

Supporting Information S13.

Identified
in two-step
but not in
one-step

METAPROTEOMICS method.

Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
1	2	2	437.255	-0.0003	EVAKEIGK	9	12.3	98.6
2	6	2	468.761	-0.0072	MLFGELVK	9	64.9	98.4
3	6	2	441.251	0.0007	QSLGAHLR	9	80.1	98.3
4	3	2	407.226	-0.0001	LNVENPK	9	87.4	98.1
5	3	2	634.853	0.0003	WLSLPGETRPL	11	88.1	96.6
6	6	2	511.751	0.0002	EHFAIYKD	8	66.1	95.5

Protein ID
Spectra
Summary Statistics

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
18.1.1.5300.1		0.0000	437.2555	0	1176	EVAKEIGK		12.4	872.4967	2

Peptide ID Hypotheses - 18.1.1.5300.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
12.4	9	1176	EVAKEIGK		872.4967	437.2556	2	-0.0003
12.4	9		DIAQELGK		872.4603	437.2375	2	0.0361
12.4	9		DLAKEIGK		872.4967	437.2556	2	-0.0003
11.4	9	220	DLAGSIIGK		872.4967	437.2556	2	-0.0003
11.4	8		DLAQELGK		872.4603	437.2375	2	0.0361

Fragmentation Evidence for Peptide

EVAKEIGK

Residue	b	b+2	y	y+2
E	130.0499	65.5286	873.5040	437.2556
V	229.1183	115.0628	744.4614	372.7343
A	300.1554	150.5813	645.3930	323.2001
K	428.2504	214.6288	574.3559	287.6816
E	557.2930	279.1501	446.2609	223.6341
I	670.3770	335.6921	317.2183	159.1128
G	727.3985	364.2029	204.1343	102.5708
K	855.4934	428.2504	147.1128	74.0600

1

Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
1	2	2	437.255	-0.0003	EVAKEIGK	9	12.3	98.6

Protein ID
Spectra
Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
18.1.1.5300.1		0.0000	437.2568	0	1059	EVAKEIGK		98.7	872.4967	2

Peptide ID Hypotheses - 18.1.1.5300.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
98.7	9	1059	EVAKEIGK		872.4967	437.2568	2	0.0023
96.9	9	204	DLAGSIIGK		872.4967	437.2568	2	0.0023
<1	7		LDAKQGIGK	Deamidated(O)@S	872.4967	437.2568	2	0.0023
<1	6		EVAKADLK		872.4967	437.2568	2	0.0023
<1	6		IDVSLAAGK		872.4967	437.2568	2	0.0023

