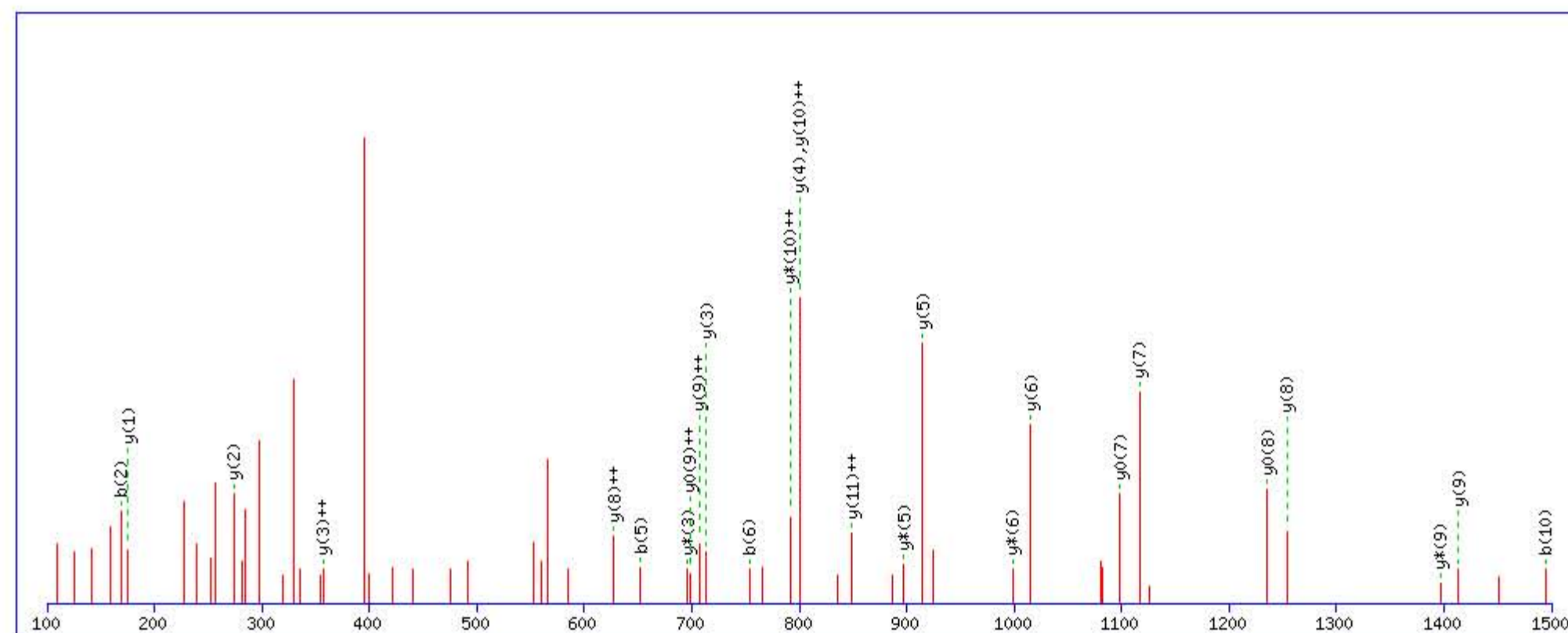
Title: Locus:1.1.1.524.8 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1766.834488

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

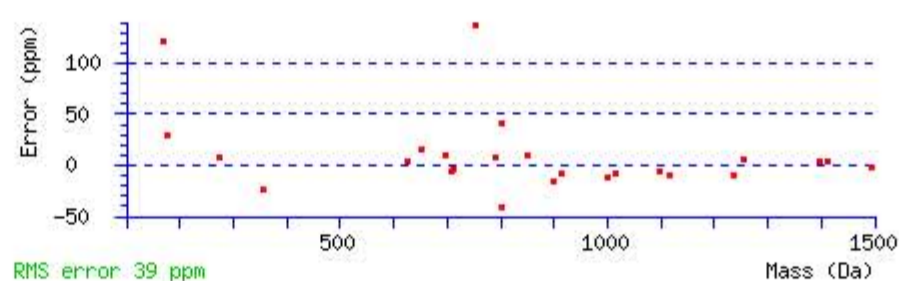
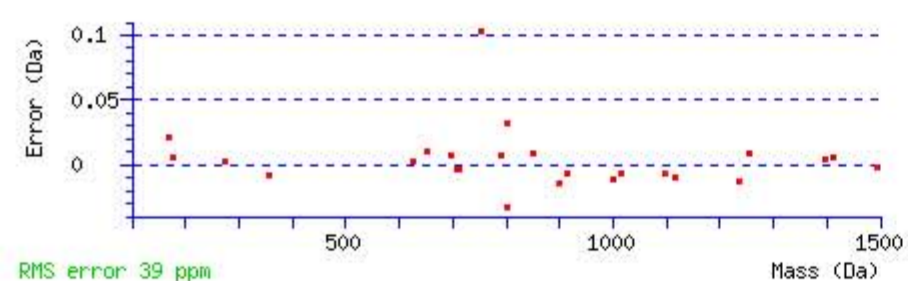
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 44 Expect: 0.00057

Matches : 26/102 fragment ions using 52 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.044390	36.525833					A							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
44.0	1766.834488	-0.008866	APWCHTTNSQVR

Mascot: <http://www.matrixscience.com/>

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **EQQCHEMAENR**

Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

Match to Query 46476: 1998.951822 from(667.324550,3+) rtinseconds(2127) index(69541)

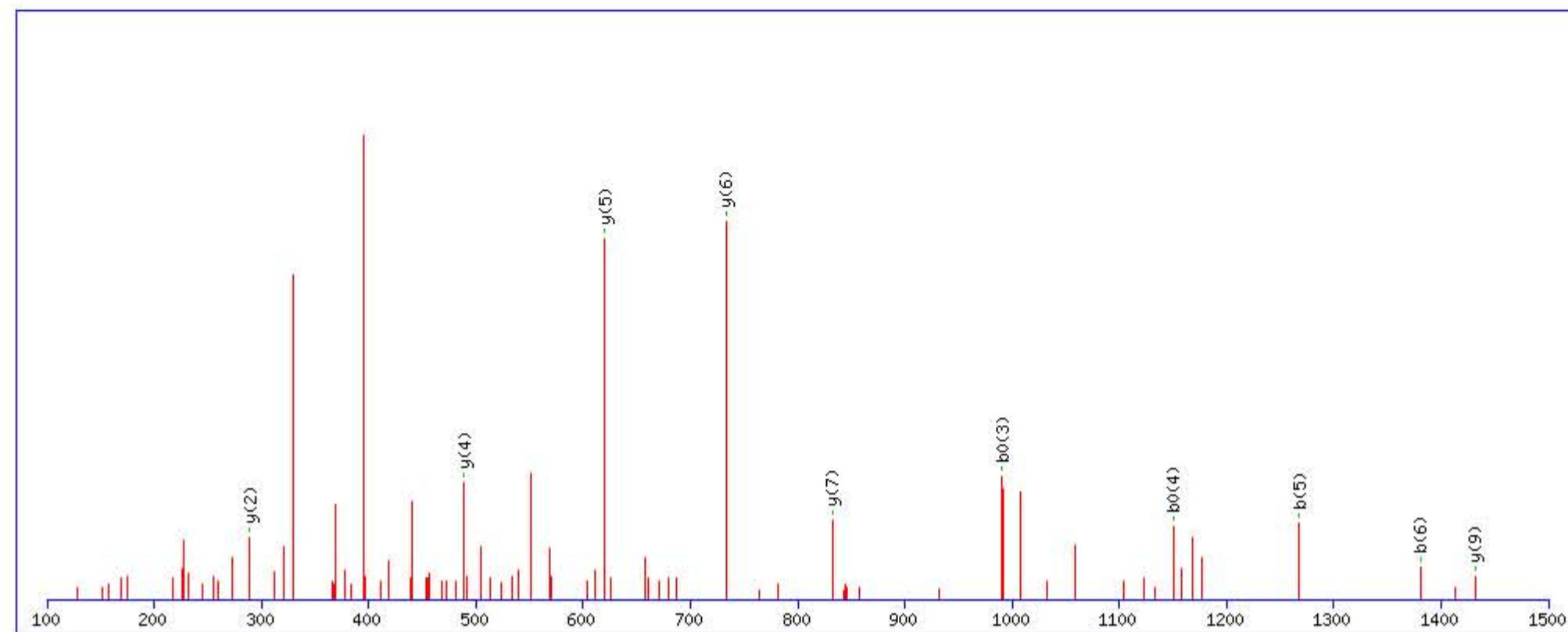
Title: Locus:1.1.1.1678.6 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1998.951141

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

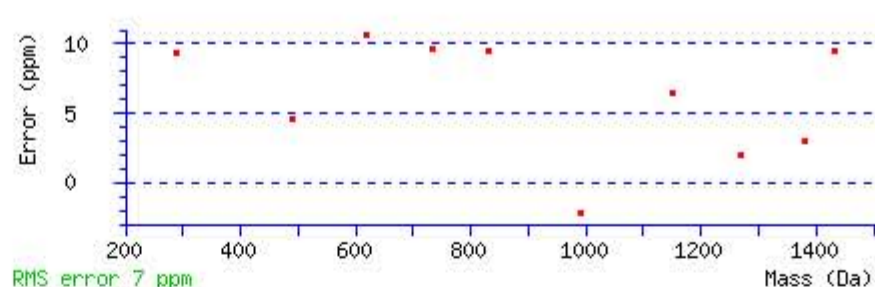
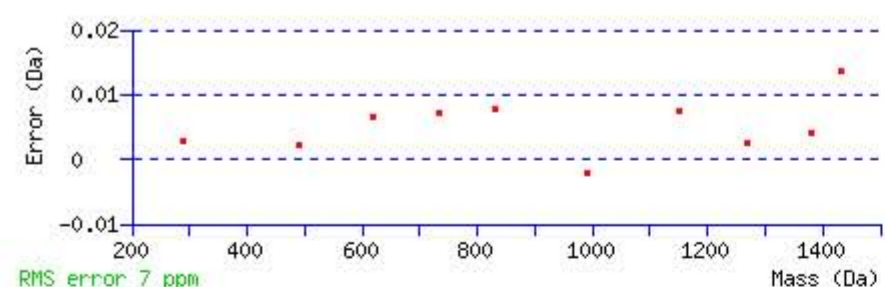
Q2 : Biotin:Thermo-21345 (Q)

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.00068

Matches : 10/114 fragment ions using 14 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	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 **EQQCHEMAENR**

(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	1998.951141	0.000681	EQQCHEMAENR
3.5	1998.979935	-0.028113	EYVLRPSYNGSFVTPDR
3.1	1998.942841	0.008981	QEEEAQAAAAAASAESR
3.1	1998.950912	0.000910	YEAQLRIFYQMYDK

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 49314: 2103.978162 from(702.333330,3+) rtinseconds(1757) index(67249)

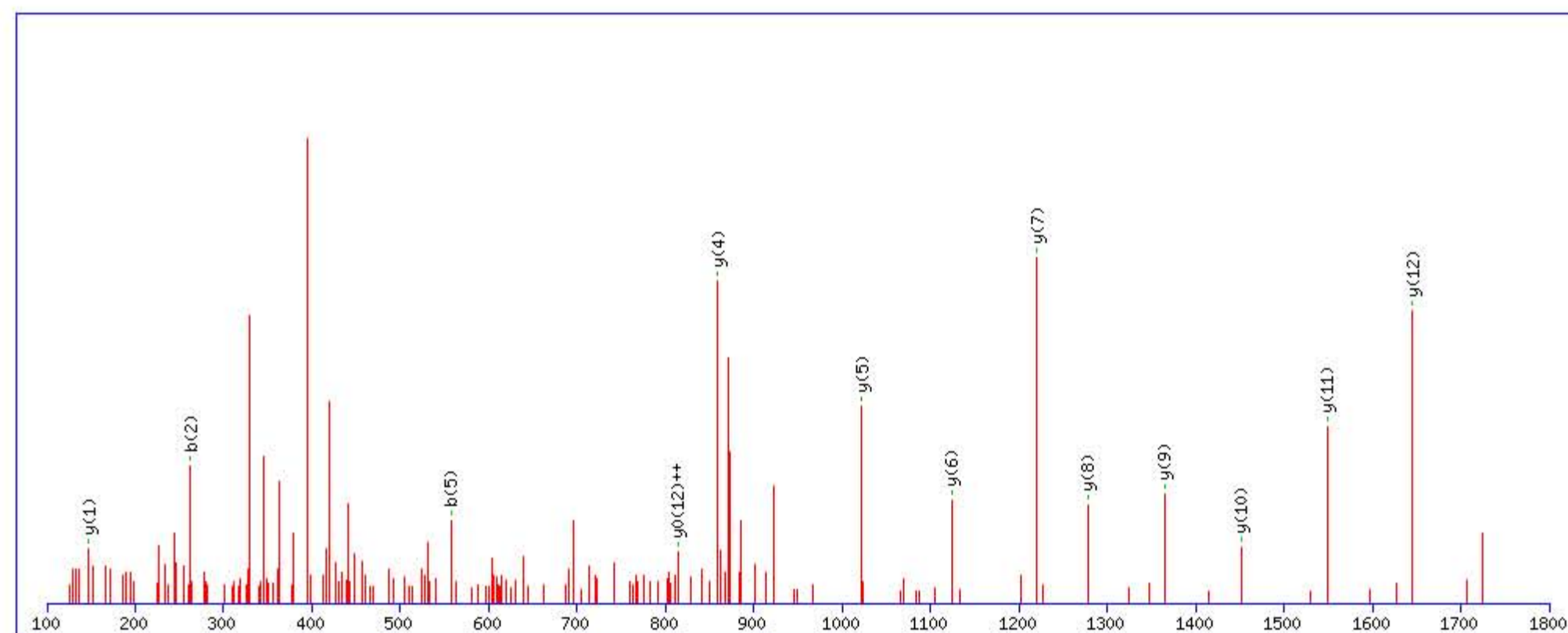
Title: Locus:1.1.1.1549.21 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2103.979172

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

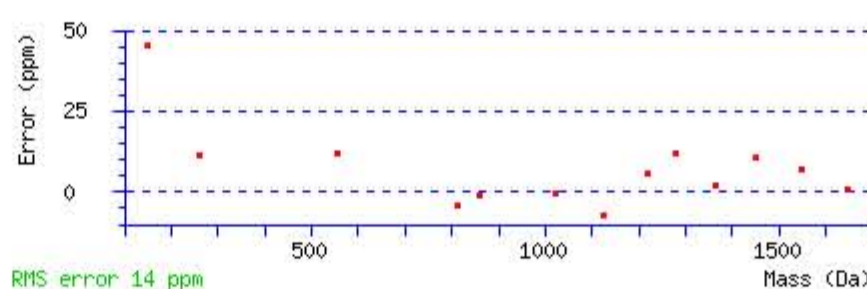
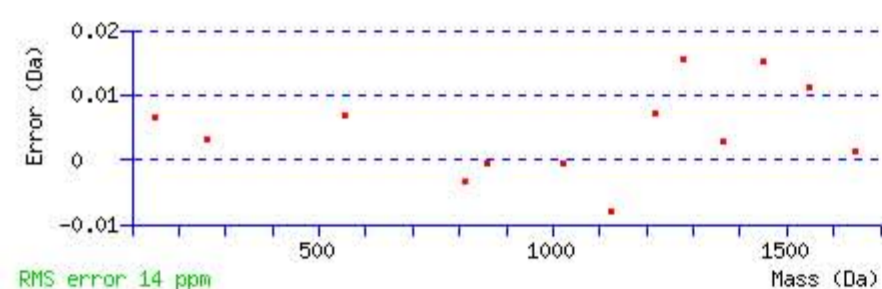
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 85 Expect: 5.1e-008

Matches : 13/144 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							16
2	262.085604	131.546440			244.075039	122.541158	T	1944.955785	972.981531	1927.929236	964.468256	1926.945220	963.976248	15
3	363.133283	182.070280			345.122718	173.064997	T	1843.908106	922.457691	1826.881557	913.944417	1825.897541	913.452409	14
4	460.186047	230.596661			442.175482	221.591379	P	1742.860427	871.933852	1725.833878	863.420577	1724.849862	862.928569	13
5	557.238811	279.123044			539.228246	270.117761	P	1645.807663	823.407470	1628.781114	814.894195	1627.797098	814.402187	12
6	654.291575	327.649426			636.281010	318.644143	P	1548.754899	774.881088	1531.728350	766.367813	1530.744334	765.875805	11
7	741.323603	371.165440			723.313038	362.160157	S	1451.702135	726.354706	1434.675586	717.841431	1433.691570	717.349423	10
8	828.355631	414.681454			810.345066	405.676171	S	1364.670107	682.838692	1347.643558	674.325417	1346.659542	673.833409	9
9	885.377095	443.192186			867.366530	434.186903	G	1277.638079	639.322678	1260.611530	630.809403	1259.627514	630.317395	8
10	982.429859	491.718568			964.419294	482.713285	P	1220.616615	610.811946	1203.590066	602.298671	1202.606050	601.806663	7
11	1083.477538	542.242407			1065.466973	533.237125	T	1123.563851	562.285564	1106.537302	553.772289	1105.553286	553.280281	6
12	1246.540867	623.774072			1228.530302	614.768789	Y	1022.516172	511.761724	1005.489623	503.248450			5
13	1685.766193	843.386735	1668.739644	834.873460	1667.755628	834.381452	Q	859.452843	430.230060	842.426294	421.716785			4
14	1845.796842	923.402059	1828.770293	914.888785	1827.786277	914.396777	C	420.227517	210.617396	403.200968	202.104122			3
15	1958.880906	979.944091	1941.854357	971.430817	1940.870341	970.938809	L	260.196868	130.602072	243.170319	122.088797			2
16							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [CTTPPPSSGPTYQCLK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
84.9	2103.979172	-0.001010	CTTPPPSSGPTYQCLK
14.9	2103.964554	0.013608	TAADTPAIMNWDLFFTMK

MASCOT Search Results

Peptide View

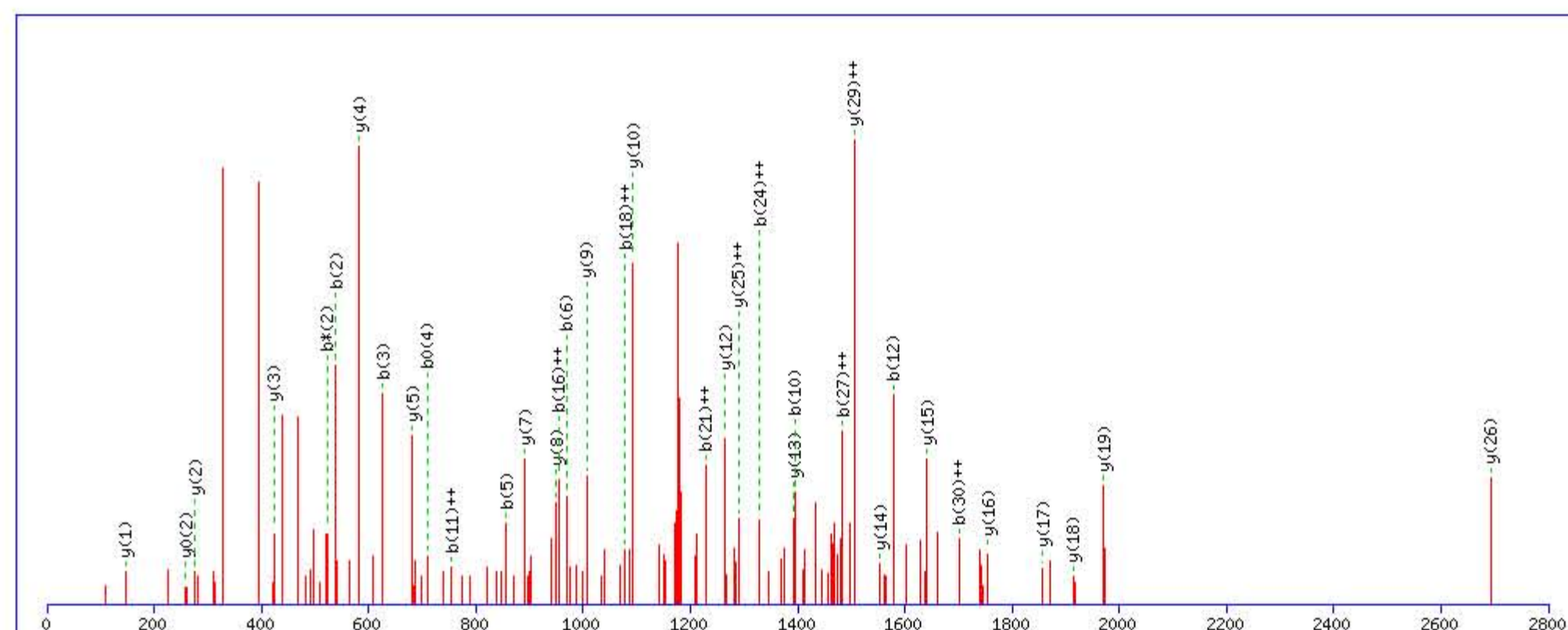
MS/MS Fragmentation of **VQSTELCAGHLAGGTDSCQGDSSGGPLVCFEK**
 Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 53919: 3547.565772 from(1183.529200,3+) rtinseconds(2154) index(69692)
 Title: Locus:1.1.1.1687.20 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

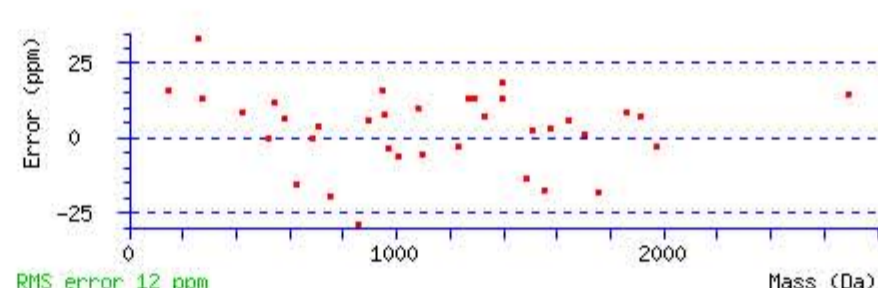
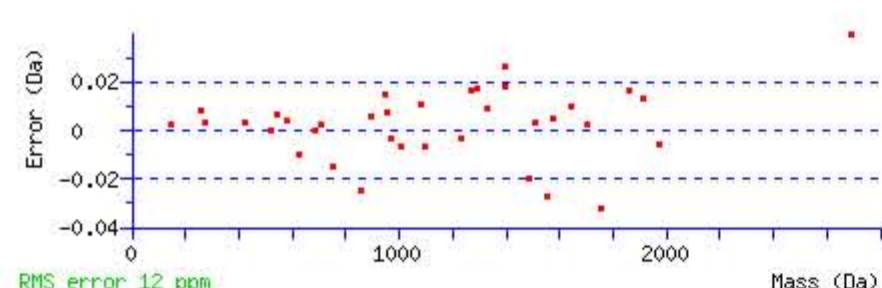
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3547.584061
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q2 : Biotin:Thermo-21345 (Q)
 Ions Score: 96 Expect: 3.8e-009
 Matches : 36/352 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	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 **VQSTELCAGHLAGGTDSCQGDSSGGPLVCFEK**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
95.7	3547.584061	-0.018289	VQSTELCAGHLAGGTDSCQGDSSGGPLVCFEK
11.9	3547.584061	-0.018289	VQSTELCAGHLAGGTDSCQGDSSGGPLVCFEK

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 55119: 2436.130242 from(813.050690,3+) rtinseconds(1869) index(67790)

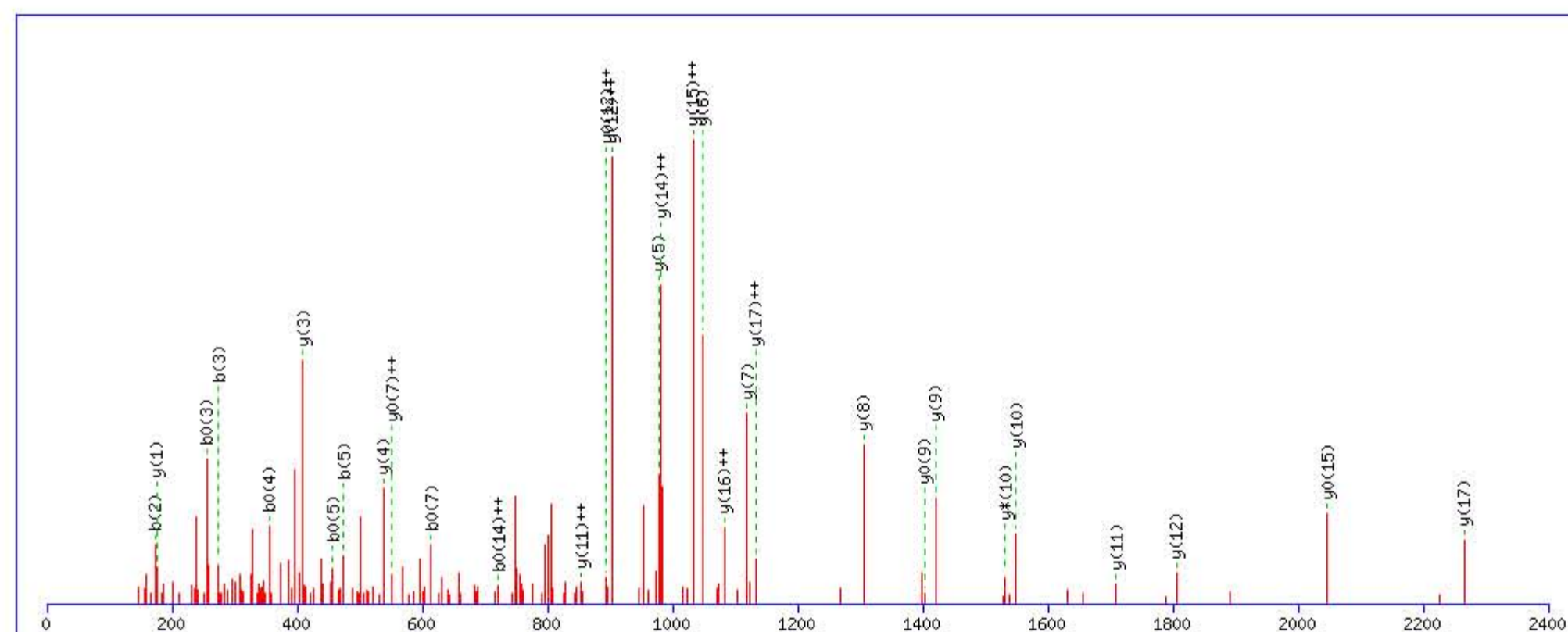
Title: Locus:1.1.1.1588.17 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2436.131470

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

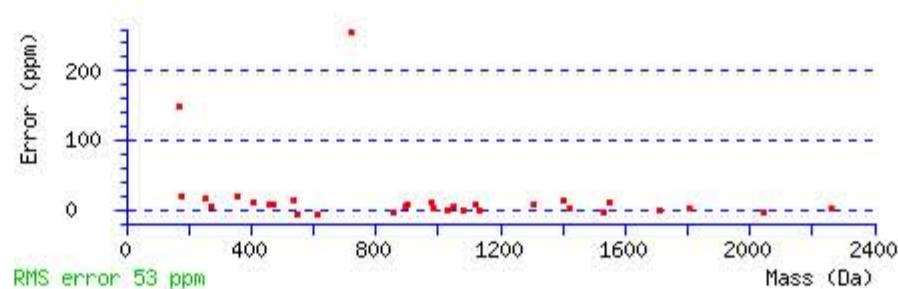
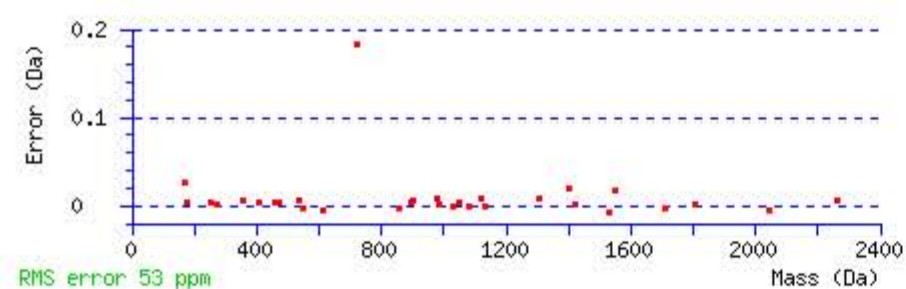
Variable modifications:

Q15 : Biotin:Thermo-21345 (Q)

Ions Score: 62 Expect: 8.9e-006

Matches : 31/190 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	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
62.1	2436.131470	-0.001228	ATTVTGTPCQDWAAQEPHR
24.3	2436.131470	-0.001228	ATTVTGTPCQDWAAQEPHR

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 56154: 2482.252602 from(828.424810,3+) rtinseconds(2211) index(70029)

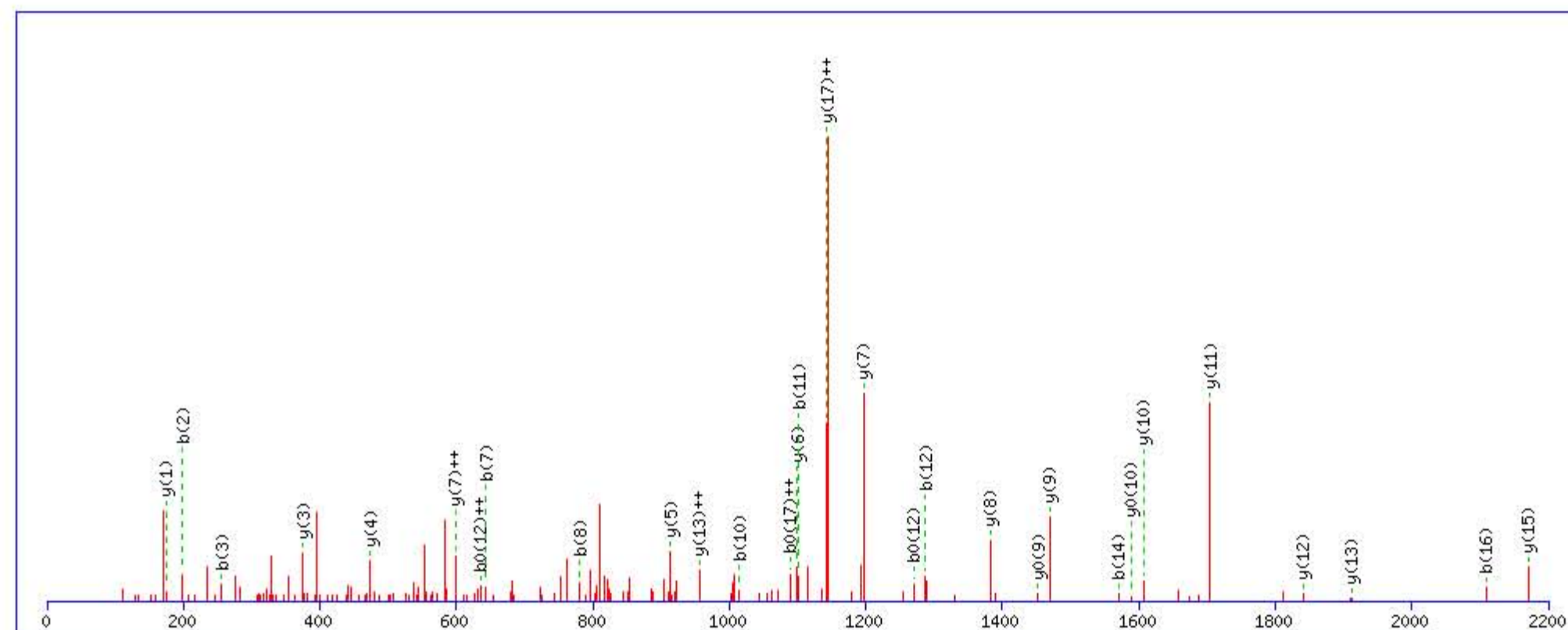
Title: Locus:1.1.1.1707.12 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2482.251480

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

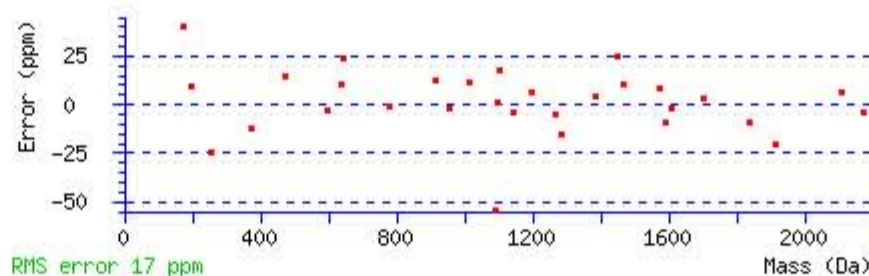
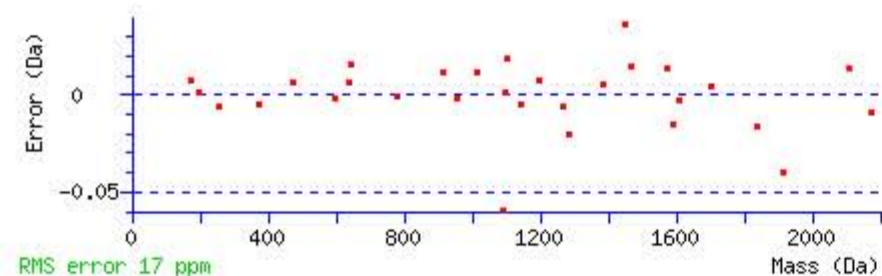
Variable modifications:

Q15 : Biotin:Thermo-21345 (Q)

Ions Score: 59 Expect: 4.3e-005

Matches : 30/164 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							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
58.8	2482.251480	0.001122	VVGGCVAHPHSWPWQVSLR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **NPDNDPQGPWCYTTDPEKR**

Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 57648: 2600.140332 from(867.720720,3+) rtinseconds(1971) index(68570)

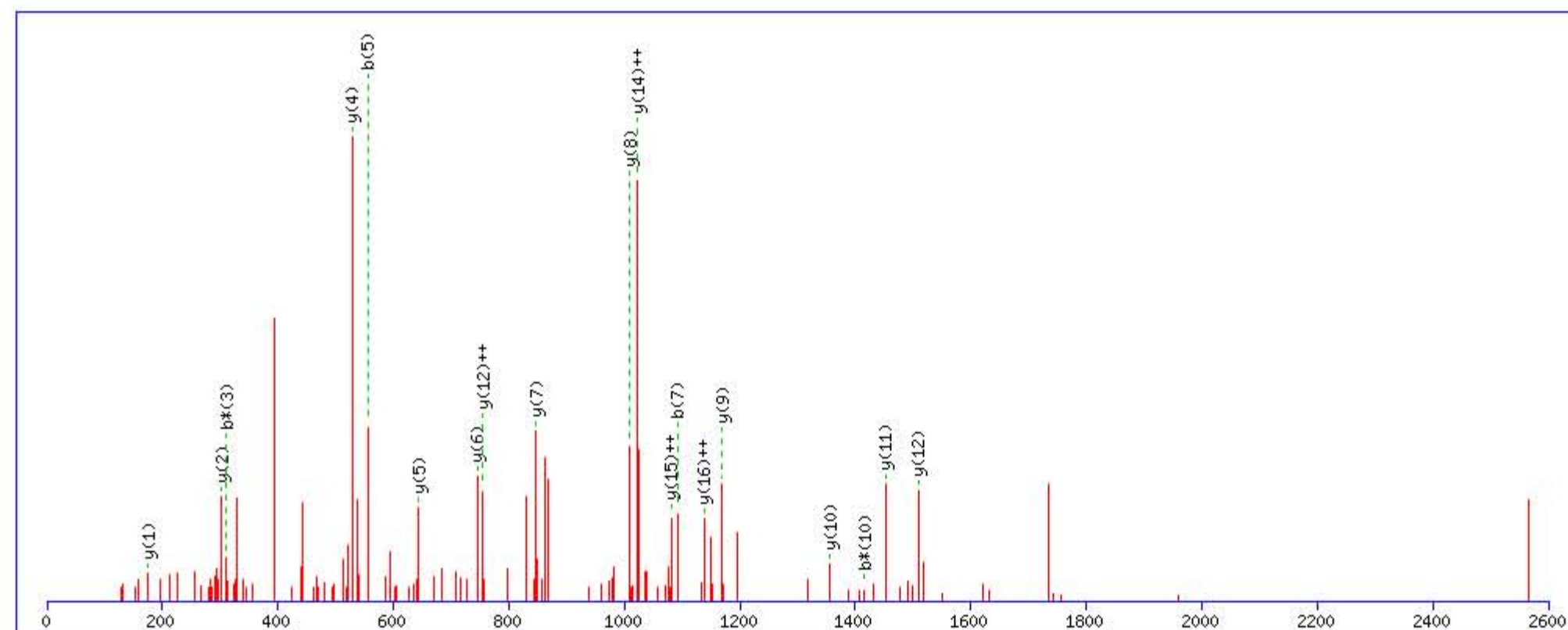
Title: Locus:1.1.1.1623.26 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2600.142410

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

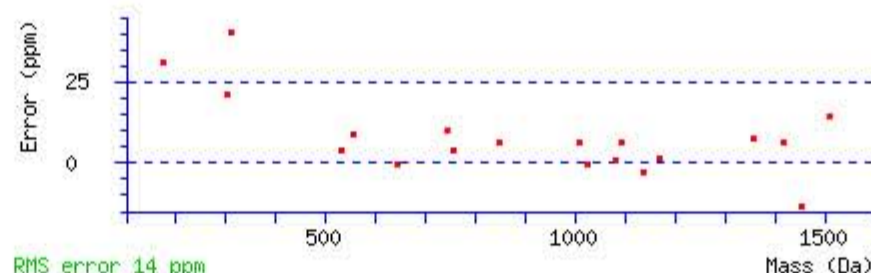
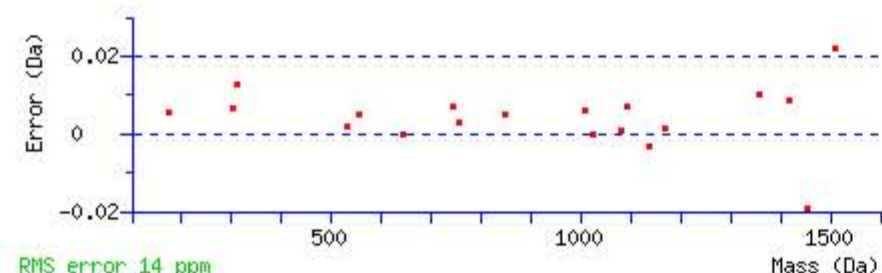
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 66 Expect: 1.6e-006

Matches : 19/208 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	115.050203	58.028740	98.023654	49.515465			N							19
2	212.102967	106.555121	195.076418	98.041847			P	2487.106759	1244.057017	2470.080210	1235.543743	2469.096194	1235.051735	18
3	327.129910	164.068593	310.103361	155.555319	309.119345	155.063311	D	2390.053995	1195.530635	2373.027446	1187.017361	2372.043430	1186.525353	17
4	441.172837	221.090057	424.146288	212.576782	423.162272	212.084774	N	2275.027052	1138.017164	2258.000503	1129.503889	2257.016487	1129.011881	16
5	556.199780	278.603528	539.173231	270.090254	538.189215	269.598246	D	2160.984125	1080.995700	2143.957576	1072.482426	2142.973560	1071.990418	15
6	653.252544	327.129910	636.225995	318.616636	635.241979	318.124628	P	2045.957182	1023.482229	2028.930633	1014.968955	2027.946617	1014.476946	14
7	1092.477870	546.742573	1075.451321	538.229299	1074.467305	537.737290	Q	1948.904418	974.955847	1931.877869	966.442572	1930.893853	965.950564	13
8	1149.499334	575.253305	1132.472785	566.740030	1131.488769	566.248022	G	1509.679092	755.343184	1492.652543	746.829910	1491.668527	746.337902	12
9	1246.552098	623.779687	1229.525549	615.266413	1228.541533	614.774404	P	1452.657628	726.832452	1435.631079	718.319178	1434.647063	717.827170	11
10	1432.631411	716.819343	1415.604862	708.306069	1414.620846	707.814061	W	1355.604864	678.306070	1338.578315	669.792796	1337.594299	669.300788	10
11	1592.662060	796.834668	1575.635511	788.321394	1574.651495	787.829385	C	1169.525551	585.266414	1152.499002	576.753139	1151.514986	576.261131	9
12	1755.725389	878.366333	1738.698840	869.853058	1737.714824	869.361050	Y	1009.494902	505.251089	992.468353	496.737815	991.484337	496.245807	8
13	1856.773068	928.890172	1839.746519	920.376898	1838.762503	919.884889	T	846.431573	423.719425	829.405024	415.206150	828.421008	414.714142	7
14	1957.820747	979.414012	1940.794198	970.900737	1939.810182	970.408729	T	745.383894	373.195585	728.357345	364.682311	727.373329	364.190303	6
15	2072.847690	1036.927483	2055.821141	1028.414208	2054.837125	1027.922200	D	644.336215	322.671746	627.309666	314.158471	626.325650	313.666463	5
16	2169.900454	1085.453865	2152.873905	1076.940590	2151.889889	1076.448582	P	529.309272	265.158274	512.282723	256.645000	511.298707	256.152992	4
17	2298.943047	1149.975161	2281.916498	1141.461887	2280.932482	1140.969879	E	432.256508	216.631892	415.229959	208.118618	414.245943	207.626610	3
18	2427.038010	1214.022643	2410.011461	1205.509368	2409.027445	1205.017360	K	303.213915	152.110595	286.187366	143.597321			2
19							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [NPDNDPQGPWCYTTDPEKR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.5	2600.142410	-0.002078	NPDNDPQGPWCYTTDPEKR

Mascot: <http://www.matrixscience.com/>

Peptide View

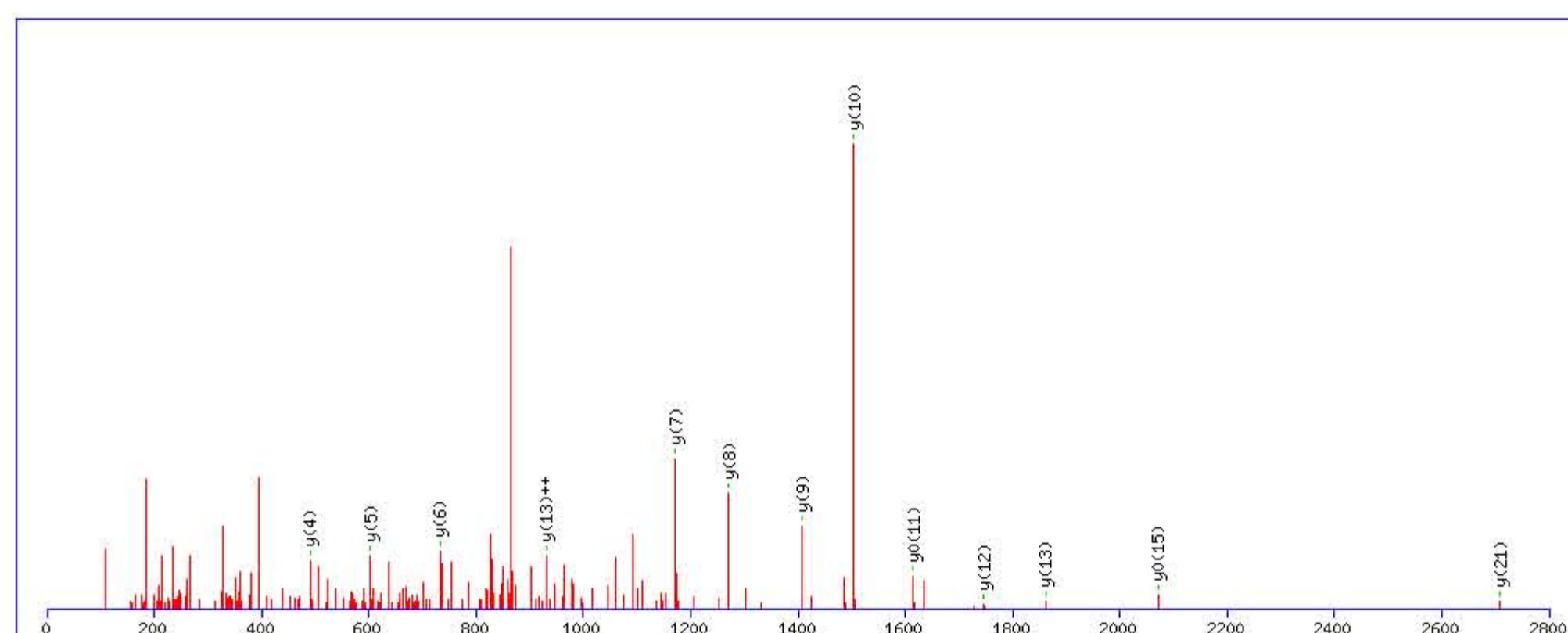
MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
 Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 59495: 2806.475496 from(702.626150,4+) rtinseconds(2056) index(69147)
 Title: Locus:1.1.1.1653.11 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

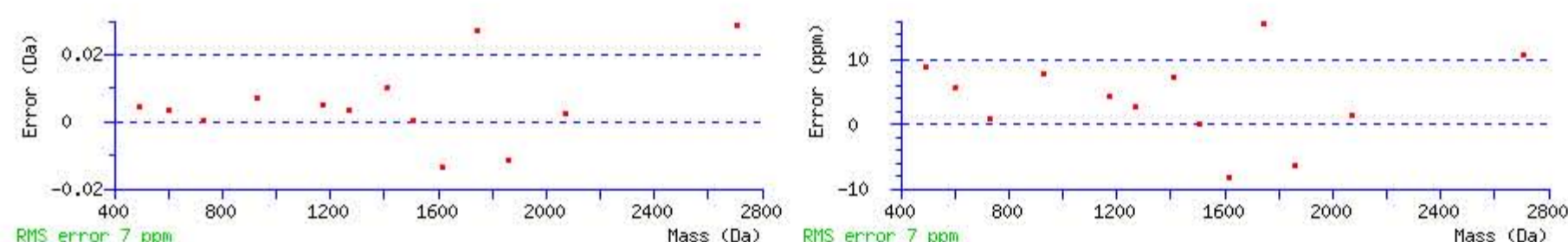
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2806.479965
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q16 : Biotin:Thermo-21345 (Q)
 Ions Score: 63 Expect: 1.3e-005
 Matches : 13/224 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	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
62.6	2806.479965	-0.004469	VILGAHQEVNLEPHVQEIEVSR

Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIIEVSR**

Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 59497: 2806.477212 from(936.499680,3+) rtinseconds(2097) index(69351)

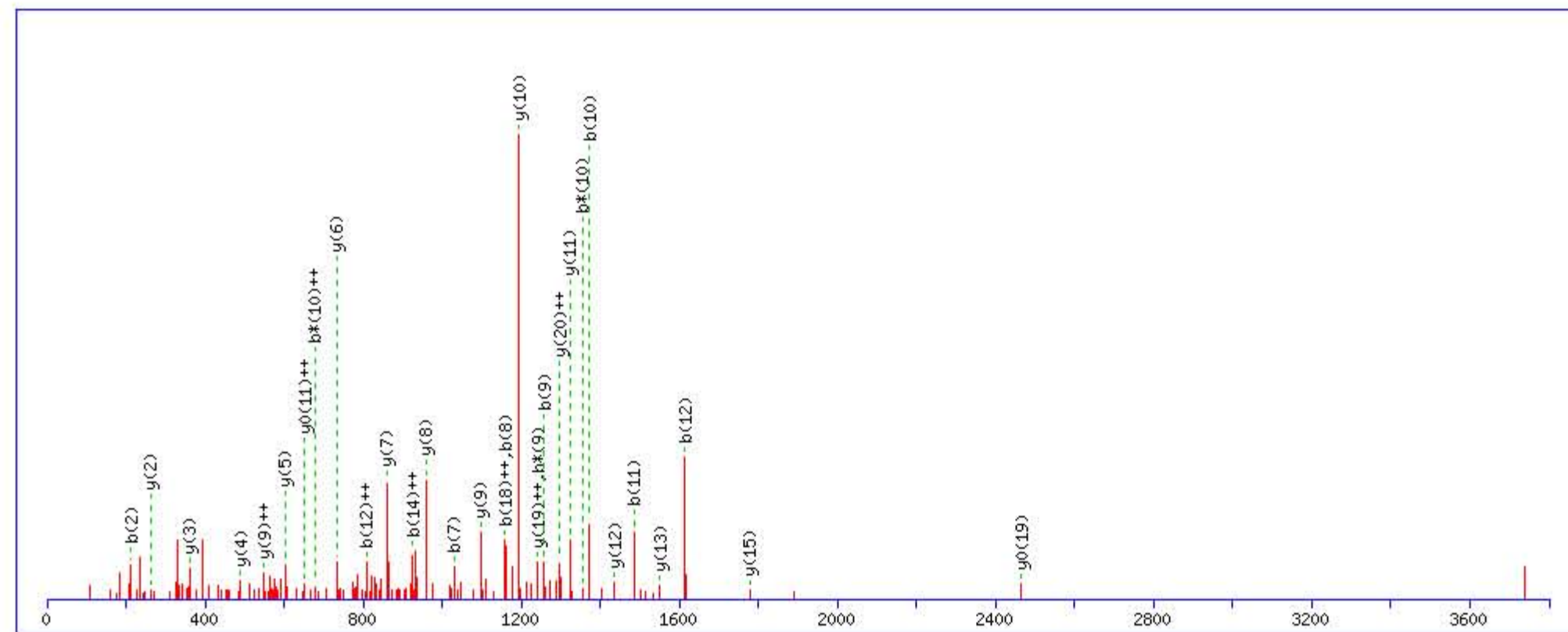
Title: Locus:1.1.1.1667.22 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2806.479965

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

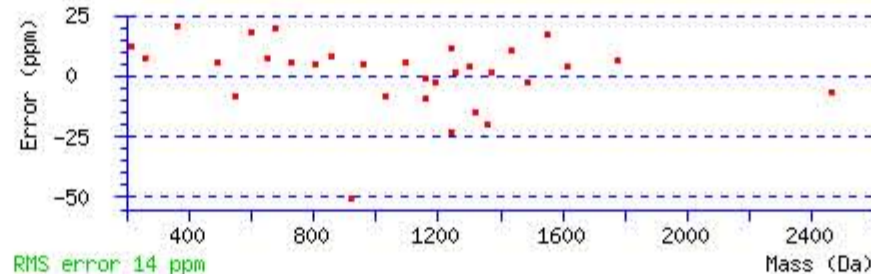
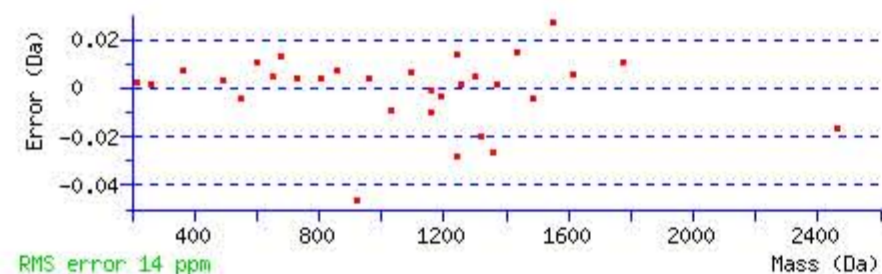
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 76 Expect: 6e-007

Matches : 31/224 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							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 [VILGAHQEVNLEPHVQEIIEVSR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.7	2806.479965	-0.002753	VILGAHQEVNLEPHVQEIIEVSR
6.3	2806.479965	-0.002753	VILGAHQEVNLEPHVQEIIEVSR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **TMSGLECAWDSQSPHAHGYPISK**

Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 61677: 2997.356896 from(750.346500,4+) rtinseconds(1996) index(68772)

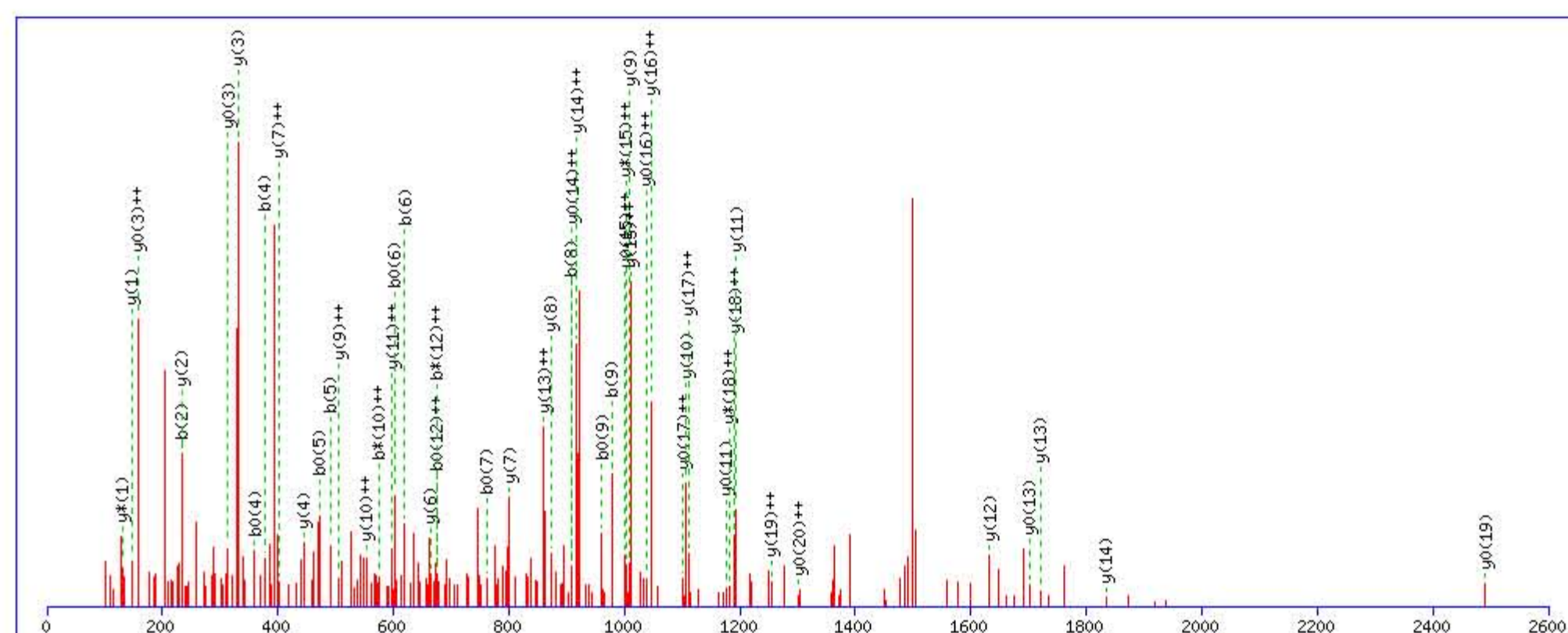
Title: Locus:1.1.1.1632.20 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2997.357162

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

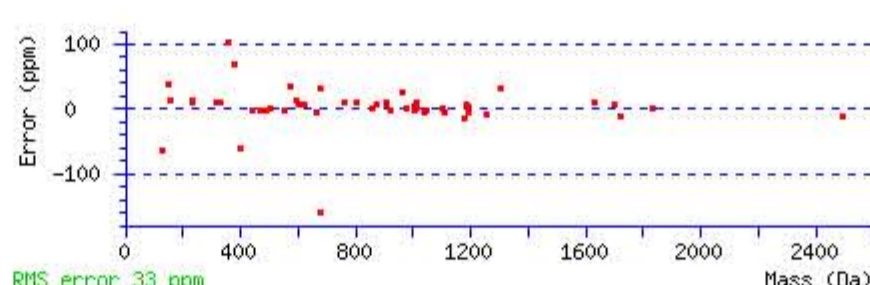
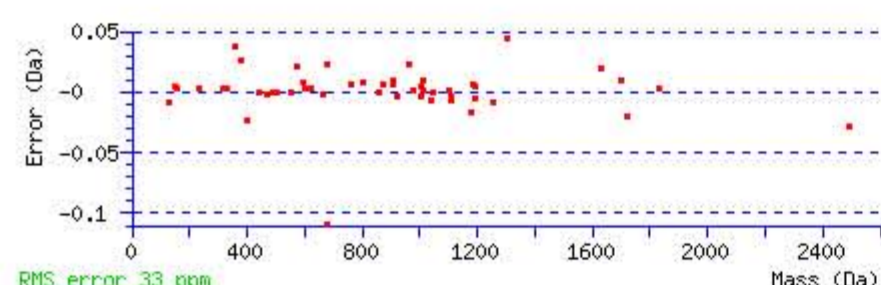
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 40 Expect: 0.001

Matches : 51/260 fragment ions using 154 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.054955	51.531116			84.044390	42.525833	T							24
2	233.095440	117.051358			215.084875	108.046076	M	2897.316768	1449.162022	2880.290219	1440.648748	2879.306203	1440.156740	23
3	320.127468	160.567372			302.116903	151.562089	S	2766.276283	1383.641780	2749.249734	1375.128505	2748.265718	1374.636497	22
4	377.148932	189.078104			359.138367	180.072821	G	2679.244255	1340.125766	2662.217706	1331.612491	2661.233690	1331.120483	21
5	490.232996	245.620136			472.222431	236.614853	L	2622.222791	1311.615034	2605.196242	1303.101759	2604.212226	1302.609751	20
6	619.275589	310.141433			601.265024	301.136150	E	2509.138727	1255.073002	2492.112178	1246.559727	2491.128162	1246.067719	19
7	779.306238	390.156757			761.295673	381.151475	C	2380.096134	1190.551705	2363.069585	1182.038431	2362.085569	1181.546423	18
8	907.364816	454.186046	890.338267	445.672772	889.354251	445.180764	Q	2220.065485	1110.536381	2203.038936	1102.023106	2202.054920	1101.531098	17
9	978.401930	489.704603	961.375381	481.191329	960.391365	480.699321	A	2092.006907	1046.507092	2074.980358	1037.993817	2073.996342	1037.501809	16
10	1164.481243	582.744260	1147.454694	574.230985	1146.470678	573.738977	W	2020.969793	1010.988535	2003.943244	1002.475260	2002.959228	1001.983252	15
11	1279.508186	640.257731	1262.481637	631.744457	1261.497621	631.252449	D	1834.890480	917.948878	1817.863931	909.435604	1816.879915	908.943596	14
12	1366.540214	683.773745	1349.513665	675.260471	1348.529649	674.768463	S	1719.863537	860.435407	1702.836988	851.922132	1701.852972	851.430124	13
13	1805.765540	903.386408	1788.738991	894.873134	1787.754975	894.381126	Q	1632.831509	816.919393	1615.804960	808.406118	1614.820944	807.914110	12
14	1892.797568	946.902422	1875.771019	938.389148	1874.787003	937.897140	S	1193.606183	597.306730	1176.579634	588.793455	1175.595618	588.301447	11
15	1989.850332	995.428804	1972.823783	986.915530	1971.839767	986.423522	P	1106.574155	553.790716	1089.547606	545.277441	1088.563590	544.785433	10
16	2126.909244	1063.958260	2109.882695	1055.444986	2108.898679	1054.952978	H	1009.521391	505.264334	992.494842	496.751059	991.510826	496.259051	9
17	2197.946358	1099.476817	2180.919809	1090.963543	2179.935793	1090.471535	A	872.462479	436.734878	855.435930	428.221603	854.451914	427.729595	8
18	2335.005270	1168.006273	2317.978721	1159.492999	2316.994705	1159.000991	H	801.425365	401.216321	784.398816	392.703046	783.414800	392.211038	7
19	2392.026734	1196.517005	2375.000185	1188.003731	2374.016169	1187.511723	G	664.366453	332.686865	647.339904	324.173590	646.355888	323.681582	6
20	2555.090063	1278.048670	2538.063514	1269.535395	2537.079498	1269.043387	Y	607.344989	304.176133	590.318440	295.662858	589.334424	295.170850	5
21	2668.174127	1334.590702	2651.147578	1326.077427	2650.163562	1325.585419	I	444.281660	222.644468	427.255111	214.131194	426.271095	213.639186	4
22	2765.226891	1383.117084	2748.200342	1374.603809	2747.216326	1374.111801	P	331.197596	166.102436	314.171047	157.589162	313.187031	157.097154	3
23	2852.258919	1426.633098	2835.232370	1418.119823	2834.248354	1417.627815	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
24							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **TMSGLECAWDSQSPHAHGYPISK**