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

EVAKEIGK

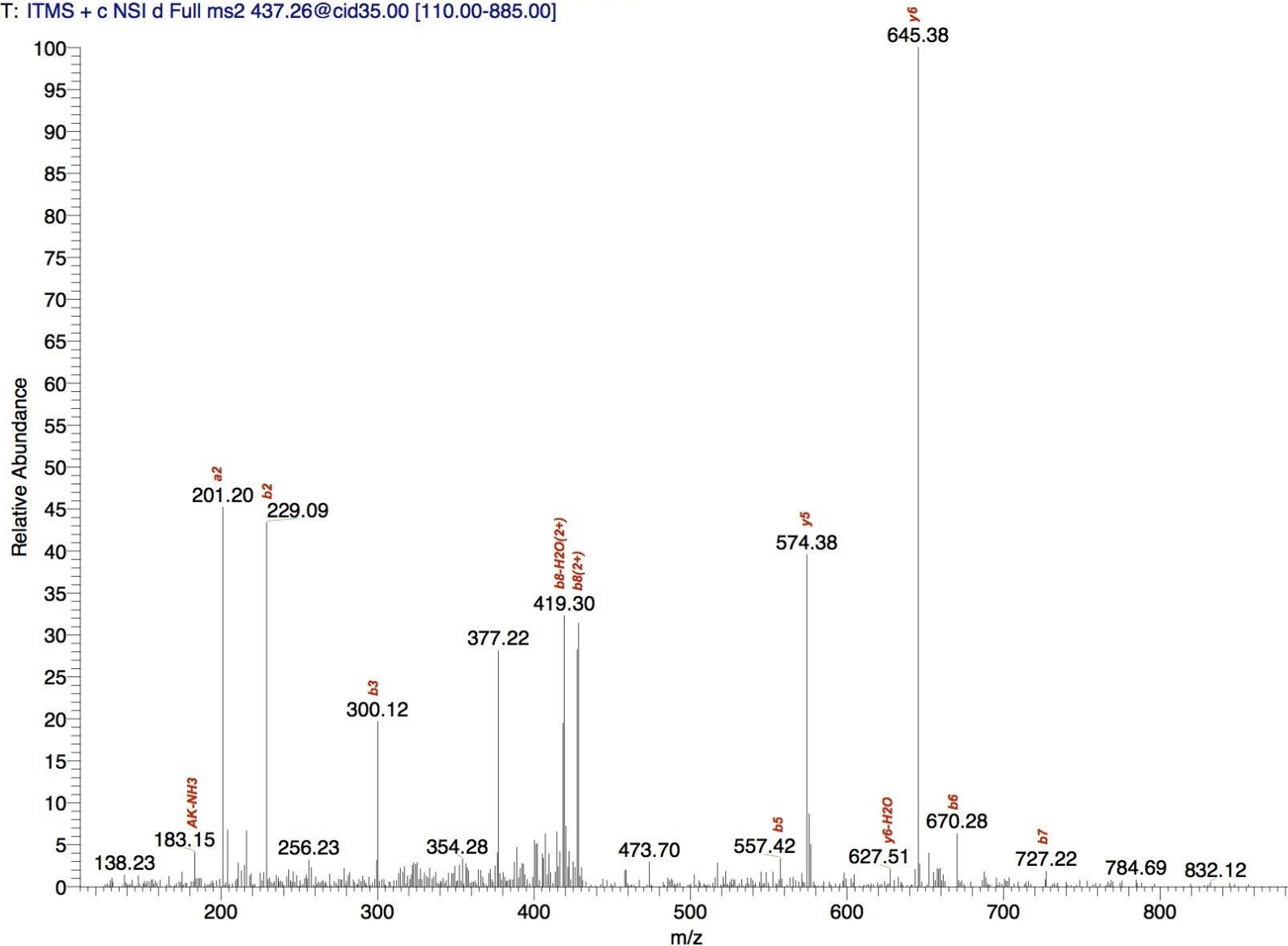
Residue	b	b+2	y	y+2
E	130.0499	65.5286	873.5040	437.2568
V	229.1183	115.0628	744.4614	372.7343
A	300.1554	150.5813	645.3939	323.2001
K	428.2504	214.6288	574.3559	287.6816
E	557.2930	279.1501	446.2609	223.6341
I	670.3770	335.6921	317.2183	159.1128
G	727.3985	364.2029	204.1343	102.5708
K	855.4934	428.2504	147.1128	74.0600

1

Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
1	2	2	437.255	-0.0003	EVAKEIGK	9	12.3	98.6

tgriffin_koore004_051211_PIC2 #5300 RT: 42.31 AV: 1 NL: 3.16E3

T: ITMS + c NSI d Full ms2 437.26@cid35.00 [110.00-885.00]



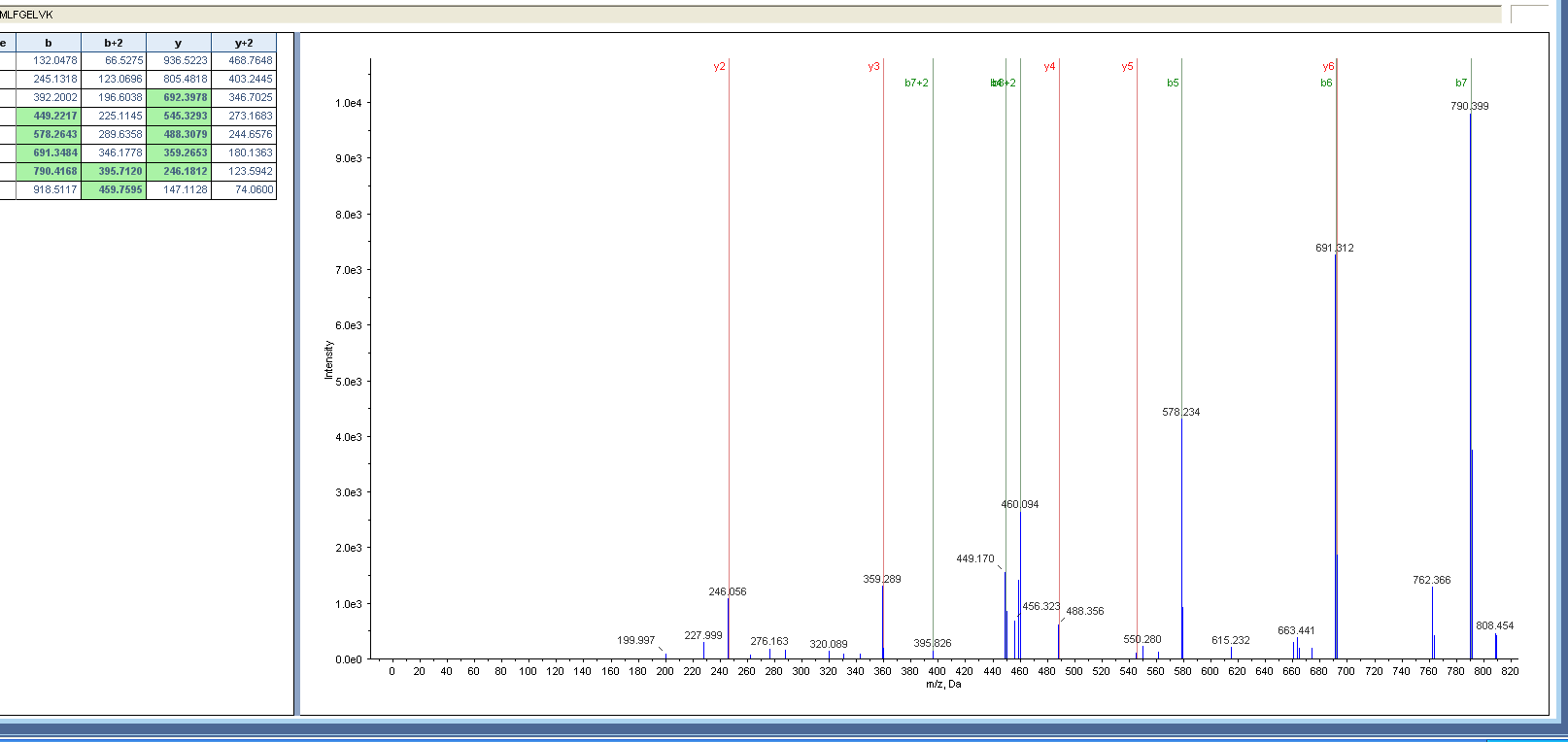
Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
1	2	2	437.255	-0.0003	EVAKEIGK	9	12.3	98.6

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
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- Peptide Summary...
- Protein Summary...

Protein ID		Spectra		Summary Statistics						
Spectrum List										
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
41.1.1.2428.1		935.5078	468.7612	2	1589	MLFGELVK		64.9	935.5150	2

Peptide ID Hypotheses - 41.1.1.2428.1										
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass	Precursor MS Region	
64.9	9	1589	MLFGELVK		935.5150	468.7648	2	-0.0072	No Data Showing	
<1	8	111	RYEEIVK		935.5076	468.7611	2	0.0002		
<1	8		AFTEEIVK		935.4964	468.7555	2	0.0114		
<1	8		EYVYELVK		935.4964	468.7555	2	0.0114		
<1	8		RYEELVK		935.5076	468.7611	2	0.0002		



2

Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	6	2	468.761	-0.0072	MLFGELVK	9	64.9	98.4

Protein ID
Spectra
Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
41.1.1.2428.1		935.5078	468.7612	2	1123	MLFGELVK		98.4	935.5150	2

Peptide ID Hypotheses - 41.1.1.2428.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
98.4	9	1123	MLFGELVK		935.5150	468.7648	2	-0.0072
19.1	8	88	RYEEIVK		935.5076	468.7611	2	0.0002
<1	7		DHVPFLVK		935.5076	468.7611	2	0.0002
<1	7		TAVIELAR		935.5076	468.7611	2	0.0002
<1	6		FVETTAIR		935.5076	468.7611	2	0.0002

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

MLFGELVK

Residue	b	b+2	y	y+2
M	132.0478	66.5275	936.5223	468.7648
L	245.1318	123.0696	805.4818	403.2445
F	392.2002	196.6038	692.3978	346.7025
G	449.2217	225.1145	545.3293	273.1683
E	578.2643	289.6358	488.3079	244.6576
L	691.3484	346.1778	359.2653	180.1363
V	790.4168	395.7120	246.1812	123.5942
K	918.5117	459.7595	147.1128	74.0600