(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	2997.357162	-0.000266	TMSGLECAWDSQSPHAHGYPISK
11.1	2997.357162	-0.000266	TMSGLECAWDSQSPHAHGYPISK

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 62322: 3092.446164 from(516.414970,6+) rtinseconds(1418) index(65249)

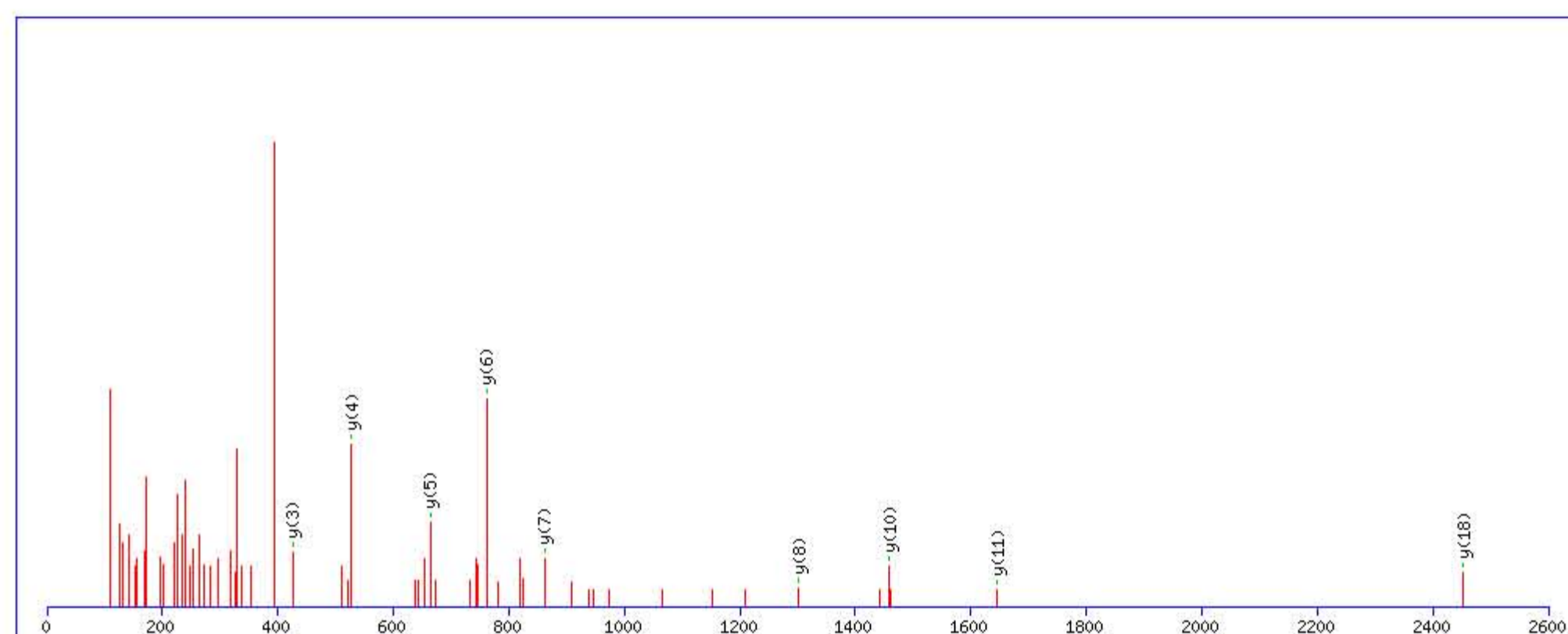
Title: Locus:1.1.1.1431.13 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3092.457016

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

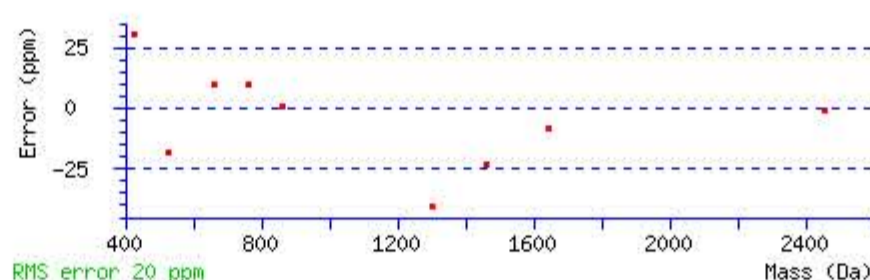
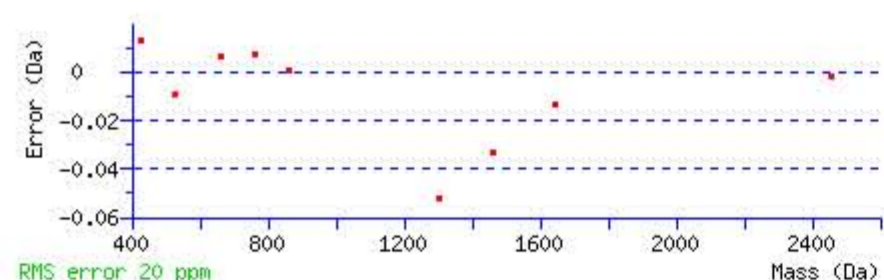
Variable modifications:

Q18 : Biotin:Thermo-21345 (Q)

Ions Score: 51 Expect: 0.00013

Matches : 9/270 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							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
51.0	3092.457016	-0.010852	GNVAVTVSGHTCQHWSAQTPHTHNR
21.1	3092.457016	-0.010852	GNVAVTVSGHTCQHWSAQTPHTHNR

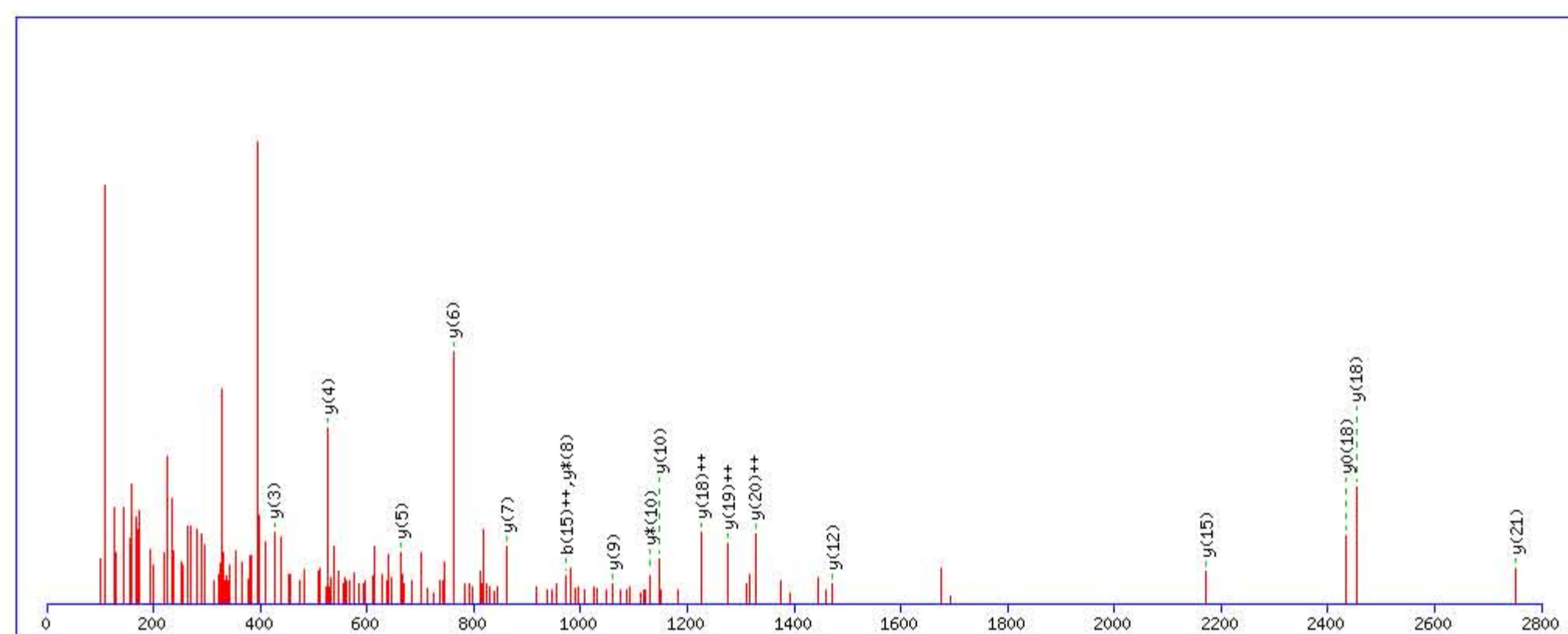
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
 Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

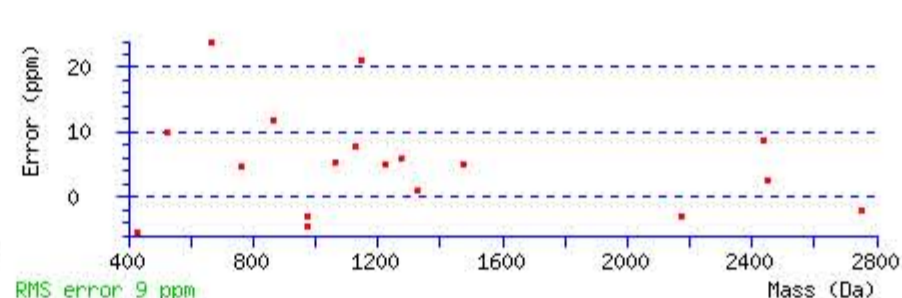
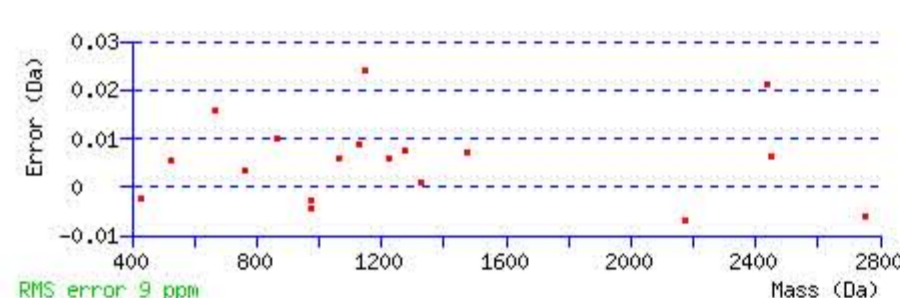
Match to Query 62328: 3092.449044 from(516.415450,6+) rtinseconds(1453) index(65507)
 Title: Locus:1.1.1.1443.15 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3092.457016
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q13 : Biotin:Thermo-21345 (Q)
 Ions Score: 52 Expect: 0.00011
 Matches : 18/270 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							25
2	172.071667	86.539471	155.045118	78.026197			N	3036.442790	1518.725033	3019.416241	1510.211758	3018.432225	1509.719750	24
3	271.140081	136.073679	254.113532	127.560404			V	2922.399863	1461.703569	2905.373314	1453.190295	2904.389298	1452.698287	23
4	342.177195	171.592236	325.150646	163.078961			A	2823.331449	1412.169362	2806.304900	1403.656088	2805.320884	1403.164080	22
5	441.245609	221.126443	424.219060	212.613168			V	2752.294335	1376.650805	2735.267786	1368.137531	2734.283770	1367.645523	21
6	542.293288	271.650282	525.266739	263.137008	524.282723	262.645000	T	2653.225921	1327.116598	2636.199372	1318.603324	2635.215356	1318.111316	20
7	641.361702	321.184489	624.335153	312.671215	623.351137	312.179207	V	2552.178242	1276.592759	2535.151693	1268.079484	2534.167677	1267.587476	19
8	728.393730	364.700503	711.367181	356.187229	710.383165	355.695221	S	2453.109828	1227.058552	2436.083279	1218.545277	2435.099263	1218.053269	18
9	785.415194	393.211235	768.388645	384.697961	767.404629	384.205953	G	2366.077800	1183.542538	2349.051251	1175.029263	2348.067235	1174.537255	17
10	922.474106	461.740691	905.447557	453.227417	904.463541	452.735409	H	2309.056336	1155.031806	2292.029787	1146.518531	2291.045771	1146.026523	16
11	1023.521785	512.264530	1006.495236	503.751256	1005.511220	503.259248	T	2171.997424	1086.502350	2154.970875	1077.989075	2153.986859	1077.497067	15
12	1183.552434	592.279855	1166.525885	583.766581	1165.541869	583.274572	C	2070.949745	1035.978510	2053.923196	1027.465236	2052.939180	1026.973228	14
13	1622.777760	811.892518	1605.751211	803.379244	1604.767195	802.887236	Q	1910.919096	955.963186	1893.892547	947.449911	1892.908531	946.957903	13
14	1759.836672	880.421974	1742.810123	871.908700	1741.826107	871.416692	H	1471.693770	736.350523	1454.667221	727.837248	1453.683205	727.345240	12
15	1945.915985	973.461631	1928.889436	964.948356	1927.905420	964.456348	W	1334.634858	667.821067	1317.608309	659.307792	1316.624293	658.815784	11
16	2032.948013	1016.977645	2015.921464	1008.464370	2014.937448	1007.972362	S	1148.555545	574.781410	1131.528996	566.268136	1130.544980	565.776128	10
17	2103.985127	1052.496201	2086.958578	1043.982927	2085.974562	1043.490919	A	1061.523517	531.265396	1044.496968	522.752122	1043.512952	522.260114	9
18	2232.043705	1116.525490	2215.017156	1108.012216	2214.033140	1107.520208	Q	990.486403	495.746839	973.459854	487.233565	972.475838	486.741557	8
19	2333.091384	1167.049330	2316.064835	1158.536055	2315.080819	1158.044047	T	862.427825	431.717550	845.401276	423.204276	844.417260	422.712268	7
20	2430.144148	1215.575712	2413.117599	1207.062437	2412.133583	1206.570429	P	761.380146	381.193711	744.353597	372.680436	743.369581	372.188428	6
21	2567.203060	1284.105168	2550.176511	1275.591893	2549.192495	1275.099885	H	664.327382	332.667329	647.300833	324.154054	646.316817	323.662046	5
22	2668.250739	1334.629007	2651.224190	1326.115733	2650.240174	1325.623725	T	527.268470	264.137873	510.241921	255.624598	509.257905	255.132590	4
23	2805.309651	1403.158463	2788.283102	1394.645189	2787.299086	1394.153181	H	426.220791	213.614033	409.194242	205.100759			3
24	2919.352578	1460.179927	2902.326029	1451.666652	2901.342013	1451.174644	N	289.161879	145.084577	272.135330	136.571303			2
25							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **GNVAVTVSGHTCQHWSAQTPHTHNR**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.8	3092.457016	-0.007972	GNVAVTVSGHTCQHWSAQTPHTHNR
22.2	3092.457016	-0.007972	GNVAVTVSGHTCQHWSAQTPHTHNR

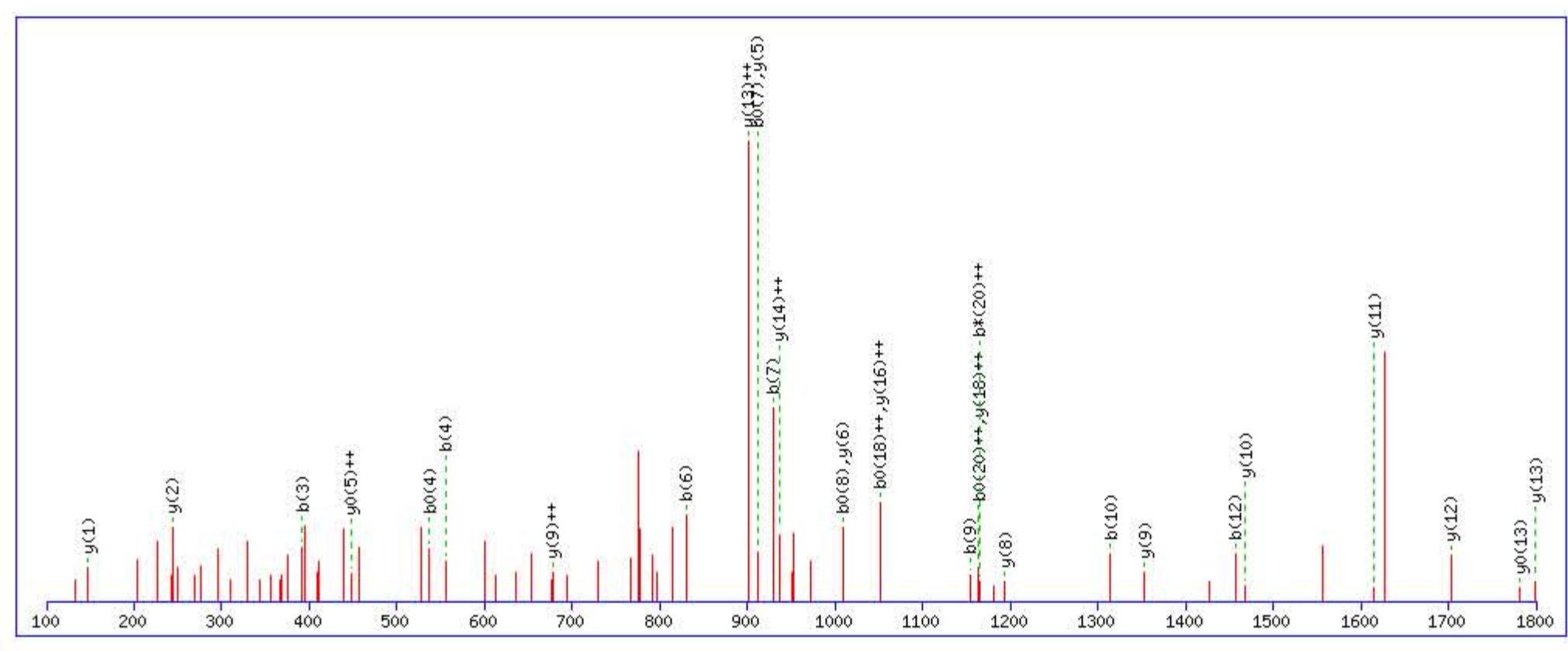
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYDYCDVPQCAAPSFDCGKQPVEPK**
 Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

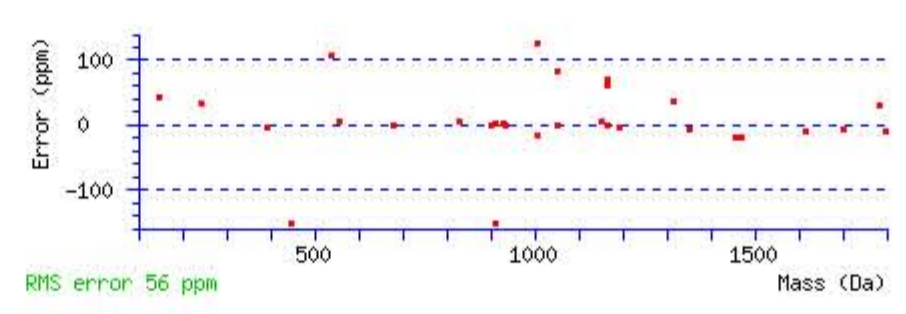
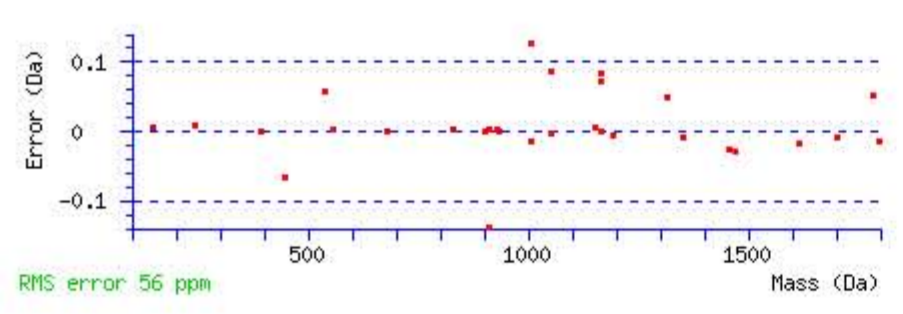
Match to Query 64976: 3254.446776 from(814.618970,4+) rtinseconds(2054) index(69136)
 Title: Locus:1.1.1.1652.25 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3254.454514
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q21 : Biotin:Thermo-21345 (Q)
 Ions Score: 52 Expect: 4.8e-005
 Matches : 30/264 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	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 **LYDYCDVPQCAAPSFDCGKQPVEPK**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.7	3254.454514	-0.007738	LYDYCDVPQCAAPSFDCGKQPVEPK

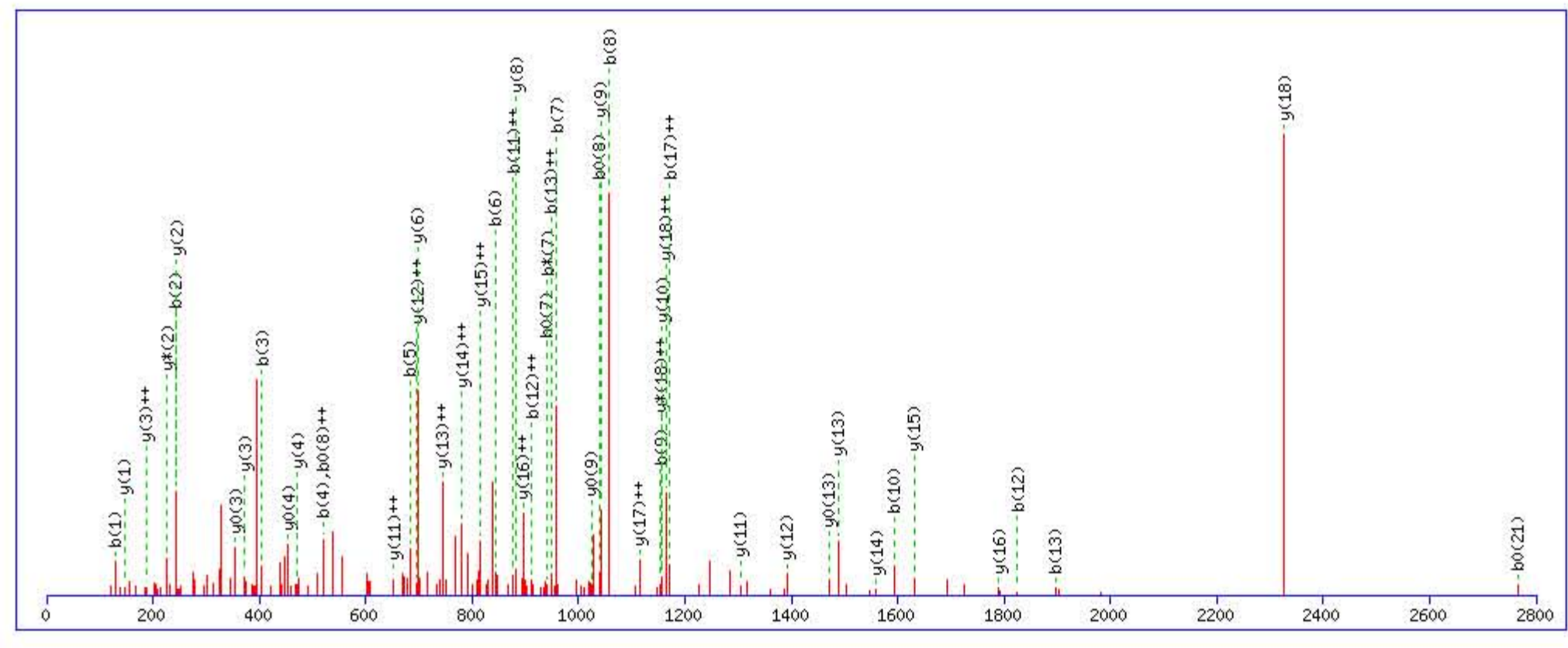
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **KLYDYCDVPQCAAPSFDCGKQPVEPK**
 Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

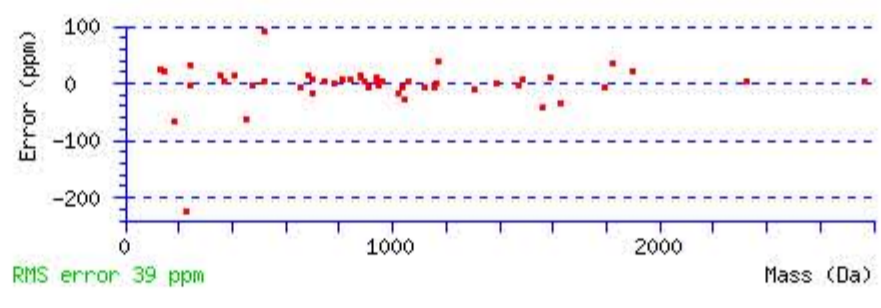
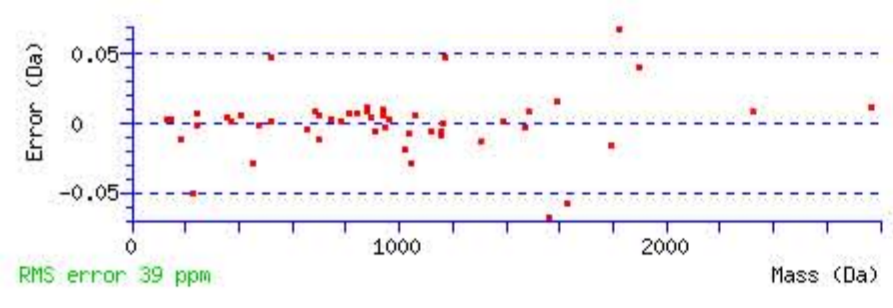
Match to Query 66110: 3382.550016 from(846.644780,4+) rtinseconds(1988) index(68710)
 Title: Locus:1.1.1.1629.16 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3382.549469
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q10 : Biotin:Thermo-21345 (Q)
 Ions Score: 67 Expect: 5.4e-007
 Matches : 51/290 fragment ions using 133 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 **KLYDYCDVPQCAAPSFDCGKQPVEPK**
 (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	3382.549469	0.000547	KLYDYCDVPQCAAPSFDCGKQPVEPK
8.0	3382.549469	0.000547	KLYDYCDVPQCAAPSFDCGKQPVEPK
0.1	3382.580414	-0.030398	HLYPNTPYAYTFWYMMNARSKNVGWR
0.1	3382.580414	-0.030398	HLYPNTPYAYTFWYMMNARSKNVGWR

MASCOT Search Results

Peptide View

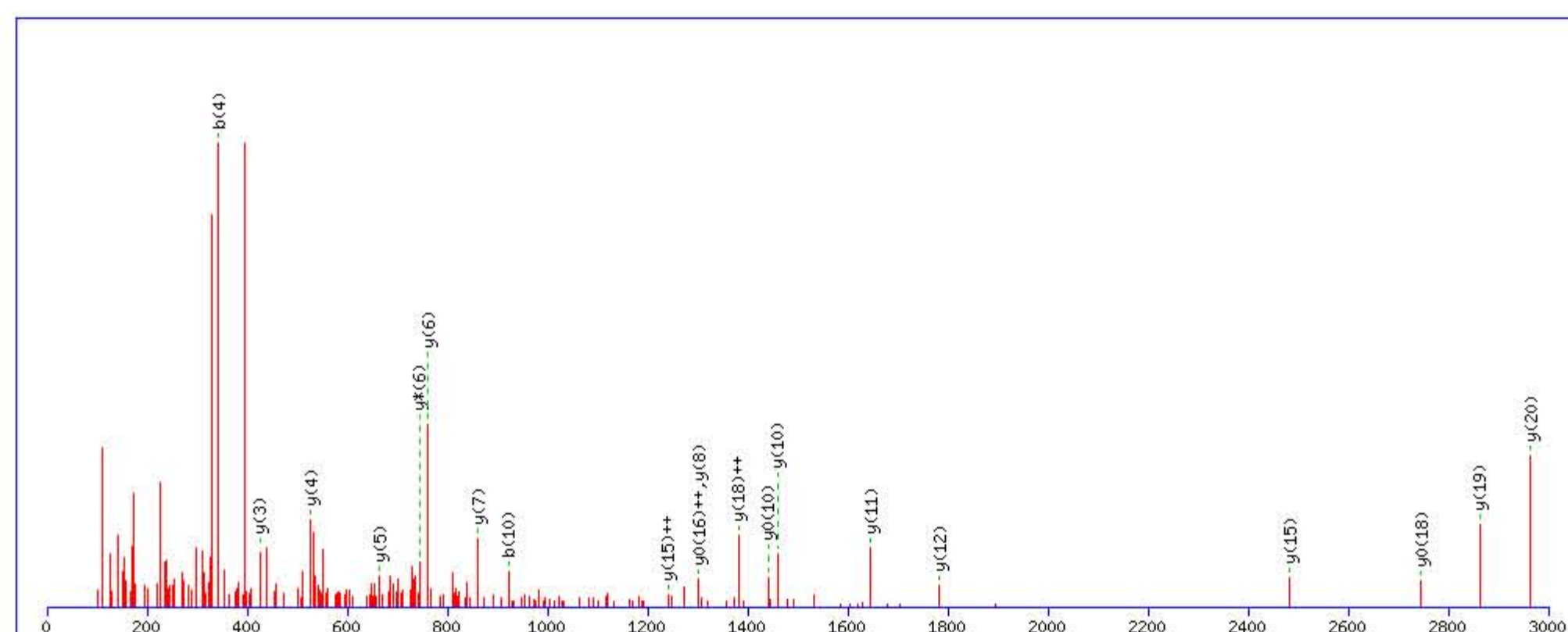
MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHITHNR**
 Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

Match to Query 66349: 3403.614324 from(568.276330,6+) rtinseconds(1654) index(66674)
 Title: Locus:1.1.1.1513.8 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

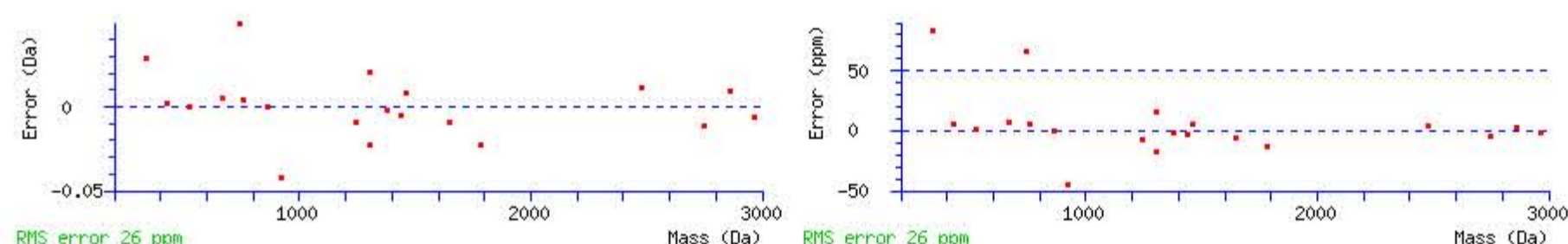
Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 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: 56 Expect: 7.7e-006
 Matches : 20/270 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							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 **GNVAVTVSGHTCQHWSAQTPHITHNR**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.8	3403.623764	-0.009440	GNVAVTVSGHTCQHWSAQTPHITHNR
1.3	3403.604858	0.009466	TQVPMVVMPhGGPHSSFVTAWMLFPAMLCK
0.7	3403.604858	0.009466	TQVPMVVMPhGGPHSSFVTAWMLFPAMLCK

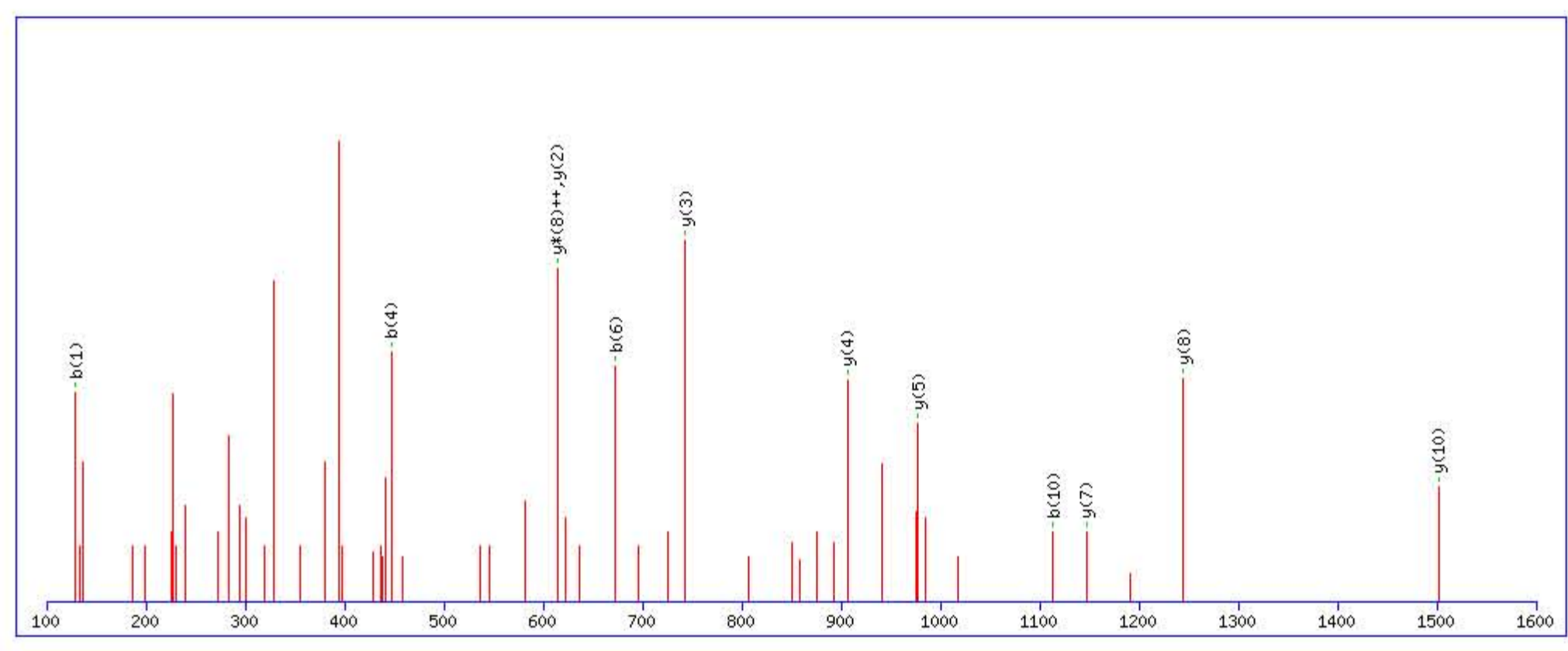
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KCSAPEPSQKPPGKPCPGLAYEQR**
 Found in **PROP_HUMAN**, Properdin OS=Homo sapiens GN=CFP PE=1 SV=2

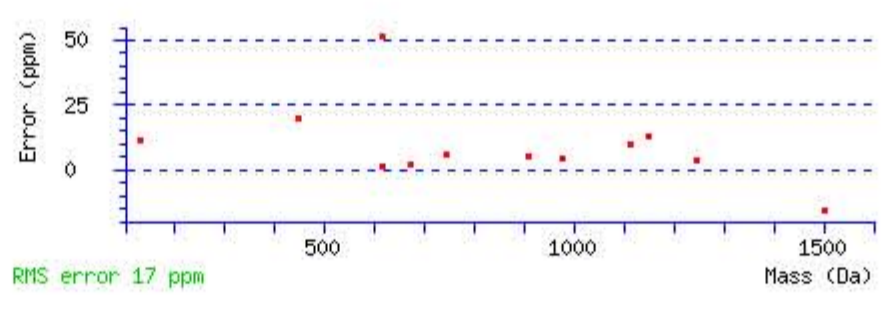
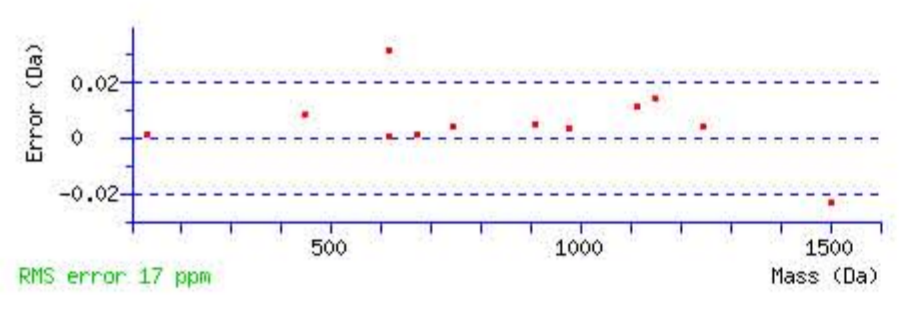
Match to Query 61642: 2992.466020 from(599.500480,5+) rtinseconds(1445) index(65442)
 Title: Locus:1.1.1.1440.23 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2992.472107
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q23 : Biotin:Thermo-21345 (Q)
 Ions Score: 57 Expect: 4.7e-006
 Matches : 12/268 fragment ions using 13 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.102239	65.054757	112.075690	56.541483			K							24
2	289.132888	145.070082	272.106339	136.556808			C	2865.384455	1433.195865	2848.357906	1424.682591	2847.373890	1424.190583	23
3	376.164916	188.586096	359.138367	180.072822	358.154351	179.580814	S	2705.353806	1353.180541	2688.327257	1344.667266	2687.343241	1344.175258	22
4	447.202030	224.104653	430.175481	215.591378	429.191465	215.099370	A	2618.321778	1309.664527	2601.295229	1301.151252	2600.311213	1300.659244	21
5	544.254794	272.631035	527.228245	264.117761	526.244229	263.625753	P	2547.284664	1274.145970	2530.258115	1265.632695	2529.274099	1265.140687	20
6	673.297387	337.152332	656.270838	328.639057	655.286822	328.147049	E	2450.231900	1225.619588	2433.205351	1217.106313	2432.221335	1216.614305	19
7	770.350151	385.678714	753.323602	377.165439	752.339586	376.673431	P	2321.189307	1161.098292	2304.162758	1152.585017	2303.178742	1152.093009	18
8	857.382179	429.194728	840.355630	420.681453	839.371614	420.189445	S	2224.136543	1112.571909	2207.109994	1104.058635	2206.125978	1103.566627	17
9	985.440757	493.224017	968.414208	484.710742	967.430192	484.218734	Q	2137.104515	1069.055895	2120.077966	1060.542621	2119.093950	1060.050613	16
10	1113.535720	557.271498	1096.509171	548.758224	1095.525155	548.266216	K	2009.045937	1005.026607	1992.019388	996.513332	1991.035372	996.021324	15
11	1210.588484	605.797880	1193.561935	597.284606	1192.577919	596.792598	P	1880.950974	940.979125	1863.924425	932.465851	1862.940409	931.973843	14
12	1307.641248	654.324262	1290.614699	645.810988	1289.630683	645.318980	P	1783.898210	892.452743	1766.871661	883.939469	1765.887645	883.447461	13
13	1364.662712	682.834994	1347.636163	674.321720	1346.652147	673.829712	G	1686.845446	843.926361	1669.818897	835.413087	1668.834881	834.921079	12
14	1492.757675	746.882476	1475.731126	738.369201	1474.747110	737.877193	K	1629.823982	815.415629	1612.797433	806.902355	1611.813417	806.410347	11
15	1589.810439	795.408858	1572.783890	786.895583	1571.799874	786.403575	P	1501.729019	751.368148	1484.702470	742.854873	1483.718454	742.362865	10
16	1749.841088	875.424182	1732.814539	866.910908	1731.830523	866.418900	C	1404.676255	702.841766	1387.649706	694.328491	1386.665690	693.836483	9
17	1846.893852	923.950564	1829.867303	915.437290	1828.883287	914.945282	P	1244.645606	622.826441	1227.619057	614.313167	1226.635041	613.821159	8
18	1903.915316	952.461296	1886.888767	943.948022	1885.904751	943.456014	G	1147.592842	574.300059	1130.566293	565.786785	1129.582277	565.294777	7
19	2016.999380	1009.003328	1999.972831	1000.490054	1998.988815	999.998045	L	1090.571378	545.789327	1073.544829	537.276053	1072.560813	536.784045	6
20	2088.036494	1044.521885	2071.009945	1036.008610	2070.025929	1035.516602	A	977.487314	489.247295	960.460765	480.734021	959.476749	480.242013	5
21	2251.099823	1126.053549	2234.073274	1117.540275	2233.089258	1117.048267	Y	906.450200	453.728738	889.423651	445.215464	888.439635	444.723456	4
22	2380.142416	1190.574846	2363.115867	1182.061571	2362.131851	1181.569564	E	743.386871	372.197074	726.360322	363.683799	725.376306	363.191791	3
23	2819.367742	1410.187509	2802.341193	1401.674235	2801.357177	1401.182227	Q	614.344278	307.675777	597.317729	299.162503			2
24							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **KCSAPEPSQKPPGKPCPGLAYEQR**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.3	2992.472107	-0.006087	KCSAPEPSQKPPGKPCPGLAYEQR
0.4	2992.422989	0.043031	MPSTASLTRKSNVNNQQCPASTPSSEVIS

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 25483: 1276.567968 from(639.291260,2+) rtinseconds(1454) index(32957)

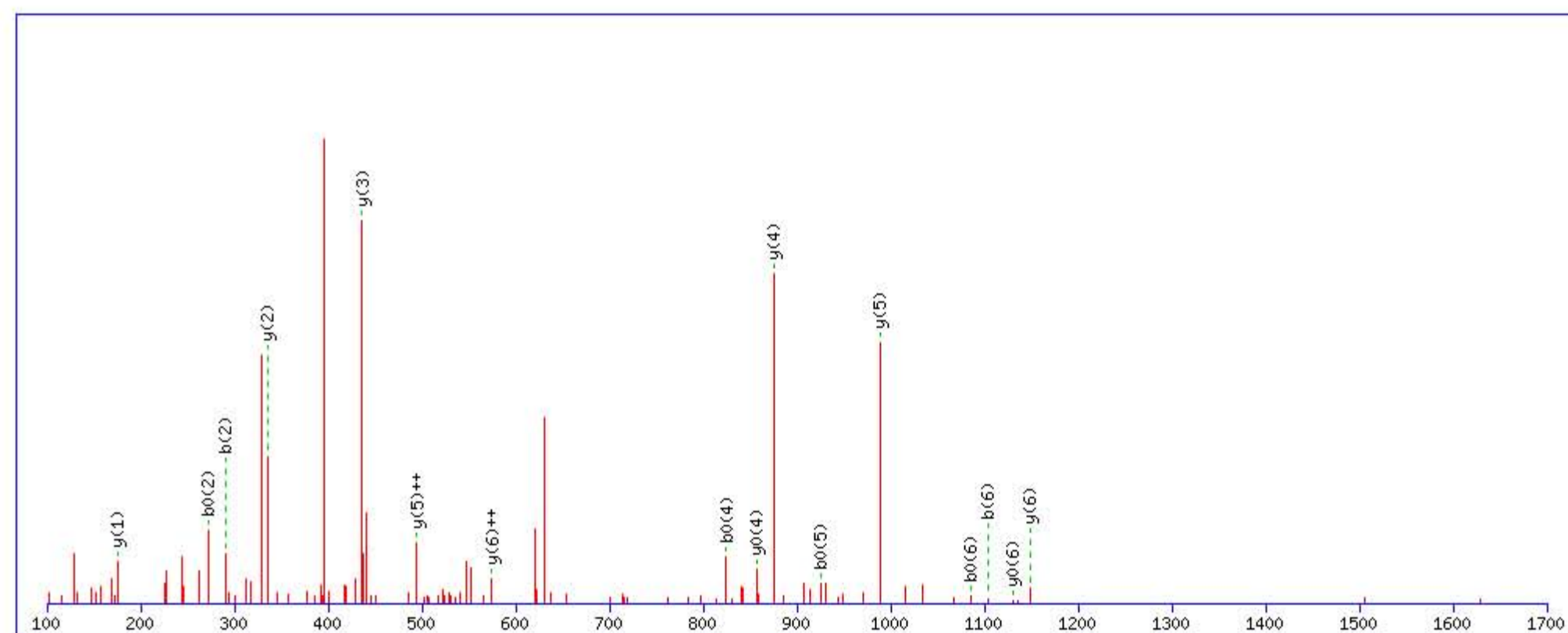
Title: Locus:1.1.1.2925.23 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1276.572632

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

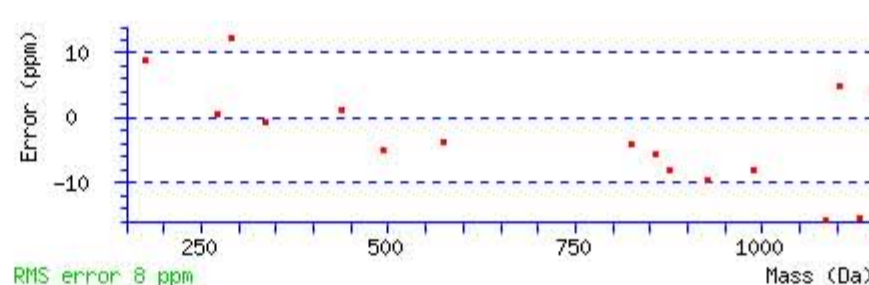
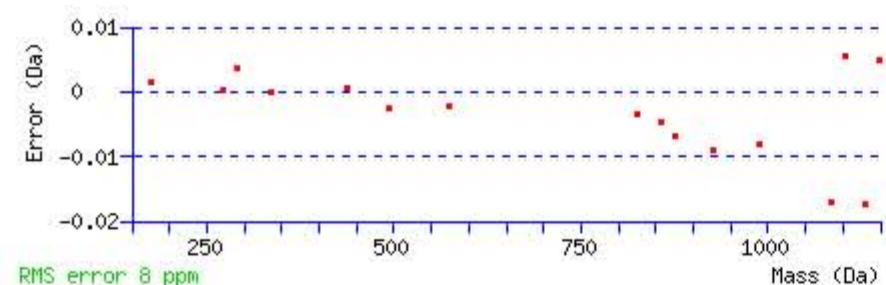
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.0031

Matches : 16/62 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	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
32.8	1276.572632	-0.004664	ECLQTCR
11.9	1276.553116	0.014852	EDLDNASKDDR
7.1	1276.583862	-0.015894	KMSLSCHVCR
6.4	1276.579605	-0.011637	EEQRSPFNDR
5.8	1276.587006	-0.019038	EDGTWAPMRSK
5.2	1276.571762	-0.003794	AGAESPTMSVDGR
3.8	1276.569275	-0.001307	MPMWAGGVGSPR
3.0	1276.569229	-0.001261	MTGRYEMYAR
0.5	1276.560516	0.007452	DEAEMSPVVER
0.3	1276.579132	-0.011164	MPMNAALGEPK

Mascot: <http://www.matrixscience.com/>

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 51672: 2230.117572 from(744.379800,3+) rtinseconds(2285) index(38156)

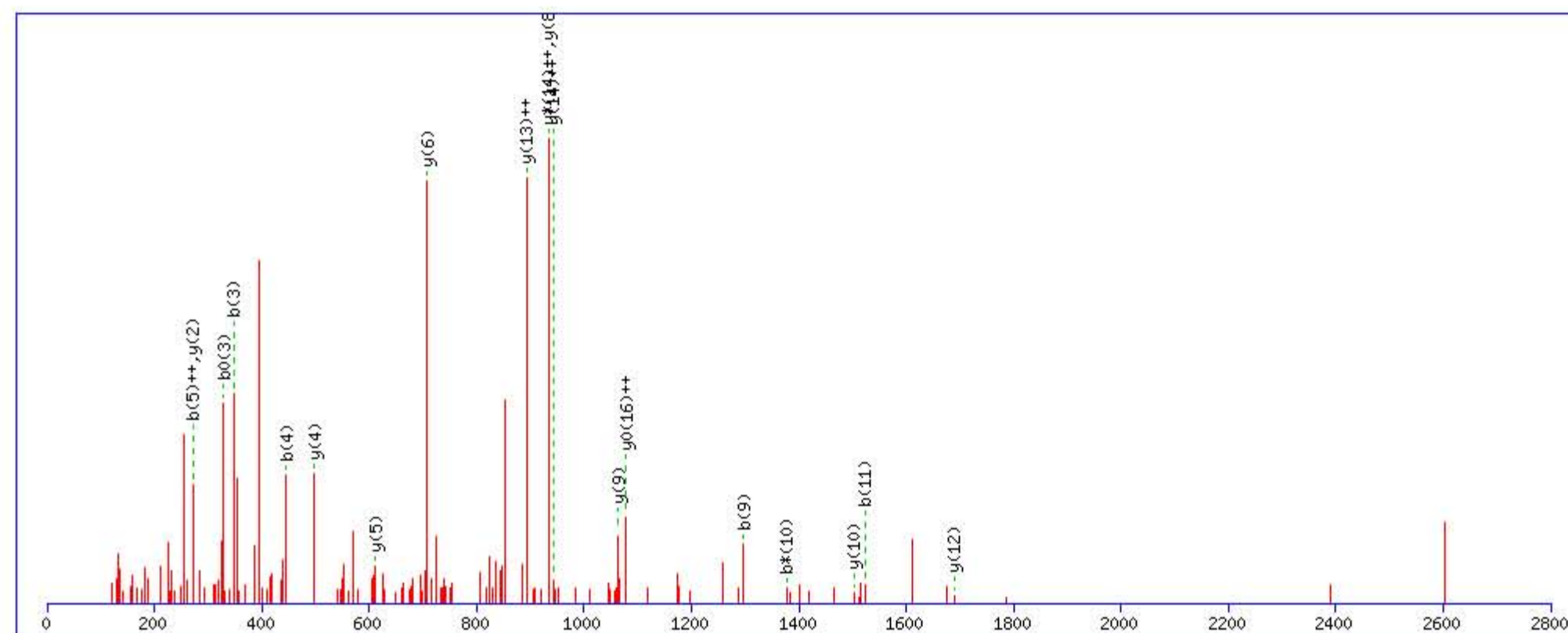
Title: Locus:1.1.1.3215.15 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2230.112595

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

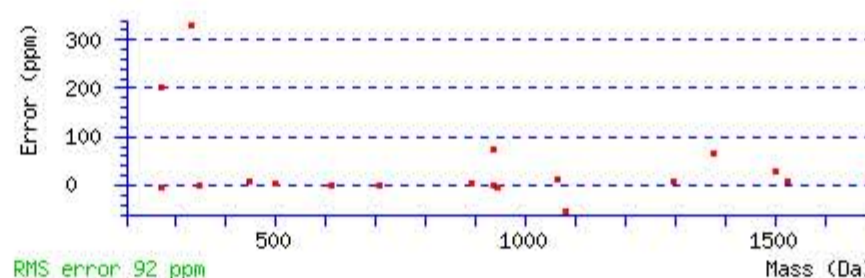
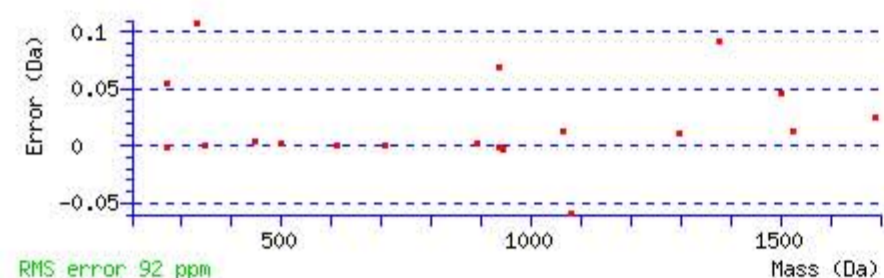
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 25 Expect: 0.093

Matches : 19/164 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							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
25.1	2230.112595	0.004977	GECVPGEQEPEPILIPR

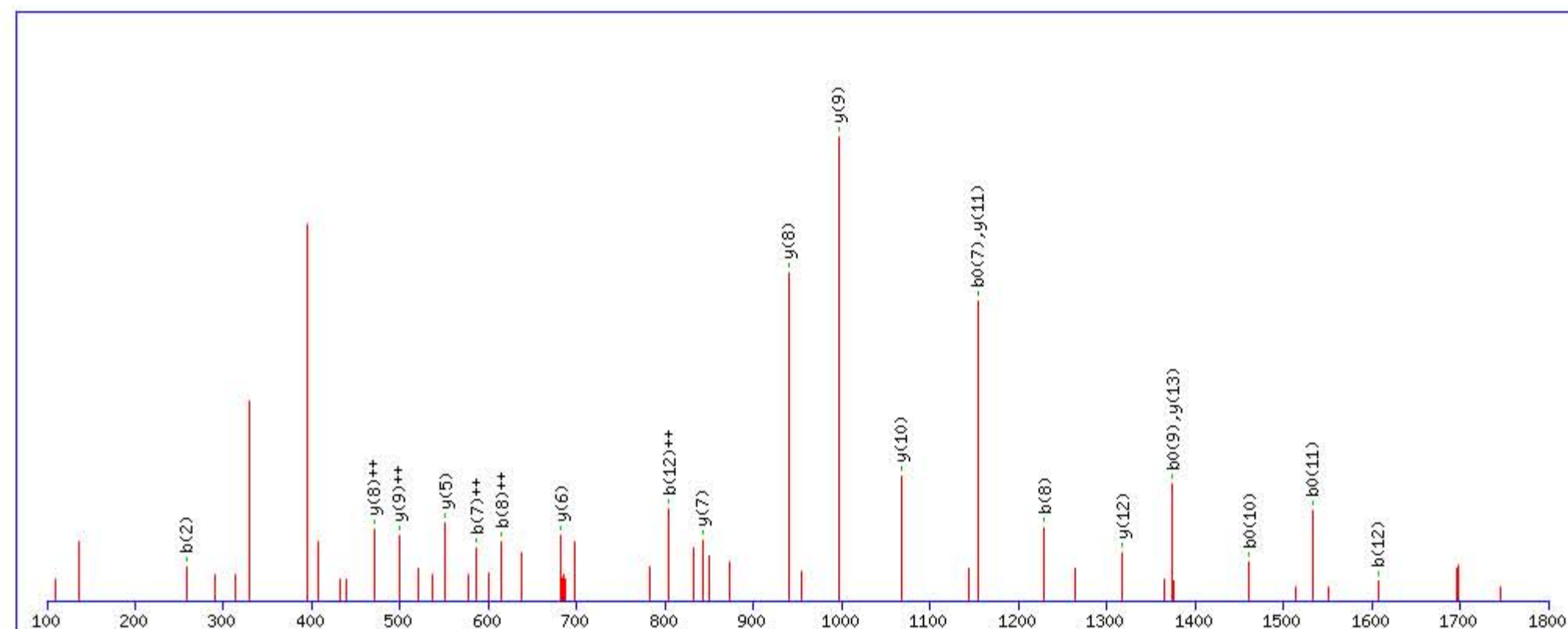
Mascot: <http://www.matrixscience.com/>

Peptide View

MS/MS Fragmentation of **KEDSCQLGYSAGPCMGMTSR**
 Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

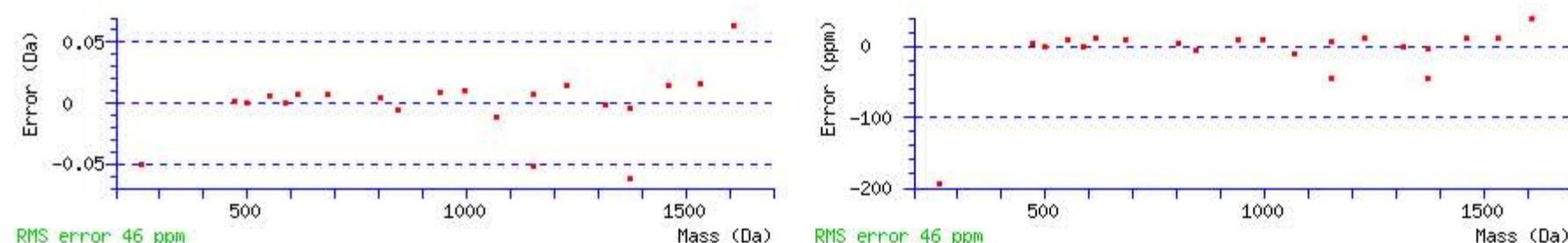
Match to Query 57202: 2545.106742 from(849.376190,3+) rtinseconds(1926) index(52273)
 Title: Locus:1.1.1.1286.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

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): 2545.089188
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q6 : Biotin:Thermo-21345 (Q)
 Ions Score: 54 Expect: 1.9e-005
 Matches : 21/224 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							20
2	258.144832	129.576054	241.118283	121.062780	240.134267	120.570772	E	2418.001508	1209.504392	2400.974959	1200.991117	2399.990943	1200.499109	19
3	373.171775	187.089526	356.145226	178.576251	355.161210	178.084243	D	2288.958915	1144.983095	2271.932366	1136.469821	2270.948350	1135.977813	18
4	460.203803	230.605540	443.177254	222.092265	442.193238	221.600257	S	2173.931972	1087.469624	2156.905423	1078.956349	2155.921407	1078.464341	17
5	620.234452	310.620864	603.207903	302.107590	602.223887	301.615582	C	2086.899944	1043.953610	2069.873395	1035.440335	2068.889379	1034.948327	16
6	1059.459778	530.233527	1042.433229	521.720253	1041.449213	521.228245	Q	1926.869295	963.938286	1909.842746	955.425011	1908.858730	954.933003	15
7	1172.543842	586.775559	1155.517293	578.262285	1154.533277	577.770277	L	1487.643969	744.325623	1470.617420	735.812348	1469.633404	735.320340	14
8	1229.565306	615.286291	1212.538757	606.773017	1211.554741	606.281008	G	1374.559905	687.783591	1357.533356	679.270316	1356.549340	678.778308	13
9	1392.628635	696.817956	1375.602086	688.304681	1374.618070	687.812673	Y	1317.538441	659.272859	1300.511892	650.759584	1299.527876	650.267576	12
10	1479.660663	740.333970	1462.634114	731.820695	1461.650098	731.328687	S	1154.475112	577.741194	1137.448563	569.227920	1136.464547	568.735912	11
11	1550.697777	775.852527	1533.671228	767.339252	1532.687212	766.847244	A	1067.443084	534.225180	1050.416535	525.711906	1049.432519	525.219898	10
12	1607.719241	804.363259	1590.692692	795.849984	1589.708676	795.357976	G	996.405970	498.706623	979.379421	490.193349	978.395405	489.701341	9
13	1704.772005	852.889641	1687.745456	844.376366	1686.761440	843.884358	P	939.384506	470.195891	922.357957	461.682617	921.373941	461.190609	8
14	1864.802654	932.904965	1847.776105	924.391691	1846.792089	923.899683	C	842.331742	421.669509	825.305193	413.156235	824.321177	412.664227	7
15	1995.843139	998.425208	1978.816590	989.911933	1977.832574	989.419925	M	682.301093	341.654185	665.274544	333.140910	664.290528	332.648902	6
16	2052.864603	1026.935939	2035.838054	1018.422665	2034.854038	1017.930657	G	551.260608	276.133942	534.234059	267.620668	533.250043	267.128660	5
17	2183.905088	1092.456182	2166.878539	1083.942907	2165.894523	1083.450899	M	494.239144	247.623210	477.212595	239.109935	476.228579	238.617927	4
18	2284.952767	1142.980021	2267.926218	1134.466747	2266.942202	1133.974739	T	363.198659	182.102967	346.172110	173.589693	345.188094	173.097685	3
19	2371.984795	1186.496035	2354.958246	1177.982761	2353.974230	1177.490753	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
20							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **KEDSCQLGYSAGPCMGMTSR**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.1	2545.089188	0.017554	KEDSCQLGYSAGPCMGMTSR

MASCOT 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 21773: 1153.660648 from(577.837600,2+) rtinseconds(1917) index(35812)