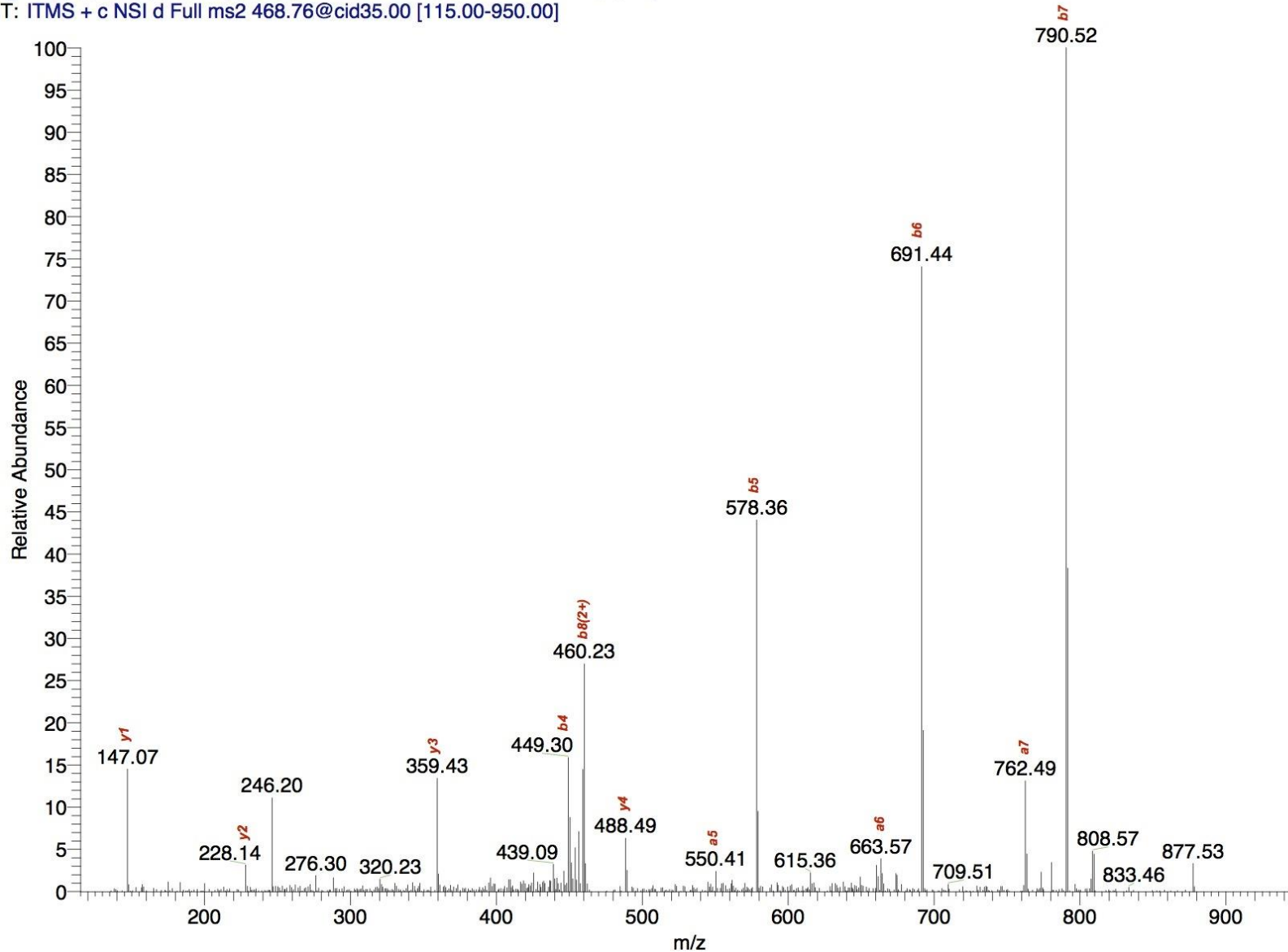


Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	6	2	468.761	-0.0072	MLFGELVK	9	64.9	98.4

MLFGELVK

tgriffin_koore004_060611_P6C_6 #2428 RT: 19.84 AV: 1 NL: 9.81E3

T: ITMS+ c NSI d Full ms2 468.76@cid35.00 [115.00-950.00]



Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	6	2	468.761	-0.0072	MLFGELVK	9	64.9	98.4

Workflow Tasks

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- Spot-Based (MS and MS/MS)...
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- Analysis Log...
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- Peptide Summary...
- Protein Summary...