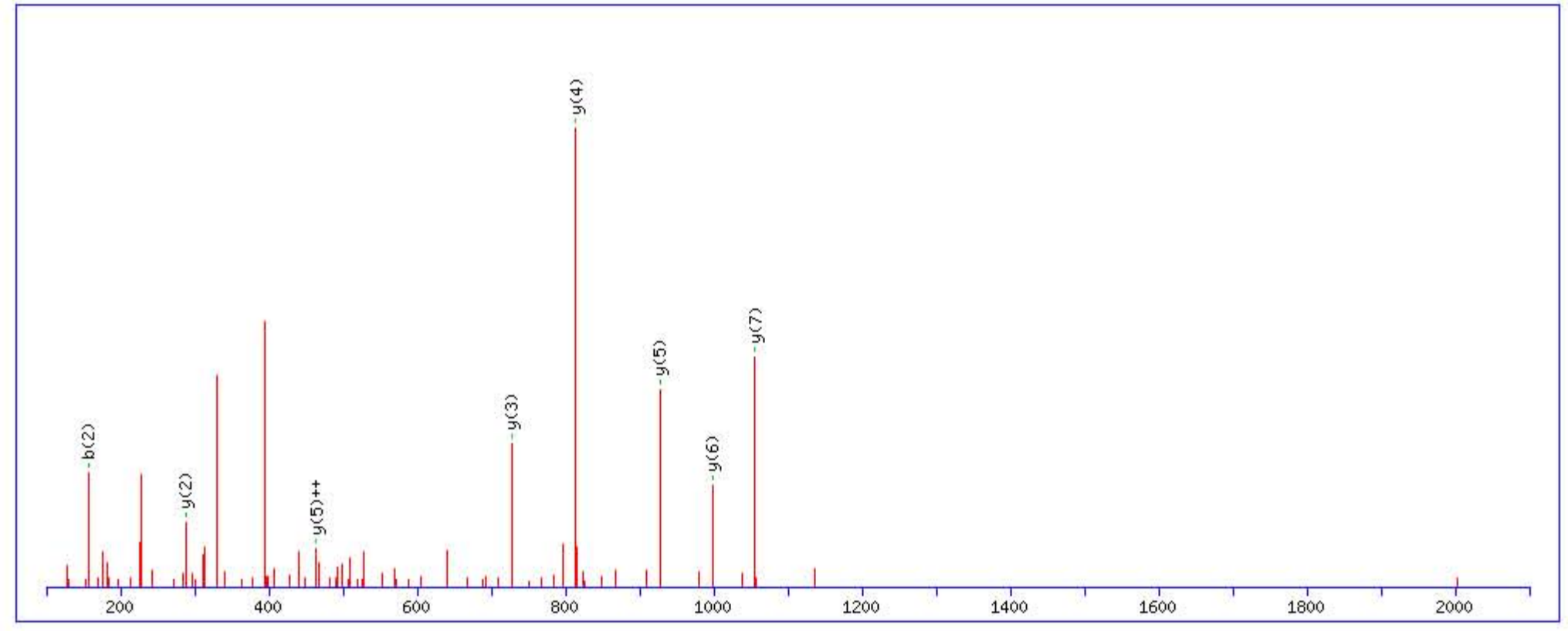
Title: Locus:1.1.1.3087.14 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1153.664139

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

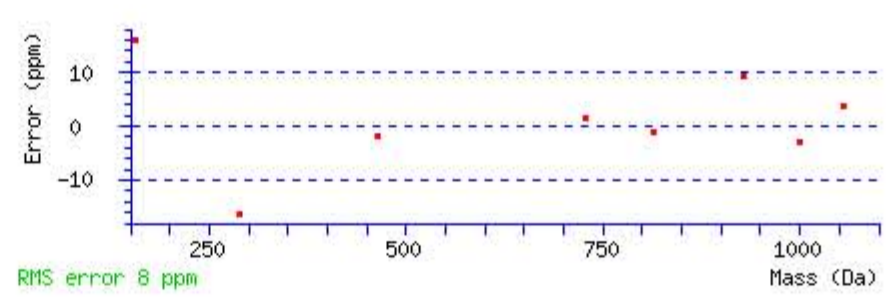
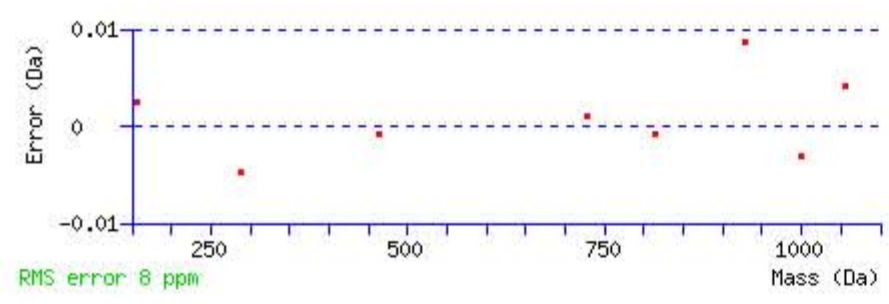
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 57 Expect: 3.3e-005

Matches : 8/60 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	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
56.7	1153.664139	-0.003491	VGALSQLR
23.6	1153.667953	-0.007305	RANPNSIRVK
20.9	1153.645477	0.015171	RALAAPVAEEK
14.2	1153.675354	-0.014706	RALLSQR
14.2	1153.675369	-0.014721	RALTVQR
13.1	1153.664124	-0.003476	VKQEALR
7.2	1153.675369	-0.014721	QTVRALR
6.5	1153.656723	0.003925	RPSADPGKKAK
4.3	1153.645493	0.015155	NLLKLDAPDR
3.1	1153.664124	-0.003476	LKVEQAR

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 35366: 1561.829268 from(781.921910,2+) rtinseconds(2161) index(53983)

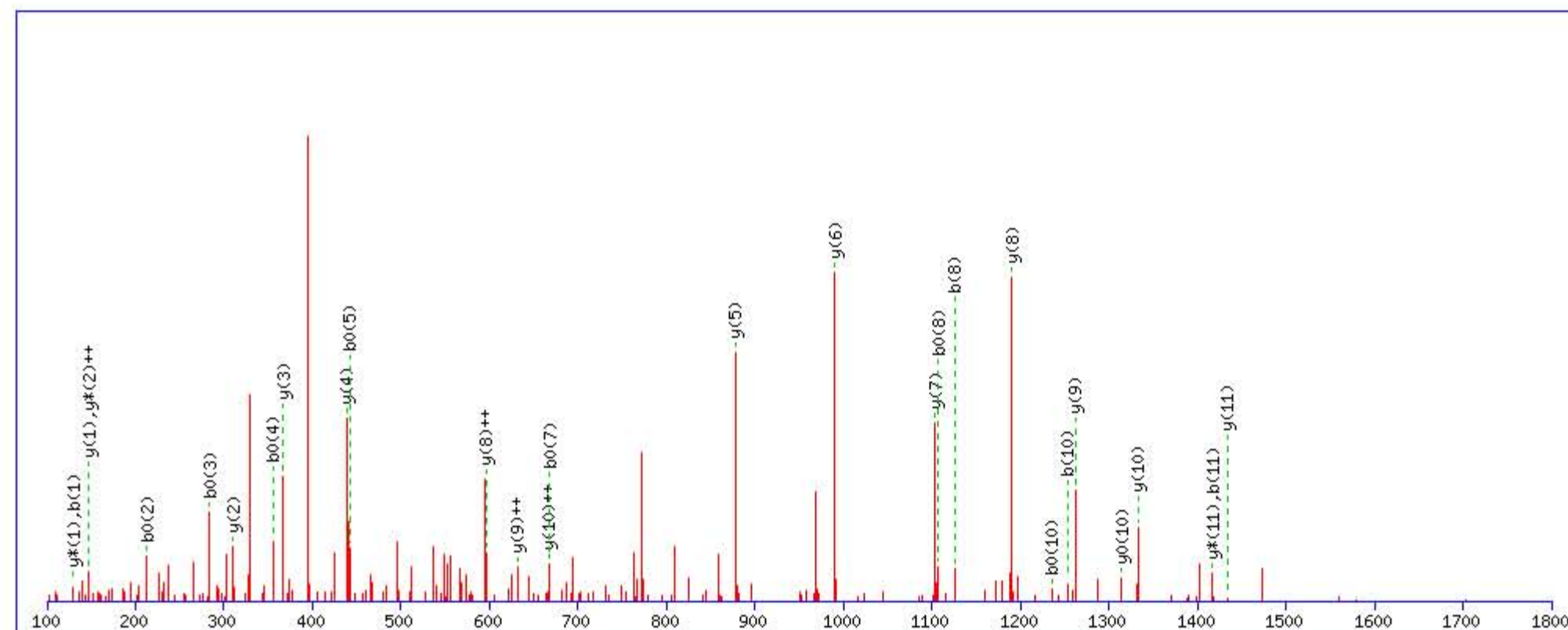
Title: Locus:1.1.1.1367.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1561.817383

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

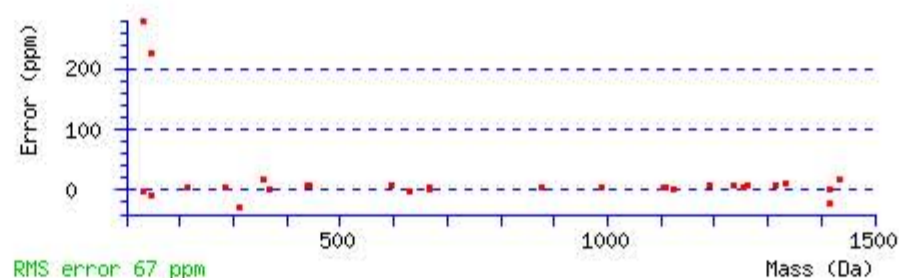
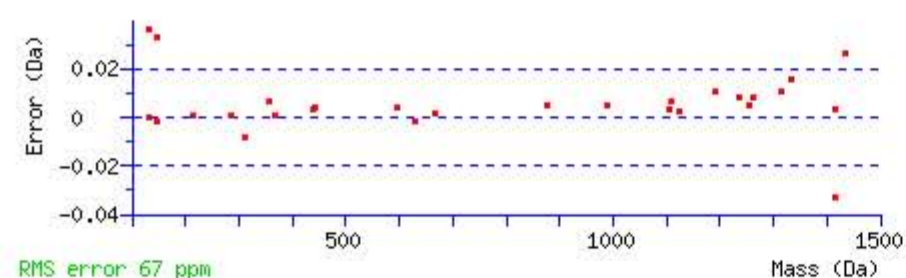
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 54 Expect: 1.8e-005

Matches : 29/104 fragment ions using 71 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							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
54.0	1561.817383	0.011885	ETAASLLQAGYK
3.4	1561.817398	0.011870	VLPEVLEKQCGYK

Mascot: <http://www.matrixscience.com/>

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TATSEYQTFNPR**

Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

Match to Query 44163: 1871.894352 from(624.972060,3+) rtinseconds(2281) index(54733)

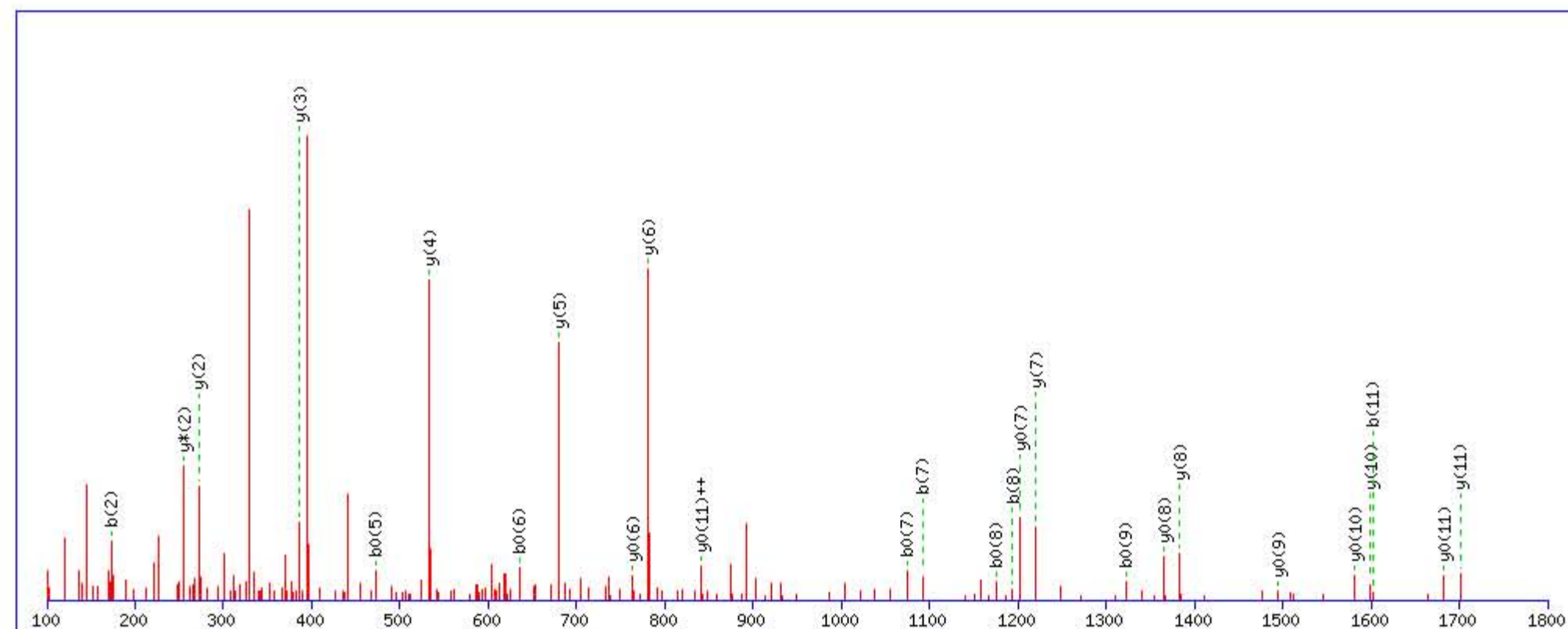
Title: Locus:1.1.1.1409.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1871.887619

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

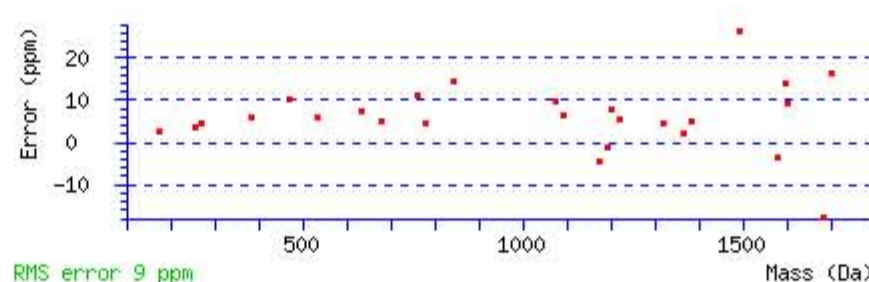
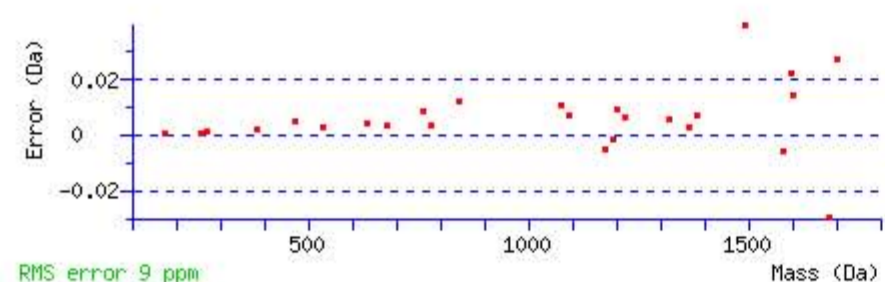
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 47 Expect: 0.00038

Matches : 26/122 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	102.054955	51.531116			84.044390	42.525833	T							13
2	173.092069	87.049672			155.081504	78.044390	A	1771.847219	886.427248	1754.820670	877.913973	1753.836654	877.421965	12
3	274.139748	137.573512			256.129183	128.568230	T	1700.810105	850.908691	1683.783556	842.395416	1682.799540	841.903408	11
4	361.171776	181.089526			343.161211	172.084243	S	1599.762426	800.384851	1582.735877	791.871577	1581.751861	791.379569	10
5	490.214369	245.610822			472.203804	236.605540	E	1512.730398	756.868837	1495.703849	748.355563	1494.719833	747.863555	9
6	653.277698	327.142487			635.267133	318.137205	Y	1383.687805	692.347541	1366.661256	683.834266	1365.677240	683.342258	8
7	1092.503024	546.755150	1075.476475	538.241876	1074.492459	537.749868	Q	1220.624476	610.815876	1203.597927	602.302602	1202.613911	601.810594	7
8	1193.550703	597.278990	1176.524154	588.765715	1175.540138	588.273707	T	781.399150	391.203213	764.372601	382.689939	763.388585	382.197931	6
9	1340.619117	670.813197	1323.592568	662.299922	1322.608552	661.807914	F	680.351471	340.679374	663.324922	332.166099			5
10	1487.687531	744.347404	1470.660982	735.834129	1469.676966	735.342121	F	533.283057	267.145167	516.256508	258.631892			4
11	1601.730458	801.368867	1584.703909	792.855593	1583.719893	792.363585	N	386.214643	193.610959	369.188094	185.097685			3
12	1698.783222	849.895249	1681.756673	841.381975	1680.772657	840.889967	P	272.171716	136.589496	255.145167	128.076221			2
13							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **TATSEYQTFNPR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.8	1871.887619	0.006733	TATSEYQTFNPR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SPQELLCGASLISDR**

Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

Match to Query 45649: 1956.003388 from(979.008970,2+) rtinseconds(2515) index(55984)

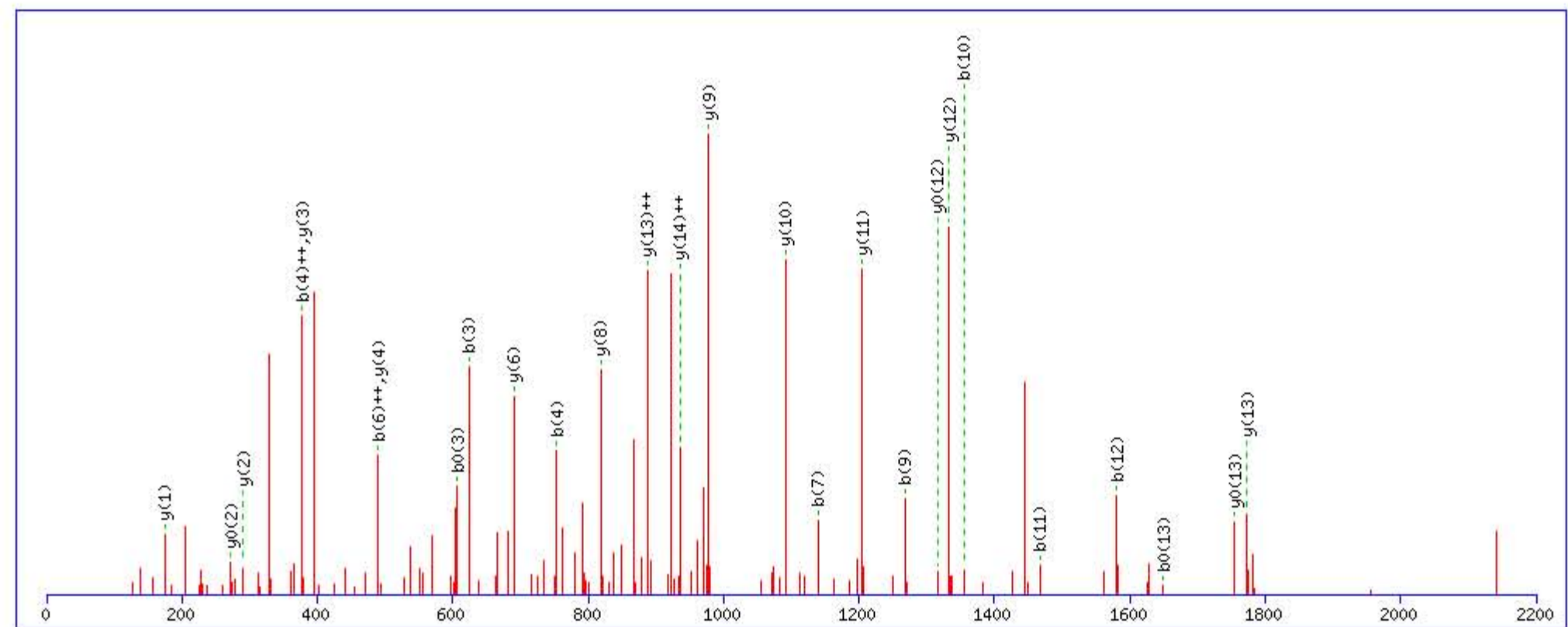
Title: Locus:1.1.1.1490.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1955.980850

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

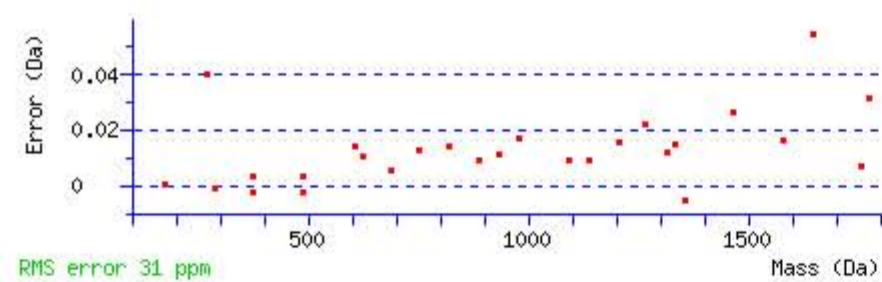
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

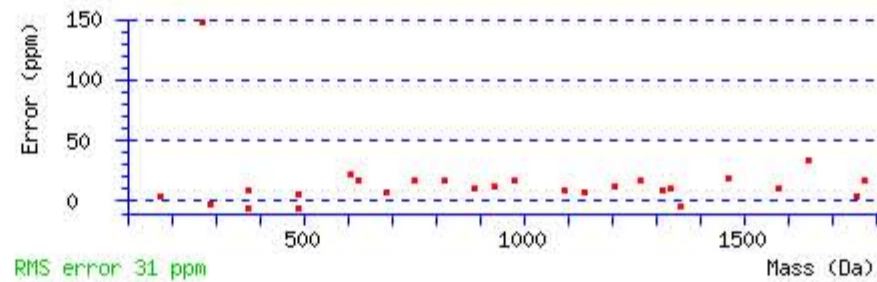
Ions Score: 86 Expect: 6.9e-008

Matches : 27/162 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	88.039304	44.523290			70.028739	35.518008	S							15
2	185.092068	93.049672			167.081503	84.044389	P	1869.956117	935.481697	1852.929568	926.968422	1851.945552	926.476414	14
3	624.317394	312.662335	607.290845	304.149061	606.306829	303.657053	Q	1772.903353	886.955314	1755.876804	878.442040	1754.892788	877.950032	13
4	753.359987	377.183632	736.333438	368.670357	735.349422	368.178349	E	1333.678027	667.342652	1316.651478	658.829377	1315.667462	658.337369	12
5	866.444051	433.725664	849.417502	425.212389	848.433486	424.720381	L	1204.635434	602.821355	1187.608885	594.308081	1186.624869	593.816073	11
6	979.528115	490.267696	962.501566	481.754421	961.517550	481.262413	L	1091.551370	546.279323	1074.524821	537.766049	1073.540805	537.274040	10
7	1139.558764	570.283020	1122.532215	561.769746	1121.548199	561.277738	C	978.467306	489.737291	961.440757	481.224017	960.456741	480.732009	9
8	1196.580228	598.793752	1179.553679	590.280478	1178.569663	589.788470	G	818.436657	409.721967	801.410108	401.208692	800.426092	400.716684	8
9	1267.617342	634.312309	1250.590793	625.799035	1249.606777	625.307027	A	761.415193	381.211235	744.388644	372.697960	743.404628	372.205952	7
10	1354.649370	677.828323	1337.622821	669.315049	1336.638805	668.823041	S	690.378079	345.692678	673.351530	337.179403	672.367514	336.687395	6
11	1467.733434	734.370355	1450.706885	725.857081	1449.722869	725.365073	L	603.346051	302.176664	586.319502	293.663389	585.335486	293.171381	5
12	1580.817498	790.912387	1563.790949	782.399113	1562.806933	781.907104	I	490.261987	245.634631	473.235438	237.121357	472.251422	236.629349	4
13	1667.849526	834.428401	1650.822977	825.915127	1649.838961	825.423118	S	377.177923	189.092600	360.151374	180.579325	359.167358	180.087317	3
14	1782.876469	891.941873	1765.849920	883.428598	1764.865904	882.936590	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



RMS error 31 ppm



RMS error 31 ppm

NCBI BLAST search of [SPQELLCGASLISDR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
86.2	1955.980850	0.022538	SPQELLCGASLISDR
17.8	1956.006470	-0.003082	AILRVAELSSDDFHLDR
2.4	1955.975464	0.027924	QHSLHSAQWFAGAFILR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **HQDFNSAVQLVENFCR**

Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

Match to Query 52519: 2274.074502 from(759.032110,3+) rtinseconds(2457) index(71300)

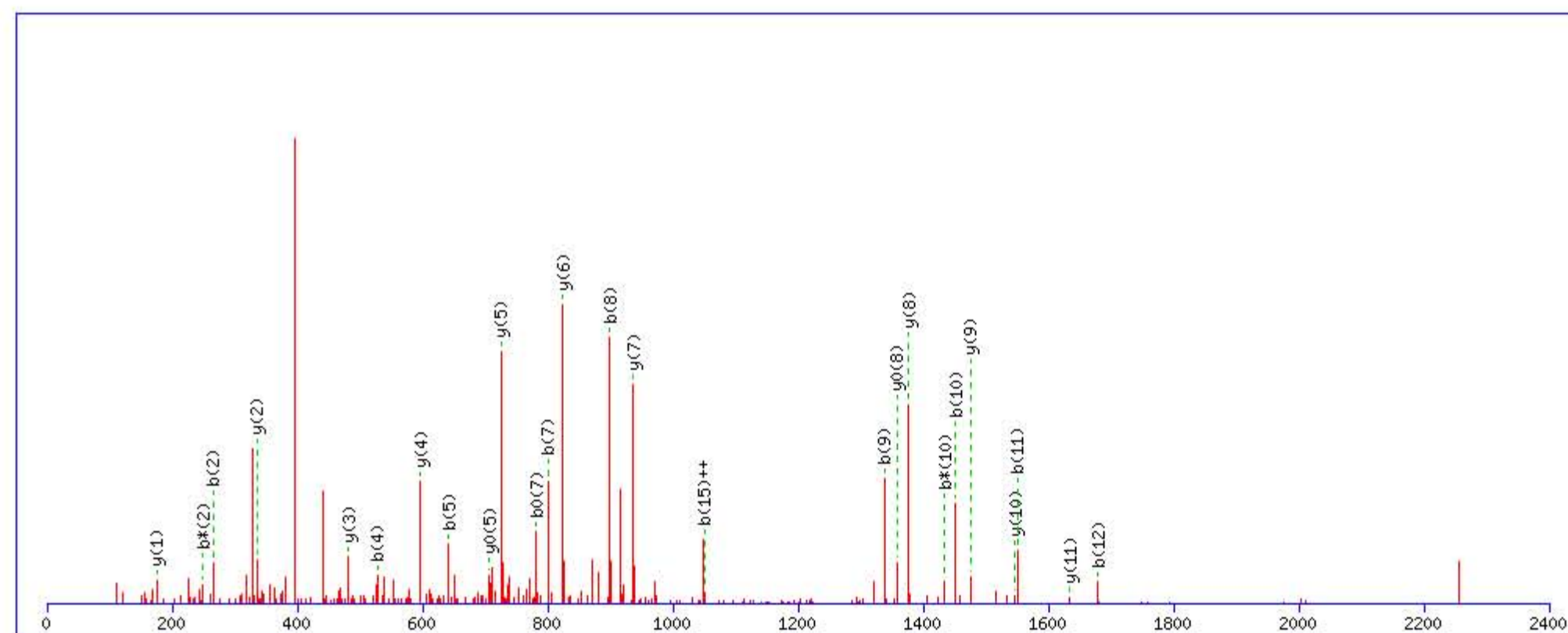
Title: Locus:1.1.1.1793.6 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2274.067398

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

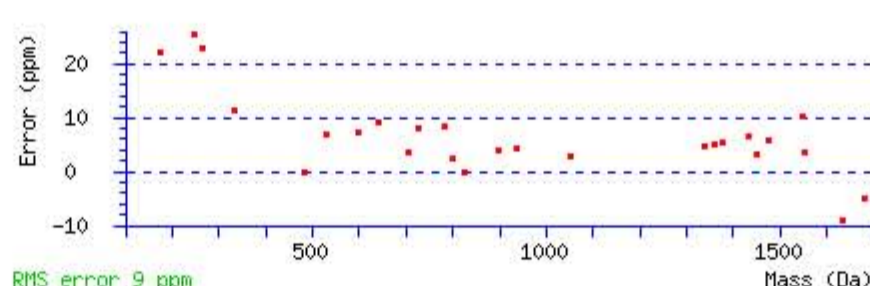
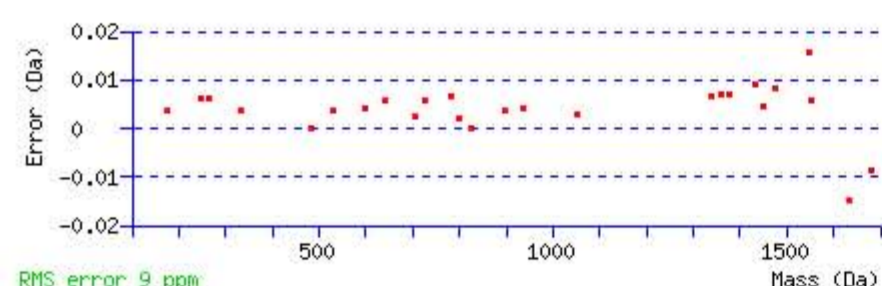
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 55 Expect: 5.7e-005

Matches : 26/166 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							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
55.3	2274.067398	0.007104	HQDFNSAVQLVENFCR
17.6	2274.067398	0.007104	HQDFNSAVQLVENFCR

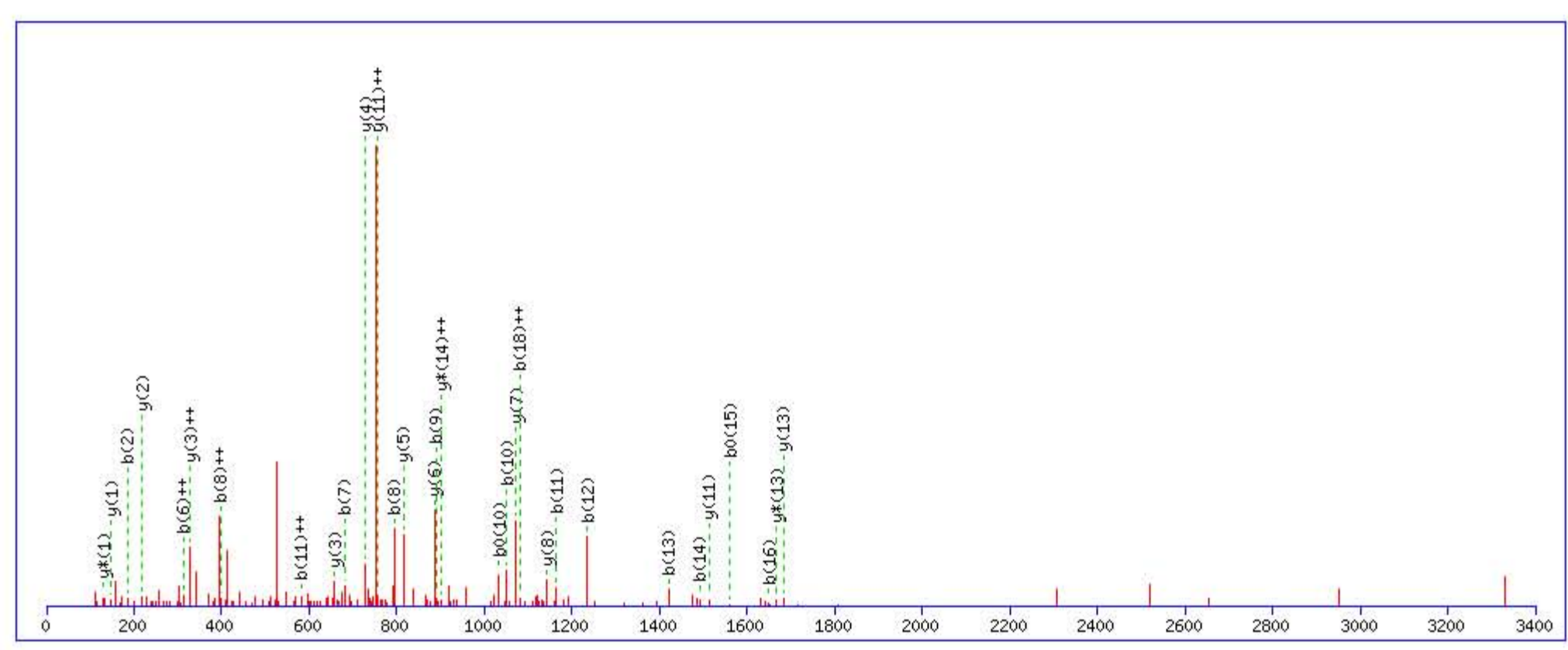
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **LAVTTHGLPCLAWASAQAK**
 Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

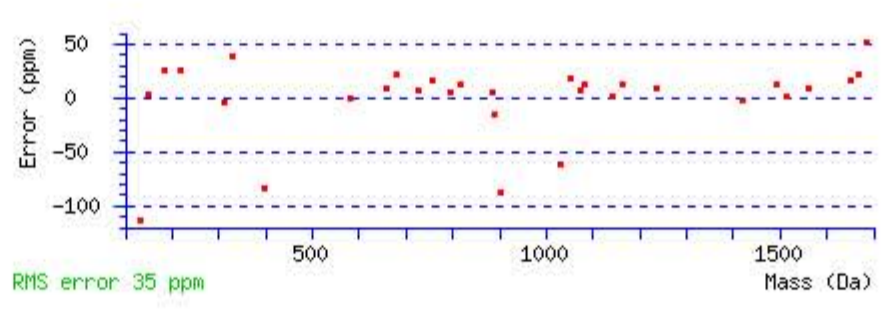
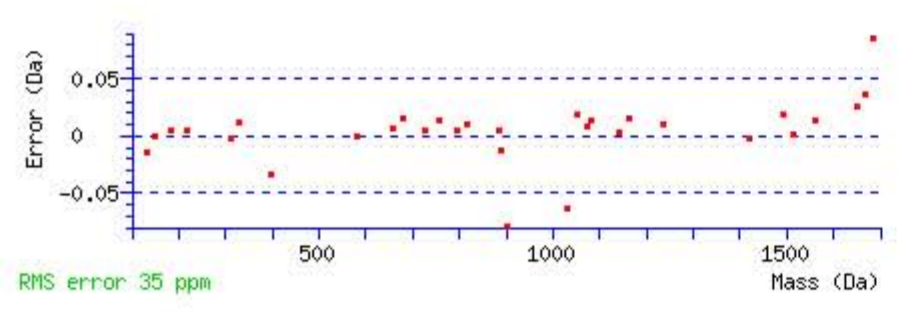
Match to Query 53098: 2305.229082 from(769.416970,3+) rtinseconds(2417) index(55489)
 Title: Locus:1.1.1.1456.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2305.207504
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q17 : Biotin:Thermo-21345 (Q)
 Ions Score: 34 Expect: 0.009
 Matches : 31/170 fragment ions using 98 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							19
2	185.128454	93.067865					A	2193.130730	1097.069003	2176.104181	1088.555728	2175.120165	1088.063720	18
3	284.196868	142.602072					V	2122.093616	1061.550446	2105.067067	1053.037171	2104.083051	1052.545163	17
4	385.244547	193.125912			367.233982	184.120629	T	2023.025202	1012.016239	2005.998653	1003.502965	2005.014637	1003.010957	16
5	486.292226	243.649751			468.281661	234.644469	T	1921.977523	961.492400	1904.950974	952.979125	1903.966958	952.487117	15
6	623.351138	312.179207			605.340573	303.173925	H	1820.929844	910.968560	1803.903295	902.455286	1802.919279	901.963278	14
7	680.372602	340.689939			662.362037	331.684657	G	1683.870932	842.439104	1666.844383	833.925830	1665.860367	833.433822	13
8	793.456666	397.231971			775.446101	388.226689	L	1626.849468	813.928372	1609.822919	805.415098	1608.838903	804.923090	12
9	890.509430	445.758353			872.498865	436.753071	P	1513.765404	757.386340	1496.738855	748.873066	1495.754839	748.381058	11
10	1050.540079	525.773678			1032.529514	516.768395	C	1416.712640	708.859958	1399.686091	700.346684	1398.702075	699.854675	10
11	1163.624143	582.315710			1145.613578	573.310427	L	1256.681991	628.844634	1239.655442	620.331359	1238.671426	619.839351	9
12	1234.661257	617.834267			1216.650692	608.828984	A	1143.597927	572.302602	1126.571378	563.789327	1125.587362	563.297319	8
13	1420.740570	710.873923			1402.730005	701.868640	W	1072.560813	536.784045	1055.534264	528.270770	1054.550248	527.778762	7
14	1491.777684	746.392480			1473.767119	737.387197	A	886.481500	443.744388	869.454951	435.231114	868.470935	434.739106	6
15	1578.809712	789.908494			1560.799147	780.903212	S	815.444386	408.225831	798.417837	399.712557	797.433821	399.220549	5
16	1649.846826	825.427051			1631.836261	816.421768	A	728.412358	364.709817	711.385809	356.196543			4
17	2089.072152	1045.039714	2072.045603	1036.526439	2071.061587	1036.034431	Q	657.375244	329.191260	640.348695	320.677986			3
18	2160.109266	1080.558271	2143.082717	1072.044996	2142.098701	1071.552988	A	218.149918	109.578597	201.123369	101.065323			2
19							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **LAVTTHGLPCLAWASAQAK**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.0	2305.207504	0.021578	LAVTTHGLPCLAWASAQAK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SEGSSVNLSPPLEQVPDR**

Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

Match to Query 54037: 2381.154012 from(794.725280,3+) rtinseconds(2216) index(54364)

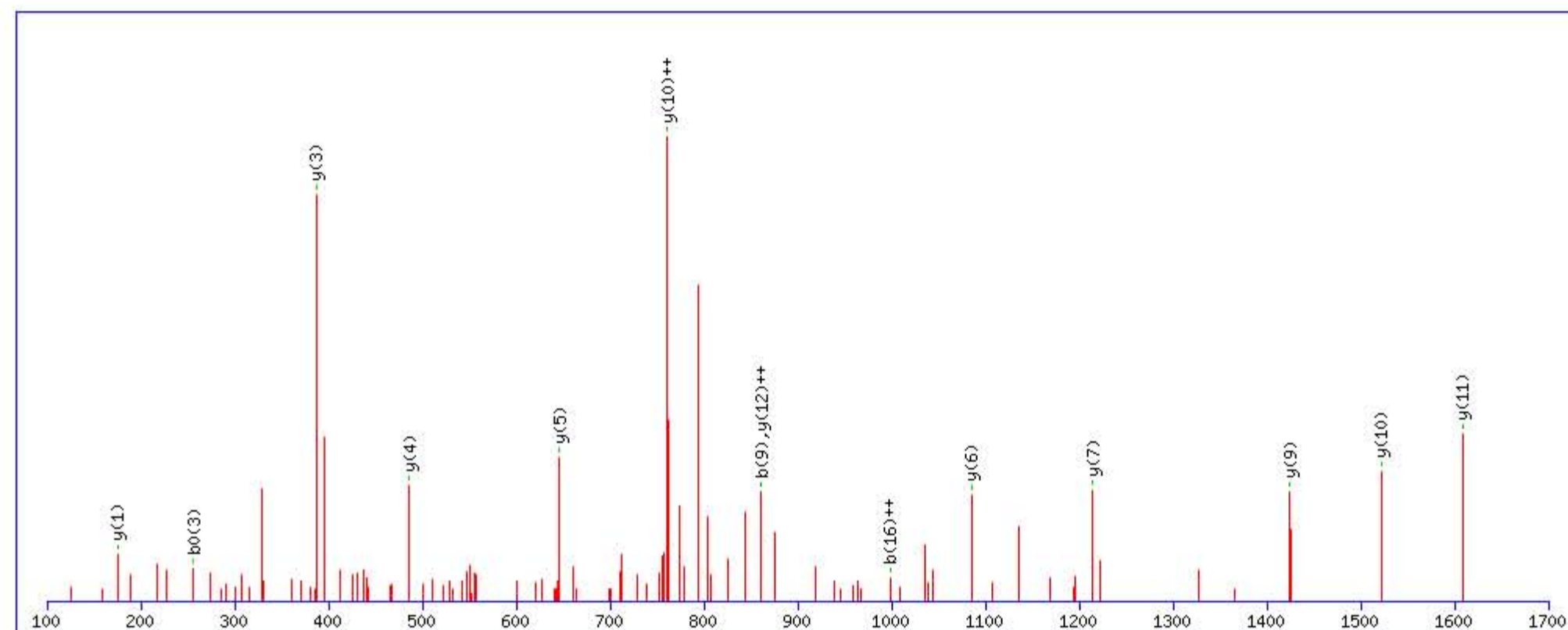
Title: Locus:1.1.1.1386.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2381.135529

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

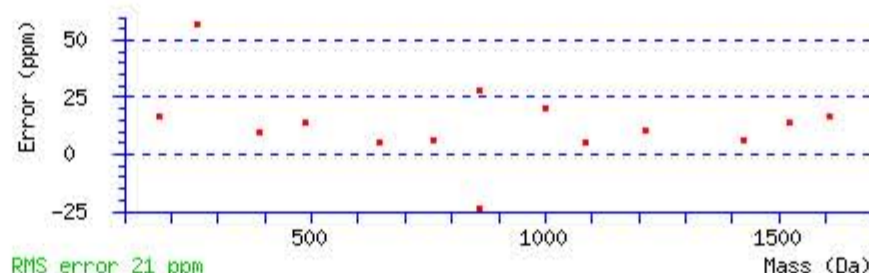
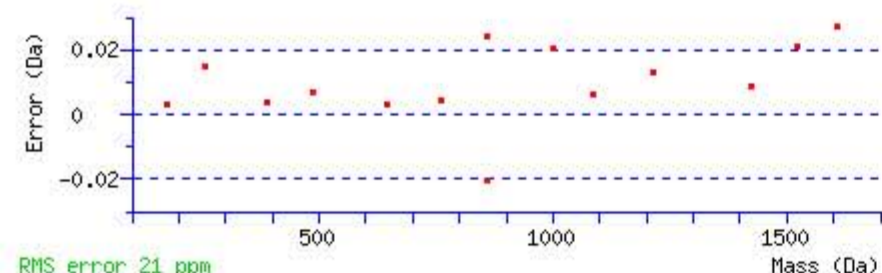
Variable modifications:

Q14 : Biotin:Thermo-21345 (Q)

Ions Score: 80 Expect: 2.5e-007

Matches : 14/202 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							19
2	217.081897	109.044586			199.071332	100.039304	E	2295.110779	1148.059027	2278.084230	1139.545753	2277.100214	1139.053745	18
3	274.103361	137.555319			256.092796	128.550036	G	2166.068186	1083.537731	2149.041637	1075.024456	2148.057621	1074.532448	17
4	361.135389	181.071332			343.124824	172.066050	S	2109.046722	1055.026999	2092.020173	1046.513724	2091.036157	1046.021716	16
5	448.167417	224.587346			430.156852	215.582064	S	2022.014694	1011.510985	2004.988145	1002.997711	2004.004129	1002.505703	15
6	547.235831	274.121554			529.225266	265.116271	V	1934.982666	967.994971	1917.956117	959.481697	1916.972101	958.989689	14
7	661.278758	331.143017	644.252209	322.629742	643.268193	322.137734	N	1835.914252	918.460764	1818.887703	909.947490	1817.903687	909.455482	13
8	774.362822	387.685049	757.336273	379.171774	756.352257	378.679766	L	1721.871325	861.439301	1704.844776	852.926026	1703.860760	852.434018	12
9	861.394850	431.201063	844.368301	422.687788	843.384285	422.195780	S	1608.787261	804.897269	1591.760712	796.383994	1590.776696	795.891986	11
10	958.447614	479.727445	941.421065	471.214170	940.437049	470.722162	P	1521.755233	761.381255	1504.728684	752.867980	1503.744668	752.375972	10
11	1055.500378	528.253827	1038.473829	519.740553	1037.489813	519.248544	P	1424.702469	712.854873	1407.675920	704.341598	1406.691904	703.849590	9
12	1168.584442	584.795859	1151.557893	576.282584	1150.573877	575.790576	L	1327.649705	664.328491	1310.623156	655.815216	1309.639140	655.323208	8
13	1297.627035	649.317155	1280.600486	640.803881	1279.616470	640.311873	E	1214.565641	607.786459	1197.539092	599.273184	1196.555076	598.781176	7
14	1736.852361	868.929819	1719.825812	860.416544	1718.841796	859.924536	Q	1085.523048	543.265162	1068.496499	534.751888	1067.512483	534.259880	6
15	1896.883010	948.945143	1879.856461	940.431869	1878.872445	939.939861	C	646.297722	323.652499	629.271173	315.139225	628.287157	314.647217	5
16	1995.951424	998.479350	1978.924875	989.966076	1977.940859	989.474068	V	486.267073	243.637174	469.240524	235.123900	468.256508	234.631892	4
17	2093.004188	1047.005732	2075.977639	1038.492457	2074.993623	1038.000449	P	387.198659	194.102967	370.172110	185.589693	369.188094	185.097685	3
18	2208.031131	1104.519203	2191.004582	1096.005929	2190.020566	1095.513921	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
19							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [SEGSSVNLSPPLEQVPDR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
79.8	2381.135529	0.018483	SEGSSVNLSPPLEQVPDR

Mascot: <http://www.matrixscience.com/>

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 57176: 2542.431656 from(636.615190,4+) rtinseconds(2562) index(56325)

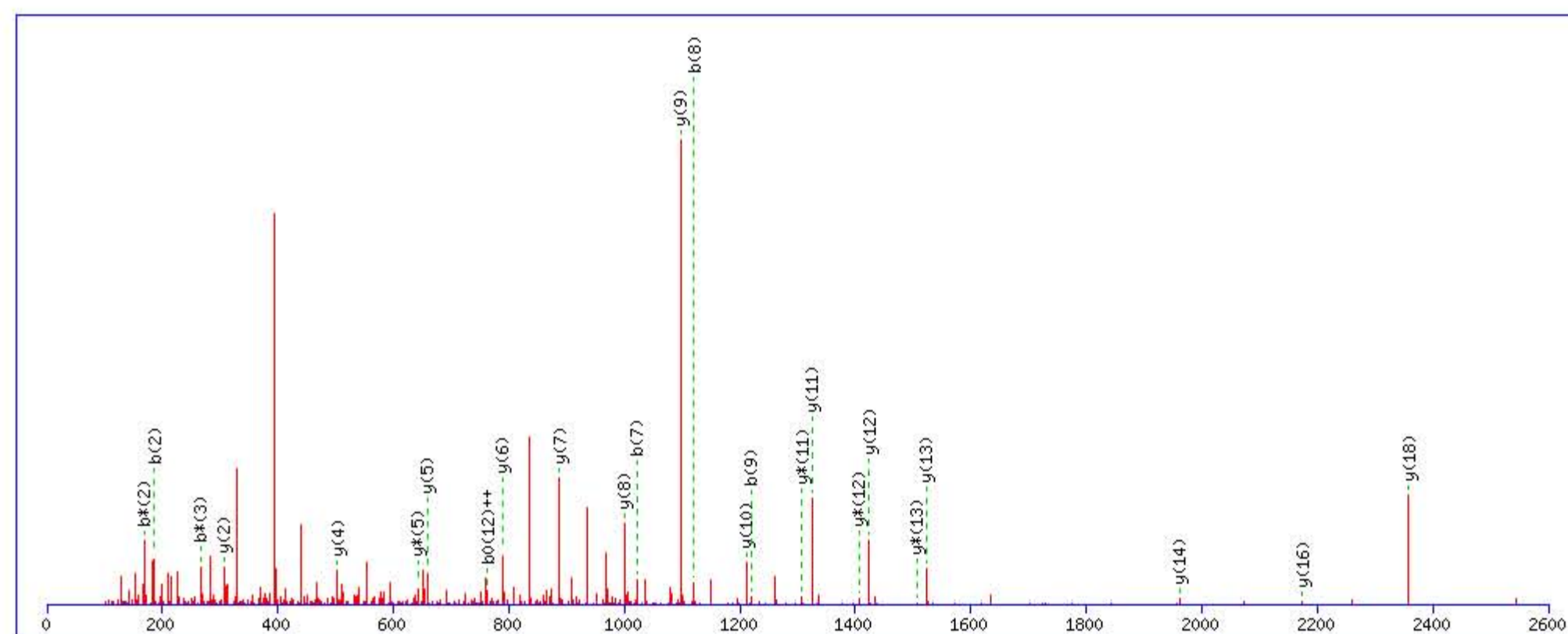
Title: Locus:1.1.1.1507.4 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2542.412766

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

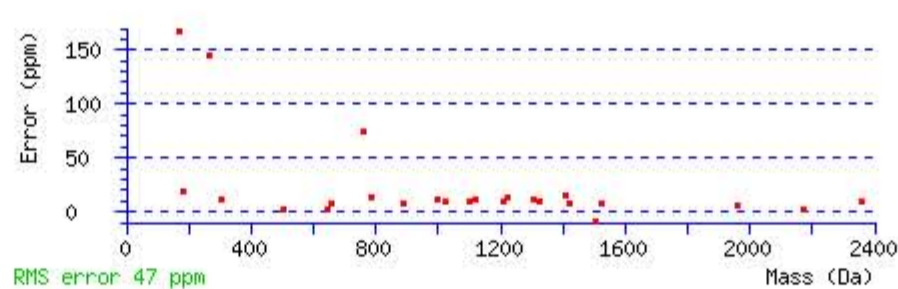
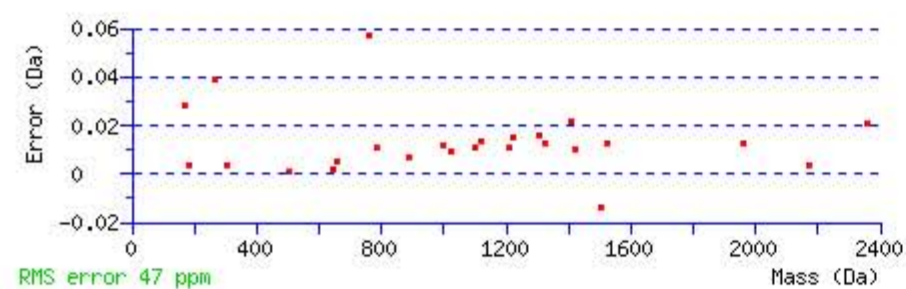
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 71 Expect: 5e-007

Matches : 25/210 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	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
71.2	2542.412766	0.018890	GQPSVLQVVNLPIVERPVCK
38.0	2542.412766	0.018890	GQPSVLQVVNLPIVERPVCK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **IVEGSDAEIGMSPWQVMLFR**

Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

Match to Query 57515: 2591.285442 from(864.769090,3+) rtinseconds(2882) index(58542)

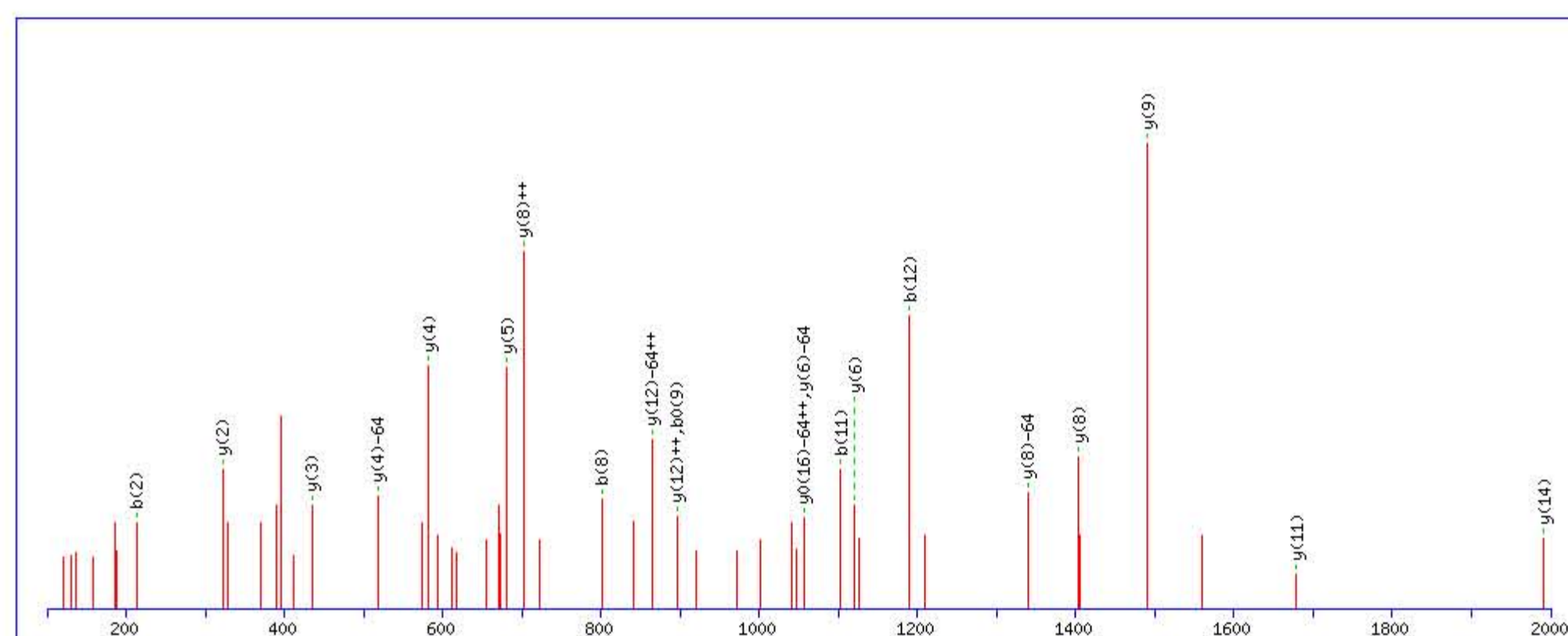
Title: Locus:1.1.1.1616.22 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2591.258621

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

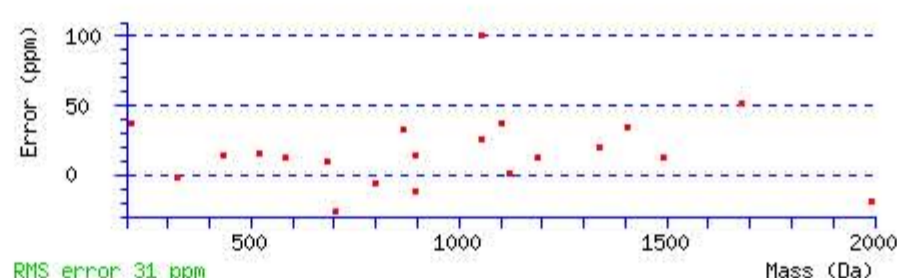
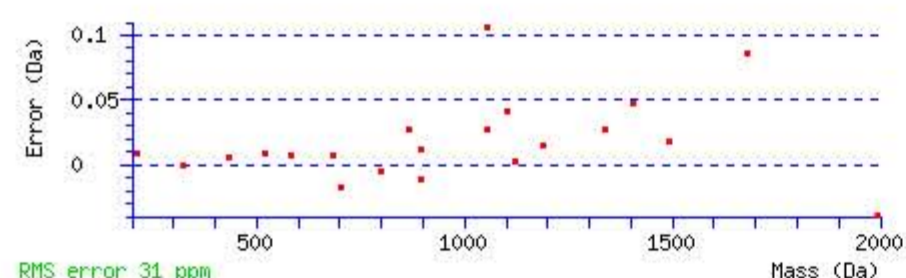
Q15 : Biotin:Thermo-21345 (Q)

M17 : Oxidation (M), with neutral losses 0.000000 (shown in table), 63.998285

Ions Score: 61 Expect: 2.6e-006

Matches : 21/284 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	114.091340	57.549308					I							20
2	213.159754	107.083515					V	2479.181837	1240.094556	2462.155288	1231.581282	2461.171272	1231.089274	19
3	342.202347	171.604811			324.191782	162.599529	E	2380.113423	1190.560349	2363.086874	1182.047075	2362.102858	1181.555067	18
4	399.223811	200.115543			381.213246	191.110261	G	2251.070830	1126.039053	2234.044281	1117.525778	2233.060265	1117.033770	17
5	486.255839	243.631557			468.245274	234.626275	S	2194.049366	1097.528321	2177.022817	1089.015046	2176.038801	1088.523038	16
6	601.282782	301.145029			583.272217	292.139747	D	2107.017338	1054.012307	2089.990789	1045.499032	2089.006773	1045.007024	15
7	672.319896	336.663586			654.309331	327.658303	A	1991.990395	996.498836	1974.963846	987.985561	1973.979830	987.493553	14
8	801.362489	401.184883			783.351924	392.179600	E	1920.953281	960.980279	1903.926732	952.467004	1902.942716	951.974996	13
9	914.446553	457.726915			896.435988	448.721632	I	1791.910688	896.458982	1774.884139	887.945708	1773.900123	887.453700	12
10	971.468017	486.237647			953.457452	477.232364	G	1678.826624	839.916950	1661.800075	831.403676	1660.816059	830.911668	11
11	1102.508502	551.757889			1084.497937	542.752606	M	1621.805160	811.406218	1604.778611	802.892944	1603.794595	802.400936	10
12	1189.540530	595.273903			1171.529965	586.268621	S	1490.764675	745.885976	1473.738126	737.372701	1472.754110	736.880693	9
13	1286.593294	643.800285			1268.582729	634.795003	P	1403.732647	702.369962	1386.706098	693.856687			8
14	1472.672607	736.839942			1454.662042	727.834659	W	1306.679883	653.843580	1289.653334	645.330305			7
15	1911.897933	956.452605	1894.871384	947.939330	1893.887368	947.447322	Q	1120.600570	560.803923	1103.574021	552.290649			6
16	2010.966347	1005.986812	1993.939798	997.473537	1992.955782	996.981529	V	681.375244	341.191260	664.348695	332.677986			5
17	2158.001747	1079.504511	2140.975198	1070.991237	2139.991182	1070.499229	M	582.306830	291.657053	565.280281	283.143779			4
18	2271.085811	1136.046543	2254.059262	1127.533269	2253.075246	1127.041261	L	435.271430	218.139353	418.244881	209.626078			3
19	2418.154225	1209.580750	2401.127676	1201.067476	2400.143660	1200.575468	F	322.187366	161.597321	305.160817	153.084046			2
20							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [IVEGSDAEIGMSPWQVMLFR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

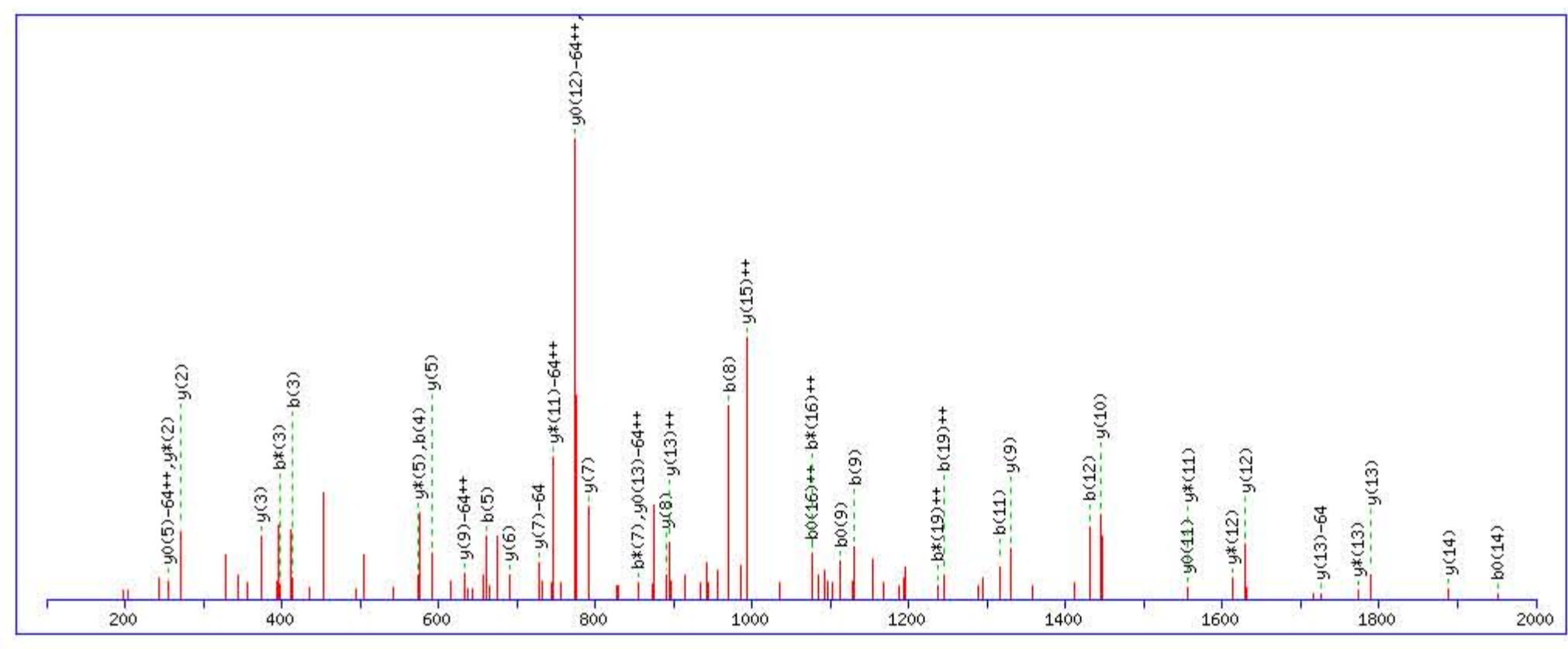
Score	Mr(calc):	Delta	Sequence
60.8	2591.258621	0.026821	IVEGSDAEIGMSPWQVMLFR
3.5	2591.258621	0.026821	IVEGSDAEIGMSPWQVMLFR
1.2	2591.315231	-0.029789	FLASDKPQEMANASLTLETPLTSK

Peptide View

MS/MS Fragmentation of **RQECSIPVCGDQVTVAMTPR**
 Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

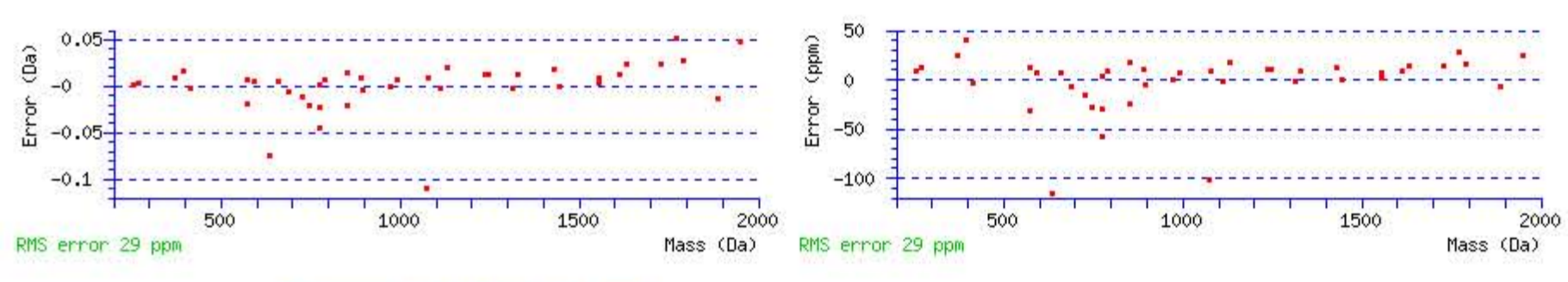
Match to Query 58963: 2758.319652 from(920.447160,3+) rtinseconds(1855) index(51875)
 Title: Locus:1.1.1.1261.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2758.302322
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q13 : Biotin:Thermo-21345 (Q)
 M18 : Oxidation (M), with neutral losses 0.000000 (shown in table), 63.998285
 Ions Score: 50 Expect: 0.0002
 Matches : 43/352 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	157.108387	79.057831	140.081838	70.544557			R							21
2	285.166965	143.087121	268.140416	134.573846			Q	2603.208466	1302.107871	2586.181917	1293.594596	2585.197901	1293.102588	20
3	414.209558	207.608417	397.183009	199.095143	396.198993	198.603135	E	2475.149888	1238.078582	2458.123339	1229.565307	2457.139323	1229.073299	19
4	574.240207	287.623742	557.213658	279.110467	556.229642	278.618459	C	2346.107295	1173.557285	2329.080746	1165.044011	2328.096730	1164.552003	18
5	661.272235	331.139756	644.245686	322.626481	643.261670	322.134473	S	2186.076646	1093.541961	2169.050097	1085.028686	2168.066081	1084.536678	17
6	774.356299	387.681788	757.329750	379.168513	756.345734	378.676505	I	2099.044618	1050.025947	2082.018069	1041.512672	2081.034053	1041.020664	16
7	871.409063	436.208170	854.382514	427.694895	853.398498	427.202887	P	1985.960554	993.483915	1968.934005	984.970641	1967.949989	984.478633	15
8	970.477477	485.742377	953.450928	477.229102	952.466912	476.737094	V	1888.907790	944.957533	1871.881241	936.444259	1870.897225	935.952251	14
9	1130.508126	565.757701	1113.481577	557.244427	1112.497561	556.752418	C	1789.839376	895.423326	1772.812827	886.910052	1771.828811	886.418044	13
10	1187.529590	594.268433	1170.503041	585.755158	1169.519025	585.263150	G	1629.808727	815.408002	1612.782178	806.894727	1611.798162	806.402719	12
11	1315.588168	658.297722	1298.561619	649.784448	1297.577603	649.292440	Q	1572.787263	786.897270	1555.760714	778.383995	1554.776698	777.891987	11
12	1430.615111	715.811194	1413.588562	707.297919	1412.604546	706.805911	D	1444.728685	722.867981	1427.702136	714.354706	1426.718120	713.862698	10
13	1869.840437	935.423857	1852.813888	926.910582	1851.829872	926.418574	Q	1329.701742	665.354509	1312.675193	656.841235	1311.691177	656.349227	9
14	1968.908851	984.958064	1951.882302	976.444789	1950.898286	975.952781	V	890.476416	445.741846	873.449867	437.228572	872.465851	436.736564	8
15	2069.956530	1035.481903	2052.929981	1026.968628	2051.945965	1026.476620	T	791.408002	396.207639	774.381453	387.694365	773.397437	387.202357	7
16	2169.024944	1085.016110	2151.998395	1076.502835	2151.014379	1076.010827	V	690.360323	345.683800	673.333774	337.170525	672.349758	336.678517	6
17	2240.062058	1120.534667	2223.035509	1112.021392	2222.051493	1111.529384	A	591.291909	296.149593	574.265360	287.636318	573.281344	287.144310	5
18	2387.097458	1194.052367	2370.070909	1185.539092	2369.086893	1185.047085	M	520.254795	260.631036	503.228246	252.117761	502.244230	251.625753	4
19	2488.145137	1244.576206	2471.118588	1236.062932	2470.134572	1235.570924	T	373.219395	187.113335	356.192846	178.600061	355.208830	178.108053	3
20	2585.197901	1293.102588	2568.171352	1284.589314	2567.187336	1284.097306	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 [RQECSIPVCGDQVTVAMTPR](#)
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.5	2758.302322	0.017330	RQECSIPVCGDQVTVAMTPR
31.7	2758.302322	0.017330	RQECSIPVCGDQVTVAMTPR

Peptide View

MS/MS Fragmentation of **RQECSIPVCGDQVTVAMTPR**

Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

Match to Query 62077: 3053.508732 from(1018.843520,3+) rtinseconds(2233) index(54449)

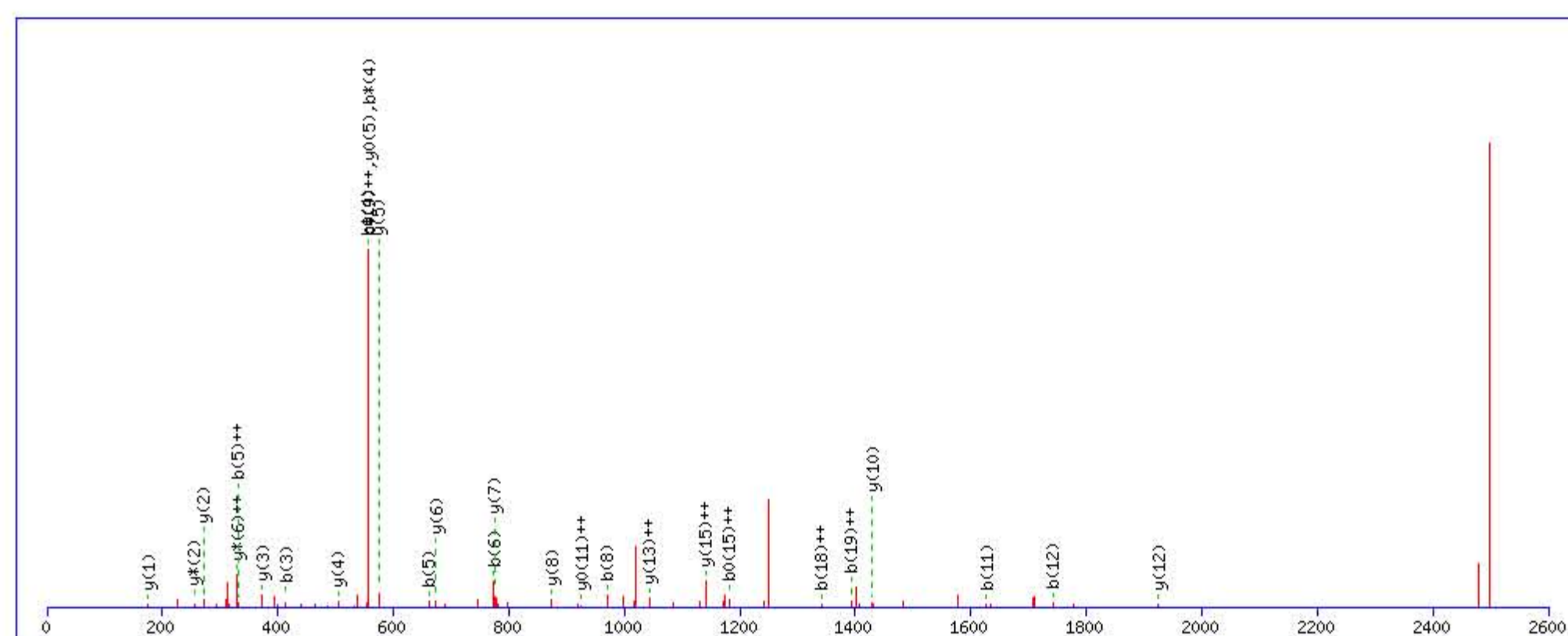
Title: Locus:1.1.1.1392.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3053.474152

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

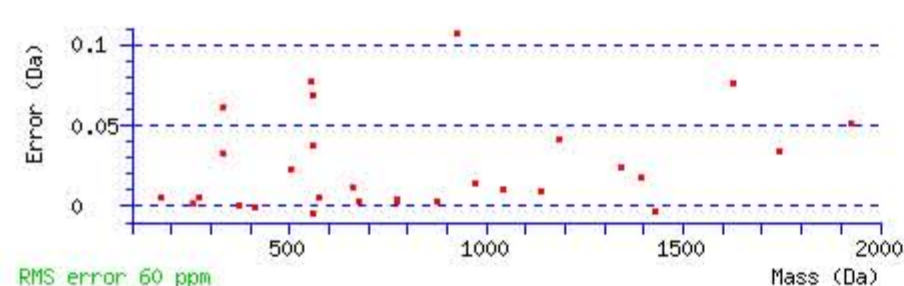
Q11 : Biotin:Thermo-21345 (Q)

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 34 Expect: 0.012

Matches : 29/232 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	157.108387	79.057831	140.081838	70.544557			R							21
2	285.166965	143.087121	268.140416	134.573846			Q	2898.380299	1449.693787	2881.353750	1441.180513	2880.369734	1440.688505	20
3	414.209558	207.608417	397.183009	199.095143	396.198993	198.603135	E	2770.321721	1385.664498	2753.295172	1377.151224	2752.311156	1376.659216	19
4	574.240207	287.623742	557.213658	279.110467	556.229642	278.618459	C	2641.279128	1321.143202	2624.252579	1312.629927	2623.268563	1312.137919	18
5	661.272235	331.139756	644.245686	322.626481	643.261670	322.134473	S	2481.248479	1241.127877	2464.221930	1232.614603	2463.237914	1232.122595	17
6	774.356299	387.681788	757.329750	379.168513	756.345734	378.676505	I	2394.216451	1197.611863	2377.189902	1189.098589	2376.205886	1188.606581	16
7	871.409063	436.208170	854.382514	427.694895	853.398498	427.202887	P	2281.132387	1141.069831	2264.105838	1132.556557	2263.121822	1132.064549	15
8	970.477477	485.742377	953.450928	477.229102	952.466912	476.737094	V	2184.079623	1092.543449	2167.053074	1084.030175	2166.069058	1083.538167	14
9	1130.508126	565.757701	1113.481577	557.244427	1112.497561	556.752418	C	2085.011209	1043.009242	2067.984660	1034.495968	2067.000644	1034.003960	13
10	1187.529590	594.268433	1170.503041	585.755158	1169.519025	585.263150	G	1924.980560	962.993918	1907.954011	954.480643	1906.969995	953.988635	12
11	1626.754916	813.881096	1609.728367	805.367822	1608.744351	804.875814	Q	1867.959096	934.483186	1850.932547	925.969911	1849.948531	925.477903	11
12	1741.781859	871.394568	1724.755310	862.881293	1723.771294	862.389285	D	1428.733770	714.870523	1411.707221	706.357248	1410.723205	705.865240	10
13	2181.007185	1091.007230	2163.980636	1082.493956	2162.996620	1082.001948	Q	1313.706827	657.357051	1296.680278	648.843777	1295.696262	648.351769	9
14	2280.075599	1140.541437	2263.049050	1132.028163	2262.065034	1131.536155	V	874.481501	437.744388	857.454952	429.231114	856.470936	428.739106	8
15	2381.123278	1191.065277	2364.096729	1182.552002	2363.112713	1182.059994	T	775.413087	388.210181	758.386538	379.696907	757.402522	379.204899	7
16	2480.191692	1240.599484	2463.165143	1232.086209	2462.181127	1231.594201	V	674.365408	337.686342	657.338859	329.173067	656.354843	328.681059	6
17	2551.228806	1276.118041	2534.202257	1267.604766	2533.218241	1267.112758	A	575.296994	288.152135	558.270445	279.638861	557.286429	279.146853	5
18	2682.269291	1341.638283	2665.242742	1333.125009	2664.258726	1332.633001	M	504.259880	252.633578	487.233331	244.120303	486.249315	243.628295	4
19	2783.316970	1392.162123	2766.290421	1383.648848	2765.306405	1383.156840	T	373.219395	187.113335	356.192846	178.600061	355.208830	178.108053	3
20	2880.369734	1440.688505	2863.343185	1432.175230	2862.359169	1431.683222	P	272.171716	136.589496	255.145167	128.076221			2
21							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [RQECSIPVCGDQVTVAMTPR](#)

(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	3053.474152	0.034580	RQECSIPVCGDQVTVAMTPR
12.0	3053.474152	0.034580	RQECSIPVCGDQVTVAMTPR
1.0	3053.474152	0.034580	RQECSIPVCGDQVTVAMTPR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **CINQLLCK**

Found in **SEPP1_HUMAN**, Selenoprotein P OS=Homo sapiens GN=SEPP1 PE=1 SV=3

Match to Query 28694: 1358.700428 from(680.357490,2+) rtinseconds(2019) index(53061)

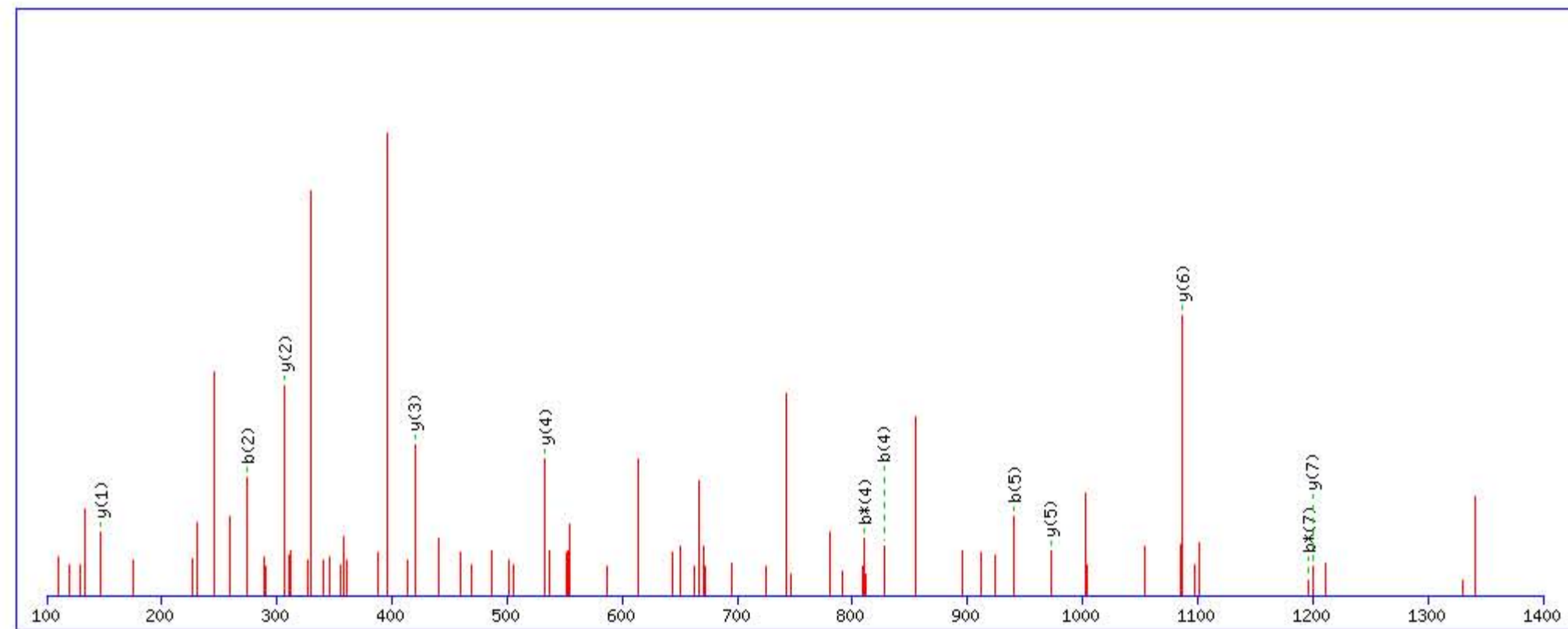
Title: Locus:1.1.1.1318.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1358.687256

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

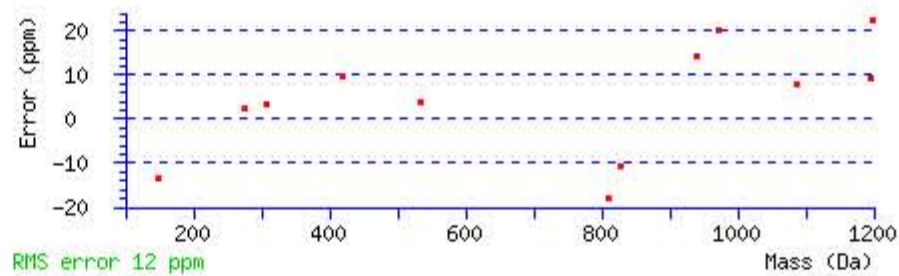
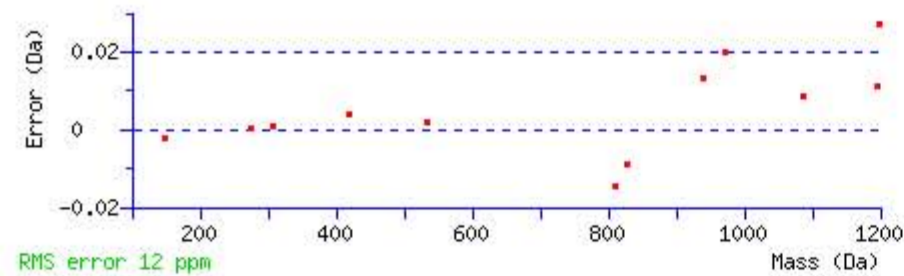
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.043

Matches : 12/52 fragment ions using 35 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	161.037925	81.022600			C					8
2	274.121989	137.564632			I	1199.663898	600.335587	1182.637349	591.822313	7
3	388.164916	194.586096	371.138367	186.072822	N	1086.579834	543.793555	1069.553285	535.280281	6
4	827.390242	414.198759	810.363693	405.685485	Q	972.536907	486.772092	955.510358	478.258817	5
5	940.474306	470.740791	923.447757	462.227517	L	533.311581	267.159429	516.285032	258.646154	4
6	1053.558370	527.282823	1036.531821	518.769549	L	420.227517	210.617396	403.200968	202.104122	3
7	1213.589019	607.298148	1196.562470	598.784873	C	307.143453	154.075365	290.116904	145.562090	2
8					K	147.112804	74.060040	130.086255	65.546765	1



NCBI BLAST search of **CINQLLCK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.2	1358.687256	0.013172	CINQLLCK
11.9	1358.701645	-0.001217	EEVFIQQR
5.6	1358.701645	-0.001217	EEVFIQQR
2.7	1358.687744	0.012684	FVKKDGHCNVR

Mascot: <http://www.matrixscience.com/>

MASCOT 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 33219: 1476.747852 from(493.256560,3+) rtinseconds(1192) index(1133)

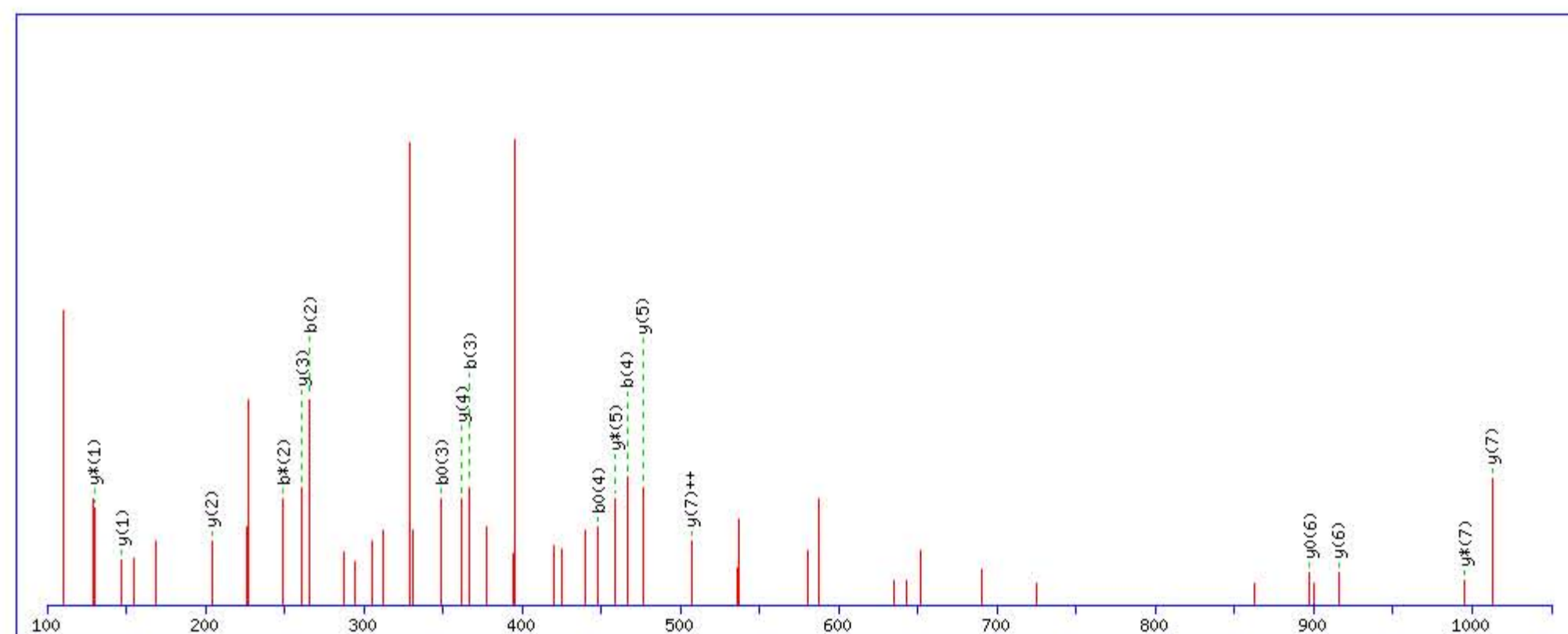
Title: Locus:1.1.1.1224.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1476.750748

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

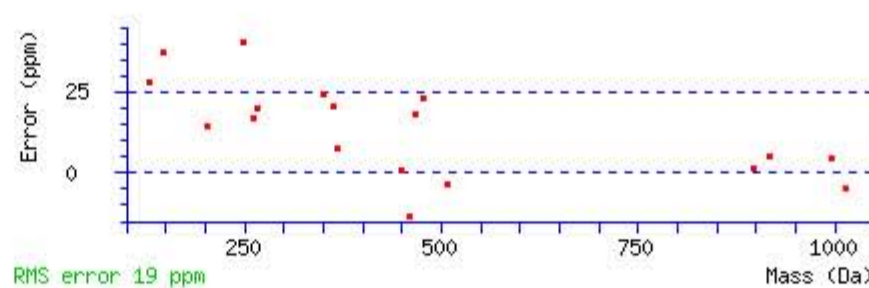
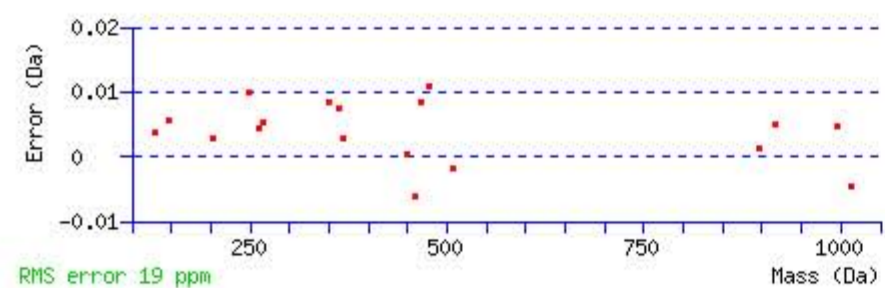
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.017

Matches : 18/108 fragment ions using 43 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	138.066188	69.536732					H							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
26.7	1476.750748	-0.002896	HQTVPQNTGGK
7.7	1476.736115	0.011737	HQEALIGQSFYFK
3.5	1476.750748	-0.002896	HQTVPQNTGGK

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 34006: 1505.709588 from(753.862070,2+) rtinseconds(2054) index(69133)

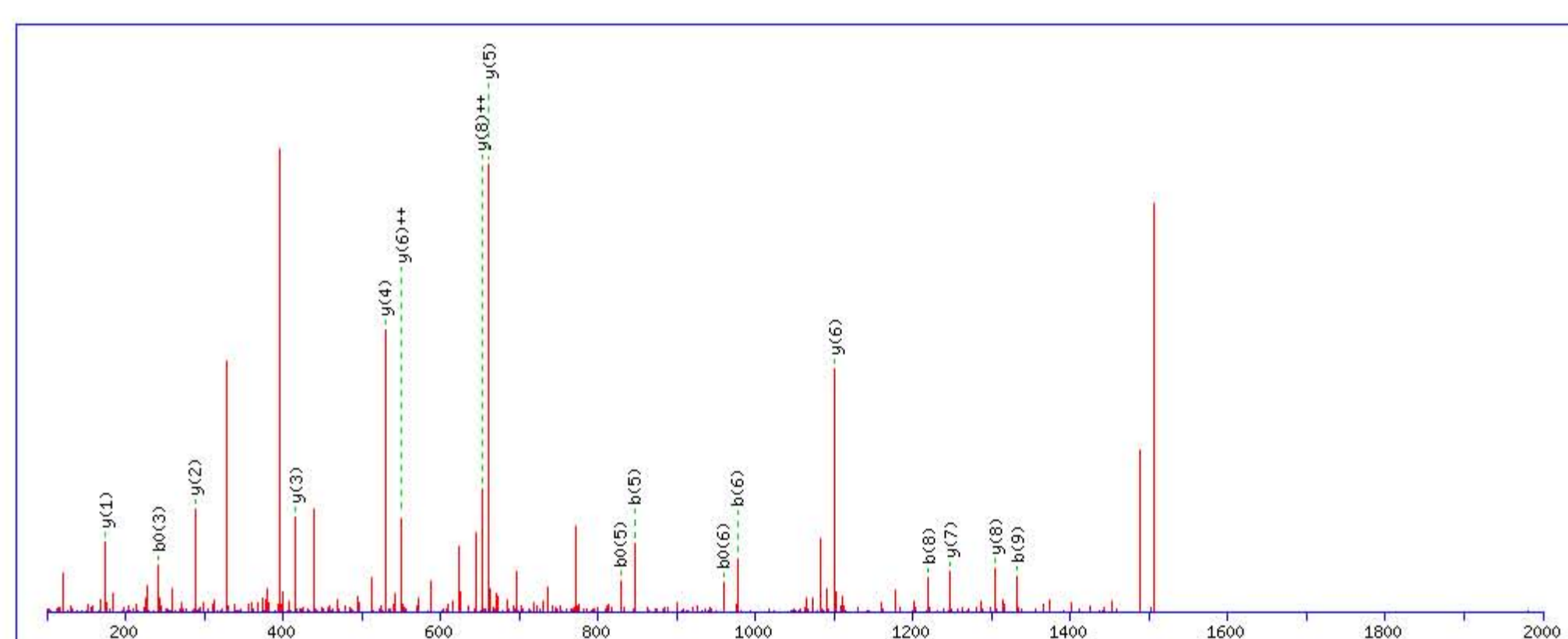
Title: Locus:1.1.1.1652.22 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1505.711899

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

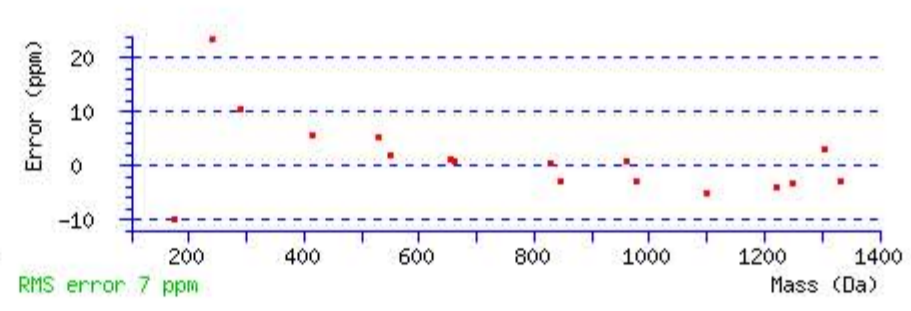
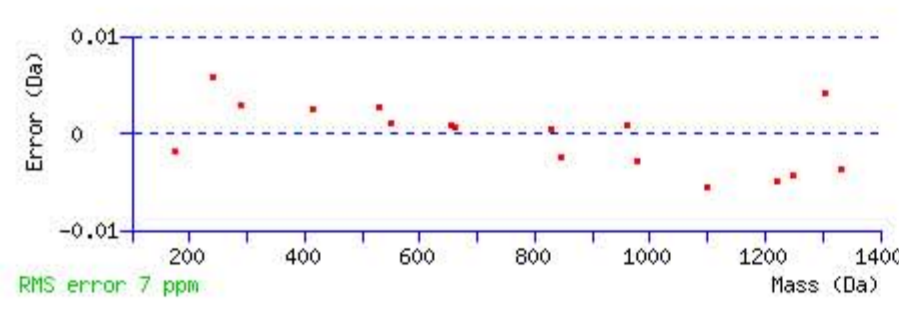
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 55 Expect: 4.6e-005

Matches : 17/84 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	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
55.0	1505.711899	-0.002311	DSGFQMNQLR
17.6	1505.711899	-0.002311	DSGFQMNQLR
15.0	1505.703140	0.006448	DETMEEQDIKLR
7.1	1505.704025	0.005563	MQMEIDQLR
1.0	1505.691910	0.017678	MEDLLDLDEELR

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 38970: 1633.802428 from(817.908490,2+) rtinseconds(1858) index(67725)

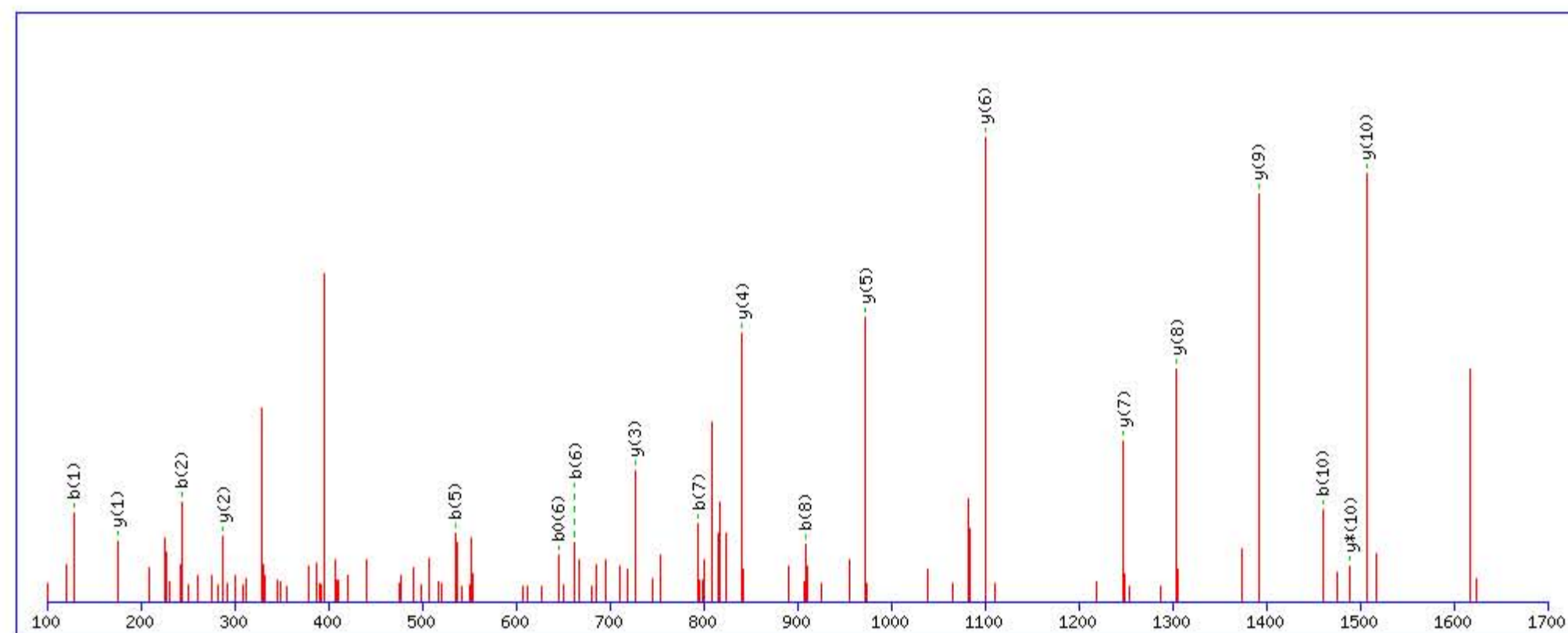
Title: Locus:1.1.1.1584.9 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1633.806854

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

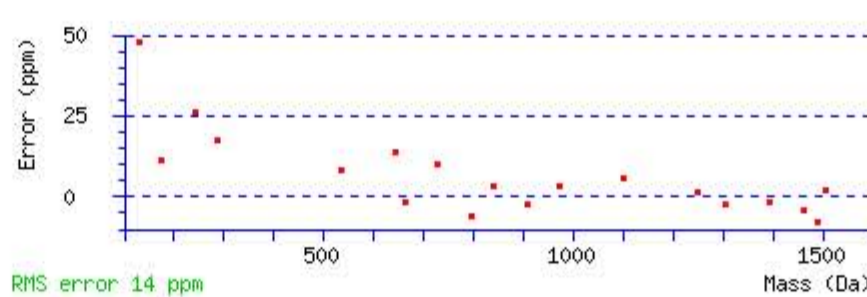
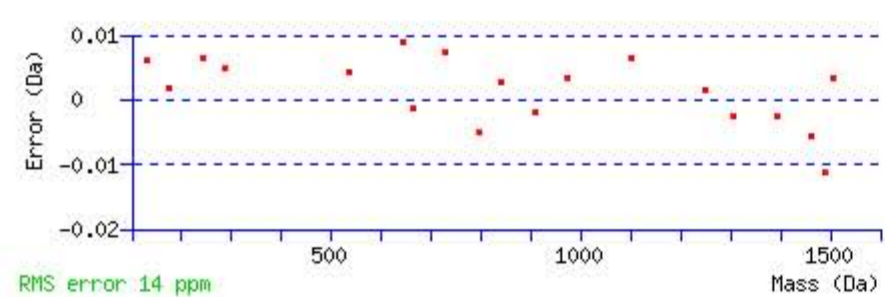
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 75 Expect: 7e-007

Matches : 19/102 fragment ions using 32 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.102239	65.054757	112.075690	56.541483			K							11
2	244.129182	122.568229	227.102633	114.054955	226.118617	113.562947	D	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	663.309666	332.158471	646.283117	323.645197	645.299101	323.153189	Q	1100.570332	550.788804	1083.543783	542.275530			6
7	794.350151	397.678714	777.323602	389.165439	776.339586	388.673431	M	972.511754	486.759515	955.485205	478.246240			5
8	908.393078	454.700177	891.366529	446.186903	890.382513	445.694895	N	841.471269	421.239272	824.444720	412.725998			4
9	1347.618404	674.312840	1330.591855	665.799566	1329.607839	665.307558	Q	727.428342	364.217809	710.401793	355.704534			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
74.9	1633.806854	-0.004426	KDSGFQMNQLR
30.9	1633.806854	-0.004426	KDSGFQMNQLR
13.7	1633.822128	-0.019700	QFMKGQVSWGR
11.2	1633.798096	0.004332	QDQEKDNMIEKLK
9.3	1633.795609	0.006819	KFMEDEQQLR
8.7	1633.799454	0.002974	DANSFKSRDQR
8.1	1633.810699	-0.008271	DQTIRIWSCSRGR
5.5	1633.784180	0.018248	QEESVQKQAMRR
3.6	1633.803482	-0.001054	QLFERDWSSR
2.6	1633.795609	0.006819	KFMEDEQQLR

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 42493: 1787.913972 from(596.978600,3+) rtinseconds(1583) index(66373)

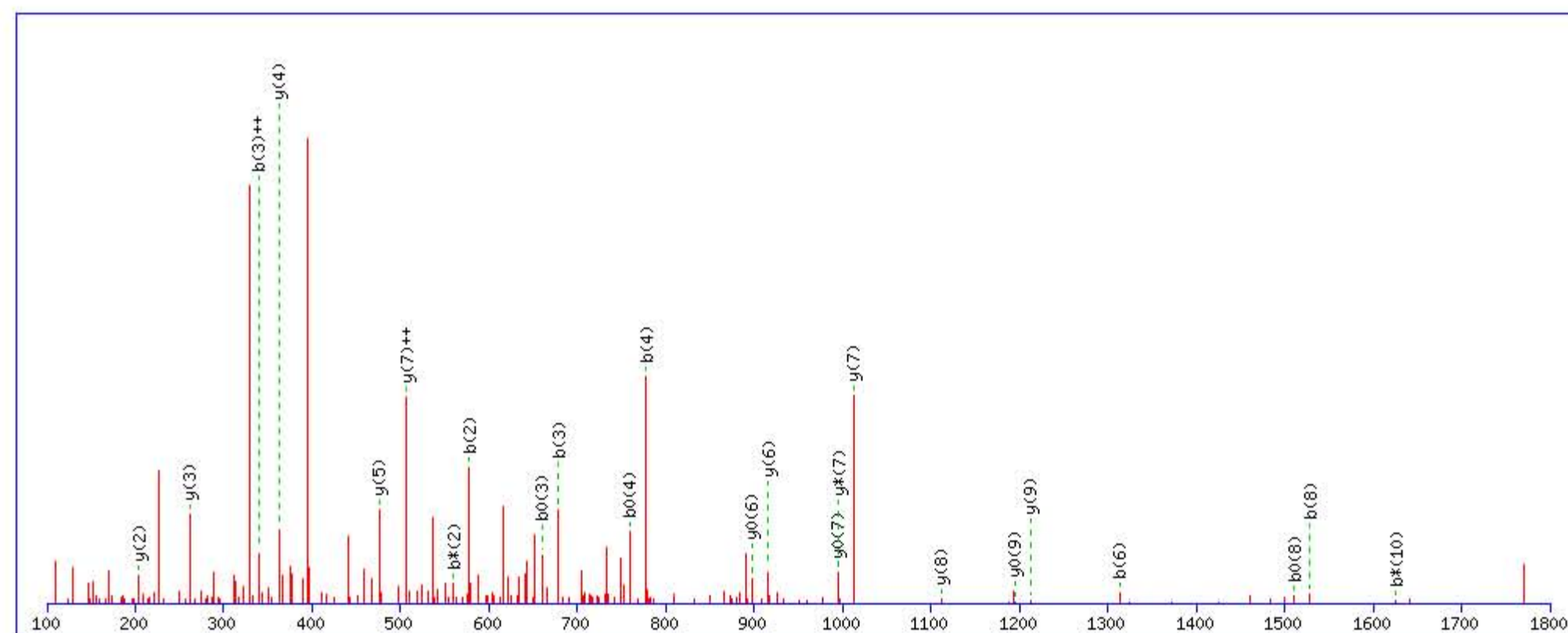
Title: Locus:1.1.1.1488.13 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1787.917496

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

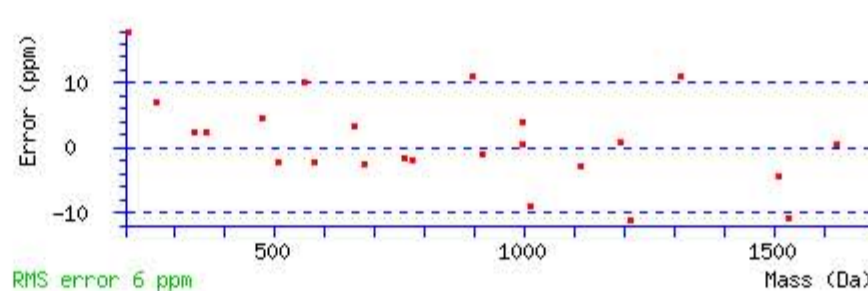
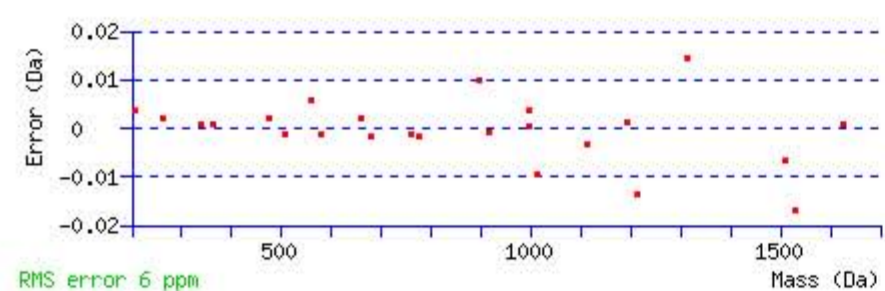
Q2 : Biotin:Thermo-21345 (Q)

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.0057

Matches : 24/108 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	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
27.9	1787.917496	-0.003524	HQTVPQNTGGK
3.8	1787.923996	-0.010024	VPLQGFAALEGMNGIQK
2.1	1787.925323	-0.011351	THRAVLAACSHYFKK
1.1	1787.935211	-0.021239	ARAYGPGIEPTGNMVKK
0.5	1787.912735	0.001237	FLLEDEKHIQEMLK

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 42737: 1801.916862 from(601.646230,3+) rtinseconds(1757) index(67246)

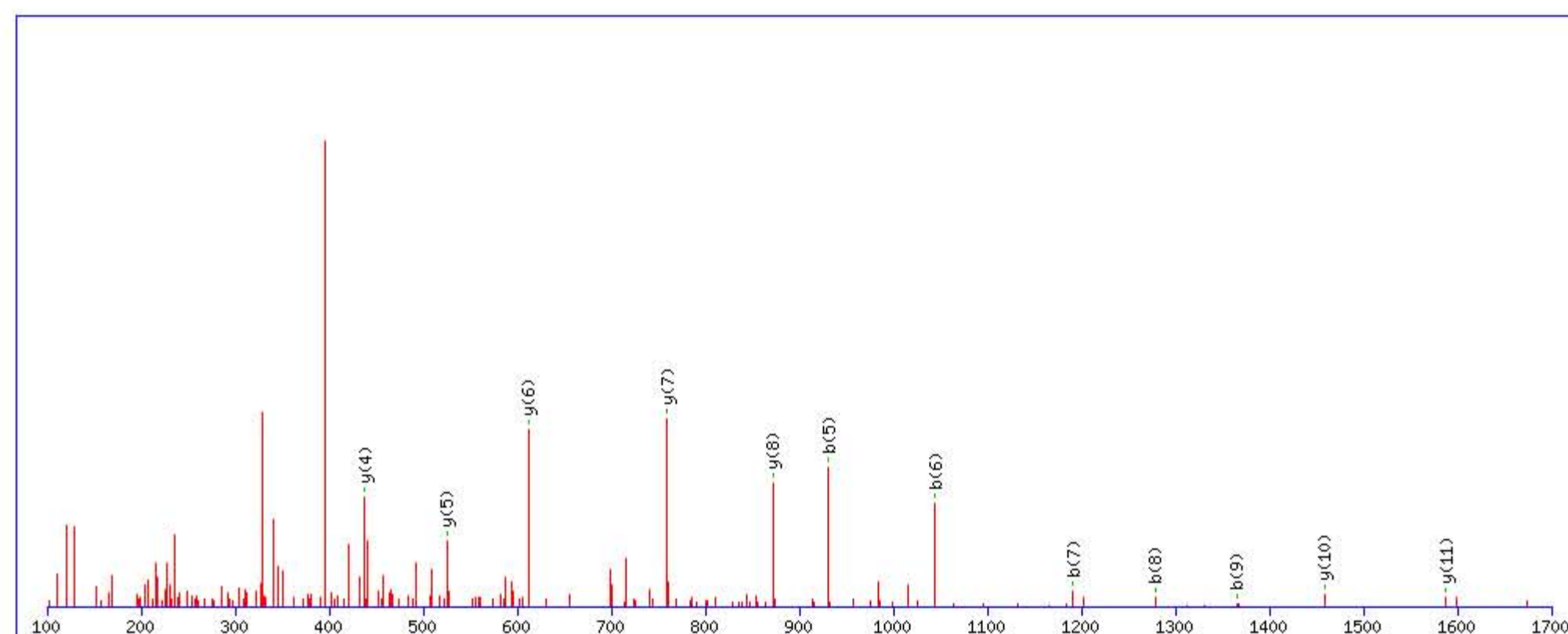
Title: Locus:1.1.1.1549.18 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1801.918518

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

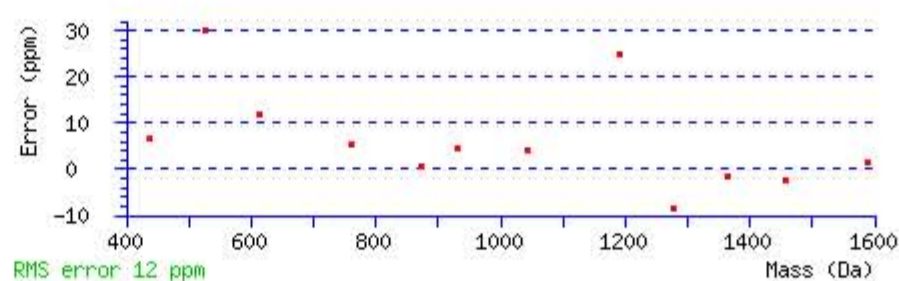
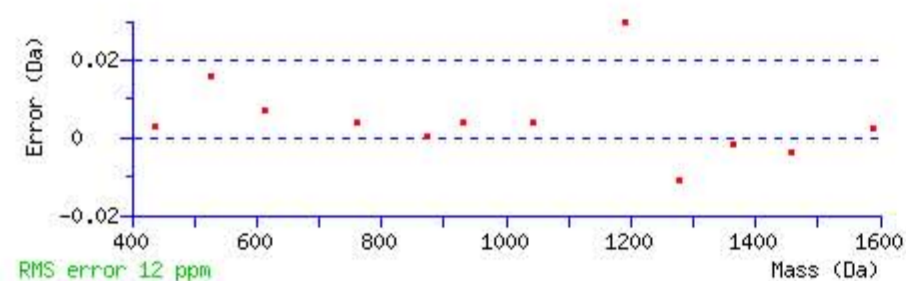
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 49 Expect: 3.9e-005

Matches : 12/134 fragment ions using 16 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							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
49.1	1801.918518	-0.001656	SKEFQLFSSPHGK
2.1	1801.914536	0.002326	QIVMTVVYGVIRYGR

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 45364: 1939.971748 from(970.993150,2+) rtinseconds(2564) index(71896)

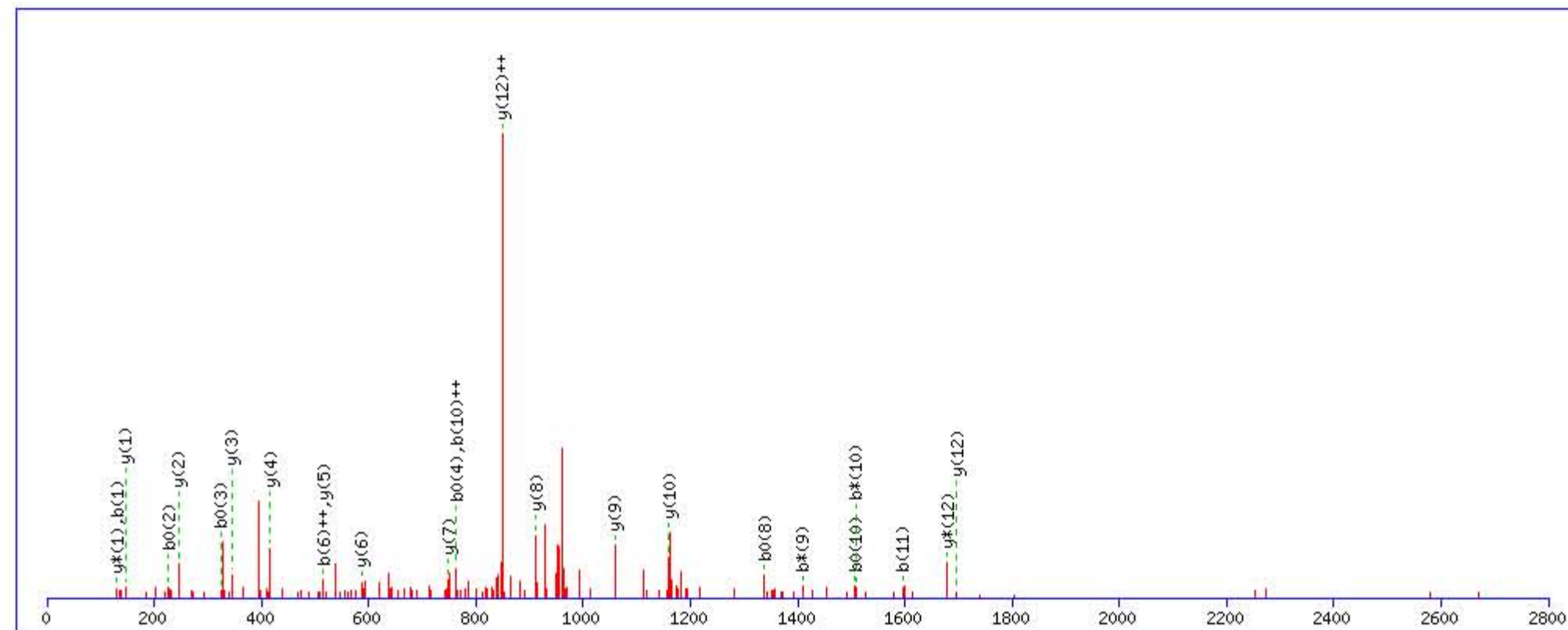
Title: Locus:1.1.1.1830.9 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1939.975372

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

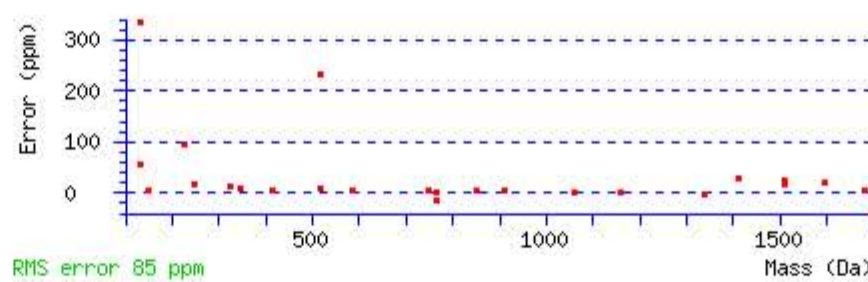
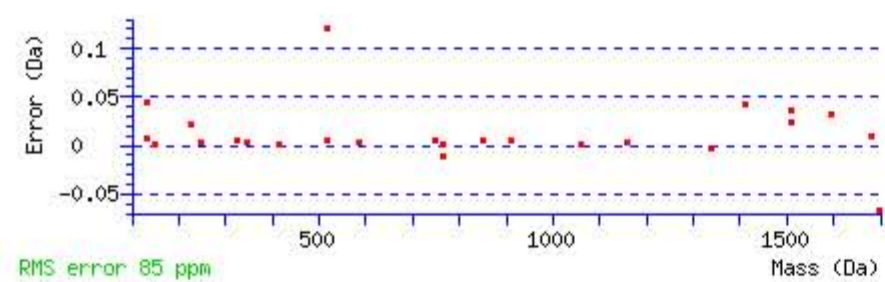
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 45 Expect: 8.9e-005

Matches : 25/132 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							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
45.2	1939.975372	-0.003624	EDPQTFYYAVAVVK
2.0	1939.992477	-0.020729	TTIYEIQDKTGSMVAVGK

Mascot: <http://www.matrixscience.com/>

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 45444: 1944.972162 from(649.331330,3+) rtinseconds(2085) index(69281)

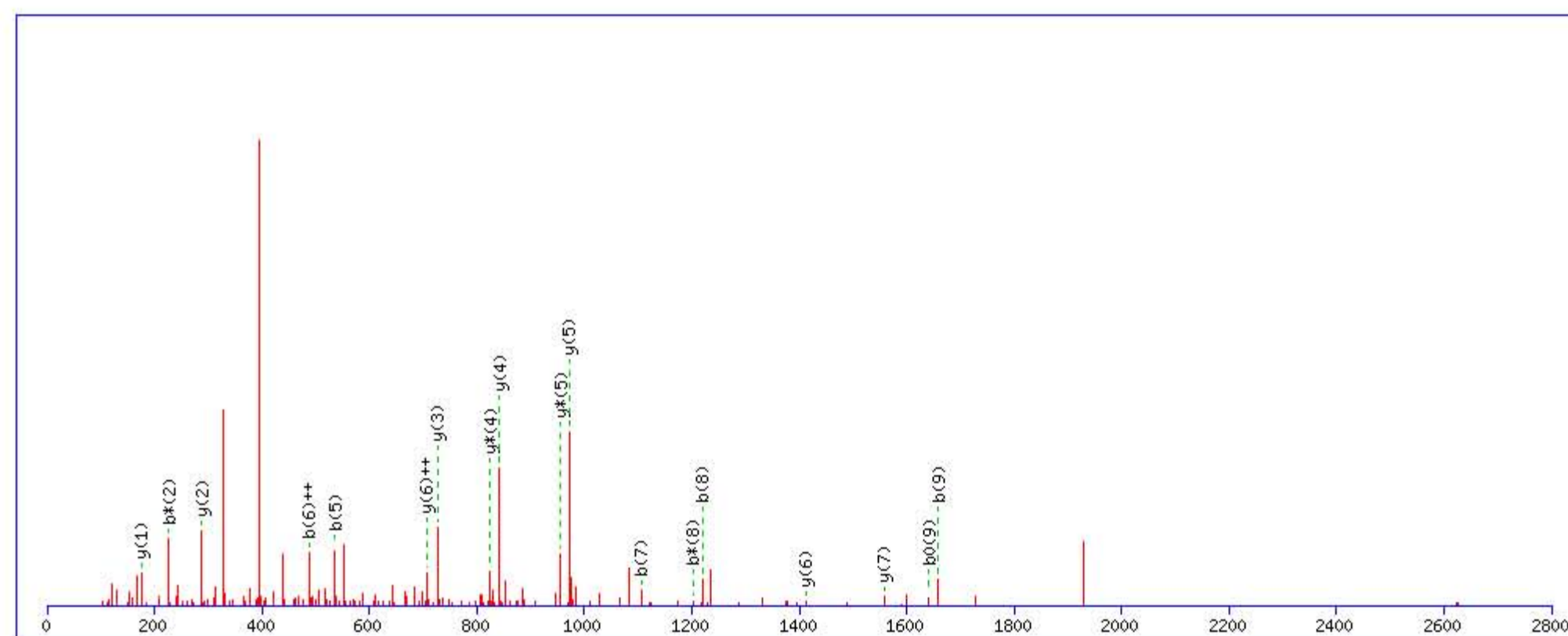
Title: Locus:1.1.1.1663.10 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1944.973602

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

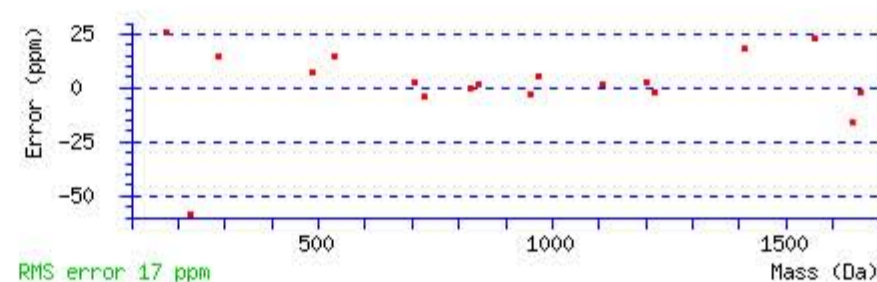
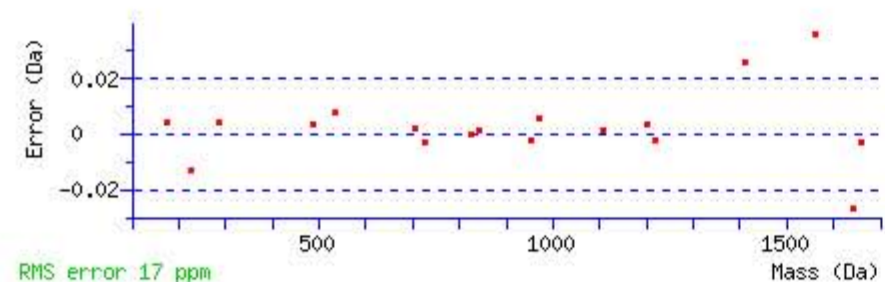
Q6 : Biotin:Thermo-21345 (Q)

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 30 Expect: 0.025

Matches : 18/102 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	129.102239	65.054757	112.075690	56.541483			K							11
2	244.129182	122.568229	227.102633	114.054955	226.118617	113.562947	D	1817.885929	909.446603	1800.859380	900.933328	1799.875364	900.441320	10
3	331.161210	166.084243	314.134661	157.570969	313.150645	157.078961	S	1702.858986	851.933131	1685.832437	843.419857	1684.848421	842.927848	9
4	388.182674	194.594975	371.156125	186.081701	370.172109	185.589693	G	1615.826958	808.417117	1598.800409	799.903843			8
5	535.251088	268.129182	518.224539	259.615908	517.240523	259.123900	F	1558.805494	779.906385	1541.778945	771.393111			7
6	974.476414	487.741845	957.449865	479.228571	956.465849	478.736563	Q	1411.737080	706.372178	1394.710531	697.858904			6
7	1105.516899	553.262088	1088.490350	544.748813	1087.506334	544.256805	M	972.511754	486.759515	955.485205	478.246241			5
8	1219.559826	610.283551	1202.533277	601.770277	1201.549261	601.278268	N	841.471269	421.239273	824.444720	412.725998			4
9	1658.785152	829.896214	1641.758603	821.382940	1640.774587	820.890932	Q	727.428342	364.217809	710.401793	355.704535			3
10	1771.869216	886.438246	1754.842667	877.924972	1753.858651	877.432964	L	288.203016	144.605146	271.176467	136.091871			2
11							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [KDSGFQMNQLR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.1	1944.973602	-0.001440	KDSGFQMNQLR