Protein ID | Spectra | Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
41.1.1.2424.1		860.4886	441.2516	2	1278	QSLGAHLR		80.1	880.4879	2

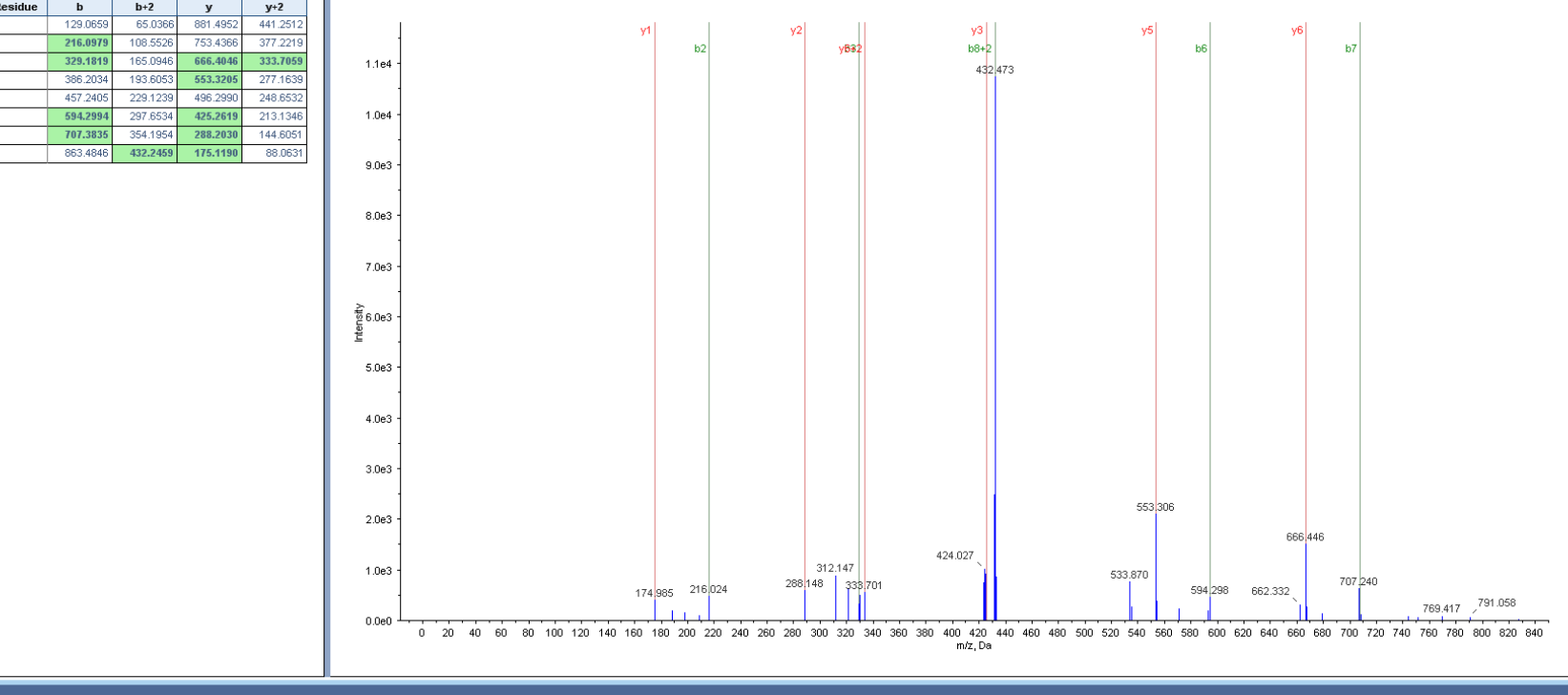
Peptide ID Hypotheses - 41.1.1.2424.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
80.1	9	1278	QSLGAHLR		880.4879	441.2512	2	0.0007
<1	8	452	NTLIQLHR		880.4879	441.2512	2	0.0007
<1	7		EKAQHILR		880.4879	441.2512	2	0.0007
<1	7		GSLAQHLR		880.4879	441.2512	2	0.0007
<1	7		ITICYILR		880.4841	441.2493	2	0.0046

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide



3

Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	6	2	441.251	0.0007	QSLGAHLR	9	80.1	98.3

Protein ID
Spectra
Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
41.1.1.2424.1		880.4886	441.2516	2	1134	QSLGAHLR		98.3	880.4879	2

Peptide ID Hypotheses - 41.1.1.2424.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
98.3	9	1134	QSLGAHLR		880.4879	441.2512	2	0.0007
17.9	8	376	NTLQLHR		880.4879	441.2512	2	0.0007
<1	5	188	FFSVYLHR		880.4807	441.2476	2	0.0079
<1	8		TWLQIHR		880.4879	441.2512	2	0.0007
<1	7		VNNHKIR	Deamidated(N)@2	880.4879	441.2512	2	0.0007