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 50929: 2192.037672 from(731.686500,3+) rtinseconds(2208) index(70015)

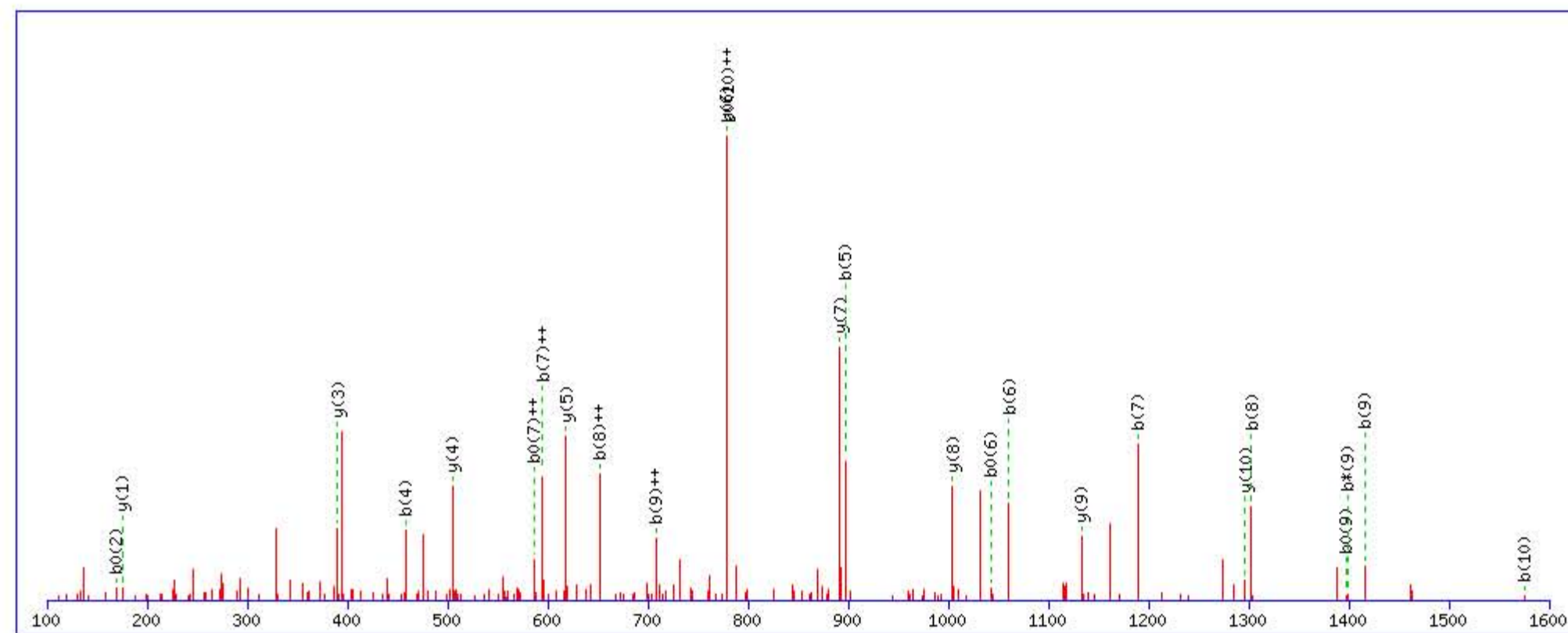
Title: Locus:1.1.1.1706.12 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2192.035400

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

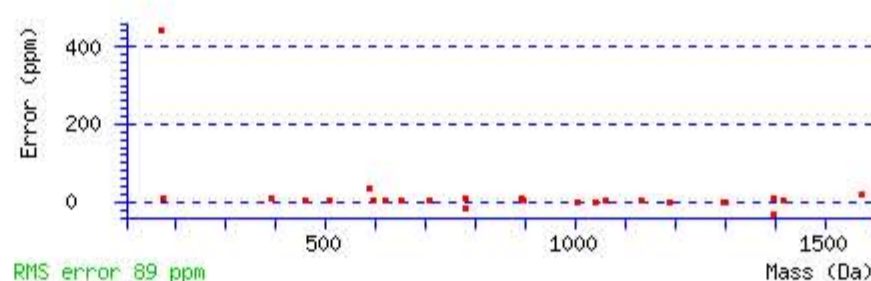
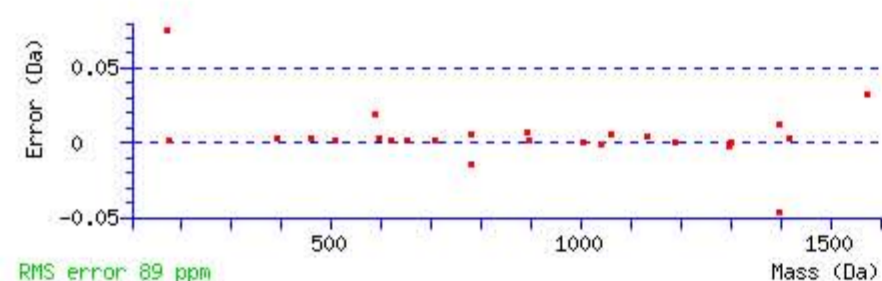
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 49 Expect: 3.7e-005

Matches : 25/160 fragment ions using 43 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.044390	36.525833					A							15
2	187.071333	94.039304			169.060768	85.034022	D	2122.005587	1061.506431	2104.979038	1052.993157	2103.995022	1052.501149	14
3	343.172444	172.089860	326.145895	163.576585	325.161879	163.084577	R	2006.978644	1003.992960	1989.952095	995.479685	1988.968079	994.987677	13
4	458.199387	229.603332	441.172838	221.090057	440.188822	220.598049	D	1850.877533	925.942404	1833.850984	917.429130	1832.866968	916.937122	12
5	897.424713	449.215995	880.398164	440.702720	879.414148	440.210712	Q	1735.850590	868.428933	1718.824041	859.915658	1717.840025	859.423650	11
6	1060.488042	530.747659	1043.461493	522.234385	1042.477477	521.742376	Y	1296.625264	648.816270	1279.598715	640.302995	1278.614699	639.810987	10
7	1189.530635	595.268955	1172.504086	586.755681	1171.520070	586.263673	E	1133.561935	567.284605	1116.535386	558.771331	1115.551370	558.279323	9
8	1302.614699	651.810987	1285.588150	643.297713	1284.604134	642.805705	L	1004.519342	502.763309	987.492793	494.250034	986.508777	493.758026	8
9	1415.698763	708.353019	1398.672214	699.839745	1397.688198	699.347737	L	891.435278	446.221277	874.408729	437.708002	873.424713	437.215994	7
10	1575.729412	788.368344	1558.702863	779.855069	1557.718847	779.363061	C	778.351214	389.679245	761.324665	381.165971	760.340649	380.673963	6
11	1688.813476	844.910376	1671.786927	836.397101	1670.802911	835.905093	L	618.320565	309.663921	601.294016	301.150646	600.310000	300.658638	5
12	1803.840419	902.423847	1786.813870	893.910573	1785.829854	893.418565	D	505.236501	253.121888	488.209952	244.608614	487.225936	244.116606	4
13	1917.883346	959.445311	1900.856797	950.932036	1899.872781	950.440028	N	390.209558	195.608417	373.183009	187.095142	372.198993	186.603134	3
14	2018.931025	1009.969150	2001.904476	1001.455876	2000.920460	1000.963868	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
15							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **ADRDQYELLCLDNTR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.6	2192.035400	0.002272	ADRDQYELLCLDNTR
1.4	2192.049973	-0.012301	AQEQLGKEMRMNENLVR

Mascot: <http://www.matrixscience.com/>

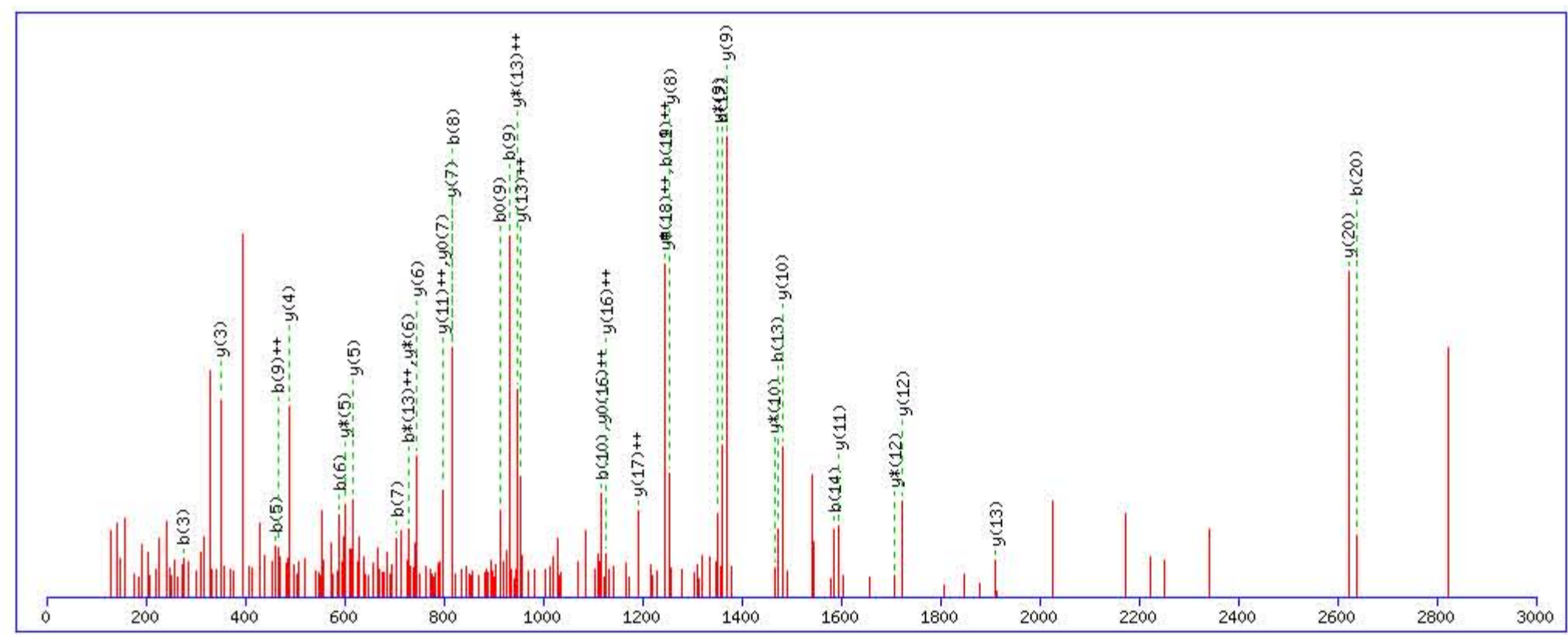
MASCOT Mascot Search Results

Peptide View

MS/MS Fragmentation of **SMGGKEDLIWELLNQAQEHFGK**
 Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

Match to Query 59908: 2840.397972 from(947.806600,3+) rtinseconds(2978) index(74988)
 Title: Locus:1.1.1.1971.6 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



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 60386: 2859.446892 from(954.156240,3+) rtinseconds(1526) index(66017)

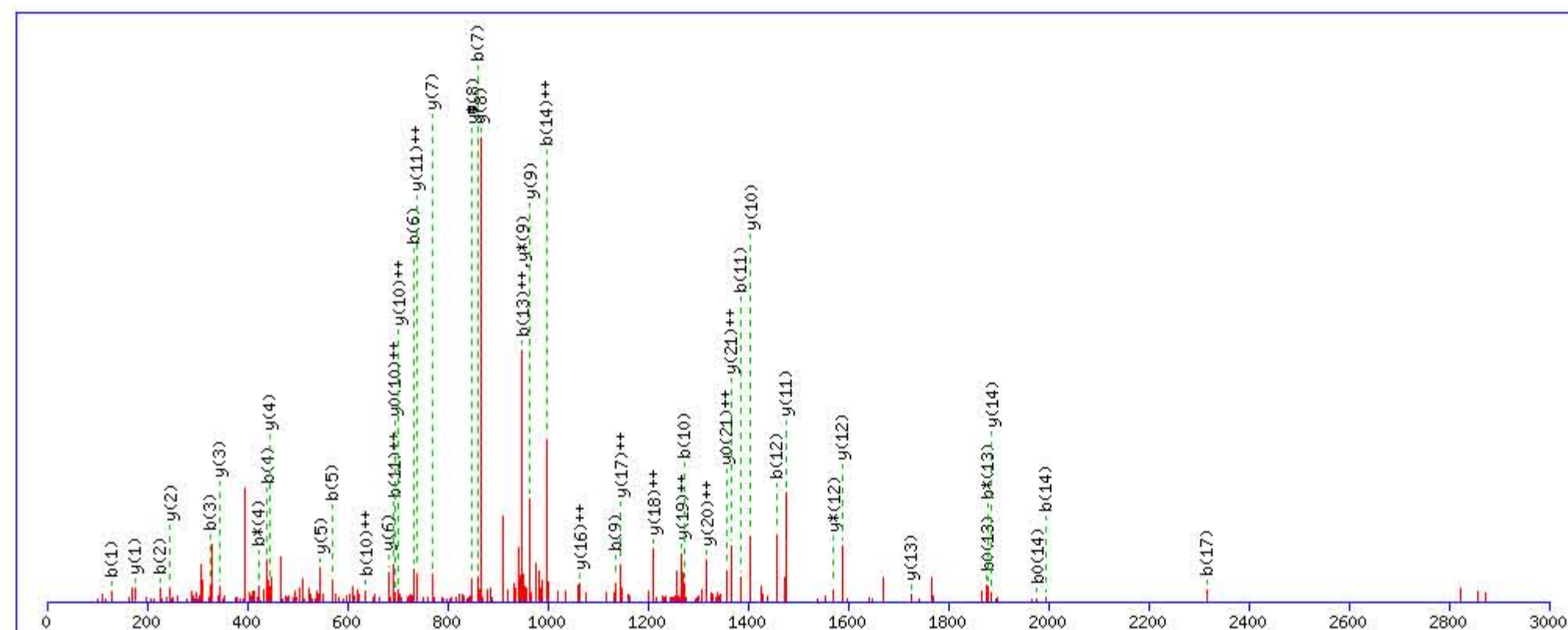
Title: Locus:1.1.1.1468.16 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2859.452393

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

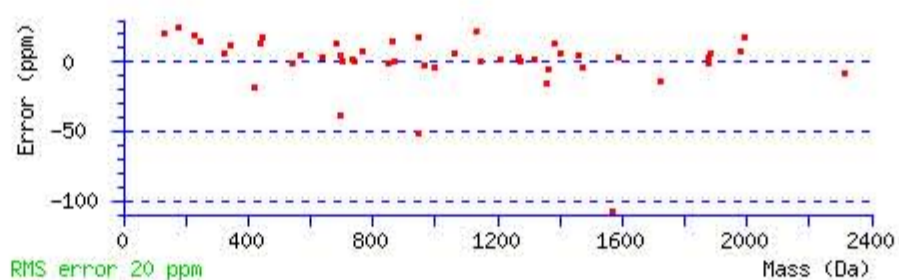
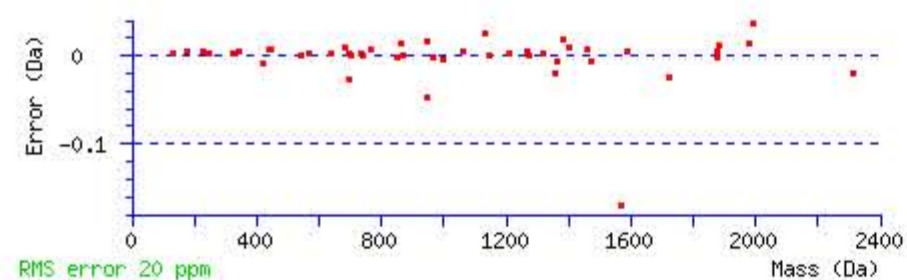
Variable modifications:

Q13 : Biotin:Thermo-21345 (Q)

Ions Score: 77 Expect: 5.5e-007

Matches : 49/238 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
77.3	2859.452393	-0.005501	KPVDEYKDCHLAQVPSHTVVAR

MASCOT 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 25354: 1270.723948 from(636.369250,2+) rtinseconds(2111) index(6516)

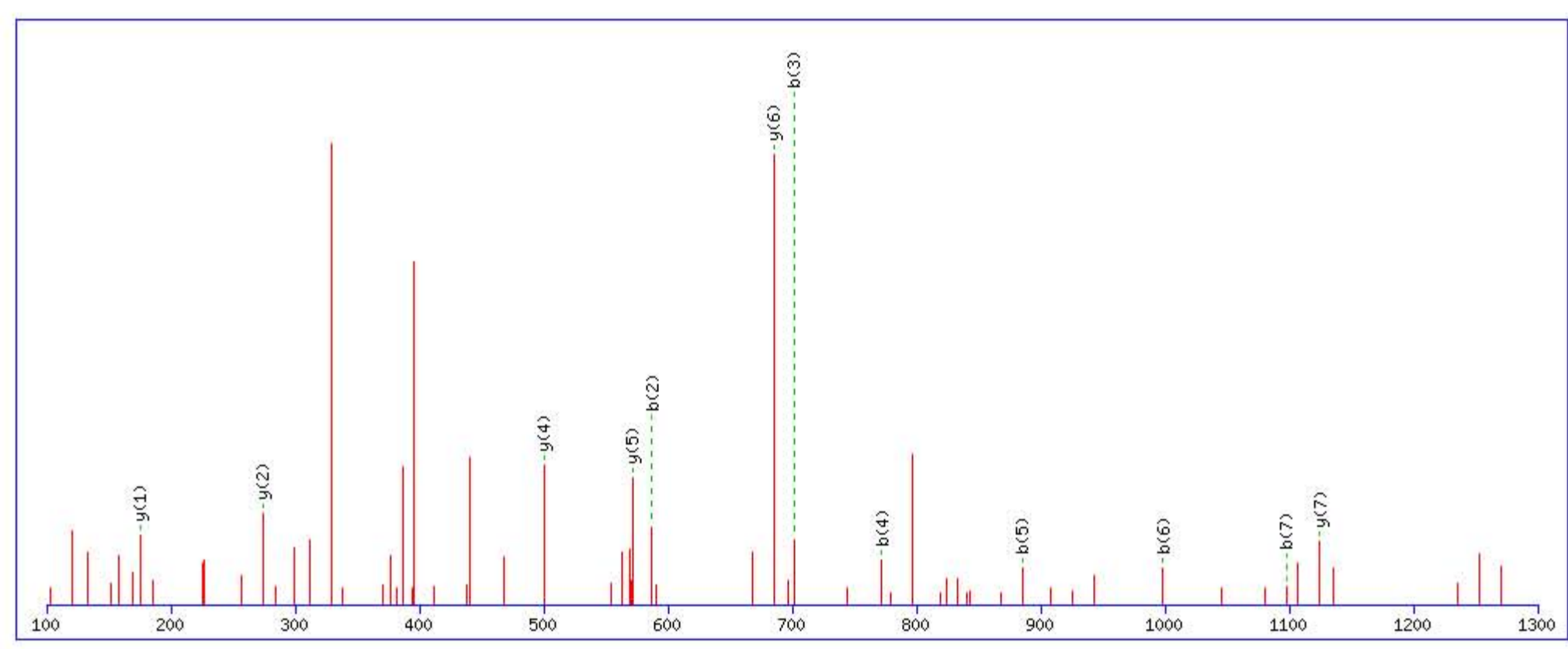
Title: Locus:1.1.1.1544.22 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1270.721985

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

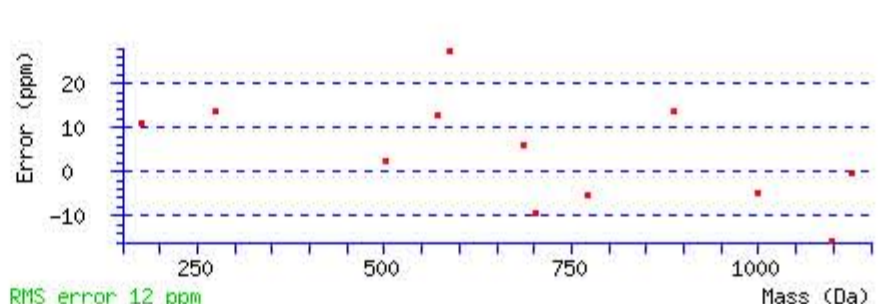
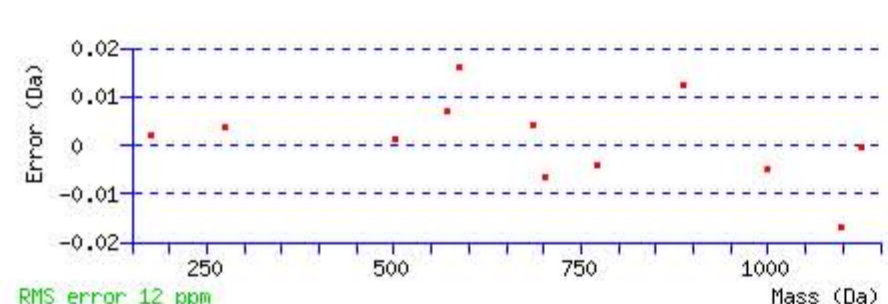
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 37 Expect: 0.0034

Matches : 12/54 fragment ions using 24 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
36.7	1270.721985	0.001963	FQNALLVR
13.3	1270.725357	-0.001409	QKVMAIVR
9.8	1270.735687	-0.011739	KEAELRSGIIR
9.5	1270.722000	0.001948	FQIAQVVR
6.9	1270.733215	-0.009267	MFHIRAVILR
6.2	1270.706711	0.017237	NMPAKTELIVR
3.3	1270.735733	-0.011785	EILGRGVSSVVR
2.9	1270.717957	0.005991	QLSRTLRSR
2.3	1270.735703	-0.011755	ASSLLAGERLVR
2.3	1270.739761	-0.015813	QVVNIPSFIVR

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 45553: 1950.092952 from(651.038260,3+) rtinseconds(1958) index(21464)

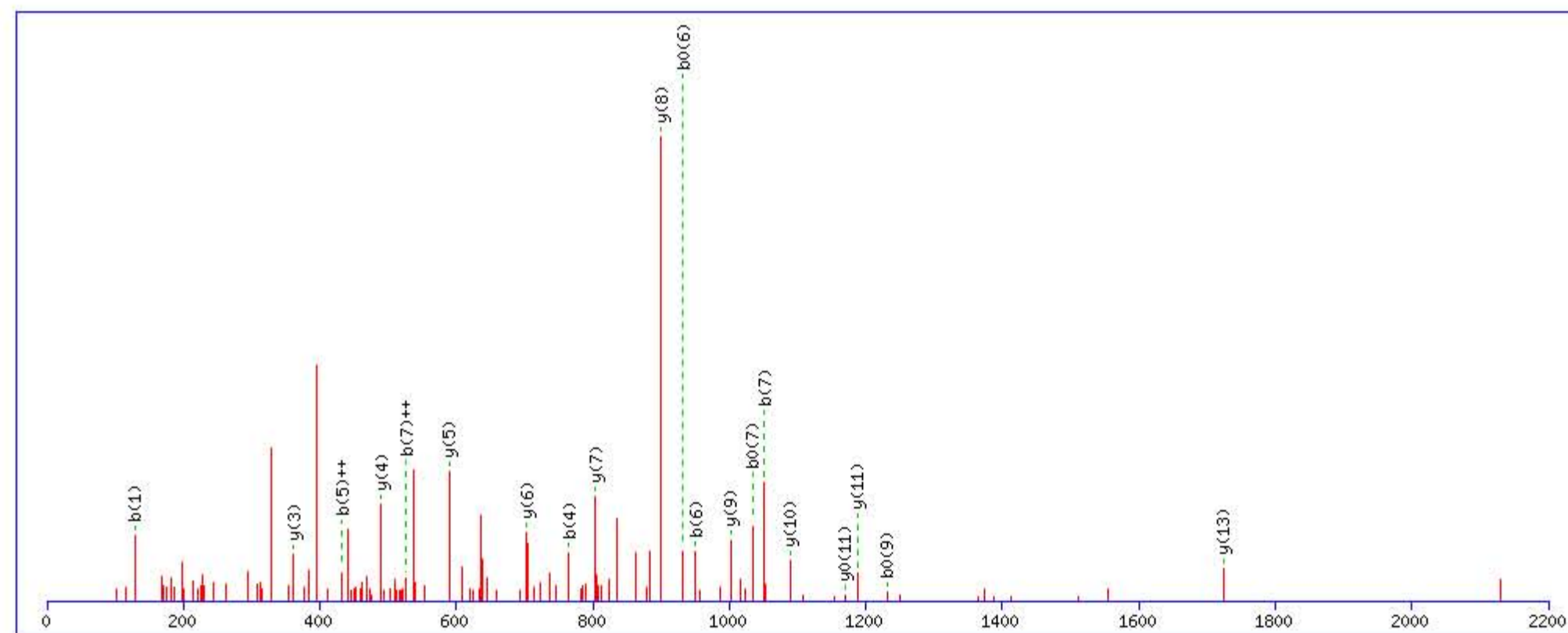
Title: Locus:1.1.1.684.4 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1950.097229

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

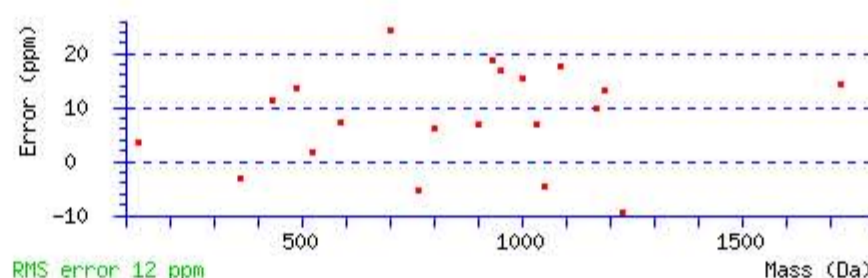
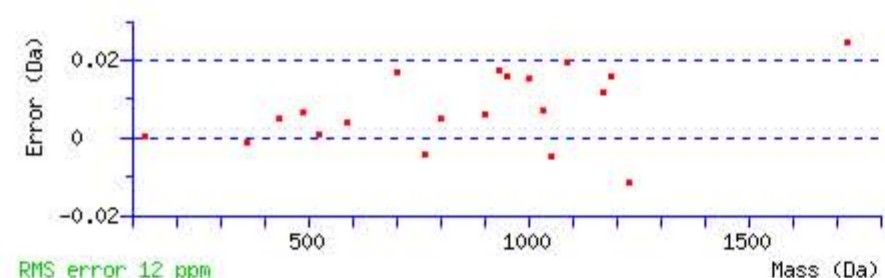
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 52 Expect: 7.1e-005

Matches : 20/156 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	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
52.3	1950.097229	-0.004277	KVPQVSTPTLVEVSR

Mascot: <http://www.matrixscience.com/>

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 31909: 1430.665782 from(477.895870,3+) rtinseconds(1148) index(31169)

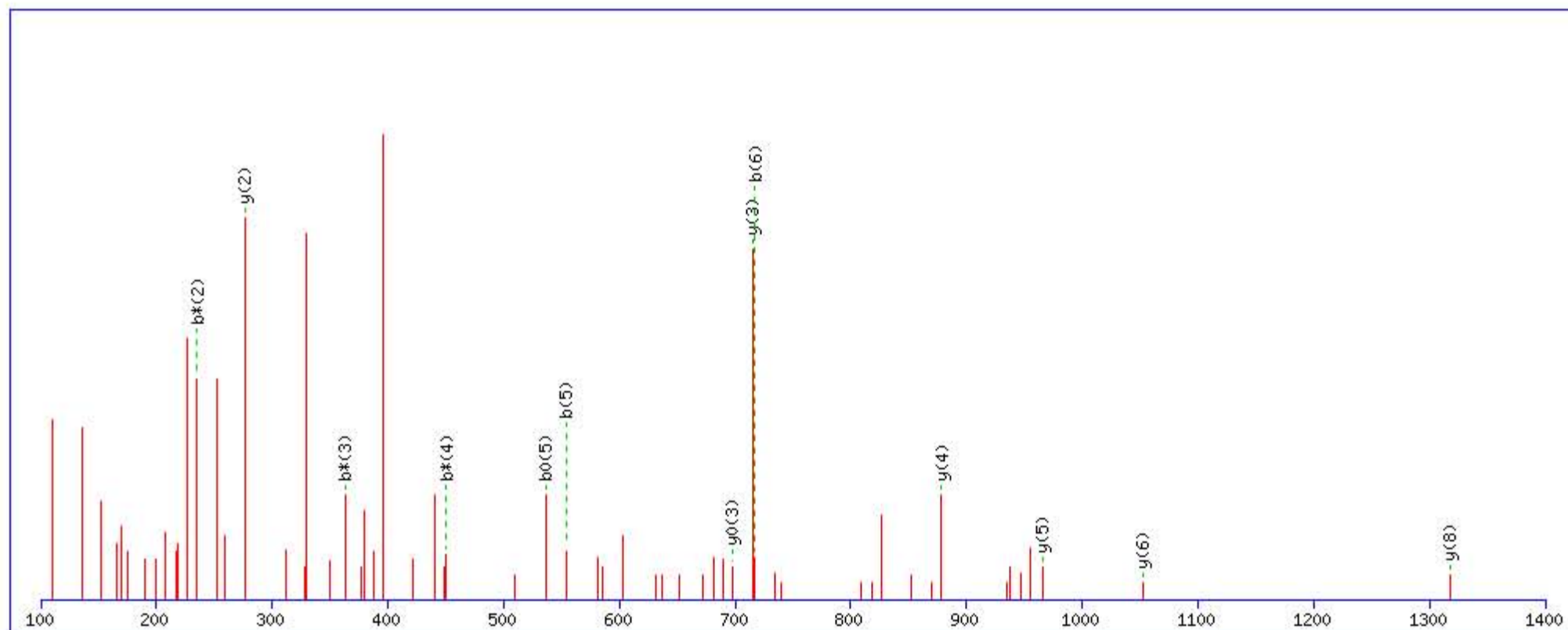
Title: Locus:1.1.1.2819.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1430.672470

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

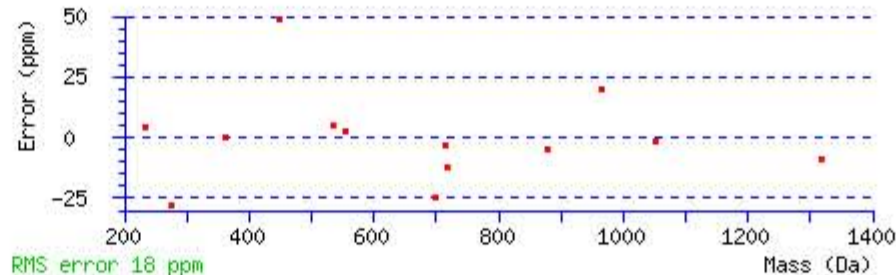
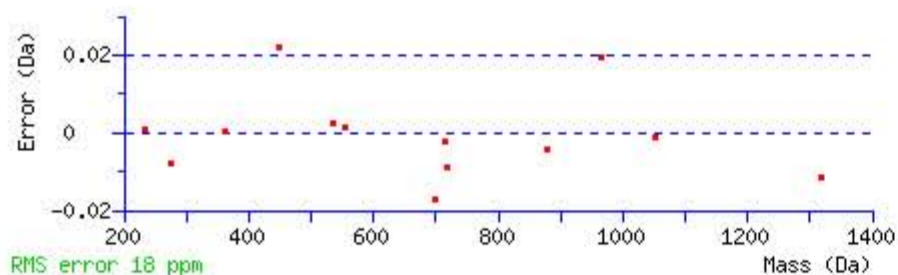
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 25 Expect: 0.036

Matches : 13/88 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	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
25.4	1430.672470	-0.006688	NHQSSYQTR

Mascot: <http://www.matrixscience.com/>

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 31911: 1430.670132 from(477.897320,3+) rtinseconds(1168) index(47659)

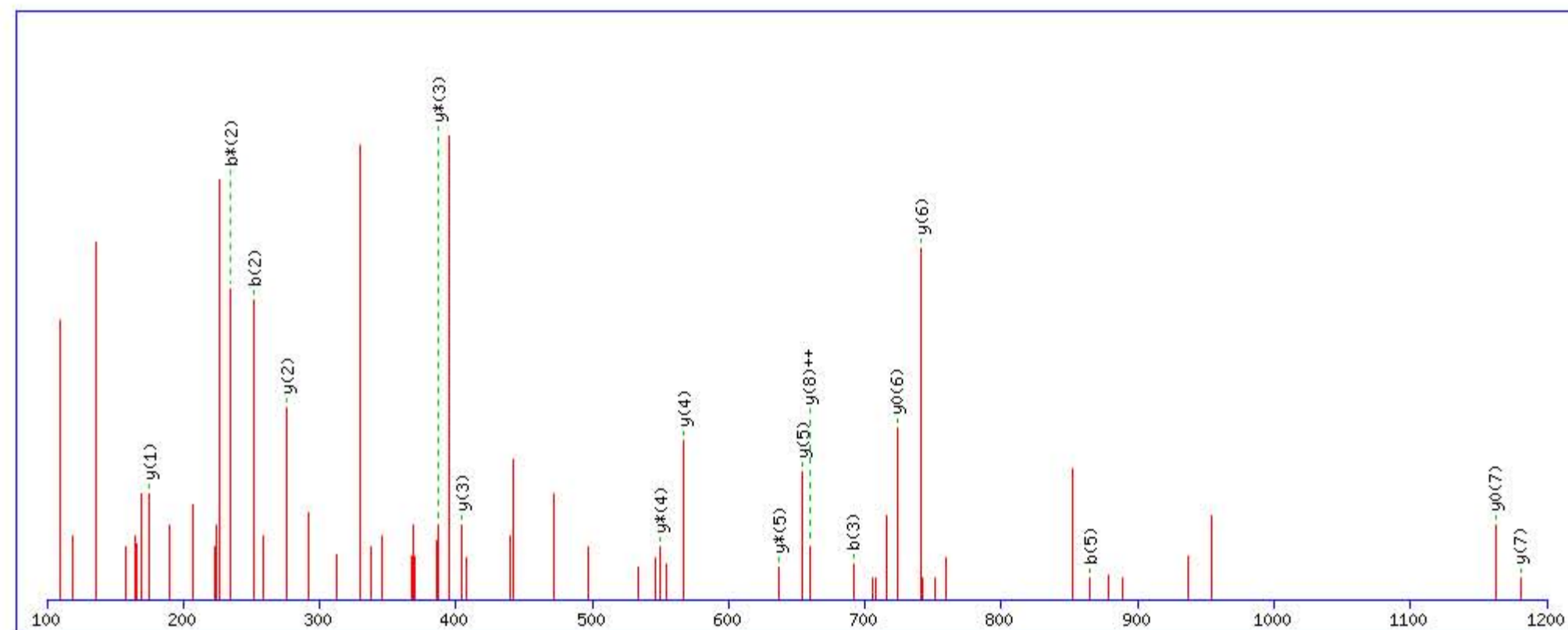
Title: Locus:1.1.1.1022.8 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1430.672470

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

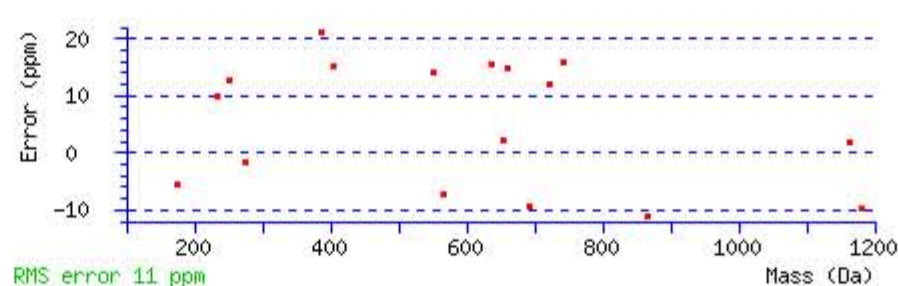
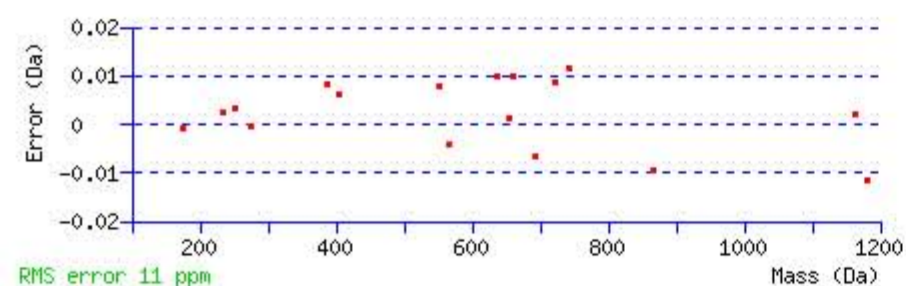
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 27 Expect: 0.027

Matches : 17/88 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							9
2	252.109115	126.558195	235.082566	118.044921			H	1317.636832	659.322054	1300.610283	650.808780	1299.626267	650.316772	8
3	691.334441	346.170859	674.307892	337.657584			Q	1180.577920	590.792598	1163.551371	582.279324	1162.567355	581.787316	7
4	778.366469	389.686872	761.339920	381.173598	760.355904	380.681590	S	741.352594	371.179935	724.326045	362.666661	723.342029	362.174653	6
5	865.398497	433.202886	848.371948	424.689612	847.387932	424.197604	S	654.320566	327.663921	637.294017	319.150647	636.310001	318.658639	5
6	1028.461826	514.734551	1011.435277	506.221276	1010.451261	505.729268	Y	567.288538	284.147907	550.261989	275.634633	549.277973	275.142625	4
7	1156.520404	578.763840	1139.493855	570.250566	1138.509839	569.758558	Q	404.225209	202.616243	387.198660	194.102968	386.214644	193.610960	3
8	1257.568083	629.287680	1240.541534	620.774405	1239.557518	620.282397	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
9							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **NHQSSYQTR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.1	1430.672470	-0.002338	NHQSSYQTR
7.6	1430.672470	-0.002338	NHQSSYQTR

Mascot: <http://www.matrixscience.com/>

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **IQNILTEEPK**

Found in **PONI_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

Match to Query 33703: 1494.801788 from(748.408170,2+) rtinseconds(2058) index(53303)

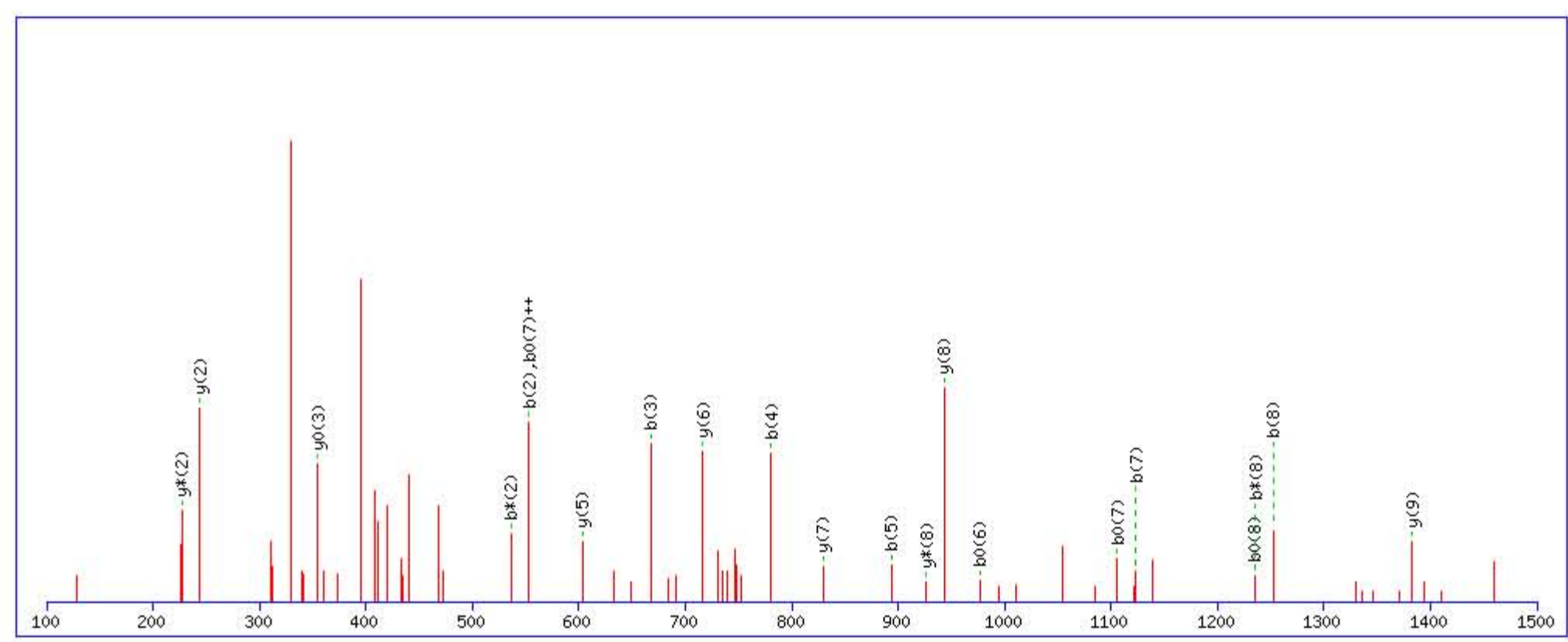
Title: Locus:1.1.1.1331.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1494.811569

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

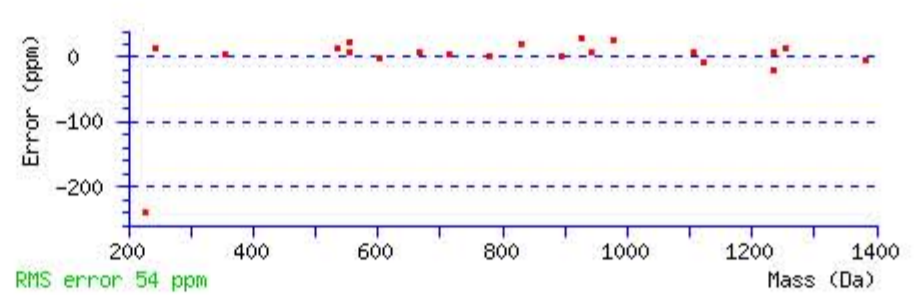
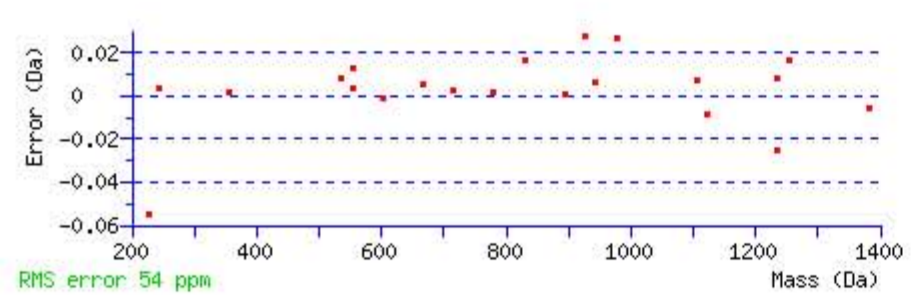
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

Ions Score: 32 Expect: 0.0029

Matches : 21/92 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					I							10
2	553.316666	277.161971	536.290117	268.648697			Q	1382.734814	691.871045	1365.708265	683.357771	1364.724249	682.865763	9
3	667.359593	334.183435	650.333044	325.670160			N	943.509488	472.258382	926.482939	463.745108	925.498923	463.253100	8
4	780.443657	390.725467	763.417108	382.212192			I	829.466561	415.236919	812.440012	406.723644	811.455996	406.231636	7
5	893.527721	447.267499	876.501172	438.754224			L	716.382497	358.694887	699.355948	350.181612	698.371932	349.689604	6
6	994.575400	497.791338	977.548851	489.278064	976.564835	488.786056	T	603.298433	302.152855	586.271884	293.639580	585.287868	293.147572	5
7	1123.617993	562.312635	1106.591444	553.799360	1105.607428	553.307352	E	502.250754	251.629015	485.224205	243.115741	484.240189	242.623733	4
8	1252.660586	626.833931	1235.634037	618.320657	1234.650021	617.828649	E	373.208161	187.107719	356.181612	178.594444	355.197596	178.102436	3
9	1349.713350	675.360313	1332.686801	666.847039	1331.702785	666.355031	P	244.165568	122.586422	227.139019	114.073148			2
10							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **IQNILTEEPK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.4	1494.811569	-0.009781	IQNILTEEPK
4.9	1494.809097	-0.007309	LQLYVFVMR
4.8	1494.779907	0.021881	QLKVMASDHR
4.0	1494.780380	0.021408	GFSHSSALRIHQK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GHQLQLDYFGACK**

Found in **SPRL1_HUMAN**, SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2

Match to Query 43588: 1846.891752 from(616.637860,3+) rtinseconds(2151) index(53896)

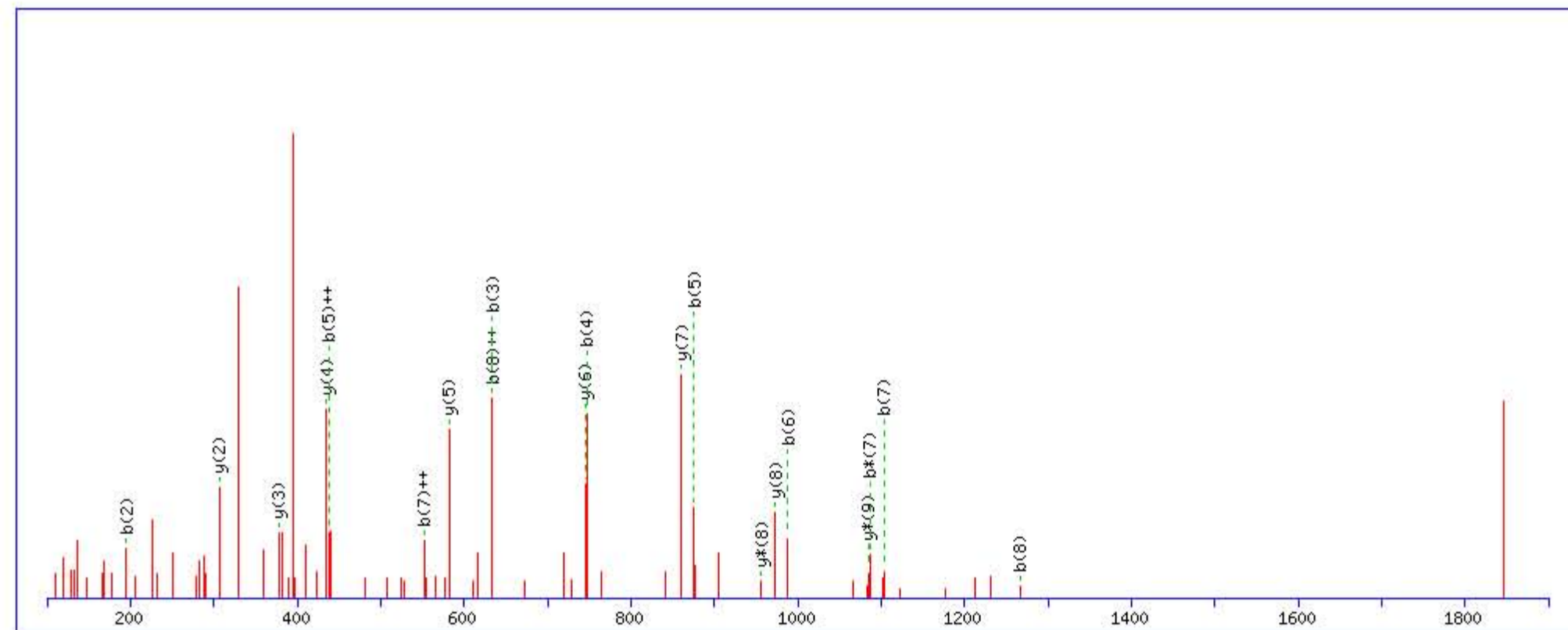
Title: Locus:1.1.1.1364.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1846.885849

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

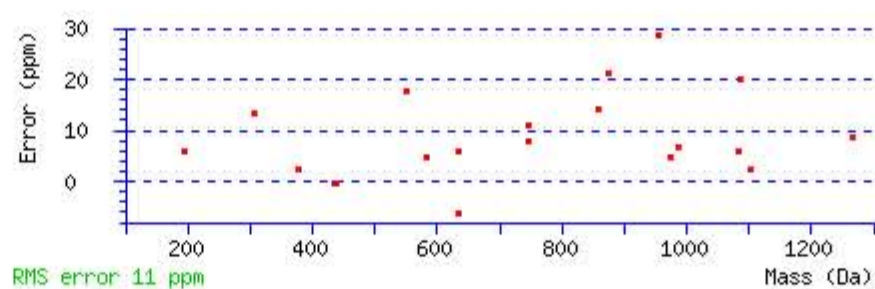
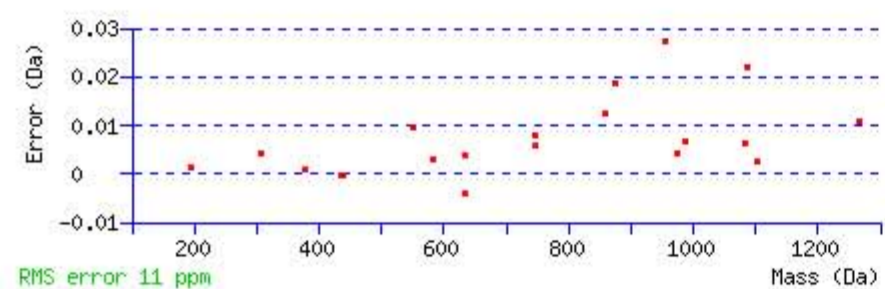
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 5.9e-005

Matches : 20/116 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	58.028740	29.518008					G							13
2	195.087652	98.047464					H	1790.871661	895.939469	1773.845112	887.426194	1772.861096	886.934186	12
3	634.312978	317.660127	617.286429	309.146853			Q	1653.812749	827.410013	1636.786200	818.896738	1635.802184	818.404730	11
4	747.397042	374.202159	730.370493	365.688885			L	1214.587423	607.797350	1197.560874	599.284075	1196.576858	598.792067	10
5	875.455620	438.231448	858.429071	429.718174			Q	1101.503359	551.255318	1084.476810	542.742043	1083.492794	542.250035	9
6	988.539684	494.773480	971.513135	486.260206			L	973.444781	487.226029	956.418232	478.712754	955.434216	478.220746	8
7	1103.566627	552.286952	1086.540078	543.773677	1085.556062	543.281669	D	860.360717	430.683997	843.334168	422.170722	842.350152	421.678714	7
8	1266.629956	633.818616	1249.603407	625.305342	1248.619391	624.813334	Y	745.333774	373.170525	728.307225	364.657251			6
9	1413.698370	707.352823	1396.671821	698.839549	1395.687805	698.347541	F	582.270445	291.638861	565.243896	283.125586			5
10	1470.719834	735.863555	1453.693285	727.350281	1452.709269	726.858273	G	435.202031	218.104653	418.175482	209.591379			4
11	1541.756948	771.382112	1524.730399	762.868838	1523.746383	762.376830	A	378.180567	189.593921	361.154018	181.080647			3
12	1701.787597	851.397437	1684.761048	842.884162	1683.777032	842.392154	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 **GHQLQLDYFGACK**

(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	1846.885849	0.005903	GHQLQLDYFGACK
30.0	1846.885849	0.005903	GHQLQLDYFGACK
1.3	1846.895721	-0.003969	LQLEETMPSYGR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GAAAHDPDSEEQQQR**

Found in **TLN1_HUMAN**, Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3

Match to Query 43356: 1833.843882 from(612.288570,3+) rtinseconds(1152) index(47598)

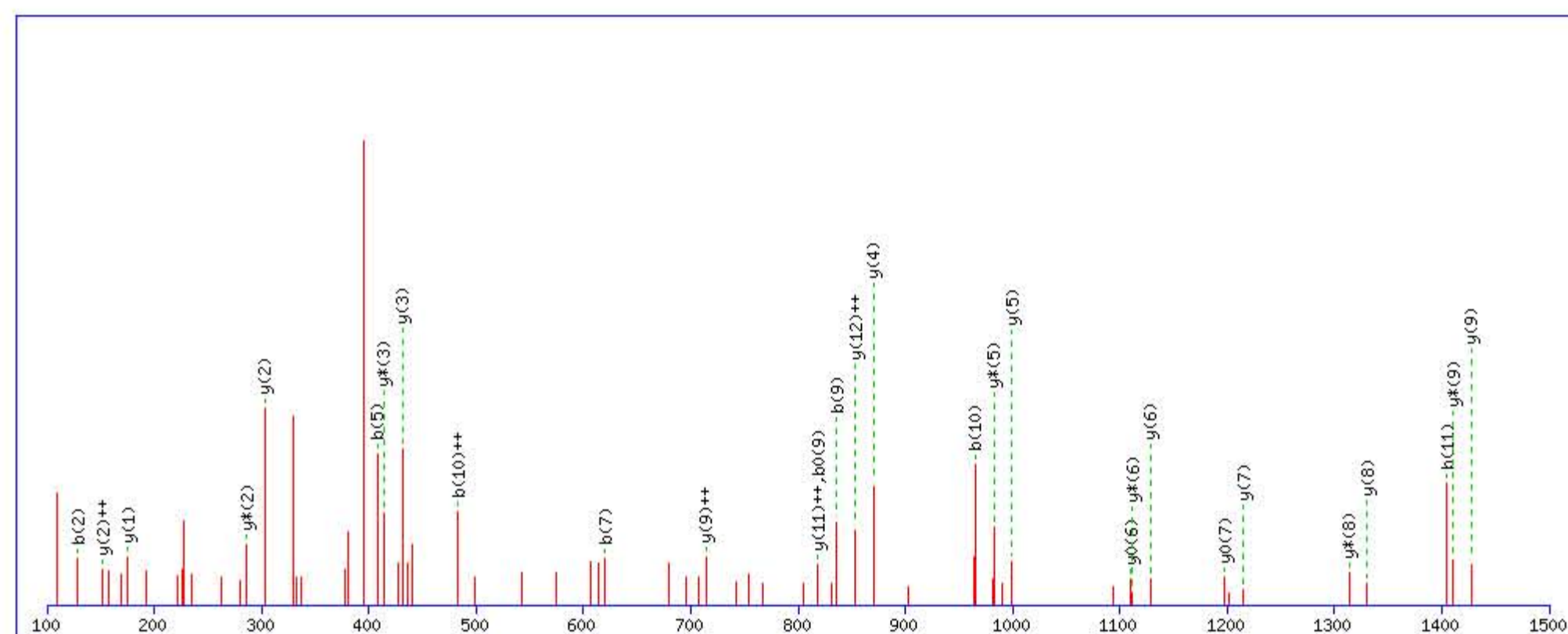
Title: Locus:1.1.1.1016.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1833.842773

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

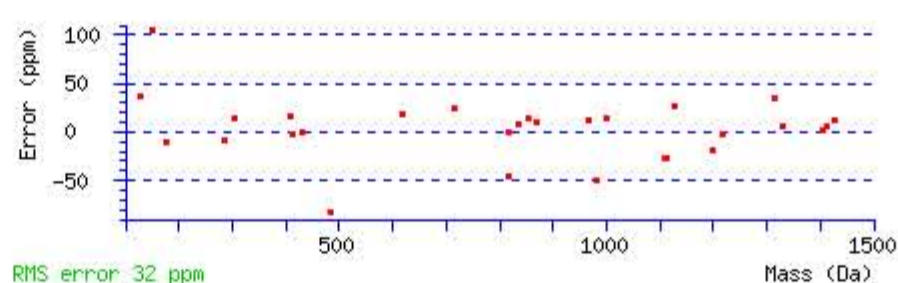
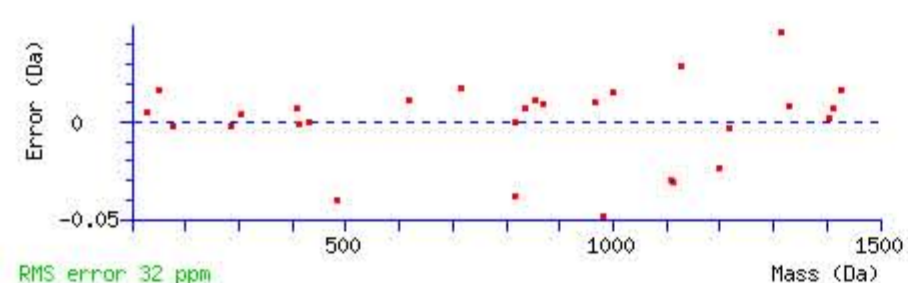
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 50 Expect: 0.00015

Matches : 29/116 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							14
2	129.065854	65.036565					A	1777.828609	889.417943	1760.802060	880.904668	1759.818044	880.412660	13
3	200.102968	100.555122					A	1706.791495	853.899386	1689.764946	845.386111	1688.780930	844.894103	12
4	271.140082	136.073679					A	1635.754381	818.380829	1618.727832	809.867554	1617.743816	809.375546	11
5	408.198994	204.603135					H	1564.717267	782.862272	1547.690718	774.348997	1546.706702	773.856989	10
6	505.251758	253.129517					P	1427.658355	714.332816	1410.631806	705.819541	1409.647790	705.327533	9
7	620.278701	310.642989			602.268136	301.637706	D	1330.605591	665.806434	1313.579042	657.293159	1312.595026	656.801151	8
8	707.310729	354.159003			689.300164	345.153720	S	1215.578648	608.292962	1198.552099	599.779688	1197.568083	599.287680	7
9	836.353322	418.680299			818.342757	409.675017	E	1128.546620	564.776948	1111.520071	556.263674	1110.536055	555.771666	6
10	965.395915	483.201596			947.385350	474.196313	E	999.504027	500.255652	982.477478	491.742377	981.493462	491.250369	5
11	1404.621241	702.814259	1387.594692	694.300984	1386.610676	693.808976	Q	870.461434	435.734355	853.434885	427.221081			4
12	1532.679819	766.843548	1515.653270	758.330273	1514.669254	757.838265	Q	431.236108	216.121692	414.209559	207.608418			3
13	1660.738397	830.872837	1643.711848	822.359562	1642.727832	821.867554	Q	303.177530	152.092403	286.150981	143.579129			2
14							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [GAAAHDPDSEEQQQR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.9	1833.842773	0.001109	GAAAHDPDSEEQQQR
47.7	1833.842773	0.001109	GAAAHDPDSEEQQQR
44.3	1833.842773	0.001109	GAAAHDPDSEEQQQR
11.5	1833.864761	-0.020879	QREQMEQMKQR
9.5	1833.864761	-0.020879	QREQMEQMKQR
8.3	1833.864761	-0.020879	QREQMEQMKQR
7.6	1833.860077	-0.016195	EDVSPGTAIGKTPEMMR
7.6	1833.860077	-0.016195	EDVSPGTAIGKTPEMMR
7.4	1833.864761	-0.020879	QREQMEQMKQR
5.0	1833.852676	-0.008794	MESSPIQSSGNSSTLGR

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 38190: 1623.934408 from(812.974480,2+) rtinseconds(2582) index(9001)

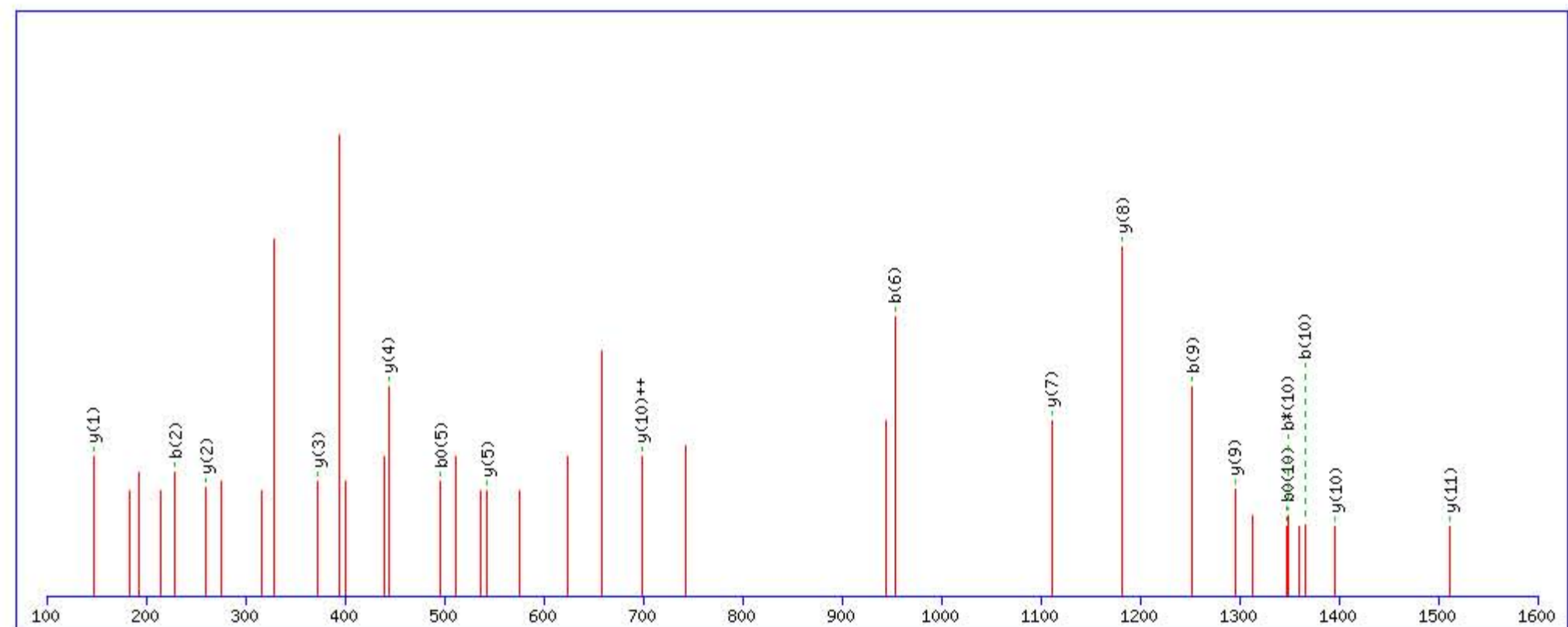
Title: Locus:1.1.1.1708.23 File:"2013-07-02 CLN FXIII 60 min 2nd F 1.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1623.926941

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

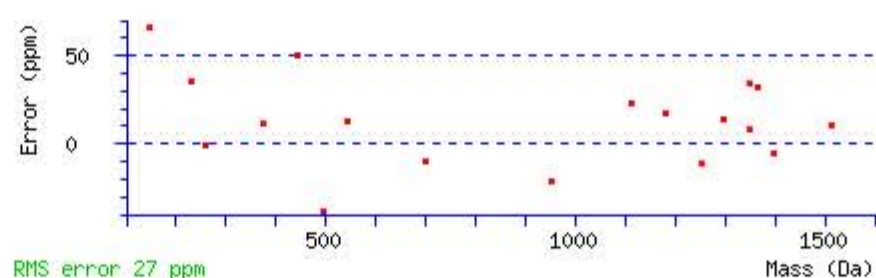
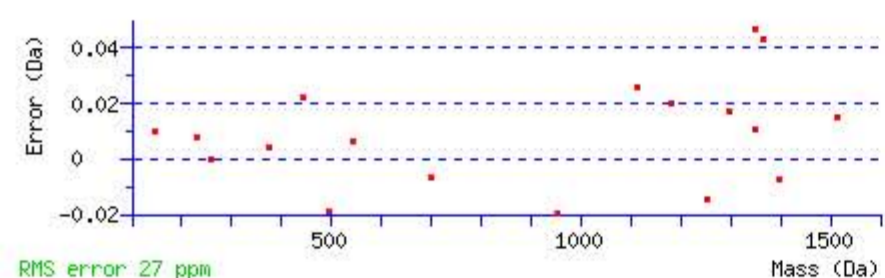
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

Ions Score: 60 Expect: 5.7e-006

Matches : 18/110 fragment ions using 36 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					L							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
59.9	1623.926941	0.007467	LDTLAQEVALLK
4.0	1623.919556	0.014852	EVSPEPIVSTVARLK

Mascot: <http://www.matrixscience.com/>

MASCOT 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 39089: 1637.866542 from(546.962790,3+) rtinseconds(1894) index(35610)

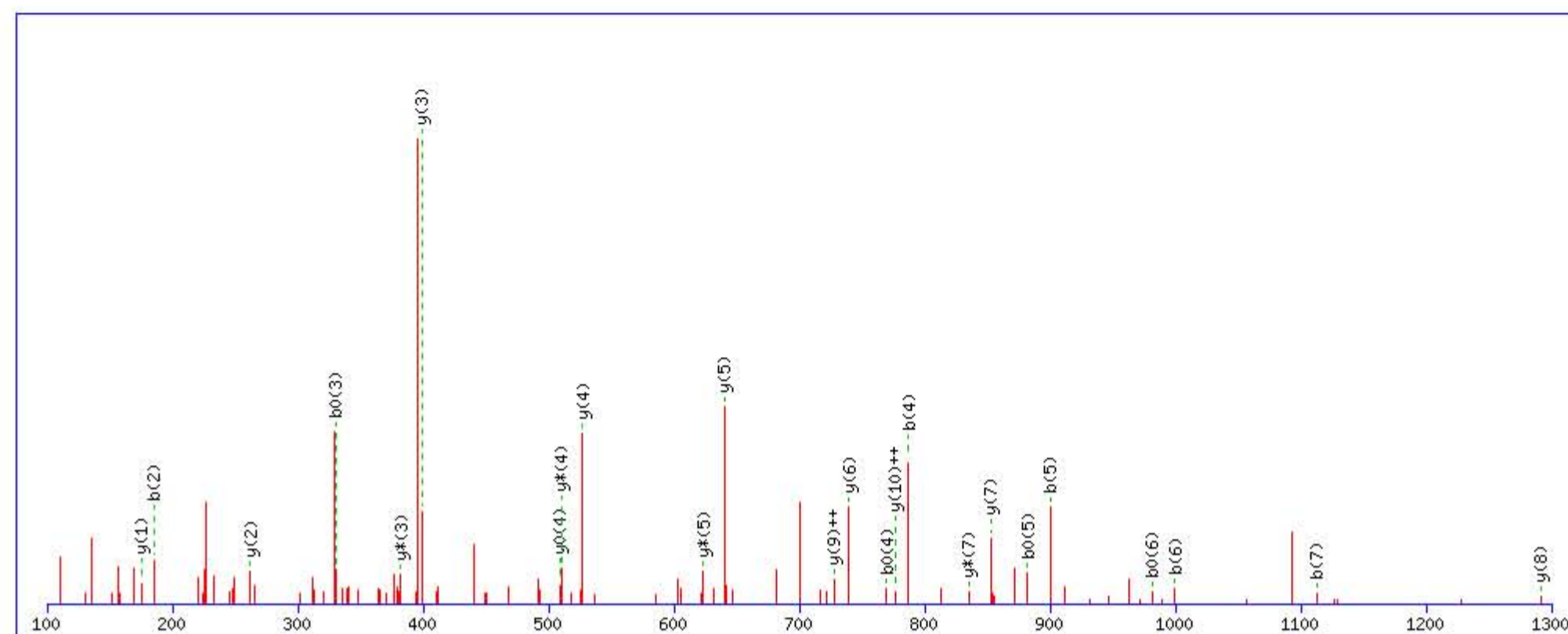
Title: Locus:1.1.1.3079.12 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1637.871170

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

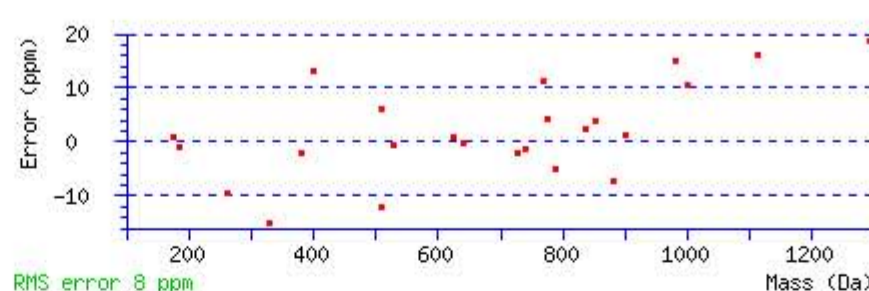
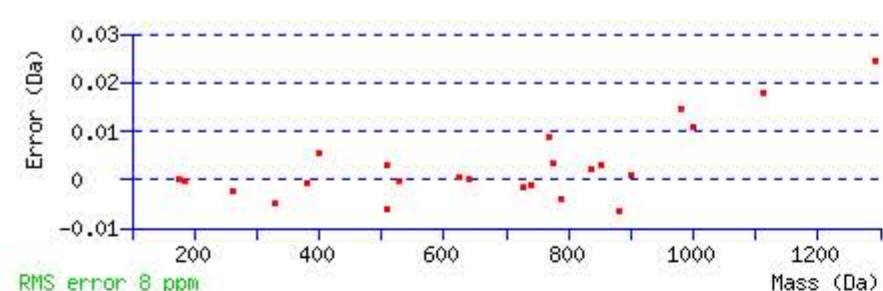
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 29 Expect: 0.025

Matches : 24/112 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							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
29.2	1637.871170	-0.004628	SPYQLVLQHSR

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **ESELQWQEEER**

Found in **TRHY_HUMAN**, Trichohyalin OS=Homo sapiens GN=TCHH PE=1 SV=2

Match to Query 42205: 1772.818908 from(887.416730,2+) rtinseconds(1835) index(20548)

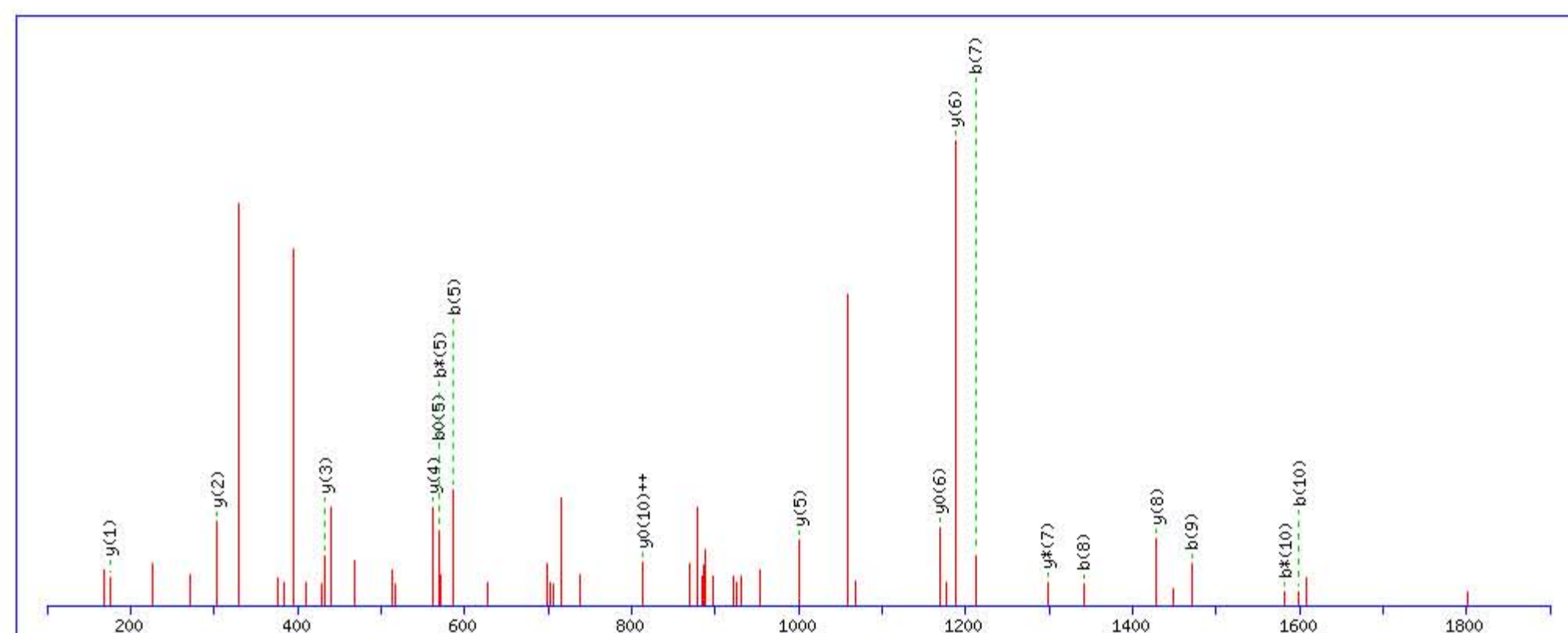
Title: Locus:1.1.1.641.15 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\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): 1772.803909

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

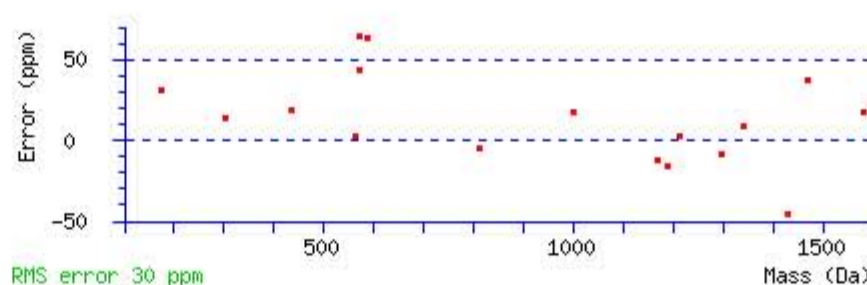
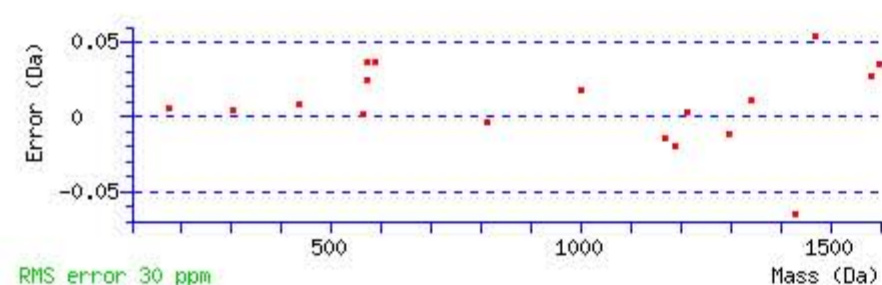
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.0093

Matches : 18/110 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							11
2	217.081897	109.044586			199.071332	100.039304	S	1644.768633	822.887955	1627.742084	814.374680	1626.758068	813.882672	10
3	346.124490	173.565883			328.113925	164.560600	E	1557.736605	779.371941	1540.710056	770.858666	1539.726040	770.366658	9
4	459.208554	230.107915			441.197989	221.102633	L	1428.694012	714.850644	1411.667463	706.337370	1410.683447	705.845362	8
5	587.267132	294.137204	570.240583	285.623930	569.256567	285.131922	Q	1315.609948	658.308612	1298.583399	649.795338	1297.599383	649.303330	7
6	773.346445	387.176861	756.319896	378.663586	755.335880	378.171578	W	1187.551370	594.279323	1170.524821	585.766049	1169.540805	585.274041	6
7	1212.571771	606.789524	1195.545222	598.276249	1194.561206	597.784241	Q	1001.472057	501.239667	984.445508	492.726392	983.461492	492.234384	5
8	1341.614364	671.310820	1324.587815	662.797546	1323.603799	662.305538	E	562.246731	281.627004	545.220182	273.113729	544.236166	272.621721	4
9	1470.656957	735.832117	1453.630408	727.318842	1452.646392	726.826834	E	433.204138	217.105707	416.177589	208.592433	415.193573	208.100425	3
10	1599.699550	800.353413	1582.673001	791.840139	1581.688985	791.348131	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 **ESELQWQEEER**

(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	1772.803909	0.014999	ESELQWQEEER
33.1	1772.822556	-0.003648	FQEGQEEER
11.1	1772.829727	-0.010819	QEEEEAMRRER
9.5	1772.803909	0.014999	ESELQWQEEER
5.3	1772.798752	0.020156	HISSCMRWPGHYSR
3.7	1772.811798	0.007110	YQTPPHQNFEDLER
3.3	1772.803909	0.014999	DMASPNWSILPEEER
3.1	1772.828873	-0.009965	QAEQEATVAREEQER
3.0	1772.819901	-0.000993	CGKSFSQSCHLVAHR
1.3	1772.836288	-0.017380	ADGSLTGGGLEAAAMAPER

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **NLHDLVDSDNQLER**

Found in **VASN_HUMAN**, Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1

Match to Query 46062: 1977.952632 from(660.324820,3+) rtinseconds(1938) index(35989)

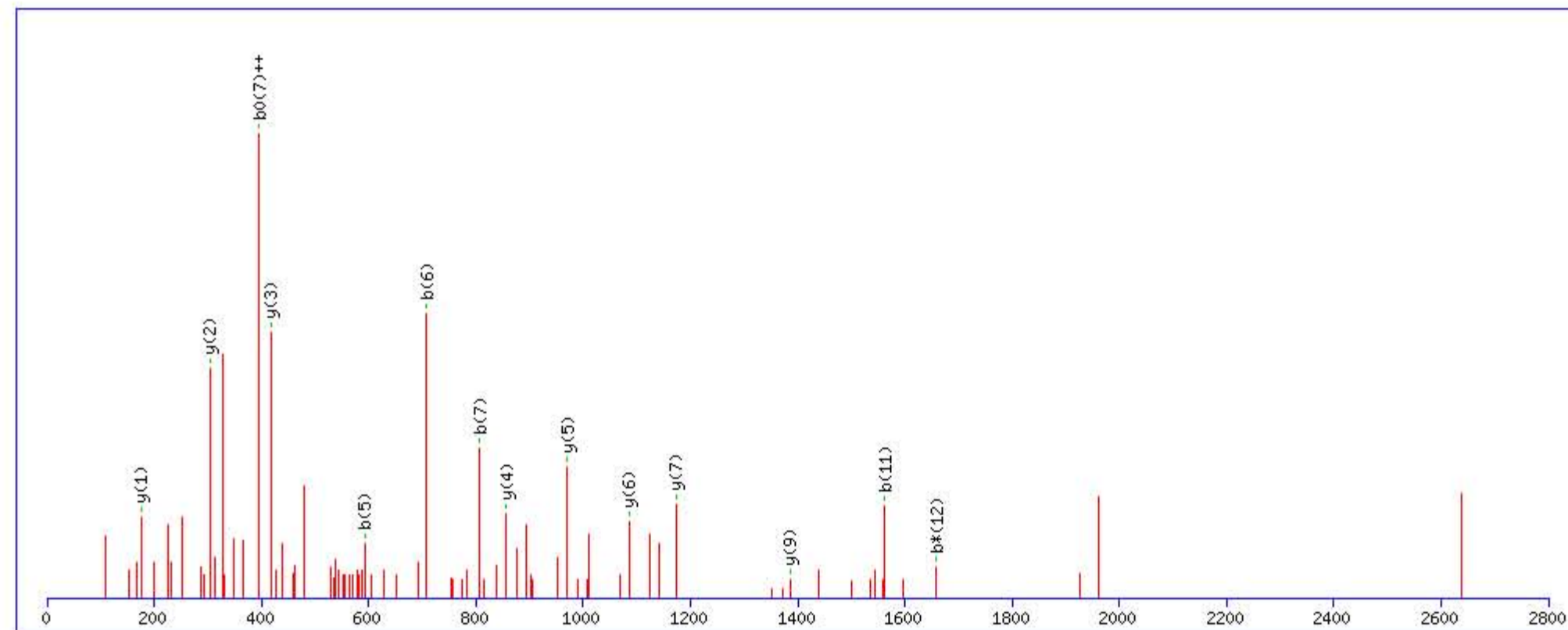
Title: Locus:1.1.1.3094.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1977.957809

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

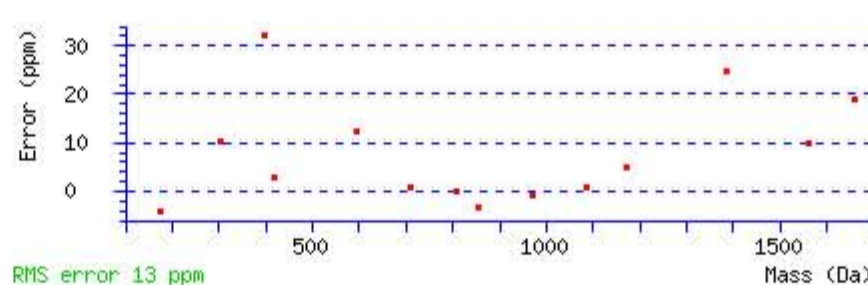
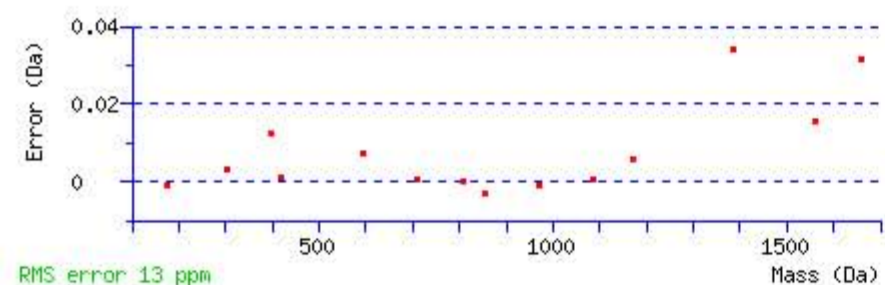
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 73 Expect: 2.8e-007

Matches : 14/148 fragment ions using 16 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.050203	58.028740	98.023654	49.515465			N							14
2	228.134267	114.570771	211.107718	106.057497			L	1864.922173	932.964724	1847.895624	924.451450	1846.911608	923.959442	13
3	365.193179	183.100227	348.166630	174.586953			H	1751.838109	876.422692	1734.811560	867.909418	1733.827544	867.417410	12
4	480.220122	240.613699	463.193573	232.100425	462.209557	231.608417	D	1614.779197	807.893236	1597.752648	799.379962	1596.768632	798.887954	11
5	593.304186	297.155731	576.277637	288.642457	575.293621	288.150449	L	1499.752254	750.379765	1482.725705	741.866490	1481.741689	741.374482	10
6	708.331129	354.669203	691.304580	346.155928	690.320564	345.663920	D	1386.668190	693.837733	1369.641641	685.324458	1368.657625	684.832450	9
7	807.399543	404.203410	790.372994	395.690135	789.388978	395.198127	V	1271.641247	636.324261	1254.614698	627.810987	1253.630682	627.318979	8
8	894.431571	447.719424	877.405022	439.206149	876.421006	438.714141	S	1172.572833	586.790054	1155.546284	578.276780	1154.562268	577.784772	7
9	1009.458514	505.232895	992.431965	496.719620	991.447949	496.227612	D	1085.540805	543.274040	1068.514256	534.760766	1067.530240	534.268758	6
10	1123.501441	562.254358	1106.474892	553.741084	1105.490876	553.249076	N	970.513862	485.760569	953.487313	477.247294	952.503297	476.755286	5
11	1562.726767	781.867021	1545.700218	773.353747	1544.716202	772.861739	Q	856.470935	428.739105	839.444386	420.225831	838.460370	419.733823	4
12	1675.810831	838.409053	1658.784282	829.895779	1657.800266	829.403771	L	417.245609	209.126442	400.219060	200.613168	399.235044	200.121160	3
13	1804.853424	902.930350	1787.826875	894.417075	1786.842859	893.925067	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
14							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **NLHDLVDSDNQLER**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.8	1977.957809	-0.005177	NLHDLVDSDNQLER
2.9	1977.979813	-0.027181	TMPRTVPGSTMKMGSLER

Mascot: <http://www.matrixscience.com/>

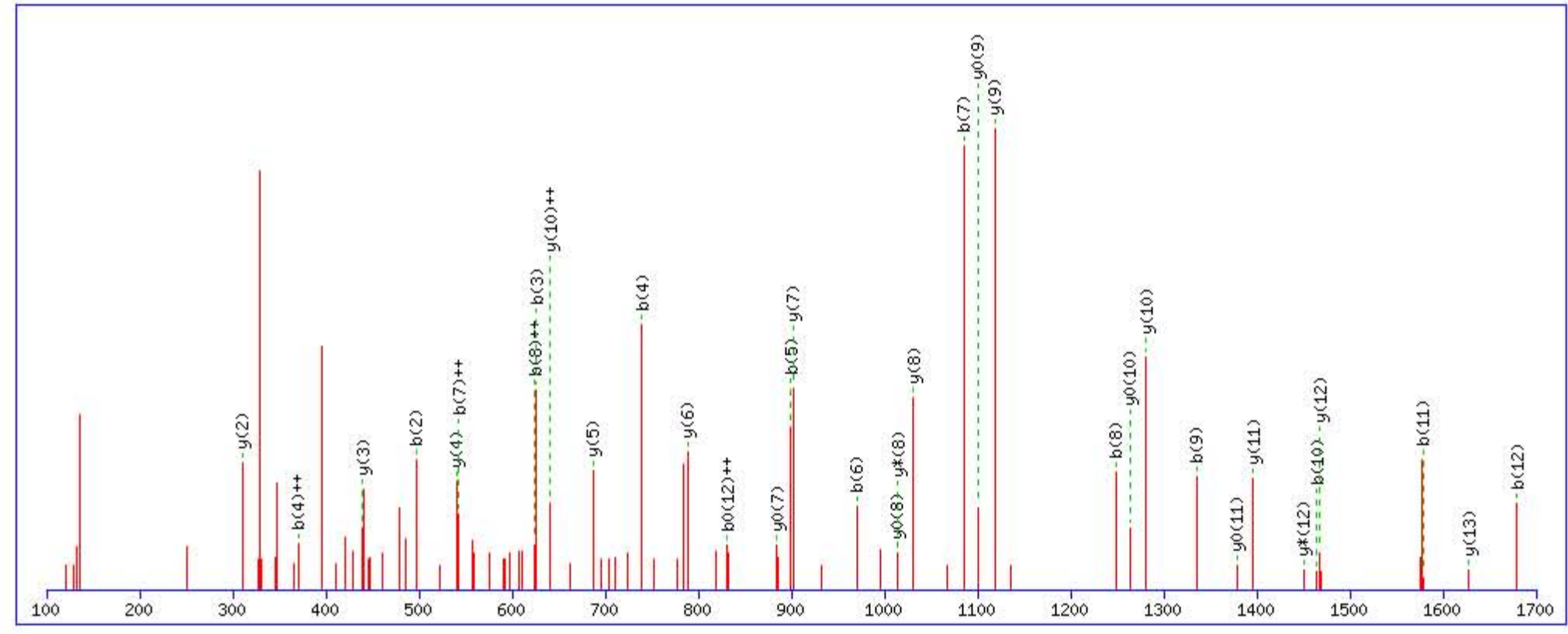
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GQELCADYSENTFTEYK**
 Found in **VTDB_HUMAN**, Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

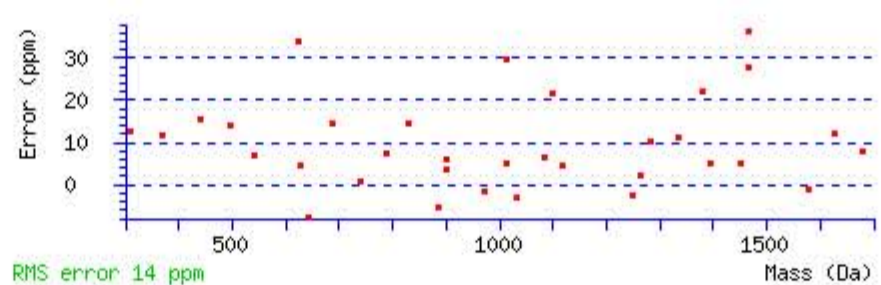
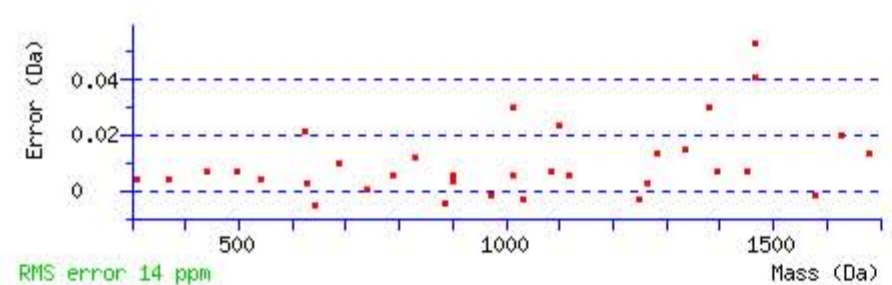
Match to Query 53918: 2365.026612 from(789.349480,3+) rtinseconds(2151) index(69672)
 Title: Locus:1.1.1.1686.25 File:"2013-07-02 CLN FXIII 60 min 2nd FT.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2365.024231
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q2 : Biotin:Thermo-21345 (Q)
 Ions Score: 78 Expect: 5.3e-008
 Matches : 35/182 fragment ions using 55 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							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
78.4	2365.024231	0.002381	GQELCADYSENTFTEYK

MATRIX SCIENCE 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 42289: 1775.911722 from(592.977850,3+) rtinseconds(1990) index(52811)

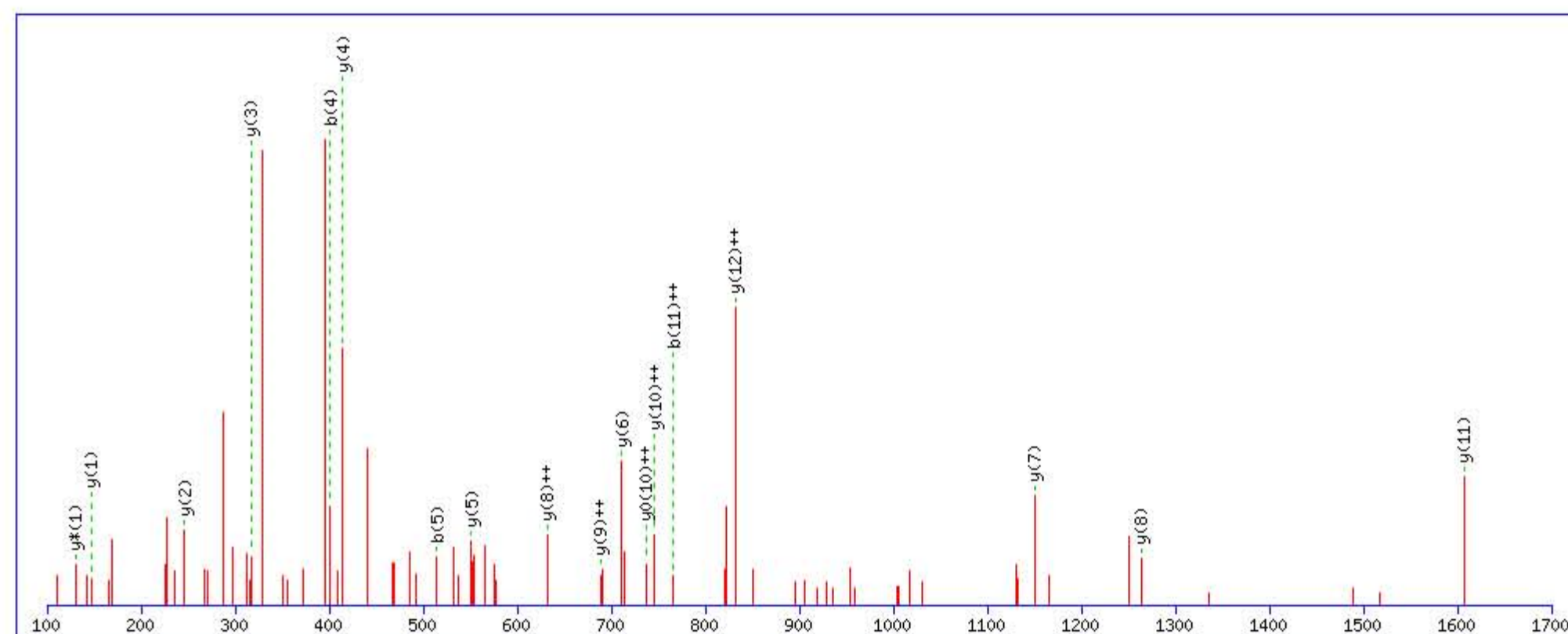
Title: Locus:1.1.1.1308.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1775.906250

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

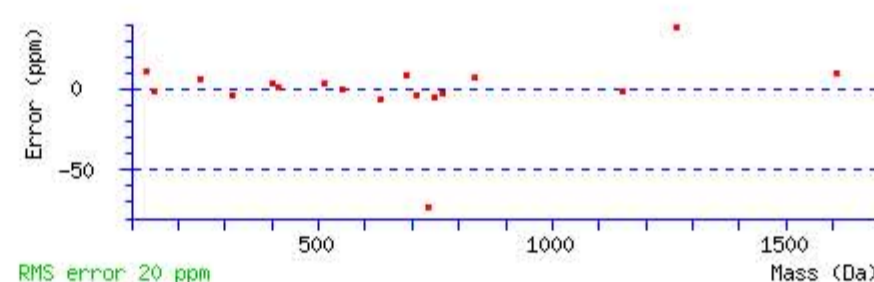
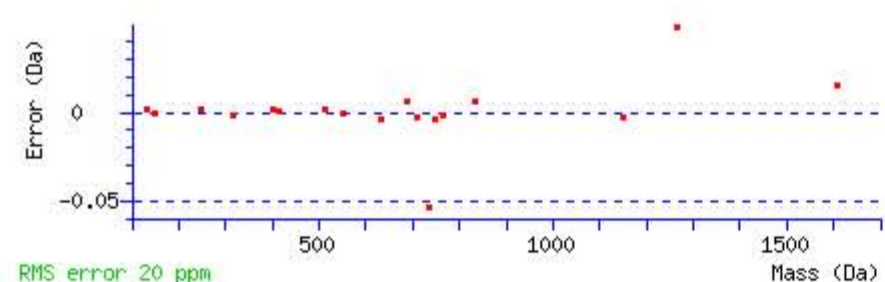
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 32 Expect: 0.017

Matches : 18/110 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							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
31.8	1775.906250	0.005472	LGDDLLQCHPAVK

Mascot: <http://www.matrixscience.com/>

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **ELNQAGQETLVTGWGYHSSR**

Found in **PROC_HUMAN**, Vitamin K-dependent protein C OS=Homo sapiens GN=PROC PE=1 SV=1

Match to Query 57183: 2543.248152 from(848.756660,3+) rtinseconds(2199) index(54222)

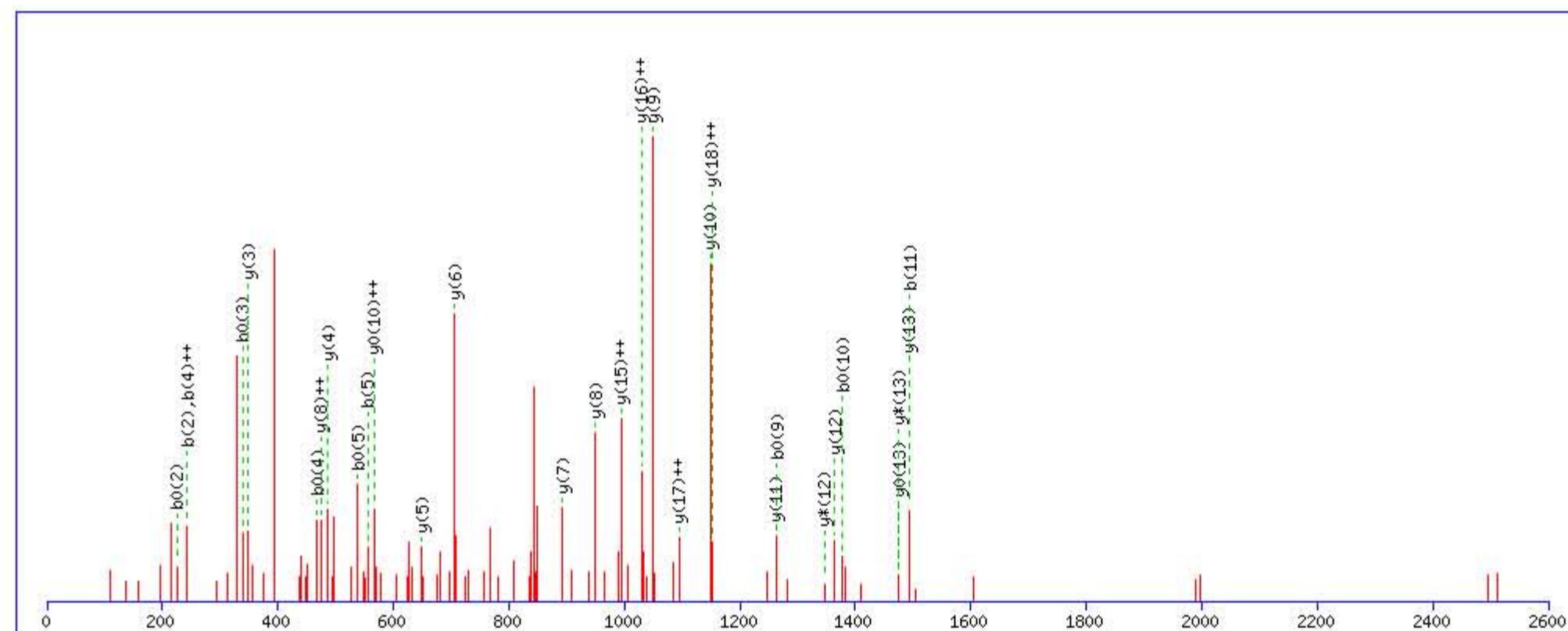
Title: Locus:1.1.1.1380.24 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2543.222702

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

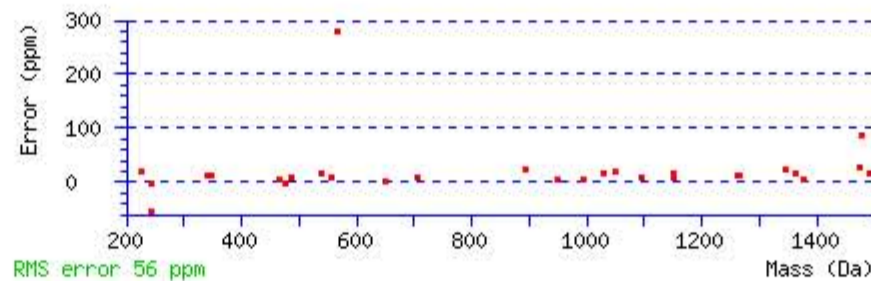
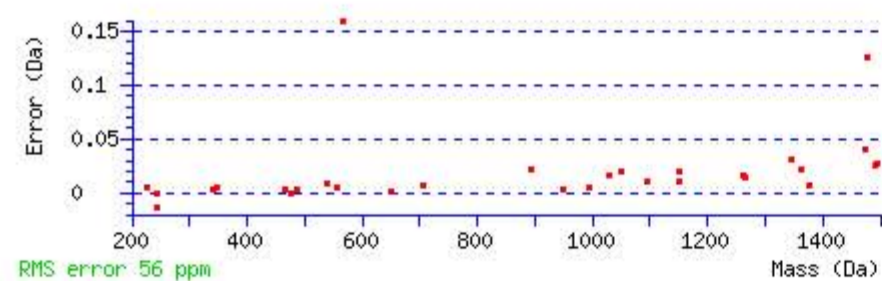
Variable modifications:

Q7 : Biotin:Thermo-21345 (Q)

Ions Score: 52 Expect: 0.00018

Matches : 30/222 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	130.049869	65.528572			112.039304	56.523290	E							20
2	243.133933	122.070605			225.123368	113.065322	L	2415.187392	1208.097334	2398.160843	1199.584059	2397.176827	1199.092051	19
3	357.176860	179.092068	340.150311	170.578794	339.166295	170.086786	N	2302.103328	1151.555302	2285.076779	1143.042027	2284.092763	1142.550019	18
4	485.235438	243.121357	468.208889	234.608083	467.224873	234.116075	Q	2188.060401	1094.533838	2171.033852	1086.020564	2170.049836	1085.528556	17
5	556.272552	278.639914	539.246003	270.126640	538.261987	269.634632	A	2060.001823	1030.504549	2042.975274	1021.991275	2041.991258	1021.499267	16
6	613.294016	307.150646	596.267467	298.637372	595.283451	298.145364	G	1988.964709	994.985993	1971.938160	986.472718	1970.954144	985.980710	15
7	1052.519342	526.763309	1035.492793	518.250035	1034.508777	517.758027	Q	1931.943245	966.475261	1914.916696	957.961986	1913.932680	957.469978	14
8	1181.561935	591.284606	1164.535386	582.771331	1163.551370	582.279323	E	1492.717919	746.862597	1475.691370	738.349323	1474.707354	737.857315	13
9	1282.609614	641.808445	1265.583065	633.295171	1264.599049	632.803163	T	1363.675326	682.341301	1346.648777	673.828026	1345.664761	673.336018	12
10	1395.693678	698.350477	1378.667129	689.837203	1377.683113	689.345195	L	1262.627647	631.817461	1245.601098	623.304187	1244.617082	622.812179	11
11	1494.762092	747.884684	1477.735543	739.371410	1476.751527	738.879402	V	1149.543583	575.275429	1132.517034	566.762155	1131.533018	566.270147	10
12	1595.809771	798.408524	1578.783222	789.895249	1577.799206	789.403241	T	1050.475169	525.741222	1033.448620	517.227948	1032.464604	516.735940	9
13	1652.831235	826.919256	1635.804686	818.405981	1634.820670	817.913973	G	949.427490	475.217383	932.400941	466.704108	931.416925	466.212100	8
14	1838.910548	919.958912	1821.883999	911.445638	1820.899983	910.953630	W	892.406026	446.706651	875.379477	438.193376	874.395461	437.701368	7
15	1895.932012	948.469644	1878.905463	939.956370	1877.921447	939.464362	G	706.326713	353.666994	689.300164	345.153720	688.316148	344.661712	6
16	2058.995341	1030.001308	2041.968792	1021.488034	2040.984776	1020.996026	Y	649.305249	325.156263	632.278700	316.642988	631.294684	316.150980	5
17	2196.054253	1098.530764	2179.027704	1090.017490	2178.043688	1089.525482	H	486.241920	243.624598	469.215371	235.111324	468.231355	234.619316	4
18	2283.086281	1142.046778	2266.059732	1133.533504	2265.075716	1133.041496	S	349.183008	175.095142	332.156459	166.581868	331.172443	166.089860	3
19	2370.118309	1185.562792	2353.091760	1177.049518	2352.107744	1176.557510	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
20							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [ELNQAGQETLVTGWGYHSSR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.7	2543.222702	0.025450	ELNQAGQETLVTGWGYHSSR
44.3	2543.222702	0.025450	ELNQAGQETLVTGWGYHSSR

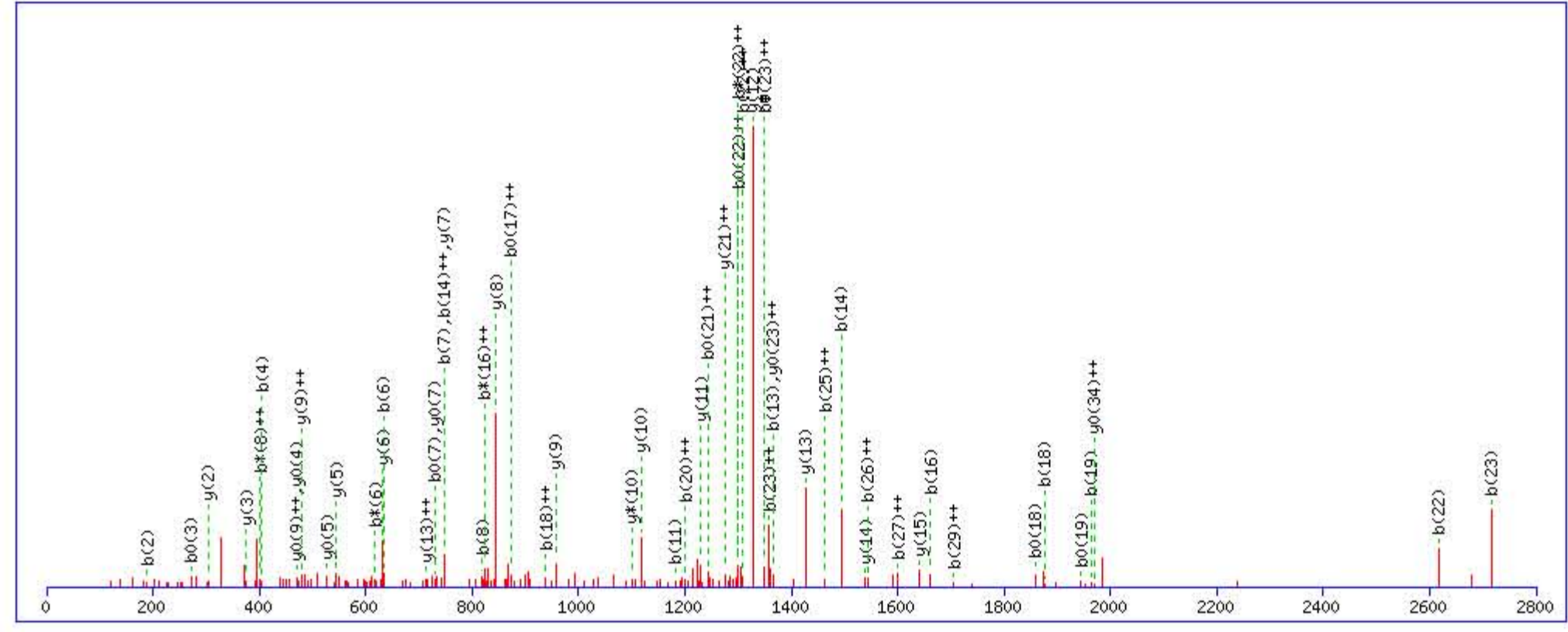
Mascot Search Results

Peptide View

MS/MS Fragmentation of **STTDNDIALHLHAQPATLSQTIVPICLPDSGLAER**
 Found in **PROC_HUMAN**, Vitamin K-dependent protein C OS=Homo sapiens GN=PROC PE=1 SV=1

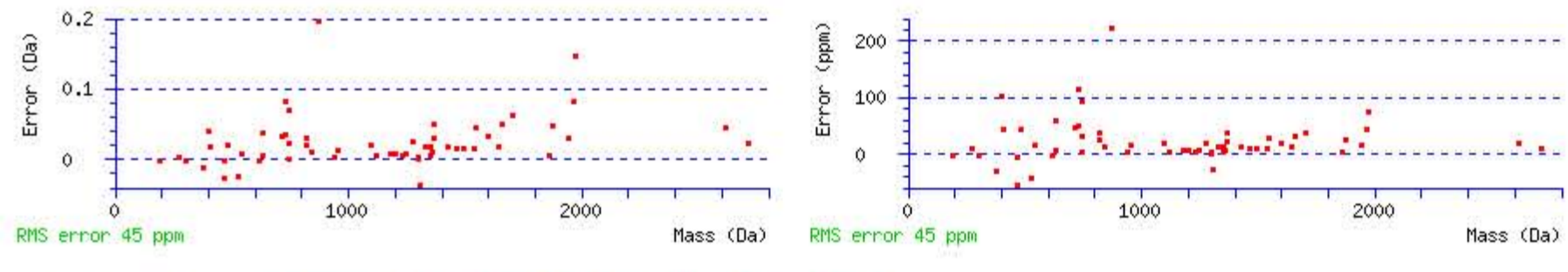
Match to Query 70147: 4041.134736 from(1011.290960,4+) rtinseconds(2998) index(59517)
 Title: Locus:1.1.1.1655.22 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 4041.091476
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q20 : Biotin:Thermo-21345 (Q)
 Ions Score: 53 Expect: 2.6e-005
 Matches : 58/398 fragment ions using 146 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							35
2	189.086983	95.047129			171.076418	86.041847	T	3955.066740	1978.037008	3938.040191	1969.523733	3937.056175	1969.031725	34
3	290.134662	145.570969			272.124097	136.565687	T	3854.019061	1927.513168	3836.992512	1918.999894	3836.008496	1918.507886	33
4	405.161605	203.084441			387.151040	194.079158	D	3752.971382	1876.989329	3735.944833	1868.476054	3734.960817	1867.984046	32
5	519.204532	260.105904	502.177983	251.592630	501.193967	251.100622	N	3637.944439	1819.475857	3620.917890	1810.962583	3619.933874	1810.470575	31
6	634.231475	317.619376	617.204926	309.106101	616.220910	308.614093	D	3523.901512	1762.454394	3506.874963	1753.941119	3505.890947	1753.449111	30
7	747.315539	374.161408	730.288990	365.648133	729.304974	365.156125	I	3408.874569	1704.940922	3391.848020	1696.427648	3390.864004	1695.935640	29
8	818.352653	409.679965	801.326104	401.166690	800.342088	400.674682	A	3295.790505	1648.398890	3278.763956	1639.885616	3277.779940	1639.393608	28
9	931.436717	466.221997	914.410168	457.708722	913.426152	457.216714	L	3224.753391	1612.880333	3207.726842	1604.367059	3206.742826	1603.875051	27
10	1044.520781	522.764028	1027.494232	514.250754	1026.510216	513.758746	L	3111.669327	1556.338301	3094.642778	1547.825027	3093.658762	1547.333019	26
11	1181.579693	591.293484	1164.553144	582.780210	1163.569128	582.288202	H	2998.585263	1499.796269	2981.558714	1491.282995	2980.574698	1490.790987	25
12	1294.663757	647.835516	1277.637208	639.322242	1276.653192	638.830234	L	2861.526351	1431.266813	2844.499802	1422.753539	2843.515786	1422.261531	24
13	1365.700871	683.354073	1348.674322	674.840799	1347.690306	674.348791	A	2748.442287	1374.724781	2731.415738	1366.211507	2730.431722	1365.719499	23
14	1493.759449	747.383362	1476.732900	738.870088	1475.748884	738.378080	Q	2677.405173	1339.206224	2660.378624	1330.692950	2659.394608	1330.200942	22
15	1590.812213	795.909744	1573.785664	787.396470	1572.801648	786.904462	P	2549.346595	1275.176935	2532.320046	1266.663661	2531.336030	1266.171653	21
16	1661.849327	831.428301	1644.822778	822.915027	1643.838762	822.423019	A	2452.293831	1226.650553	2435.267282	1218.137279	2434.283266	1217.645271	20
17	1762.897006	881.952141	1745.870457	873.438867	1744.886441	872.946858	T	2381.256717	1191.131996	2364.230168	1182.618722	2363.246152	1182.126714	19
18	1875.981070	938.494173	1858.954521	929.980898	1857.970505	929.488890	L	2280.209038	1140.608157	2263.182489	1132.094882	2262.198473	1131.602874	18
19	1963.013098	982.010187	1945.986549	973.496913	1945.002533	973.004904	S	2167.124974	1084.066125	2150.098425	1075.552850	2149.114409	1075.060842	17
20	2402.238424	1201.622850	2385.211875	1193.109575	2384.227859	1192.617567	Q	2080.092946	1040.550111	2063.066397	1032.036836	2062.082381	1031.544828	16
21	2503.286103	1252.146689	2486.259554	1243.633415	2485.275538	1243.141407	T	1640.867620	820.937448	1623.841071	812.424174	1622.857055	811.932166	15
22	2616.370167	1308.688721	2599.343618	1300.175447	2598.359602	1299.683439	I	1539.819941	770.413609	1522.793392	761.900334	1521.809376	761.408326	14
23	2715.438581	1358.222928	2698.412032	1349.709654	2697.428016	1349.217646	V	1426.735877	713.871577	1409.709328	705.358302	1408.725312	704.866294	13
24	2812.491345	1406.749310	2795.464796	1398.236036	2794.480780	1397.744028	P	1327.667463	664.337370	1310.640914	655.824095	1309.656898	655.332087	12
25	2925.575409	1463.291342	2908.548860	1454.778068	2907.564844	1454.286060	I	1230.614699	615.810988	1213.588150	607.297713	1212.604134	606.805705	11
26	3085.606058	1543.306667	3068.579509	1534.793392	3067.595493	1534.301384	C	1117.530635	559.268956	1100.504086	550.755681	1099.520070	550.263673	10
27	3198.690122	1599.848699	3181.663573	1591.335424	3180.679557	1590.843416	L	957.499986	479.253631	940.473437	470.740357	939.489421	470.248349	9
28	3295.742886	1648.375081	3278.716337	1639.861806	3277.732321	1639.369798	P	844.415922	422.711599	827.389373	414.198325	826.405357	413.706317	8
29	3410.769829	1705.888552	3393.743280	1697.375278	3392.759264	1696.883270	D	747.363158	374.185217	730.336609	365.671943	729.352593	365.179935	7
30	3497.801857	1749.404566	3480.775308	1740.891292	3479.791292	1740.399284	S	632.336215	316.671746	615.309666	308.158471	614.325650	307.666463	6
31	3554.823321	1777.915298	3537.796772	1769.402024	3536.812756	1768.910016	G	545.304187	273.155732	528.277638	264.642457	527.293622	264.150449	5
32	3667.907385	1834.457330	3650.880836	1825.944056	3649.896820	1825.452048	L	488.282723	244.645000	471.256174	236.131725	470.272158	235.639717	4
33	3738.944499	1869.975887	3721.917950	1861.462613	3720.933934	1860.970605	A	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
34	3867.987092	1934.497184	3850.960543	1925.983909	3849.976527	1925.491901	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
35							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **STTDNDIALHLHAQPATLSQTIVPICLPDSGLAER**
 (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	4041.091476	0.043260	STTDNDIALHLHAQPATLSQTIVPICLPDSGLAER
40.5	4041.091476	0.043260	STTDNDIALHLHAQPATLSQTIVPICLPDSGLAER
3.8	4041.127869	0.006867	TTAIVEVKGTVDIVLTPLVAEALDRYIEAMVHCASTR

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 18699: 1096.634328 from(549.324440,2+) rtinseconds(2001) index(52906)

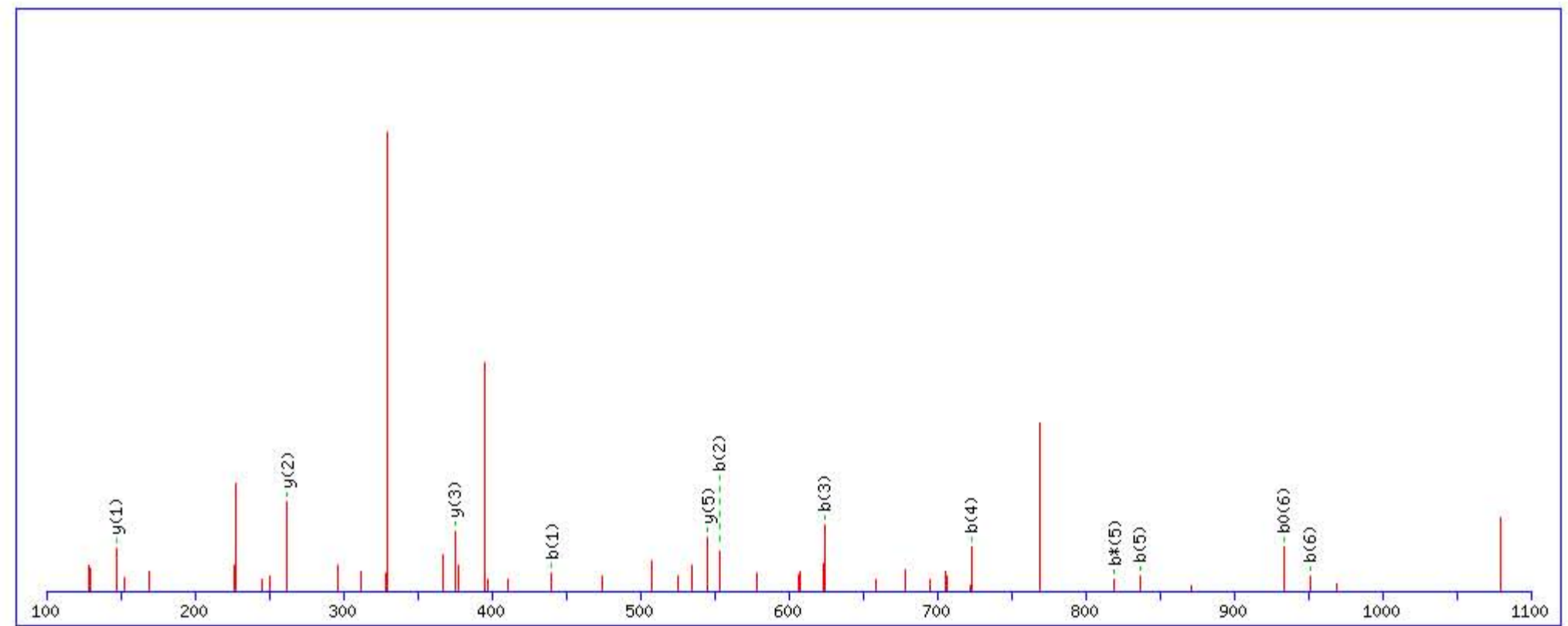
Title: Locus:1.1.1.1312.6 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1096.631439

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

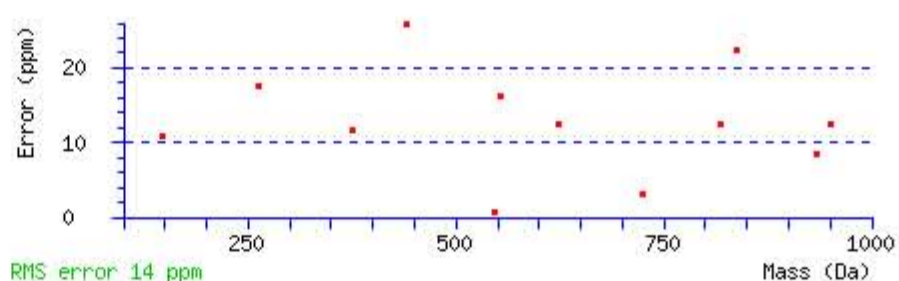
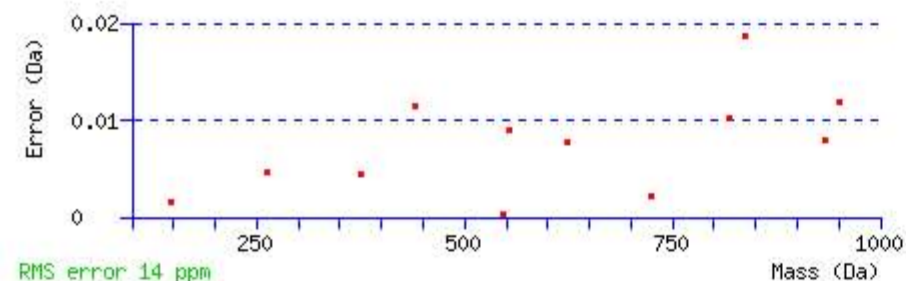
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 32 Expect: 0.0096

Matches : 12/60 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							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
31.9	1096.631439	0.002889	QLAVLDK
18.1	1096.624054	0.010274	KPVDSVPLSR
9.3	1096.624023	0.010305	IPRENLLDK
8.8	1096.635269	-0.000941	SSSLVIHKAR
5.3	1096.631439	0.002889	GILQLDK
2.2	1096.631439	0.002889	QIDVAIK
2.0	1096.628067	0.006261	YIFVSLLSR
1.6	1096.642654	-0.008326	NITMHLK
0.9	1096.646500	-0.012172	KPDQARVRK
0.7	1096.631439	0.002889	QIEGLVK

Mascot: <http://www.matrixscience.com/>

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 33148: 1474.723168 from(738.368860,2+) rtinseconds(1754) index(34795)

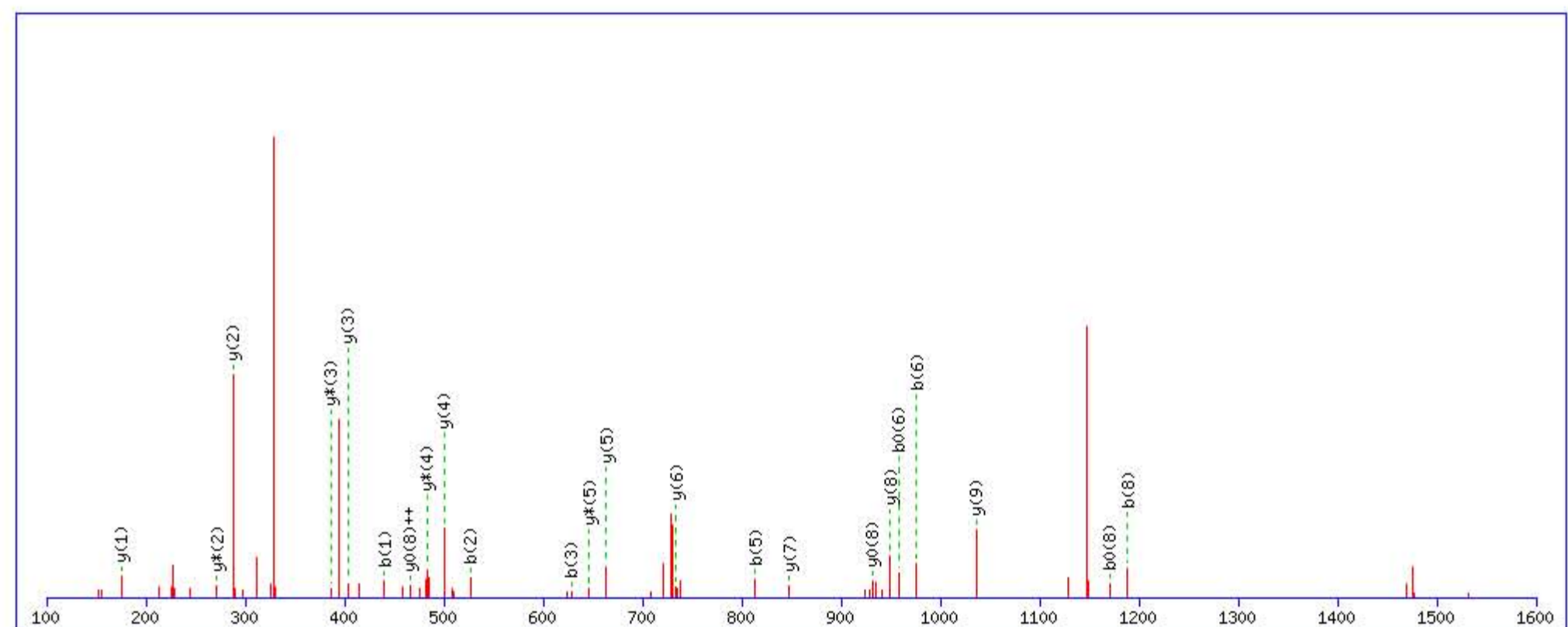
Title: Locus:1.1.1.3030.16 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1474.723831

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

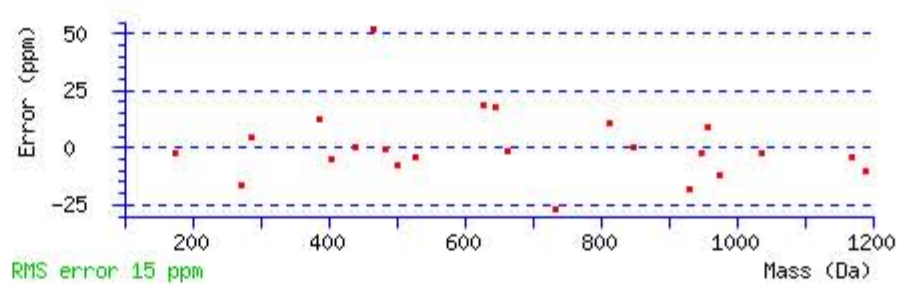
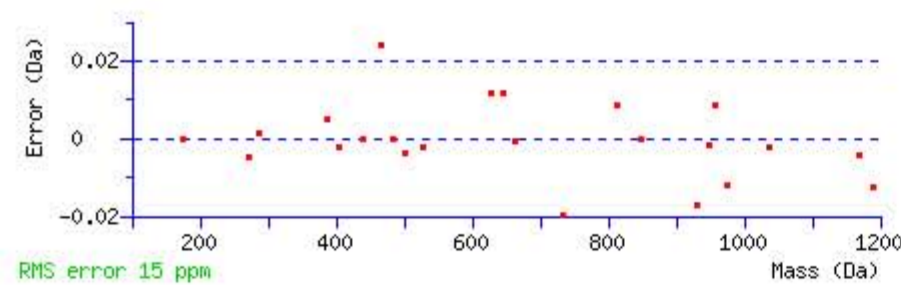
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 46 Expect: 0.00052

Matches : 23/102 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	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
46.1	1474.723831	-0.000663	QSTNAYPDLR
15.1	1474.721161	0.002007	QSTHGERGHR
9.3	1474.741592	-0.018424	SSLEHGSDVYLLR
6.4	1474.744934	-0.021766	LSKEELIQNMDR
4.0	1474.727661	-0.004493	SSATLWNSPSRNR
2.4	1474.731033	-0.007865	RGDGGKMAAAGALER
1.4	1474.719788	0.003380	QQEELEQMRLR
0.8	1474.742462	-0.019294	QCKSEFPPIR
0.6	1474.735092	-0.011924	SFCVLSQLTQHR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **SFQTGLFTAAR**

Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

Match to Query 34207: 1508.785028 from(755.399790,2+) rtinseconds(2294) index(38209)

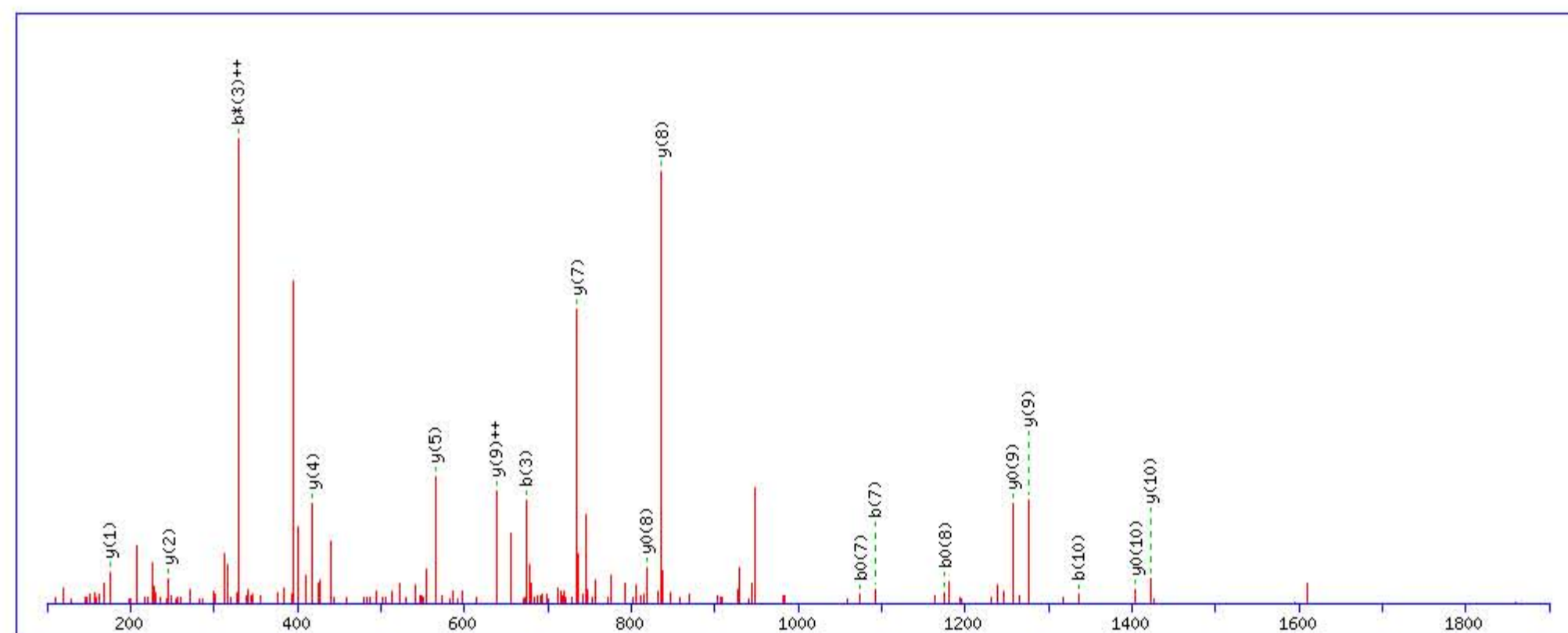
Title: Locus:1.1.1.3218.15 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1508.780975

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

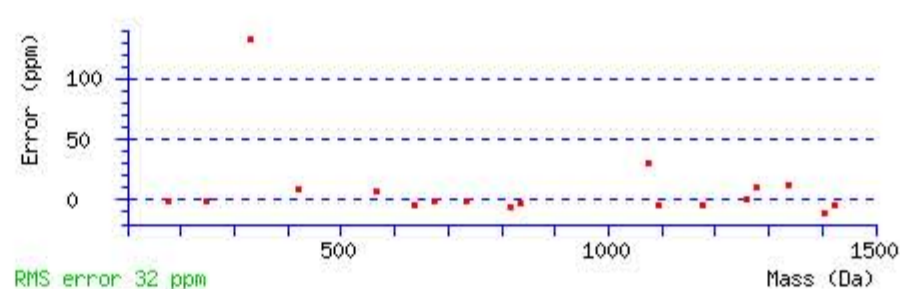
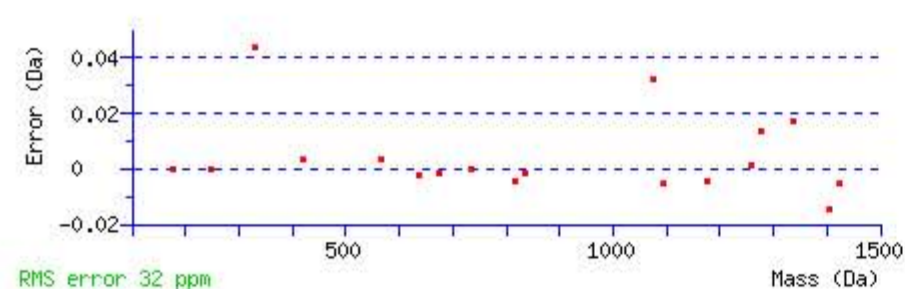
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 55 Expect: 3.5e-005

Matches : 18/110 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	88.039304	44.523290			70.028739	35.518008	S							11
2	235.107718	118.057497			217.097153	109.052214	F	1422.756220	711.881748	1405.729671	703.368474	1404.745655	702.876465	10
3	674.333044	337.670160	657.306495	329.156885	656.322479	328.664877	Q	1275.687806	638.347541	1258.661257	629.834267	1257.677241	629.342259	9
4	775.380723	388.194000	758.354174	379.680725	757.370158	379.188717	T	836.462480	418.734878	819.435931	410.221604	818.451915	409.729596	8
5	832.402187	416.704732	815.375638	408.191457	814.391622	407.699449	G	735.414801	368.211039	718.388252	359.697764	717.404236	359.205756	7
6	945.486251	473.246764	928.459702	464.733489	927.475686	464.241481	L	678.393337	339.700307	661.366788	331.187032	660.382772	330.695024	6
7	1092.554665	546.780971	1075.528116	538.267696	1074.544100	537.775688	F	565.309273	283.158275	548.282724	274.645000	547.298708	274.152992	5
8	1193.602344	597.304810	1176.575795	588.791536	1175.591779	588.299528	T	418.240859	209.624067	401.214310	201.110793	400.230294	200.618785	4
9	1264.639458	632.823367	1247.612909	624.310093	1246.628893	623.818085	A	317.193180	159.100228	300.166631	150.586953			3
10	1335.676572	668.341924	1318.650023	659.828650	1317.666007	659.336642	A	246.156066	123.581671	229.129517	115.068396			2
11							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **SFQTGLFTAAR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.0	1508.780975	0.004053	SFQTGLFTAAR
7.1	1508.798721	-0.013693	SSYGVAAPVDFLRK
5.2	1508.805893	-0.020865	RLELPRASDAEPR
4.7	1508.780960	0.004068	TQPPPENLFR
4.6	1508.776932	0.008096	LMGADSLQLFRSR
2.1	1508.805939	-0.020911	SSPEHTTILRGGVR
0.3	1508.765701	0.019327	TKPLSMLYVDNGR
0.0	1508.794708	-0.009680	SGKSGPSPTTPQPLR

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 39436: 1650.846148 from(826.430350,2+) rtinseconds(1682) index(50712)

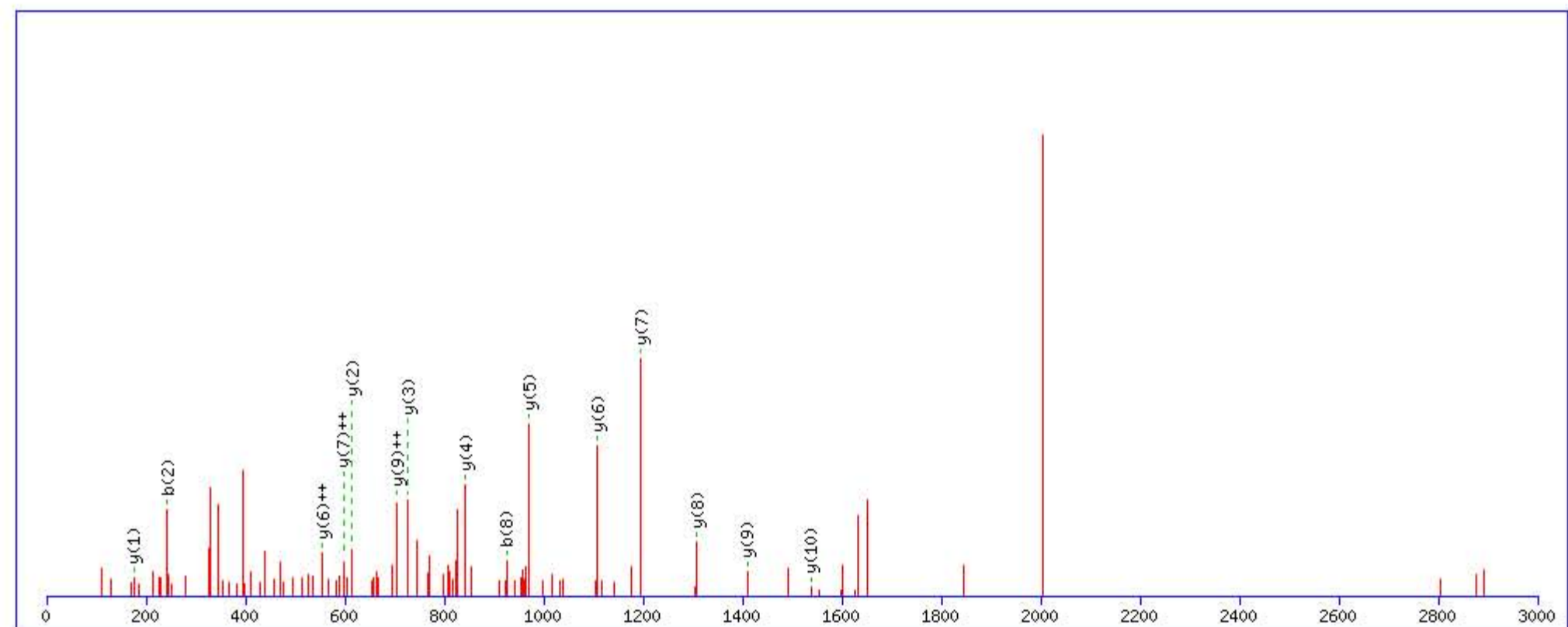
Title: Locus:1.1.1.1201.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1650.839920

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

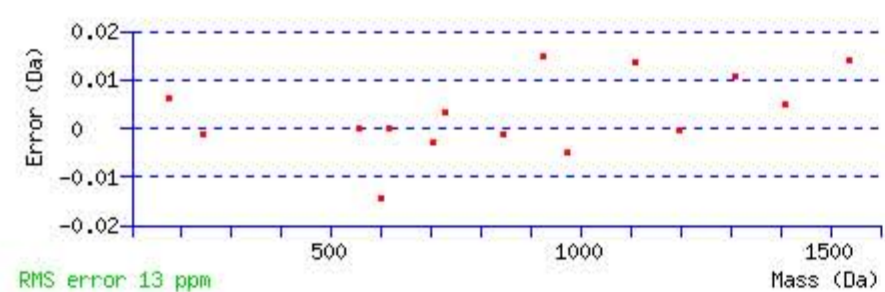
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

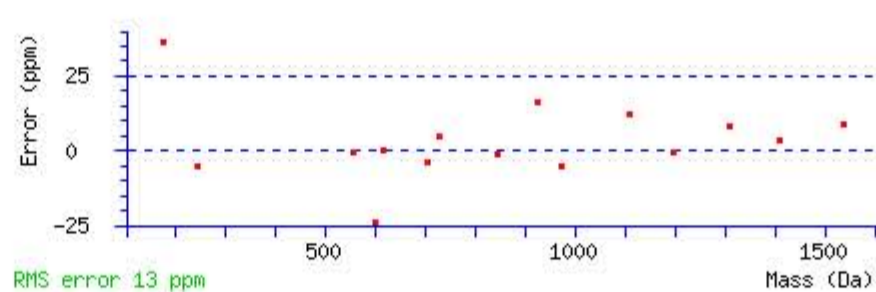
Ions Score: 66 Expect: 8.8e-007

Matches : 15/94 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	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



RMS error 13 ppm



RMS error 13 ppm

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
66.1	1650.839920	0.006228	IETISHEDLQR
1.5	1650.833389	0.012759	QQLEHIMATNR
0.3	1650.868896	-0.022748	LELLELDHEQTRR

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 53679: 2342.164332 from(781.728720,3+) rtinseconds(2162) index(22699)

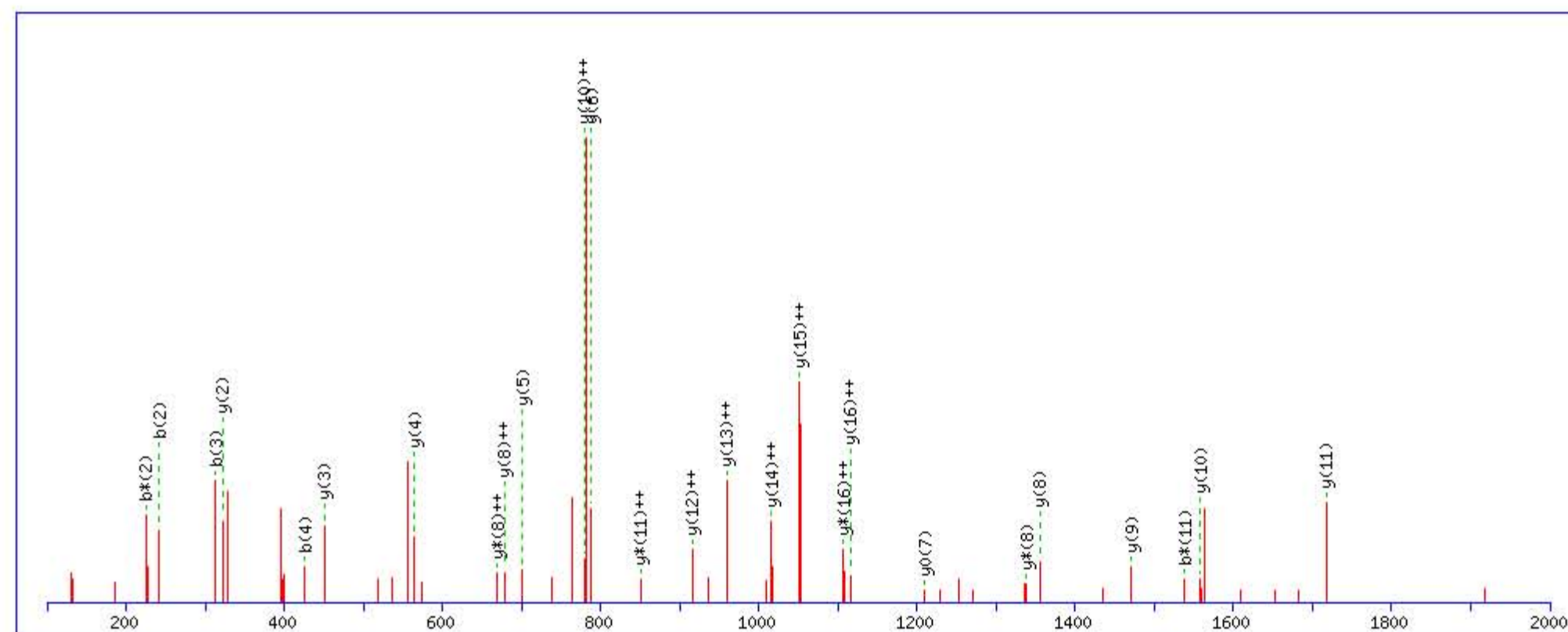
Title: Locus:1.1.1.755.9 File:"2013-07-02 CLN FXIII 60 min 2nd F 2.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2342.151108

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

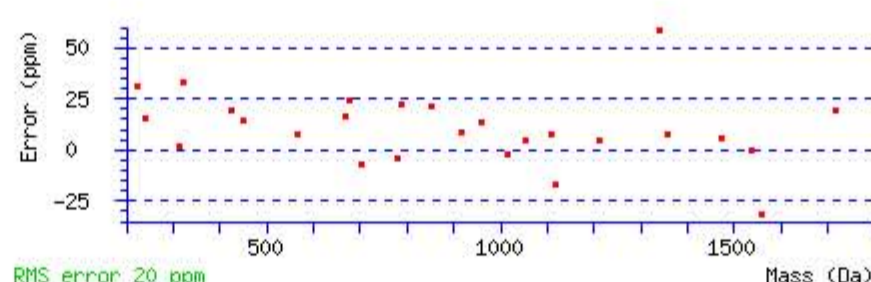
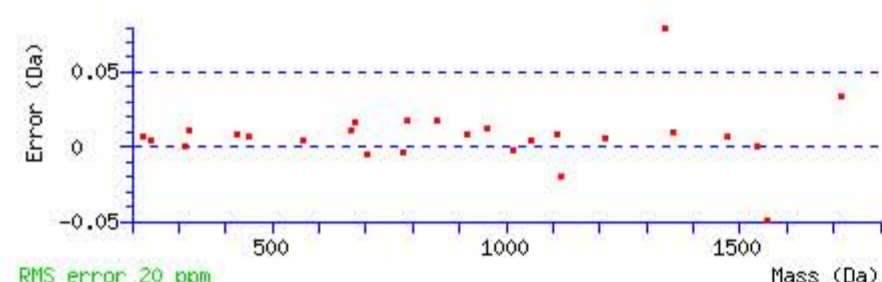
Variable modifications:

Q11 : Biotin:Thermo-21345 (Q)

Ions Score: 44 Expect: 0.0012

Matches : 26/178 fragment ions using 60 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308					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
44.1	2342.151108	0.013224	IQALSLCSDQQSHLEFR
42.9	2342.151108	0.013224	IQALSLCSDQQSHLEFR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **TDGCQHFCLPGQESYTCSCAQGYR**

Found in **PROZ_HUMAN**, Vitamin K-dependent protein Z OS=Homo sapiens GN=PROZ PE=1 SV=2

Match to Query 49654: 3192.327132 from(1065.116320,3+) rtinseconds(2067) index(53359)

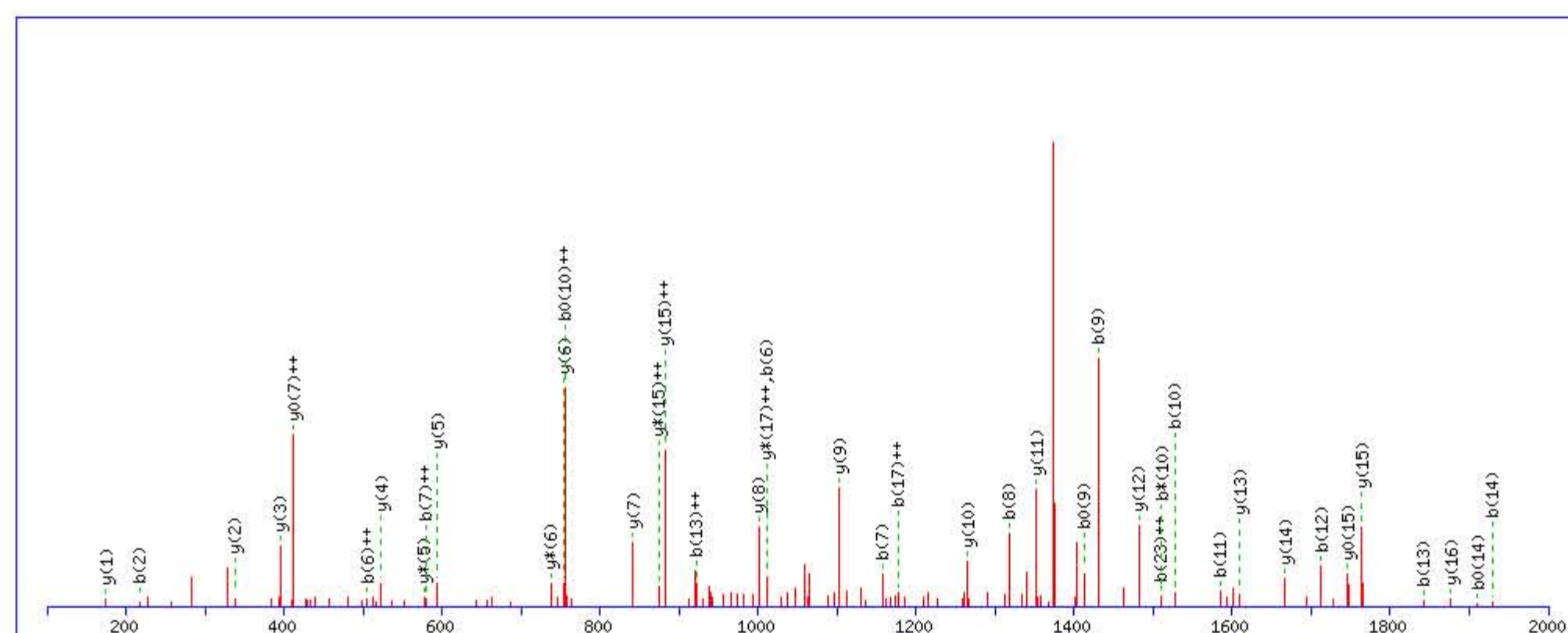
Title: Locus:1.1.1.1334.13 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3192.298050

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

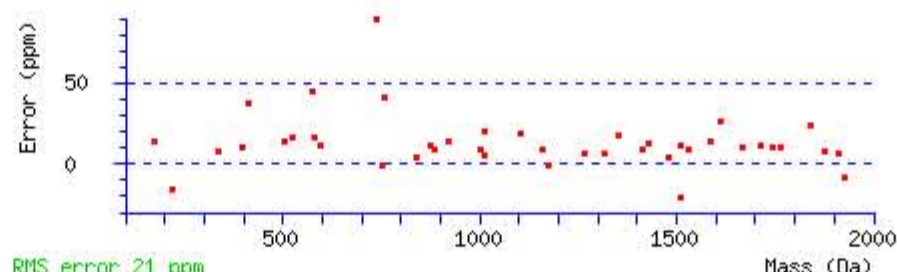
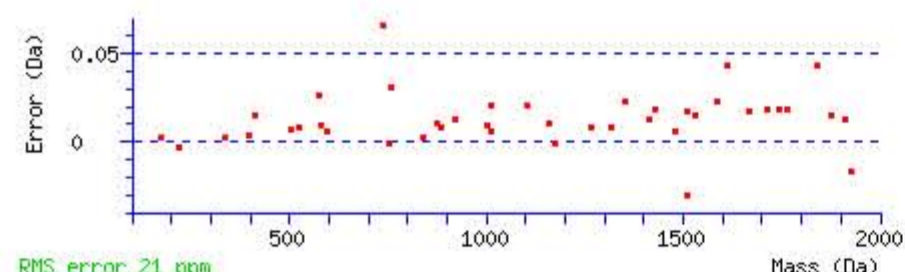
Variable modifications:

Q5 : Biotin:Thermo-21345 (Q)

Ions Score: 99 Expect: 1.1e-009

Matches : 42/256 fragment ions using 65 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.054955	51.531116			84.044390	42.525833	T							24
2	217.081898	109.044587			199.071333	100.039304	D	3092.257619	1546.632447	3075.231070	1538.119173	3074.247054	1537.627165	23
3	274.103362	137.555319			256.092797	128.550037	G	2977.230676	1489.118976	2960.204127	1480.605701	2959.220111	1480.113693	22
4	434.134011	217.570644			416.123446	208.565361	C	2920.209212	1460.608244	2903.182663	1452.094969	2902.198647	1451.602961	21
5	873.359337	437.183307	856.332788	428.670032	855.348772	428.178024	Q	2760.178563	1380.592919	2743.152014	1372.079645	2742.167998	1371.587637	20
6	1010.418249	505.712763	993.391700	497.199488	992.407684	496.707480	H	2320.953237	1160.980256	2303.926688	1152.466982	2302.942672	1151.974974	19
7	1157.486663	579.246970	1140.460114	570.733695	1139.476098	570.241687	F	2183.894325	1092.450800	2166.867776	1083.937526	2165.883760	1083.445518	18
8	1317.517312	659.262294	1300.490763	650.749020	1299.506747	650.257012	C	2036.825911	1018.916594	2019.799362	1010.403319	2018.815346	1009.911311	17
9	1430.601376	715.804326	1413.574827	707.291052	1412.590811	706.799044	L	1876.795262	938.901269	1859.768713	930.387994	1858.784697	929.895986	16
10	1527.654140	764.330708	1510.627591	755.817434	1509.643575	755.325426	P	1763.711198	882.359237	1746.684649	873.845963	1745.700633	873.353954	15
11	1584.675604	792.841440	1567.649055	784.328166	1566.665039	783.836158	G	1666.658434	833.832855	1649.631885	825.319581	1648.647869	824.827572	14
12	1712.734182	856.870729	1695.707633	848.357455	1694.723617	847.865446	Q	1609.636970	805.322123	1592.610421	796.808849	1591.626405	796.316841	13
13	1841.776775	921.392026	1824.750226	912.878751	1823.766210	912.386743	E	1481.578392	741.292834	1464.551843	732.779560	1463.567827	732.287552	12
14	1928.808803	964.908040	1911.782254	956.394765	1910.798238	955.902757	S	1352.535799	676.771538	1335.509250	668.258263	1334.525234	667.766255	11
15	2091.872132	1046.439704	2074.845583	1037.926429	2073.861567	1037.434421	Y	1265.503771	633.255523	1248.477222	624.742249	1247.493206	624.250241	10
16	2192.919811	1096.963543	2175.893262	1088.450269	2174.909246	1087.958261	T	1102.440442	551.723859	1085.413893	543.210584	1084.429877	542.718576	9
17	2352.950460	1176.978868	2335.923911	1168.465593	2334.939895	1167.973585	C	1001.392763	501.200020	984.366214	492.686745	983.382198	492.194737	8
18	2439.982488	1220.494882	2422.955939	1211.981607	2421.971923	1211.489599	S	841.362114	421.184695	824.335565	412.671421	823.351549	412.179413	7
19	2600.013137	1300.510206	2582.986588	1291.996932	2582.002572	1291.504924	C	754.330086	377.668681	737.303537	369.155407			6
20	2671.050251	1336.028763	2654.023702	1327.515489	2653.039686	1327.023481	A	594.299437	297.653357	577.272888	289.140082			5
21	2799.108829	1400.058052	2782.082280	1391.544778	2781.098264	1391.052770	Q	523.262323	262.134800	506.235774	253.621525			4
22	2856.130293	1428.568784	2839.103744	1420.055510	2838.119728	1419.563502	G	395.203745	198.105510	378.177196	189.592236			3
23	3019.193622	1510.100449	3002.167073	1501.587174	3001.183057	1501.095166	Y	338.182281	169.594778	321.155732	161.081504			2
24							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **TDGCQHFCLPGQESYTCSCAQGYR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
99.1	3192.298050	0.029082	TDGCQHFCLPGQESYTCSCAQGYR
38.3	3192.298050	0.029082	TDGCQHFCLPGQESYTCSCAQGYR

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 37719: 1614.717088 from(808.365820,2+) rtinseconds(1921) index(52227)

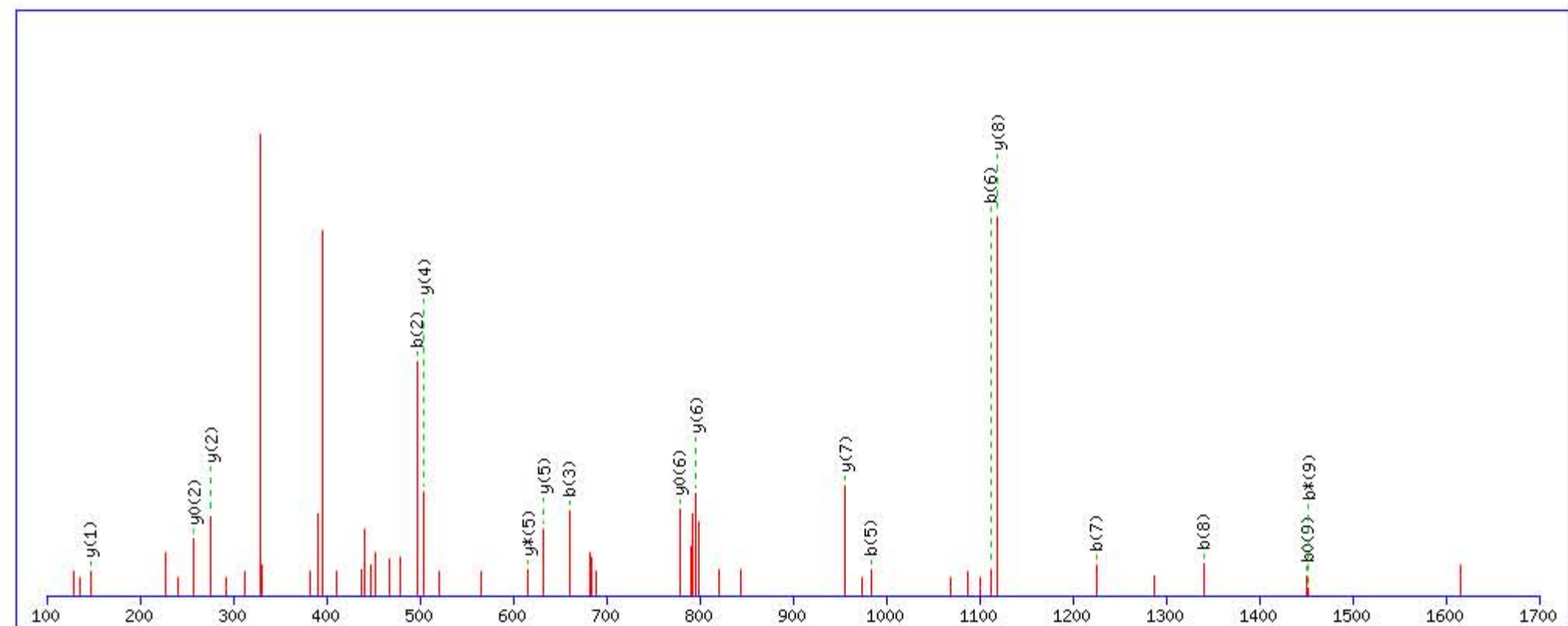
Title: Locus:1.1.1.1284.23 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1614.705795

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

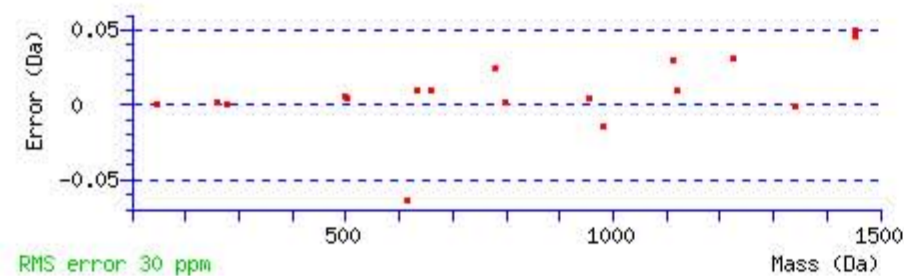
Variable modifications:

Q2 : Biotin:Thermo-21345 (Q)

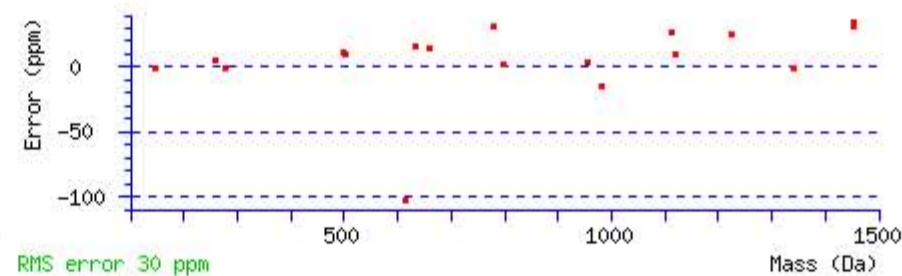
Ions Score: 52 Expect: 3e-005

Matches : 18/94 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	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



RMS error 30 ppm



RMS error 30 ppm

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
52.2	1614.705795	0.011293	GQYCYELDEK

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 46051: 1976.941452 from(659.987760,3+) rtinseconds(2165) index(37424)

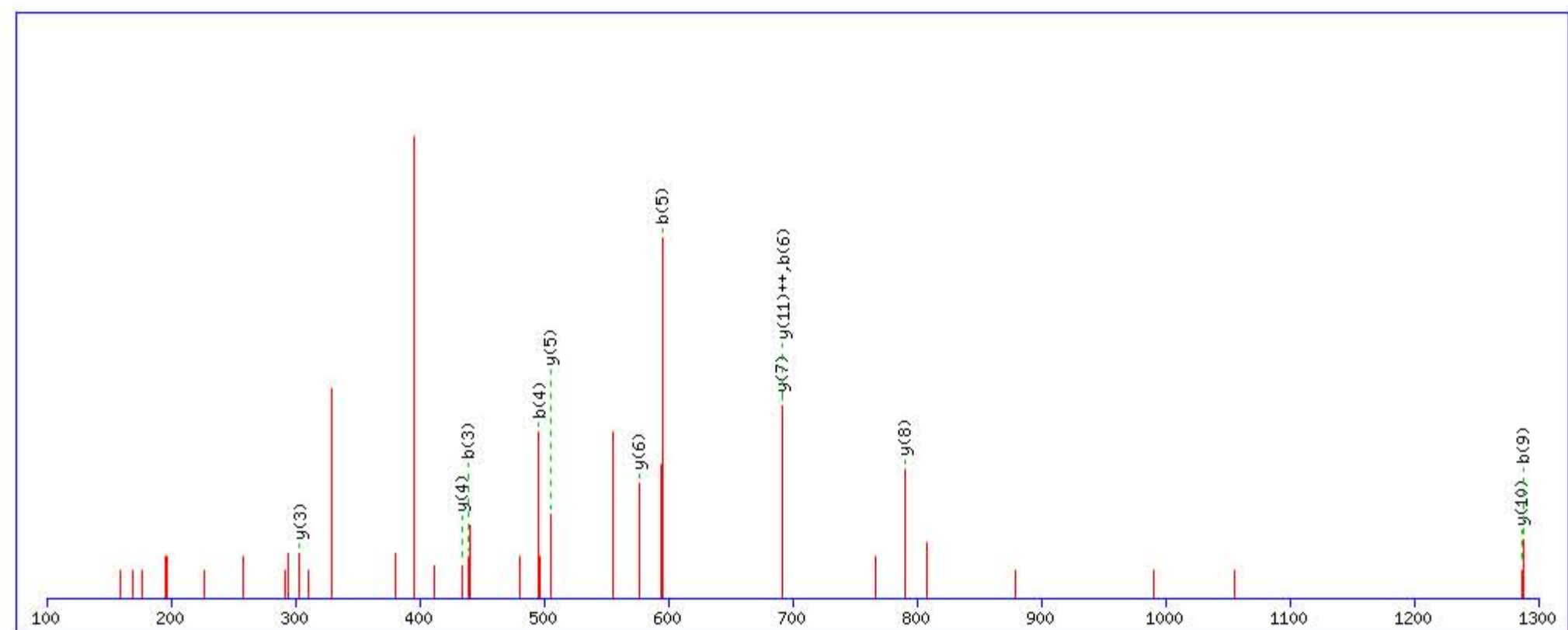
Title: Locus:1.1.1.3173.14 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1976.934937

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

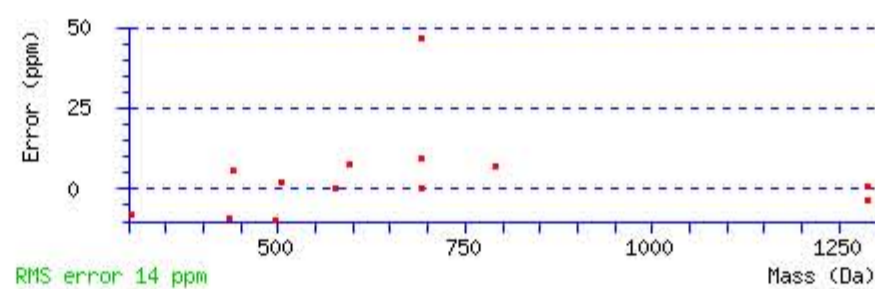
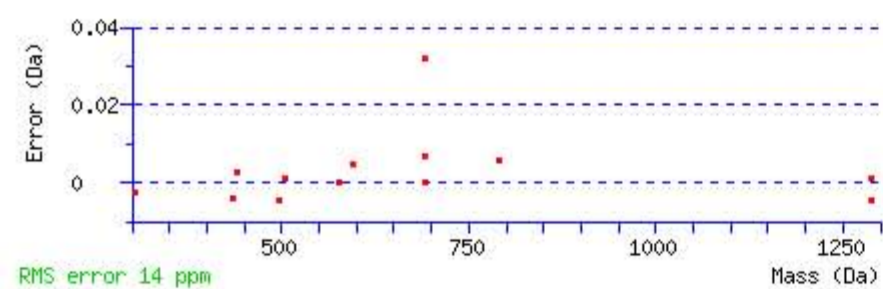
Variable modifications:

Q8 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.021

Matches : 13/154 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	116.034219	58.520748			98.023654	49.515465	D							16
2	302.113532	151.560404			284.102967	142.555122	W	1862.915257	931.961266	1845.888708	923.447992	1844.904692	922.955984	15
3	439.172444	220.089860			421.161879	211.084577	H	1676.835944	838.921610	1659.809395	830.408336	1658.825379	829.916327	14
4	496.193908	248.600592			478.183343	239.595309	G	1539.777032	770.392154	1522.750483	761.878880	1521.766467	761.386871	13
5	595.262322	298.134799			577.251757	289.129517	V	1482.755568	741.881422	1465.729019	733.368148	1464.745003	732.876140	12
6	692.315086	346.661181			674.304521	337.655899	P	1383.687154	692.347215	1366.660605	683.833941	1365.676589	683.341932	11
7	749.336550	375.171913			731.325985	366.166631	G	1286.634390	643.820833	1269.607841	635.307559	1268.623825	634.815550	10
8	1188.561876	594.784576	1171.535327	586.271302	1170.551311	585.779293	Q	1229.612926	615.310101	1212.586377	606.796827	1211.602361	606.304819	9
9	1287.630290	644.318783	1270.603741	635.805509	1269.619725	635.313501	V	790.387600	395.697438	773.361051	387.184164	772.377035	386.692156	8
10	1402.657233	701.832255	1385.630684	693.318980	1384.646668	692.826972	D	691.319186	346.163231	674.292637	337.649956	673.308621	337.157948	7
11	1473.694347	737.350812	1456.667798	728.837537	1455.683782	728.345529	A	576.292243	288.649759	559.265694	280.136485			6
12	1544.731461	772.869369	1527.704912	764.356094	1526.720896	763.864086	A	505.255129	253.131202	488.228580	244.617928			5
13	1675.771946	838.389611	1658.745397	829.876337	1657.761381	829.384329	M	434.218015	217.612645	417.191466	209.099371			4
14	1746.809060	873.908168	1729.782511	865.394894	1728.798495	864.902886	A	303.177530	152.092403	286.150981	143.579128			3
15	1803.830524	902.418900	1786.803975	893.905626	1785.819959	893.413617	G	232.140416	116.573846	215.113867	108.060571			2
16							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **DWHGVPGQVDAAMAGR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.6	1976.934937	0.006515	DWHGVPGQVDAAMAGR
9.3	1976.918793	0.022659	DDGLQYRPDVKDASDQR
1.7	1976.959854	-0.018402	HLTSRHQEAEMAQNAVR
1.4	1976.918808	0.022644	GSPGSDGPKGEKGDGPPEGPR

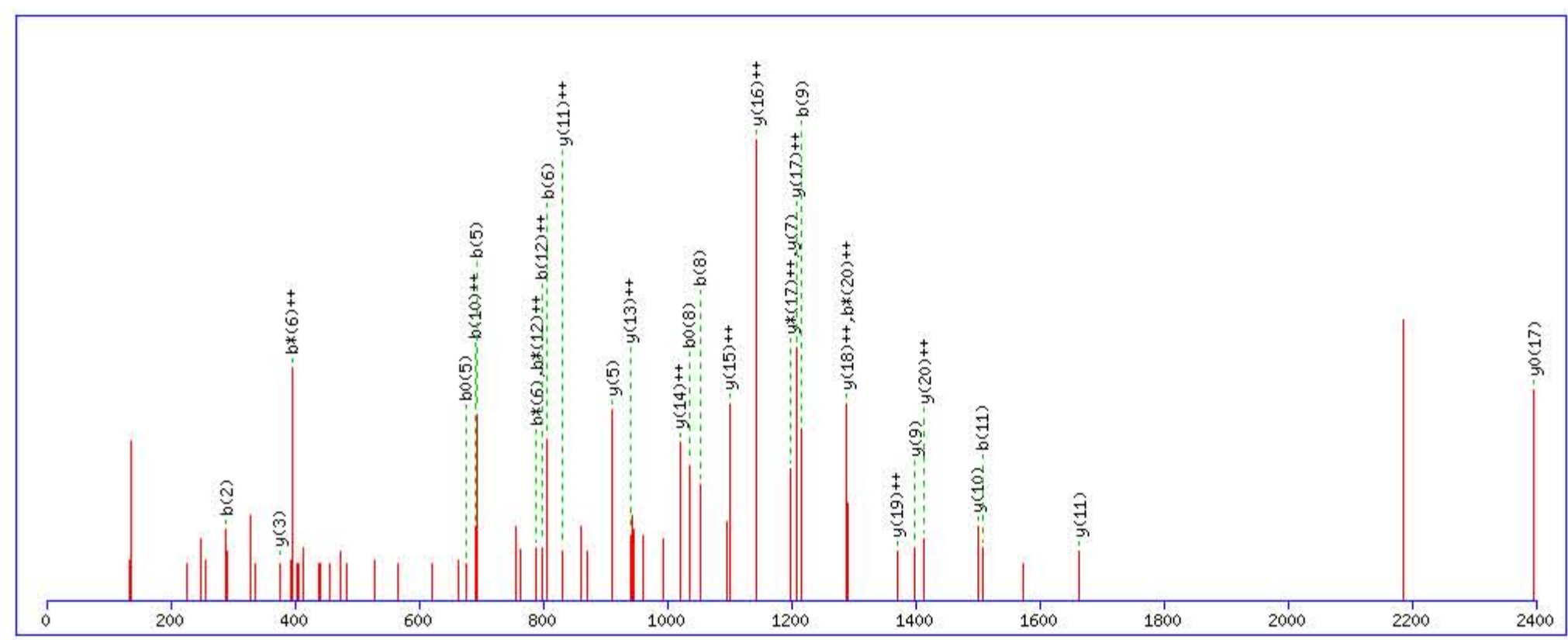
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **CQCDELCSYYQSCCTDYTAECKPQVTR**
 Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

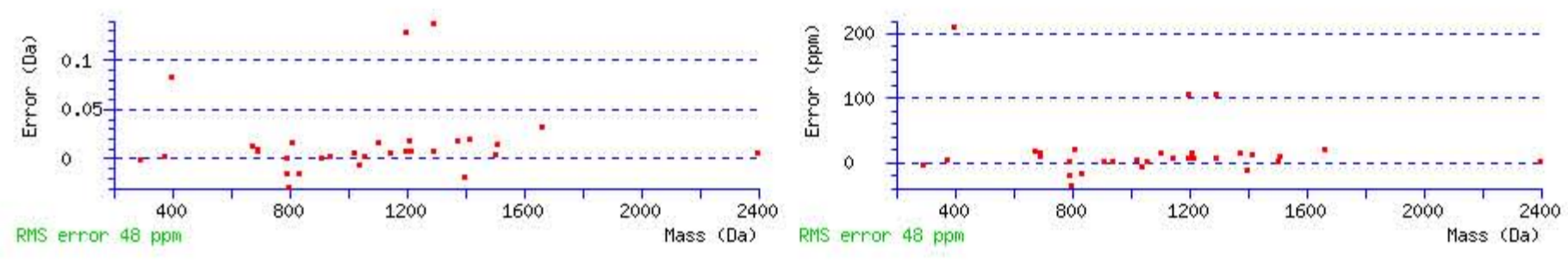
Match to Query 68758: 3792.533416 from(949.140630,4+) rtinseconds(1980) index(52726)
 Title: Locus:1.1.1.1304.26 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 3792.511536
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q24 : Biotin:Thermo-21345 (Q)
 Ions Score: 34 Expect: 0.00041
 Matches : 31/302 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	161.037925	81.022600					C							27
2	289.096503	145.051890	272.069954	136.538615			Q	3633.488150	1817.247713	3616.461601	1808.734438	3615.477585	1808.242431	26
3	449.127152	225.067214	432.100603	216.553940			C	3505.429572	1753.218424	3488.403023	1744.705149	3487.419007	1744.213141	25
4	564.154095	282.580686	547.127546	274.067411	546.143530	273.575403	D	3345.398923	1673.203099	3328.372374	1664.689825	3327.388358	1664.197817	24
5	693.196688	347.101982	676.170139	338.588708	675.186123	338.096700	E	3230.371980	1615.689628	3213.345431	1607.176353	3212.361415	1606.684345	23
6	806.280752	403.644014	789.254203	395.130740	788.270187	394.638732	L	3101.329387	1551.168331	3084.302838	1542.655057	3083.318822	1542.163049	22
7	966.311401	483.659339	949.284852	475.146064	948.300836	474.654056	C	2988.245323	1494.626299	2971.218774	1486.113025	2970.234758	1485.621017	21
8	1053.343429	527.175353	1036.316880	518.662078	1035.332864	518.170070	S	2828.214674	1414.610975	2811.188125	1406.097700	2810.204109	1405.605692	20
9	1216.406758	608.707017	1199.380209	600.193743	1198.396193	599.701735	Y	2741.182646	1371.094961	2724.156097	1362.581686	2723.172081	1362.089678	19
10	1379.470087	690.238682	1362.443538	681.725407	1361.459522	681.233399	Y	2578.119317	1289.563296	2561.092768	1281.050022	2560.108752	1280.558014	18
11	1507.528665	754.267971	1490.502116	745.754696	1489.518100	745.262688	Q	2415.055988	1208.031632	2398.029439	1199.518357	2397.045423	1199.026349	17
12	1594.560693	797.783985	1577.534144	789.270710	1576.550128	788.778702	S	2286.997410	1144.002343	2269.970861	1135.489068	2268.986845	1134.997060	16
13	1754.591342	877.799309	1737.564793	869.286035	1736.580777	868.794027	C	2199.965382	1100.486329	2182.938833	1091.973054	2181.954817	1091.481046	15
14	1914.621991	957.814634	1897.595442	949.301359	1896.611426	948.809351	C	2039.934733	1020.471005	2022.908184	1011.957730	2021.924168	1011.465722	14
15	2015.669670	1008.338473	1998.643121	999.825199	1997.659105	999.333191	T	1879.904084	940.455680	1862.877535	931.942406	1861.893519	931.450398	13
16	2130.696613	1065.851945	2113.670064	1057.338670	2112.686048	1056.846662	D	1778.856405	889.931841	1761.829856	881.418566	1760.845840	880.926558	12
17	2293.759942	1147.383609	2276.733393	1138.870335	2275.749377	1138.378327	Y	1663.829462	832.418369	1646.802913	823.905095	1645.818897	823.413086	11
18	2394.807621	1197.907449	2377.781072	1189.394174	2376.797056	1188.902166	T	1500.766133	750.886704	1483.739584	742.373430	1482.755568	741.881422	10
19	2465.844735	1233.426006	2448.818186	1224.912731	2447.834170	1224.420723	A	1399.718454	700.362865	1382.691905	691.849591	1381.707889	691.357583	9
20	2594.887328	1297.947302	2577.860779	1289.434028	2576.876763	1288.942020	E	1328.681340	664.844308	1311.654791	656.331033	1310.670775	655.839025	8
21	2754.917977	1377.962627	2737.891428	1369.449352	2736.907412	1368.957344	C	1199.638747	600.323011	1182.612198	591.809737	1181.628182	591.317729	7
22	2883.012940	1442.010108	2865.986391	1433.496834	2865.002375	1433.004826	K	1039.608098	520.307687	1022.581549	511.794412	1021.597533	511.302404	6
23	2980.065704	1490.536490	2963.039155	1482.023216	2962.055139	1481.531208	P	911.513135	456.260205	894.486586	447.746931	893.502570	447.254923	5
24	3419.291030	1710.149153	3402.264481	1701.635879	3401.280465	1701.143871	Q	814.460371	407.733823	797.433822	399.220549	796.449806	398.728541	4
25	3518.359444	1759.683360	3501.332895	1751.170086	3500.348879	1750.678078	V	375.235045	188.121160	358.208496	179.607886	357.224480	179.115878	3
26	3619.407123	1810.207200	3602.380574	1801.693925	3601.396558	1801.201917	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 **CQCDELCSYYQSCCTDYTAECKPQVTR**
 (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	3792.511536	0.021880	CQCDELCSYYQSCCTDYTAECKPQVTR
4.8	3792.511536	0.021880	CQCDELCSYYQSCCTDYTAECKPQVTR

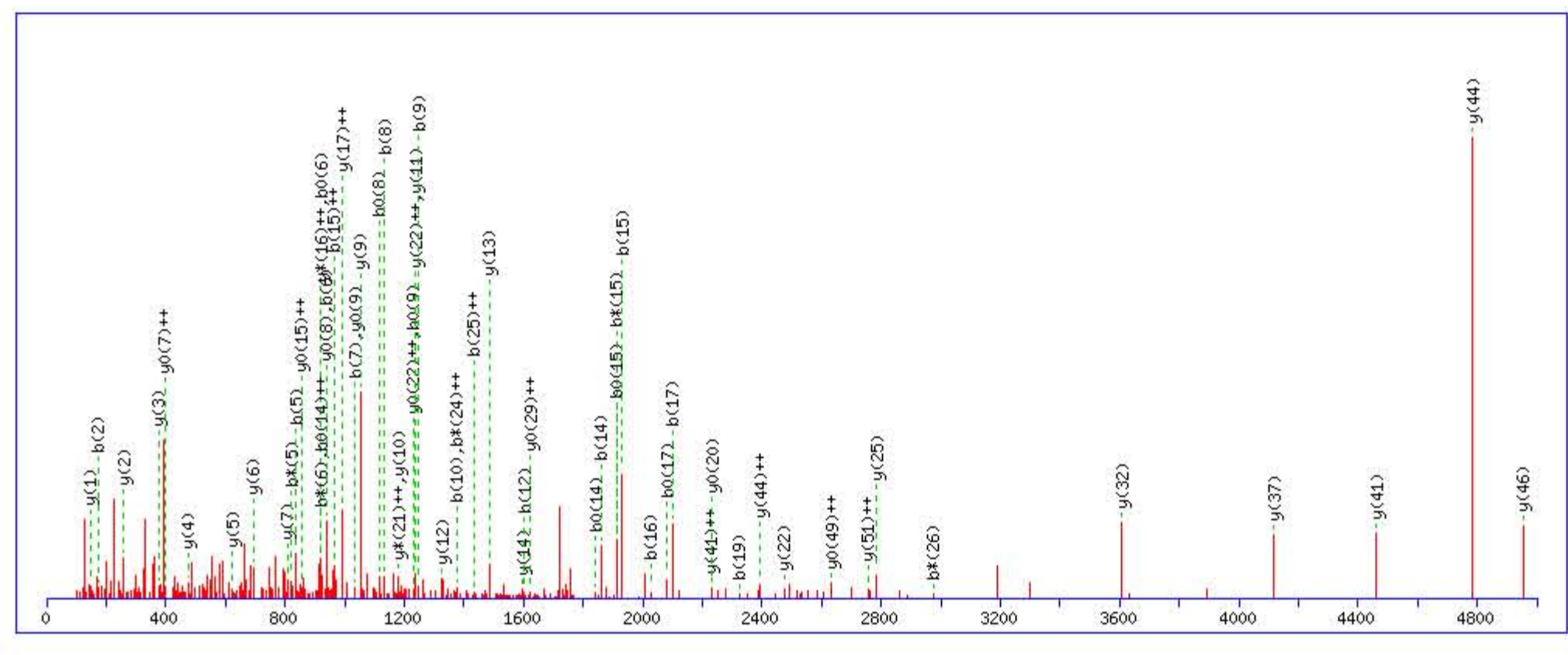
MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GNPEQTPVLKPEEEAPAVEVGASKPEGIDSRPETLHPGRPQPPAEELCSGKPFDAFTDLK**
 Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

Match to Query 77390: 6883.432352 from(861.436320,8+) rtinseconds(2117) index(53682)
 Title: Locus:1.1.1.1352.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 4.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da Full range
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 6883.374893
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q5 : Biotin:Thermo-21345 (Q)
 Ions Score: 35 Expect: 0.0034
 Matches : 62/708 fragment ions using 195 most intense peaks [\(help\)](#)

#	b	b ⁺⁺	b ⁺	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							61
2	172.071667	86.539471	155.045118	78.026197			N	6827.360757	3414.184017	6810.334208	3405.670742	6809.350192	3405.178734	60
3	269.124431	135.065854	252.097882	126.552579			P	6713.317830	3357.162553	6696.291281	3348.649279	6695.307265	3348.157271	59
4	398.167024	199.587150	381.140475	191.073876	380.156459	190.581868	E	6616.265066	3308.636171	6599.238517	3300.122897	6598.254501	3299.630889	58
5	837.392350	419.199813	820.365801	410.686539	819.381785	410.194531	Q	6487.222473	3244.114875	6470.195924	3235.601600	6469.211908	3235.109592	57
6	938.440029	469.723653	921.413480	461.210378	920.429464	460.718370	T	6047.997147	3024.502212	6030.970598	3015.988937	6029.986582	3015.496929	56
7	1035.492793	518.250035	1018.466244	509.736760	1017.482228	509.244752	P	5946.949468	2973.978372	5929.922919	2965.465098	5928.938903	2964.973090	55
8	1134.561207	567.784242	1117.534658	559.270967	1116.550642	558.778959	V	5849.896704	2925.451990	5832.870155	2916.938716	5831.886139	2916.446708	54
9	1247.645271	624.326274	1230.618722	615.812999	1229.634706	615.320991	L	5750.828290	2875.917783	5733.801741	2867.404509	5732.817725	2866.912501	53
10	1375.740234	688.373755	1358.713685	679.860481	1357.729669	679.368473	K	5637.744226	2819.375751	5620.717677	2810.862477	5619.733661	2810.370469	52
11	1472.792998	736.900137	1455.766449	728.386863	1454.782433	727.894855	P	5509.649263	2755.328270	5492.622714	2746.814995	5491.638698	2746.322987	51
12	1601.835591	801.421434	1584.809042	792.908159	1583.825026	792.416151	E	5412.596499	2706.801888	5395.569950	2698.288613	5394.585934	2697.796605	50
13	1730.878184	865.942730	1713.851635	857.429456	1712.867619	856.937448	E	5283.553906	2642.280591	5266.527357	2633.767317	5265.543341	2633.275309	49
14	1859.920777	930.464027	1842.894228	921.950752	1841.910212	921.458744	E	5154.511313	2577.759295	5137.484764	2569.246020	5136.500748	2568.754012	48
15	1930.957891	965.982584	1913.931342	957.469309	1912.947326	956.977301	A	5025.468720	2513.237998	5008.442171	2504.724724	5007.458155	2504.232716	47
16	2028.010655	1014.508966	2010.984106	1005.995691	2010.000090	1005.503683	P	4954.431606	2477.719441	4937.405057	2469.206167	4936.421041	2468.714159	46
17	2099.047769	1050.027523	2082.021220	1041.514248	2081.037204	1041.022240	A	4857.378842	2429.193059	4840.352293	2420.679785	4839.368277	2420.187777	45
18	2196.100533	1098.553905	2179.073984	1090.040630	2178.089968	1089.548622	P	4786.341728	2393.674502	4769.315179	2385.161228	4768.331163	2384.669220	44
19	2325.143126	1163.075201	2308.116577	1154.561927	2307.132561	1154.069919	E	4689.288964	2345.148120	4672.262415	2336.634846	4671.278399	2336.142838	43
20	2424.211540	1212.609408	2407.184991	1204.096134	2406.200975	1203.604126	V	4560.246371	2280.626824	4543.219822	2272.113549	4542.235806	2271.621541	42
21	2481.233004	1241.120140	2464.206455	1232.606865	2463.222439	1232.114858	G	4461.177957	2231.092617	4444.151408	2222.579342	4443.167392	2222.087334	41
22	2552.270118	1276.638697	2535.243569	1268.125423	2534.259553	1267.633415	A	4404.156493	2202.581885	4387.129944	2194.068610	4386.145928	2193.576602	40
23	2639.302146	1320.154711	2622.275597	1311.641437	2621.291581	1311.149429	S	4333.119379	2167.063328	4316.092830	2158.550053	4315.108814	2158.058045	39
24	2767.397109	1384.202193	2750.370560	1375.688918	2749.386544	1375.196910	K	4246.087351	2123.547314	4229.060802	2115.034039	4228.076786	2114.542031	38
25	2864.449873	1432.728575	2847.423324	1424.215300	2846.439308	1423.723292	P	4117.992388	2059.499832	4100.965839	2050.986558	4099.981823	2050.494550	37
26	2993.492466	1497.249871	2976.465917	1488.736597	2975.481901	1488.244589	E	4020.939624	2010.973450	4003.913075	2002.460176	4002.929059	2001.968168	36
27	3050.513930	1525.760603	3033.487381	1517.247329	3032.503365	1516.755321	G	3891.897031	1946.452154	3874.870482	1937.938879	3873.886466	1937.446871	35
28	3163.597994	1582.302635	3146.571445	1573.789361	3145.587429	1573.297353	I	3834.875567	1917.941422	3817.849018	1909.428147	3816.865002	1908.936139	34
29	3278.624937	1639.816107	3261.598388	1631.302832	3260.614372	1630.810824	D	3721.791503	1861.399390	3704.764954	1852.886115	3703.780938	1852.394107	33
30	3365.656965	1683.332121	3348.630416	1674.818846	3347.646400	1674.326838	S	3606.764560	1803.885918	3589.738011	1795.372644	3588.753995	1794.880636	32
31	3521.758076	1761.382676	3504.731527	1752.869402	3503.747511	1752.377394	R	3519.732532	1760.369904	3502.705983	1751.856630	3501.721967	1751.364622	31
32	3618.810840	1809.909058	3601.784291	1801.395784	3600.800275	1800.903776	P	3363.631421	1682.319349	3346.604872	1673.806074	3345.620856	1673.314066	30
33	3747.853433	1874.430355	3730.826884	1865.917080	3729.842868	1865.425072	E	3266.578657	1633.792967	3249.552108	1625.279692	3248.568092	1624.787684	29
34	3848.901112	1924.954194	3831.874563	1916.440920	3830.890547	1915.948912	T	3137.536064	1569.271670	3120.509515	1560.758396	3119.525499	1560.266388	28
35	3961.985176	1981.496226	3944.958627	1972.982952	3943.974611	1972.490944	L	3036.488385	1518.747831	3019.461836	1510.234556	3018.477820	1509.742548	27
36	4099.044088	2050.025682	4082.017539	2041.512408	4081.033523	2041.020400	H	2923.404321	1462.205799	2906.377772	1453.692524	2905.393756	1453.200516	26
37	4196.096852	2098.552064	4179.070303	2090.038790	4178.086287	2089.546782	P	2786.345409	1393.676343	2769.318860	1385.163068	2768.334844	1384.671060	25
38	4253.118316	2127.062796	4236.091767	2118.549522	4235.107751	2118.057514	G	2689.292645	1345.149961	2672.266096	1336.636686	2671.282080	1336.144678	24
39	4409.219427	2205.113352	4392.192878	2196.600077	4391.208862	2196.108069	R	2632.271181	1316.639229	2615.244632	1308.125954	2614.260616	1307.633946	23
40	4506.272191	2253.639734	4489.245642	2245.126459	4488.261626	2244.634451	P	2476.170070	1238.588673	2459.143521	1230.075399	2458.159505	1229.583391	22
41	4634.330769	2317.669023	4617.304220	2309.155748	4616.320204	2308.663740	Q	2379.117306	1190.062291	2362.090757	1181.549017	2361.106741	1181.057009	21
42	4731.383533	2366.195405	4714.356984	2357.682130	4713.372968	2357.190122	P	2251.058728	1126.033002	2234.032179	1117.519728	2233.048163	1117.027720	20
43	4828.436297	2414.721787	4811.409748	2406.208512	4810.425732	2405.716504	P	2154.005964	1077.506620	2136.979415	1068.993346	2135.995399	1068.501338	19
44	4899.473411	2450.240344	4882.446862	2441.727069	4881.462846	2441.235061	A	2056.953200	1028.980238	2039.926651	1020.466964	2038.942635	1019.974956	18
45	5028.516004	2514.761640	5011.489455	2506.248366	5010.505439	2505.756358	E	1985.916086	993.461681	1968.889537	984.948407	1967.905521	984.456399	17
46	5157.558597	2579.282937	5140.532048	2570.769662	5139.548032	2570.277654	E	1856.873493	928.940385	1839.846944	920.427110	1838.862928	919.935102	16
47	5286.601190	2643.804233	5269.574641	2635.290959	5268.590625	2634.798951	E	1727.830900	864.419088	1710.804351	855.905814	1709.820335	855.413806	15
48	5399.685254	2700.346265	5382.658705	2691.832991	5381.674689	2691.340983	L	1598.788307	799.897792	1581.761758	791.384517	1580.777742	790.892509	14
49	5559.715903	2780.361590	5542.689354	2771.848315	5541.705338	2771.356307	C	1485.704243	743.355760	1468.677694	734.842485	1467.693678	734.350477	13
50	5646.747931	2823.877604	5629.721382	2815.364329	5628.737366	2814.872321	S	1325.673594	663.340435	1308.647045	654.827161	1307.663029	654.335153	12
51	5703.769395	2852.388336	5686.742846	2843.875061	5685.758830	2843.383053	G	1238.641566	619.824421	1221.615017	611.311147	1220.631001	610.819139	11
52	5831.864358	2916.435817	5814.837809	2907.922543	5813.853793	2907.430535	K	1181.620102	591.313689	1164.593553	582.800415	1163.609537	582.308407	10
53	5928.917122	2964.962199	5911.890573	2956.448925	5910.906557	2955.956917	P</							

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 21859: 1157.628448 from(579.821500,2+) rtinseconds(1906) index(35717)

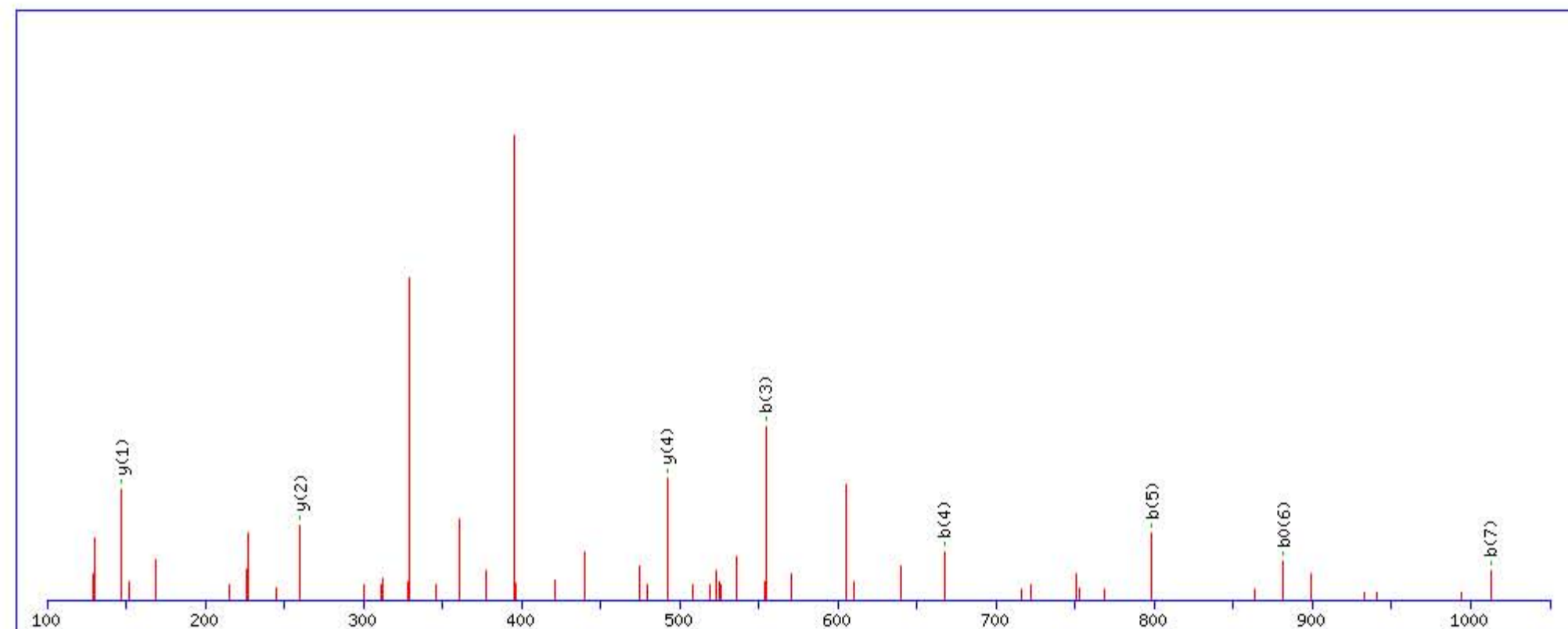
Title: Locus:1.1.1.3083.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1157.630066

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

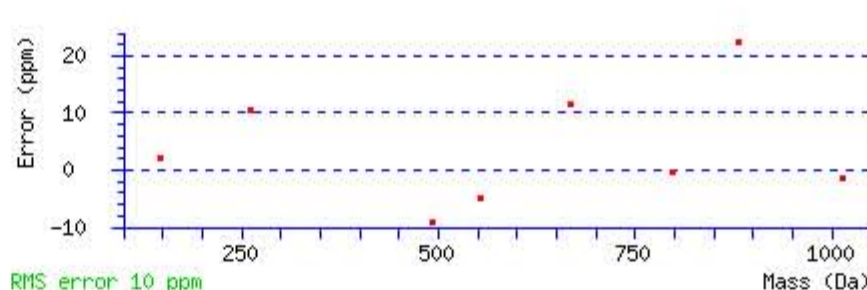
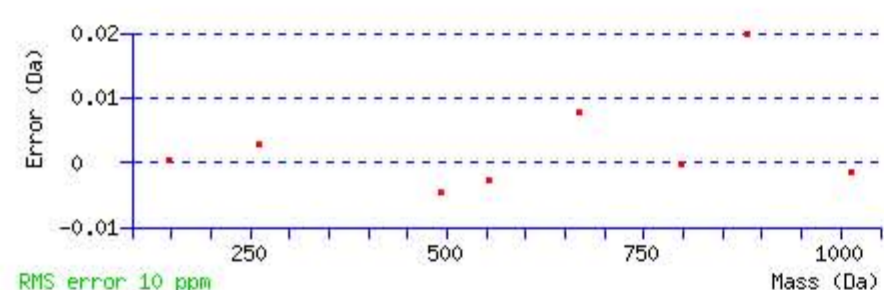
Variable modifications:

Q3 : Biotin:Thermo-21345 (Q)

Ions Score: 33 Expect: 0.015

Matches : 8/66 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							8
2	115.050204	58.028740					G	1101.615886	551.311581	1084.589337	542.798307	1083.605321	542.306299	7
3	554.275530	277.641403	537.248981	269.128129			Q	1044.594422	522.800849	1027.567873	514.287575	1026.583857	513.795567	6
4	667.359594	334.183435	650.333045	325.670161			I	605.369096	303.188186	588.342547	294.674912	587.358531	294.182904	5
5	798.400079	399.703678	781.373530	391.190403			M	492.285032	246.646154	475.258483	238.132880	474.274467	237.640872	4
6	899.447758	450.227517	882.421209	441.714243	881.437193	441.222235	T	361.244547	181.125912	344.217998	172.612637	343.233982	172.120629	3
7	1012.531822	506.769549	995.505273	498.256275	994.521257	497.764267	L	260.196868	130.602072	243.170319	122.088798			2
8							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [GGQIMTLK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.8	1157.630066	-0.001618	GGQIMTLK
12.7	1157.619293	0.009155	TNFEGPPRLK
12.4	1157.630051	-0.001603	QLSQMLK
11.9	1157.630051	-0.001603	QLSQMLK
11.3	1157.630051	-0.001603	QIKSMLQ
10.2	1157.640411	-0.011963	AQQLSSGNLK
8.4	1157.630051	-0.001603	QAGAMLLK
8.2	1157.630081	-0.001633	CVTLVQK
7.9	1157.640411	-0.011963	SPGKNSSIQLK
7.3	1157.633209	-0.004761	LLDPEPSFLK

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDSQSSWK**

Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

Match to Query 23399: 1204.553808 from(603.284180,2+) rtinseconds(1541) index(33557)

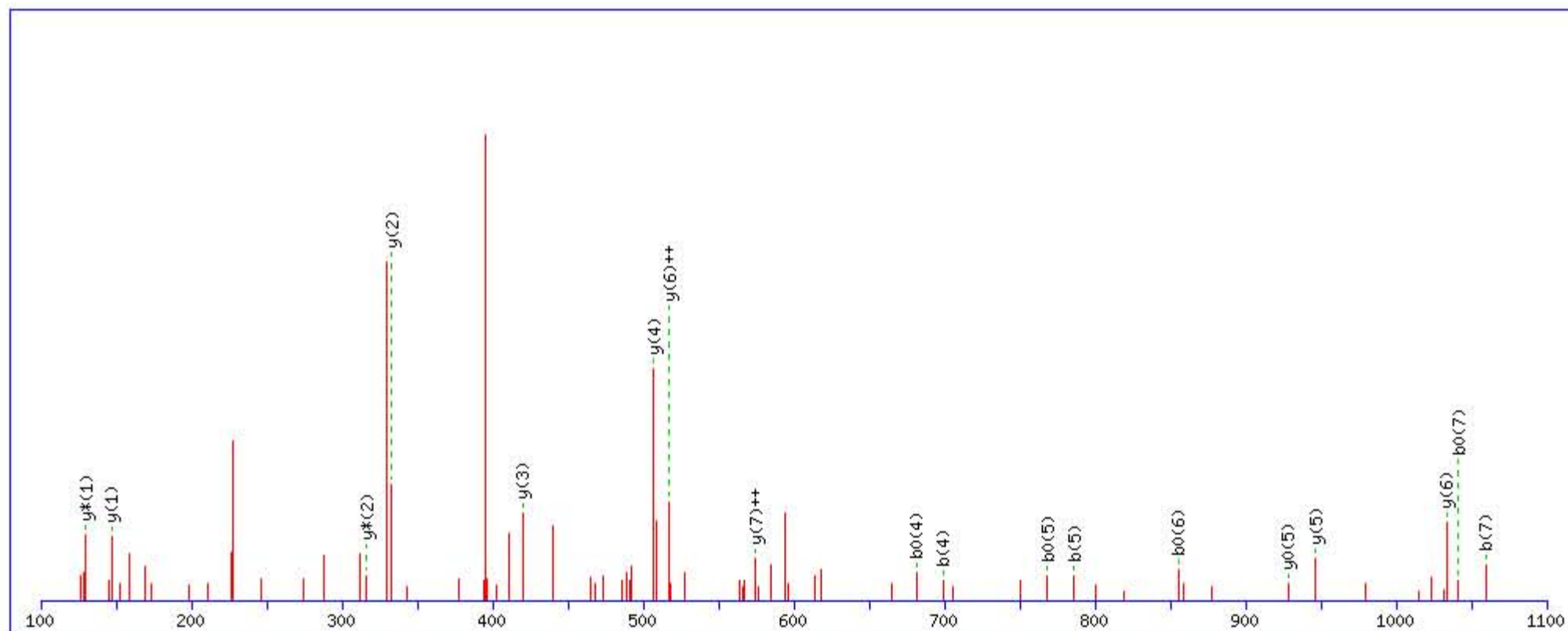
Title: Locus:1.1.1.2956.7 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1204.554657

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

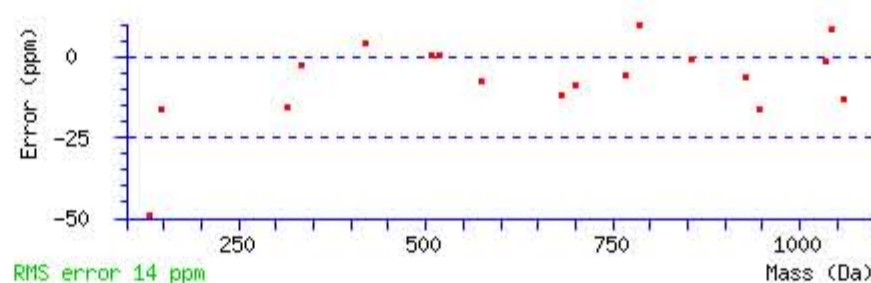
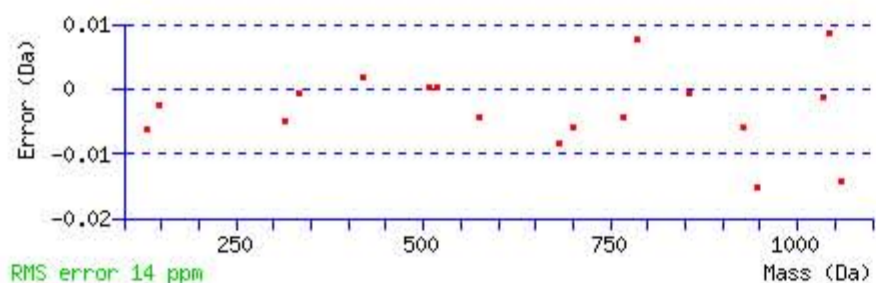
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 28 Expect: 0.0047

Matches : 18/72 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							8
2	173.055683	87.031479			155.045118	78.026197	D	1148.540470	574.773873	1131.513921	566.260599	1130.529905	565.768591	7
3	260.087711	130.547493			242.077146	121.542211	S	1033.513527	517.260402	1016.486978	508.747127	1015.502962	508.255119	6
4	699.313037	350.160157	682.286488	341.646882	681.302472	341.154874	Q	946.481499	473.744388	929.454950	465.231113	928.470934	464.739105	5
5	786.345065	393.676171	769.318516	385.162896	768.334500	384.670888	S	507.256173	254.131724	490.229624	245.618450	489.245608	245.126442	4
6	873.377093	437.192185	856.350544	428.678910	855.366528	428.186902	S	420.224145	210.615711	403.197596	202.102436	402.213580	201.610428	3
7	1059.456406	530.231841	1042.429857	521.718567	1041.445841	521.226559	W	333.192117	167.099697	316.165568	158.586422			2
8							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [GDSQSSWK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.5	1204.554657	-0.000849	GDSQSSWK
3.7	1204.540253	0.013555	QMQECAK

Mascot: <http://www.matrixscience.com/>

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 26804: 1333.612128 from(667.813340,2+) rtinseconds(1245) index(31560)

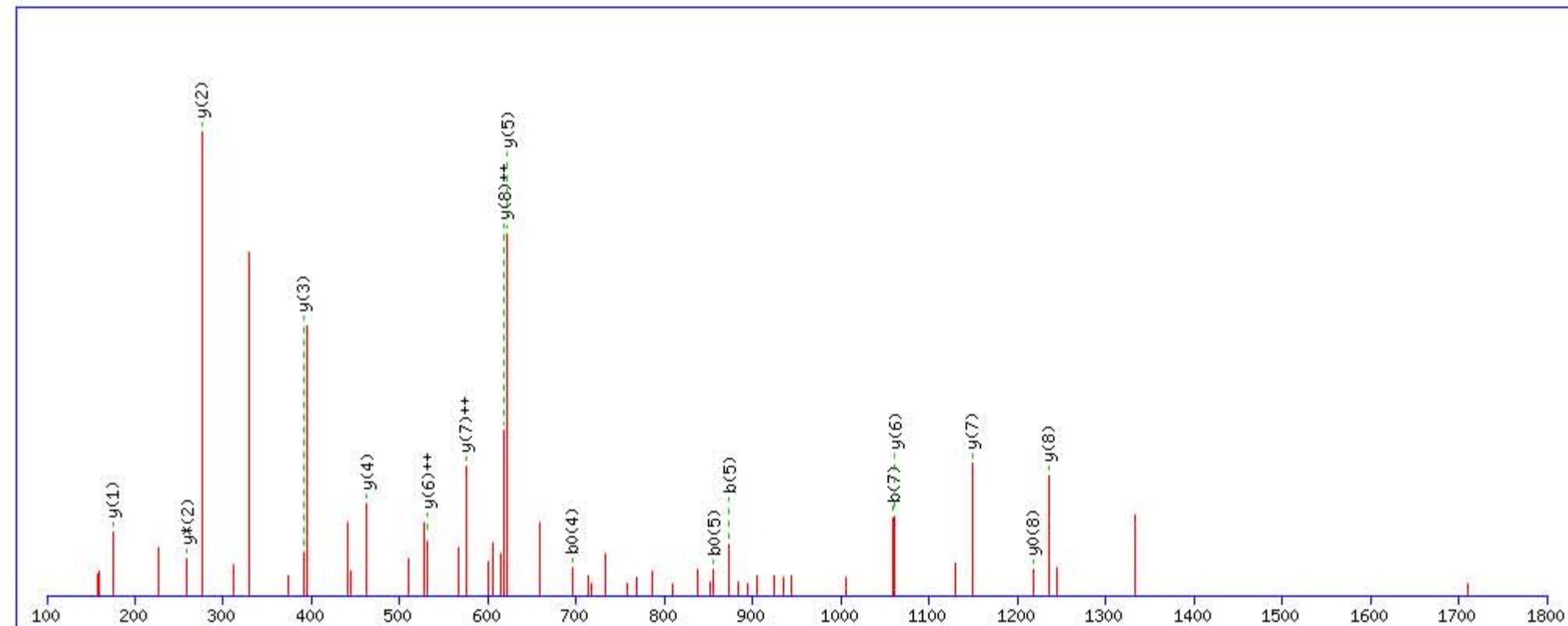
Title: Locus:1.1.1.2852.19 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1333.611862

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

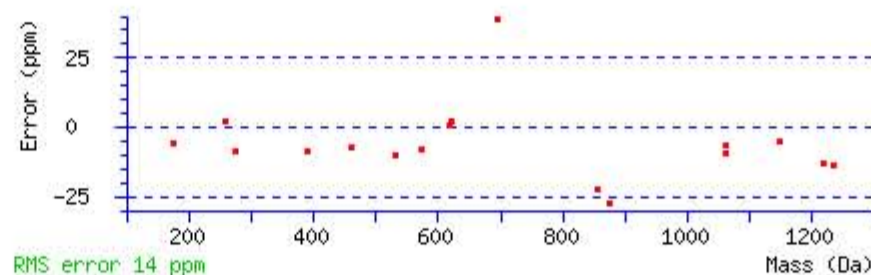
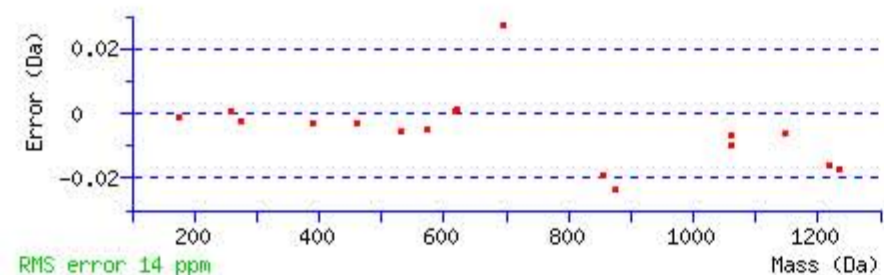
Variable modifications:

Q4 : Biotin:Thermo-21345 (Q)

Ions Score: 52 Expect: 2.1e-005

Matches : 17/86 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.075690	50.541483					V							9
2	187.107718	94.057497			169.097153	85.052214	S	1235.550719	618.278998	1218.524170	609.765723	1217.540154	609.273715	8
3	274.139746	137.573511			256.129181	128.568229	S	1148.518691	574.762984	1131.492142	566.249709	1130.508126	565.757701	7
4	713.365072	357.186174	696.338523	348.672900	695.354507	348.180892	Q	1061.486663	531.246970	1044.460114	522.733695	1043.476098	522.241687	6
5	873.395721	437.201499	856.369172	428.688224	855.385156	428.196216	C	622.261337	311.634307	605.234788	303.121032	604.250772	302.629024	5
6	944.432835	472.720056	927.406286	464.206781	926.422270	463.714773	A	462.230688	231.618982	445.204139	223.105707	444.220123	222.613700	4
7	1059.459778	530.233527	1042.433229	521.720253	1041.449213	521.228245	D	391.193574	196.100425	374.167025	187.587151	373.183009	187.095143	3
8	1160.507457	580.757367	1143.480908	572.244092	1142.496892	571.752084	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
9							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **VSSQCADTR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.5	1333.611862	0.000266	VSSQCADTR
2.6	1333.601105	0.011023	VDNRPDGFGDSR

Mascot: <http://www.matrixscience.com/>

MASCOT SEARCH RESULTS

Peptide View

MS/MS Fragmentation of **VKEEVFIQQR**

Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

Match to Query 36520: 1585.859472 from(529.627100,3+) rtinseconds(1765) index(34856)

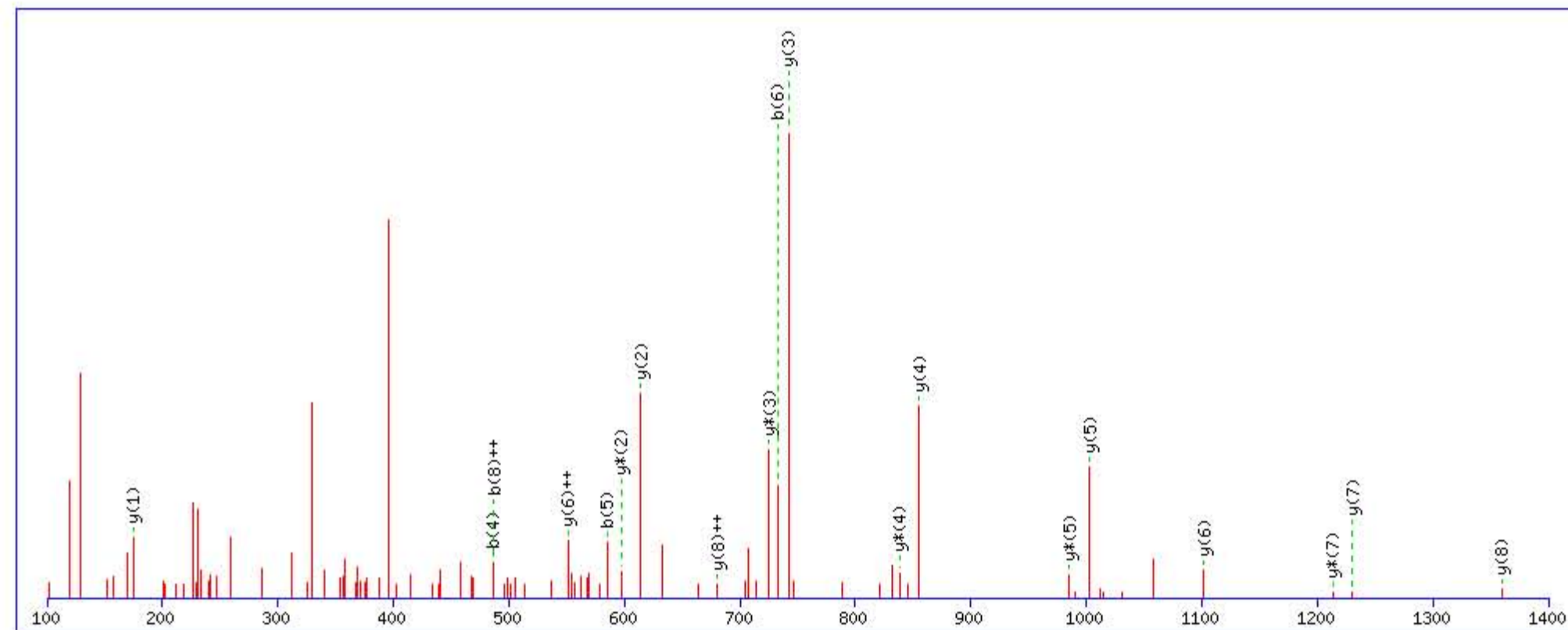
Title: Locus:1.1.1.3034.11 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1585.865021

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

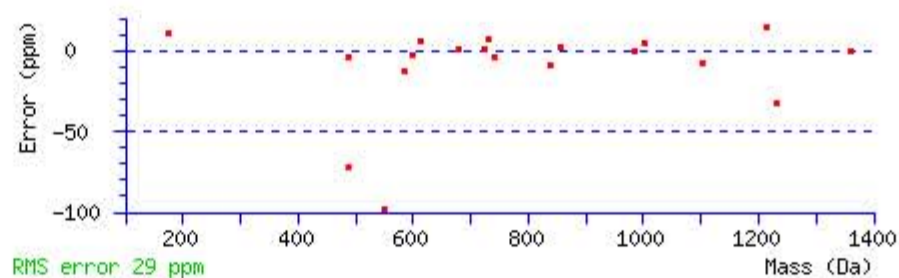
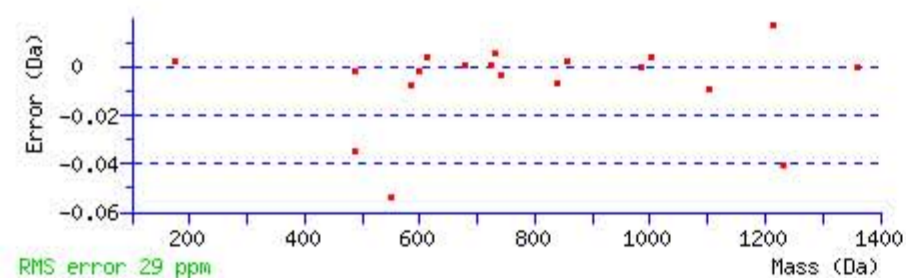
Variable modifications:

Q9 : Biotin:Thermo-21345 (Q)

Ions Score: 47 Expect: 0.00055

Matches : 19/90 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							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
46.5	1585.865021	-0.005549	VKEEVFIQQR
33.5	1585.865021	-0.005549	VKEEVFIQQR
11.6	1585.842392	0.017080	EIQTITGNQQLVR
10.3	1585.857605	0.001867	QEEVAGIRAKFPNK
1.4	1585.842361	0.017111	QSVLVKSNEEGIQR
0.6	1585.838531	0.020941	DLKEVTPEGLQMVK

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 37301: 1604.749152 from(535.923660,3+) rtinseconds(1402) index(32537)

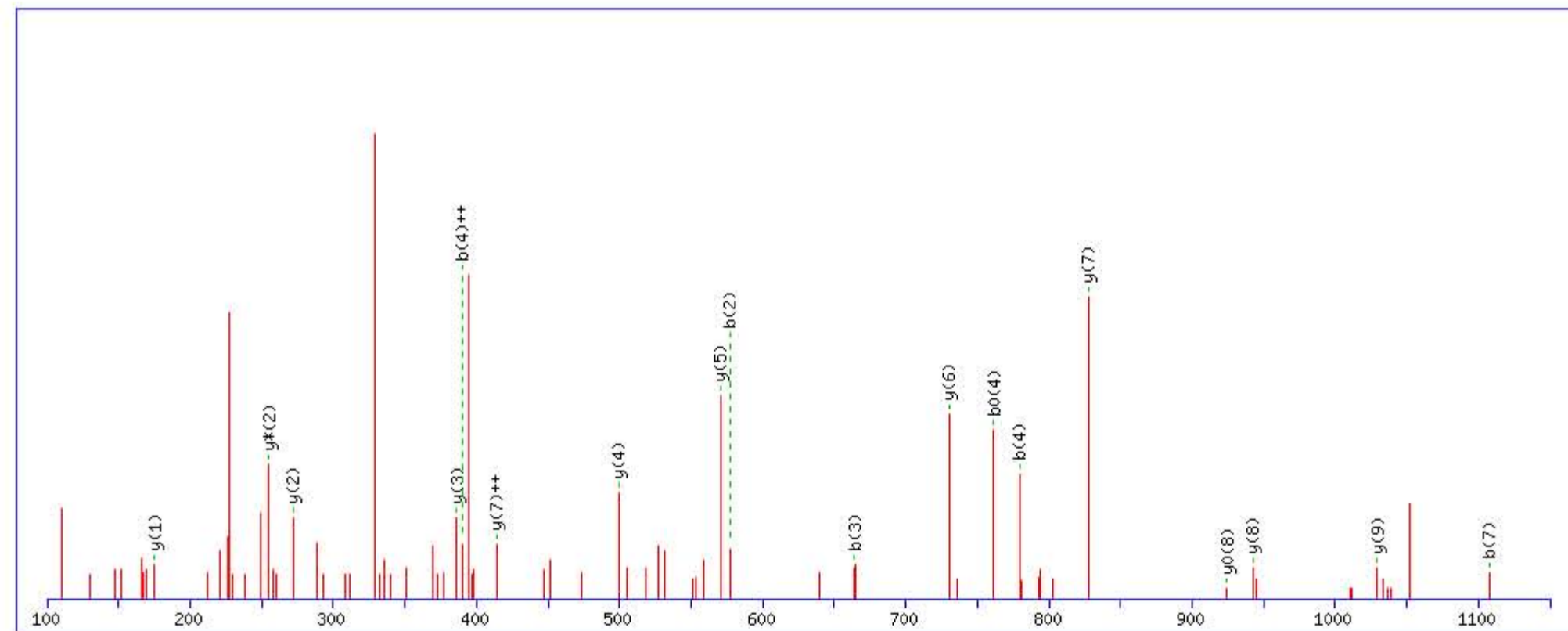
Title: Locus:1.1.1.2907.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 1604.755157

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

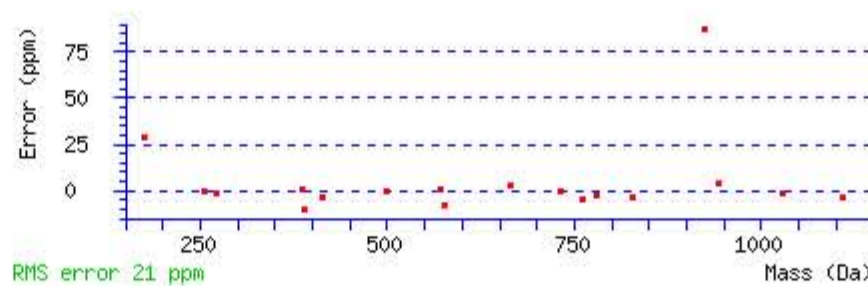
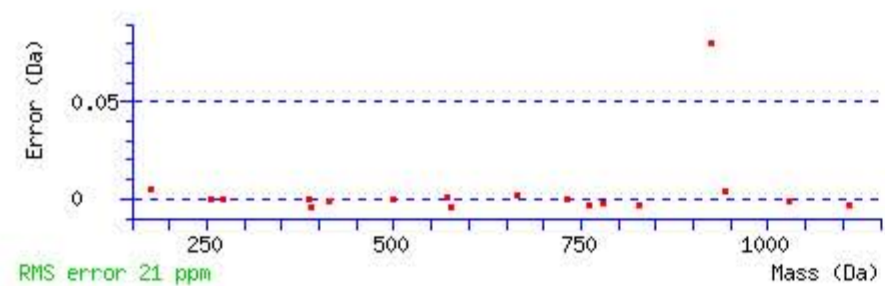
Variable modifications:

Q1 : Biotin:Thermo-21345 (Q)

Ions Score: 51 Expect: 6.7e-005

Matches : 18/102 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	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
50.6	1604.755157	-0.006005	QHSDPCALNPR
5.7	1604.736725	0.012427	EGMGWSYLVFLK
4.2	1604.732529	0.016623	GDVGDGRGDKQQGMAR
1.5	1604.772247	-0.023095	TDDIPVWDQEFLK
0.4	1604.754288	-0.005136	GPSPASSSSSSPPAHR

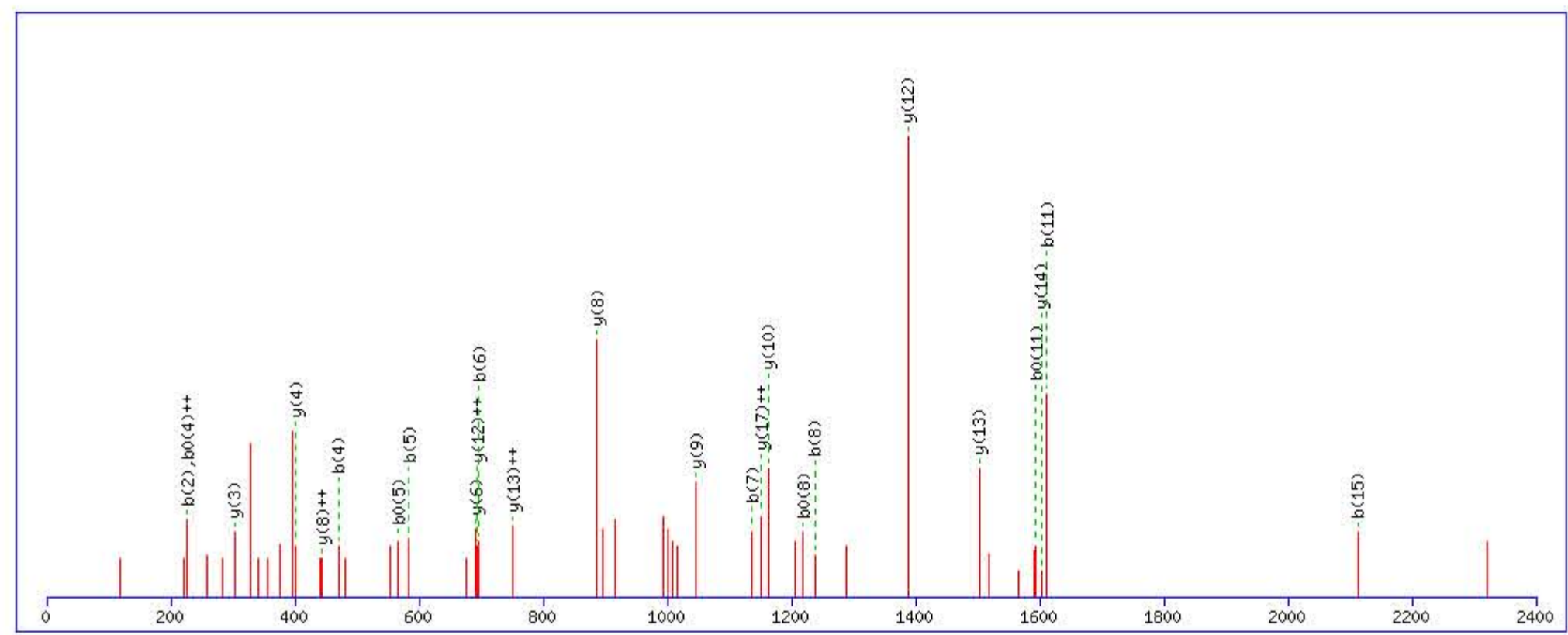
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILDELLQTCVDPEDCPVCEVAGR**
 Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

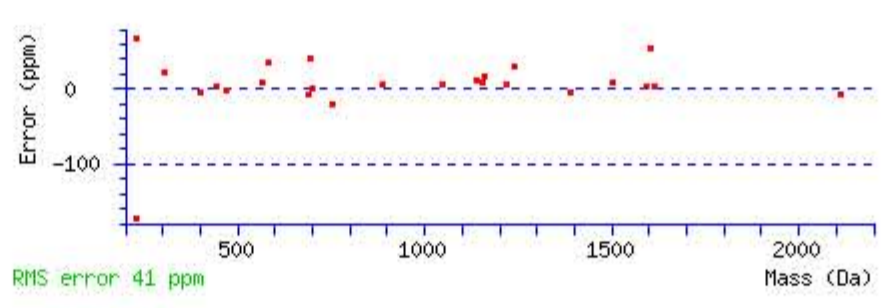
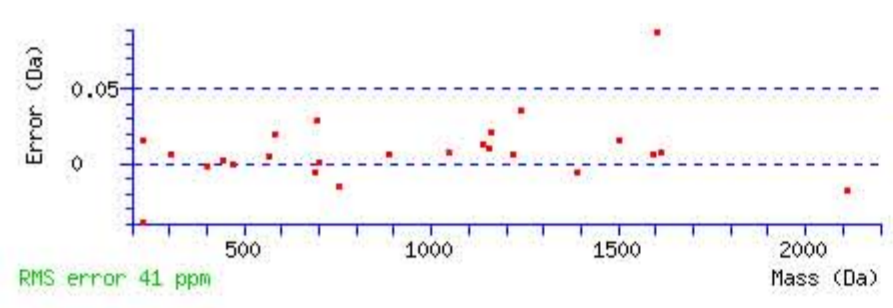
Match to Query 46475: 2998.419972 from(1000.480600,3+) rtinseconds(2606) index(40196)
 Title: Locus:1.1.1.3326.24 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"
 Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
 Or, Plot from to Da
 Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2998.390854
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Variable modifications:
 Q7 : Biotin:Thermo-21345 (Q)
 Ions Score: 52 Expect: 0.00037
 Matches : 25/240 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					I							23
2	227.175404	114.091340					L	2886.314052	1443.660664	2869.287503	1435.147389	2868.303487	1434.655381	22
3	342.202347	171.604811			324.191782	162.599529	D	2773.229988	1387.118632	2756.203439	1378.605357	2755.219423	1378.113349	21
4	471.244940	236.126108			453.234375	227.120826	E	2658.203045	1329.605160	2641.176496	1321.091886	2640.192480	1320.599878	20
5	584.329004	292.668140			566.318439	283.662858	L	2529.160452	1265.083864	2512.133903	1256.570589	2511.149887	1256.078581	19
6	697.413068	349.210172			679.402503	340.204890	L	2416.076388	1208.541832	2399.049839	1200.028557	2398.065823	1199.536549	18
7	1136.638394	568.822835	1119.611845	560.309561	1118.627829	559.817553	Q	2302.992324	1151.999800	2285.965775	1143.486525	2284.981759	1142.994517	17
8	1237.686073	619.346675	1220.659524	610.833400	1219.675508	610.341392	T	1863.766998	932.387137	1846.740449	923.873863	1845.756433	923.381855	16
9	1397.716722	699.361999	1380.690173	690.848725	1379.706157	690.356717	C	1762.719319	881.863298	1745.692770	873.350023	1744.708754	872.858015	15
10	1496.785136	748.896206	1479.758587	740.382932	1478.774571	739.890924	V	1602.688670	801.847973	1585.662121	793.334699	1584.678105	792.842691	14
11	1611.812079	806.409678	1594.785530	797.896403	1593.801514	797.404395	D	1503.620256	752.313766	1486.593707	743.800492	1485.609691	743.308483	13
12	1708.864843	854.936060	1691.838294	846.422785	1690.854278	845.930777	P	1388.593313	694.800294	1371.566764	686.287020	1370.582748	685.795012	12
13	1837.907436	919.457356	1820.880887	910.944082	1819.896871	910.452074	E	1291.540549	646.273912	1274.514000	637.760638	1273.529984	637.268630	11
14	1952.934379	976.970828	1935.907830	968.457553	1934.923814	967.965545	D	1162.497956	581.752616	1145.471407	573.239342	1144.487391	572.747333	10
15	2112.965028	1056.986152	2095.938479	1048.472877	2094.954463	1047.980869	C	1047.471013	524.239144	1030.444464	515.725870	1029.460448	515.233862	9
16	2210.017792	1105.512534	2192.991243	1096.999259	2192.007227	1096.507251	P	887.440364	444.223820	870.413815	435.710545	869.429799	435.218537	8
17	2309.086206	1155.046741	2292.059657	1146.533466	2291.075641	1146.041458	V	790.387600	395.697438	773.361051	387.184163	772.377035	386.692155	7
18	2469.116855	1235.062065	2452.090306	1226.548791	2451.106290	1226.056783	C	691.319186	346.163231	674.292637	337.649956	673.308621	337.157948	6
19	2598.159448	1299.583362	2581.132899	1291.070087	2580.148883	1290.578079	E	531.288537	266.147907	514.261988	257.634632	513.277972	257.142624	5
20	2697.227862	1349.117569	2680.201313	1340.604294	2679.217297	1340.112286	V	402.245944	201.626610	385.219395	193.113335			4
21	2768.264976	1384.636126	2751.238427	1376.122851	2750.254411	1375.630843	A	303.177530	152.092403	286.150981	143.579129			3
22	2825.286440	1413.146858	2808.259891	1404.633583	2807.275875	1404.141575	G	232.140416	116.573846	215.113867	108.060571			2
23							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **ILDELLQTCVDPEDCPVCEVAGR**
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.0	2998.390854	0.029118	ILDELLQTCVDPEDCPVCEVAGR

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAQCSQKPCEDSCR**

Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

Match to Query 47961: 2034.870492 from(679.297440,3+) rtinseconds(1158) index(31220)

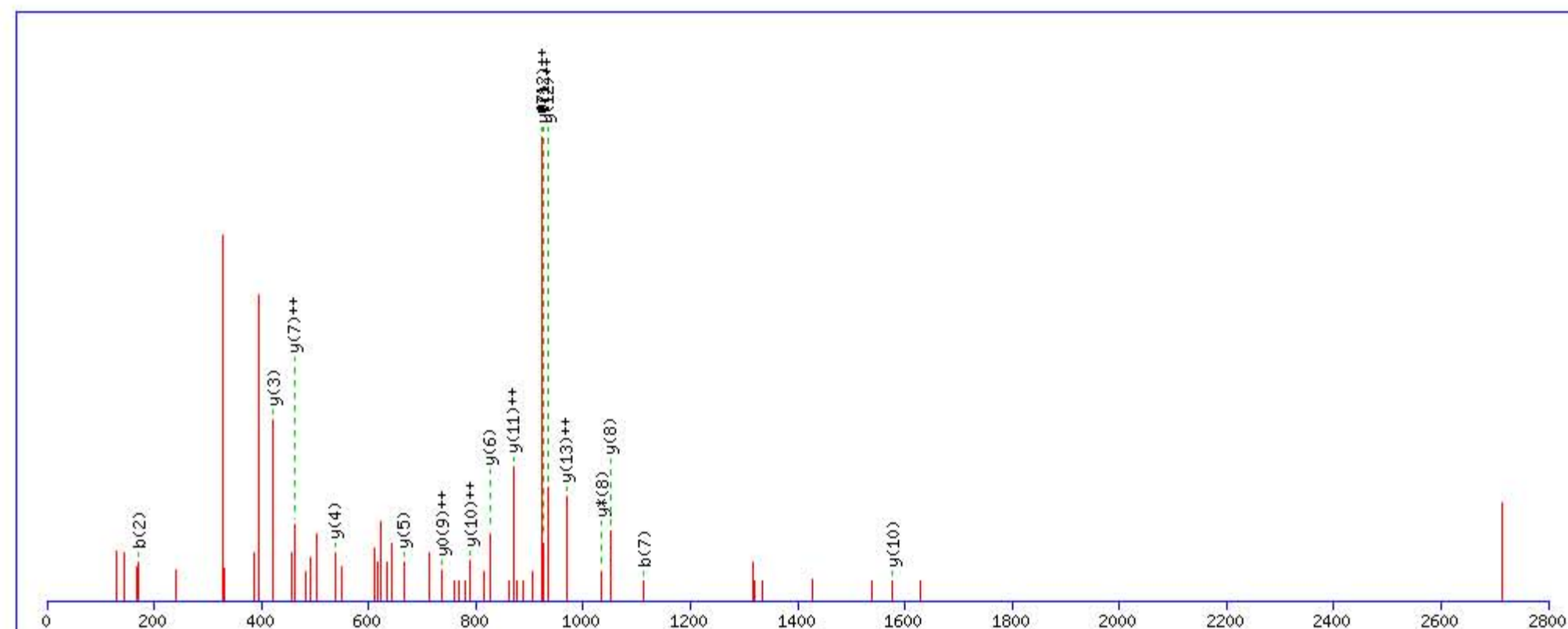
Title: Locus:1.1.1.2822.18 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2034.874374

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

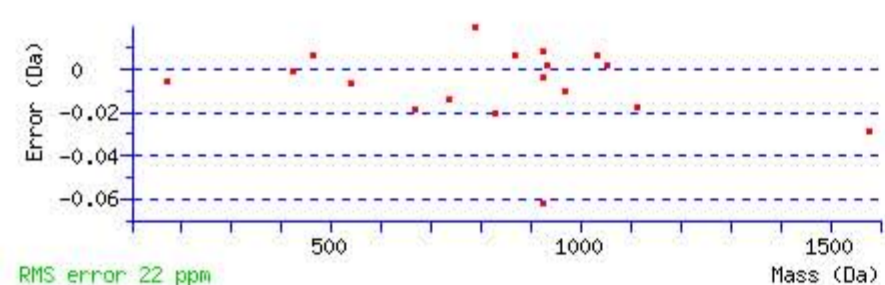
Variable modifications:

Q6 : Biotin:Thermo-21345 (Q)

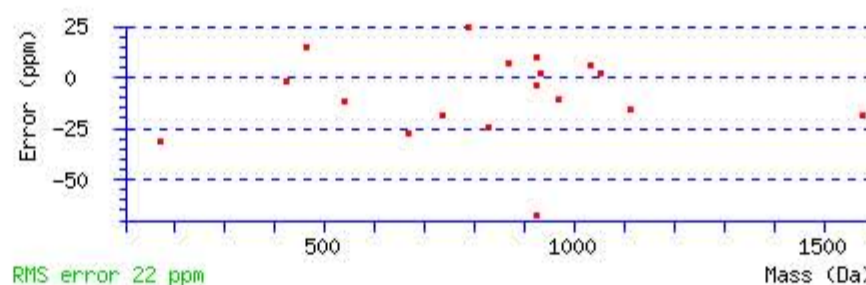
Ions Score: 30 Expect: 0.0036

Matches : 18/140 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							14
2	171.112804	86.060040					A	1936.813236	968.910256	1919.786687	960.396982	1918.802671	959.904973	13
3	299.171382	150.089329	282.144833	141.576055			Q	1865.776122	933.391699	1848.749573	924.878425	1847.765557	924.386417	12
4	459.202031	230.104653	442.175482	221.591379			C	1737.717544	869.362410	1720.690995	860.849136	1719.706979	860.357128	11
5	546.234059	273.620668	529.207510	265.107393	528.223494	264.615385	S	1577.686895	789.347086	1560.660346	780.833811	1559.676330	780.341803	10
6	985.459385	493.233331	968.432836	484.720056	967.448820	484.228048	Q	1490.654867	745.831072	1473.628318	737.317797	1472.644302	736.825789	9
7	1113.554348	557.280812	1096.527799	548.767538	1095.543783	548.275529	K	1051.429541	526.218409	1034.402992	517.705134	1033.418976	517.213126	8
8	1210.607112	605.807194	1193.580563	597.293920	1192.596547	596.801911	P	923.334578	462.170927	906.308029	453.657653	905.324013	453.165645	7
9	1370.637761	685.822519	1353.611212	677.309244	1352.627196	676.817236	C	826.281814	413.644545	809.255265	405.131271	808.271249	404.639263	6
10	1499.680354	750.343815	1482.653805	741.830540	1481.669789	741.338532	E	666.251165	333.629221	649.224616	325.115946	648.240600	324.623938	5
11	1614.707297	807.857286	1597.680748	799.344012	1596.696732	798.852004	D	537.208572	269.107924	520.182023	260.594650	519.198007	260.102642	4
12	1701.739325	851.373301	1684.712776	842.860026	1683.728760	842.368018	S	422.181629	211.594453	405.155080	203.081178	404.171064	202.589170	3
13	1861.769974	931.388625	1844.743425	922.875351	1843.759409	922.383343	C	335.149601	168.078438	318.123052	159.565164			2
14							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 22 ppm



RMS error 22 ppm

NCBI BLAST search of **VAQCSQKPCEDSCR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.1	2034.874374	-0.003882	VAQCSQKPCEDSCR
24.1	2034.874374	-0.003882	VAQCSQKPCEDSCR

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Peptide View

MS/MS Fragmentation of **HGAGVAMDGQDVQLPLLK**

Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

Match to Query 50130: 2159.133072 from(720.718300,3+) rtinseconds(2357) index(38595)

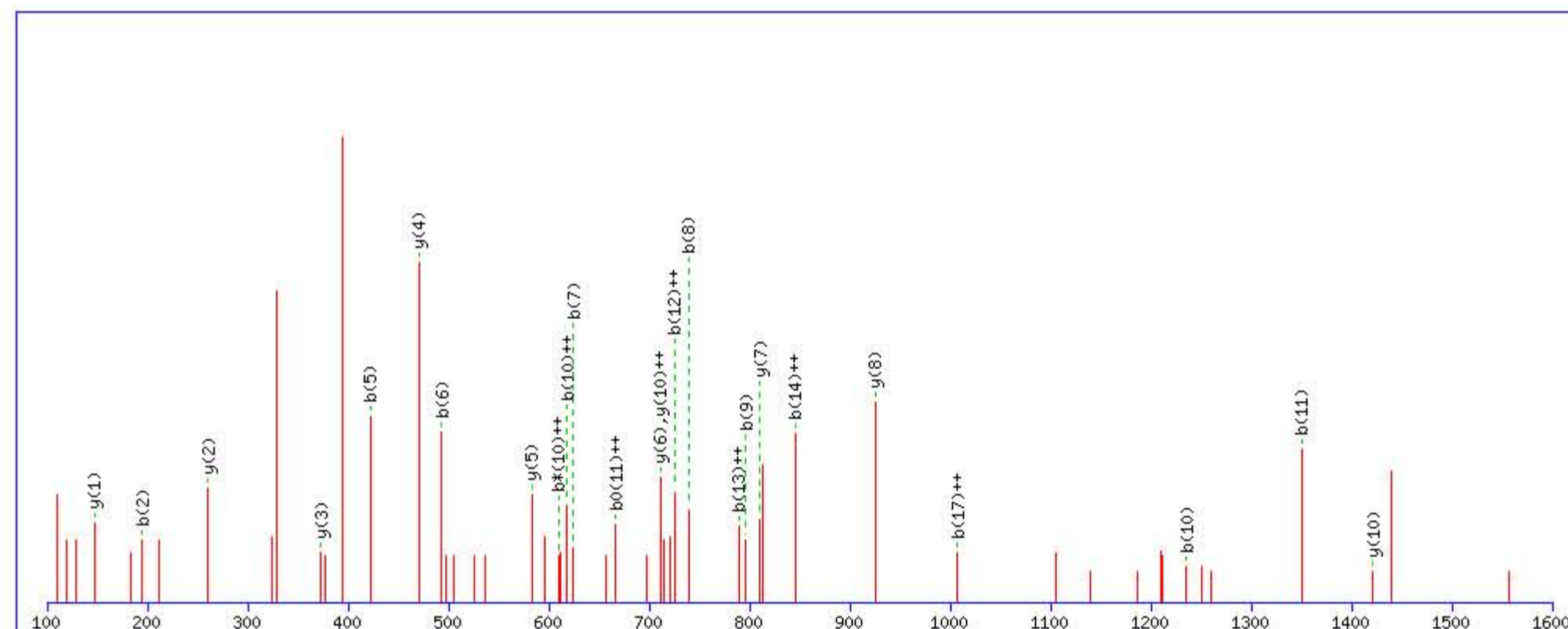
Title: Locus:1.1.1.3240.20 File:"2013-07-02 CLN FXIII 60 min 2nd F 3.wiff"

Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf5 FXIII 60 min 2nd\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



Monoisotopic mass of neutral peptide Mr(calc): 2159.123123

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

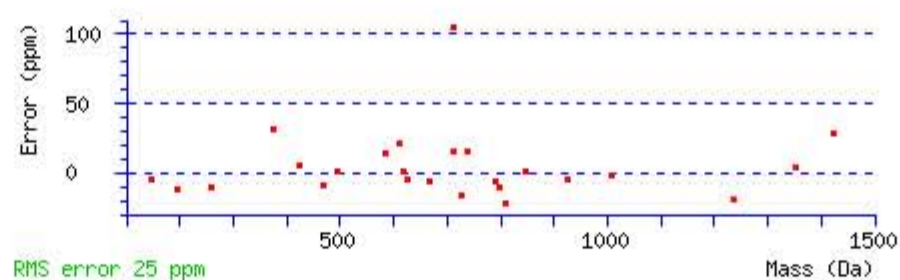
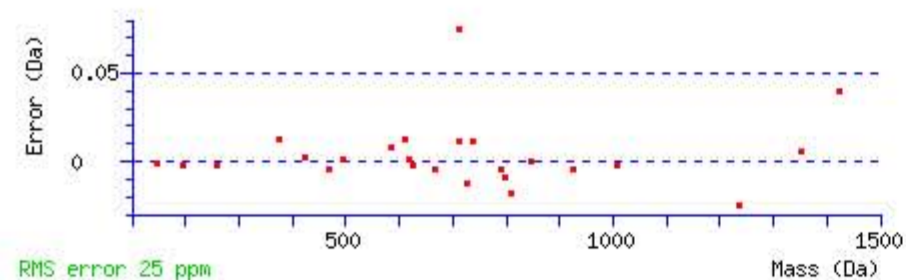
Variable modifications:

Q10 : Biotin:Thermo-21345 (Q)

Ions Score: 47 Expect: 5.6e-005

Matches : 25/158 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							18
2	195.087652	98.047464					G	2023.071483	1012.039380	2006.044934	1003.526105	2005.060918	1003.034097	17
3	266.124766	133.566021					A	1966.050019	983.528648	1949.023470	975.015373	1948.039454	974.523365	16
4	323.146230	162.076753					G	1895.012905	948.010091	1877.986356	939.496816	1877.002340	939.004808	15
5	422.214644	211.610960					V	1837.991441	919.499359	1820.964892	910.986084	1819.980876	910.494076	14
6	493.251758	247.129517					A	1738.923027	869.965152	1721.896478	861.451877	1720.912462	860.959869	13
7	624.292243	312.649760					M	1667.885913	834.446595	1650.859364	825.933320	1649.875348	825.441312	12
8	739.319186	370.163231			721.308621	361.157948	D	1536.845428	768.926352	1519.818879	760.413078	1518.834863	759.921070	11
9	796.340650	398.673963			778.330085	389.668680	G	1421.818485	711.412881	1404.791936	702.899606	1403.807920	702.407598	10
10	1235.565976	618.286626	1218.539427	609.773352	1217.555411	609.281344	Q	1364.797021	682.902149	1347.770472	674.388874	1346.786456	673.896866	9
11	1350.592919	675.800098	1333.566370	667.286823	1332.582354	666.794815	D	925.571695	463.289486	908.545146	454.776211	907.561130	454.284203	8
12	1449.661333	725.334305	1432.634784	716.821030	1431.650768	716.329022	V	810.544752	405.776014	793.518203	397.262740			7
13	1577.719911	789.363594	1560.693362	780.850319	1559.709346	780.358311	Q	711.476338	356.241807	694.449789	347.728533			6
14	1690.803975	845.905626	1673.777426	837.392351	1672.793410	836.900343	L	583.417760	292.212518	566.391211	283.699244			5
15	1787.856739	894.432008	1770.830190	885.918733	1769.846174	885.426725	P	470.333696	235.670486	453.307147	227.157212			4
16	1900.940803	950.974040	1883.914254	942.460765	1882.930238	941.968757	L	373.280932	187.144104	356.254383	178.630830			3
17	2014.024867	1007.516072	1996.998318	999.002797	1996.014302	998.510789	L	260.196868	130.602072	243.170319	122.088798			2
18							K	147.112804	74.060040	130.086255	65.546766			1



NCBI BLAST search of **HGAGVAMDGQDVQLPLLK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.0	2159.123123	0.009949	HGAGVAMDGQDVQLPLLK
20.4	2159.123123	0.009949	HGAGVAMDGQDVQLPLLK
1.6	2159.161957	-0.028885	ILQDQILTSKQKELEMAR
0.7	2159.112350	0.020722	AAQATGEFEVFNGLVHSK

Mascot: <http://www.matrixscience.com/>