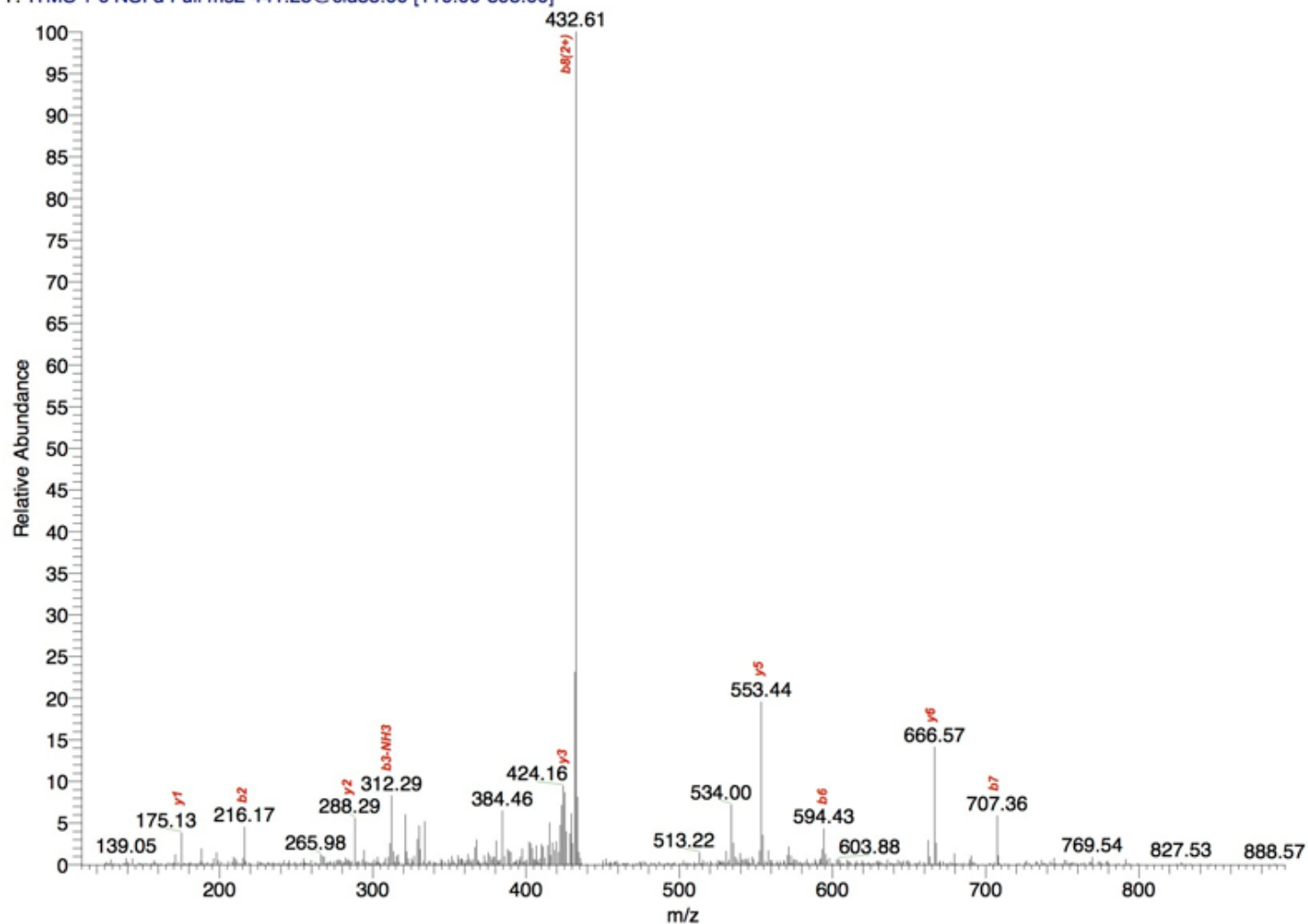
Fragmentation Evidence for Peptide

QSLGAHLR

Residue	b	b+2	y	y+2
Q	129.0659	65.0366	681.4952	441.2512
S	216.0979	108.5526	753.4366	377.2219
L	329.1819	165.0946	666.4046	333.7059
G	386.2034	193.6053	553.3295	277.1639
A	467.2405	229.1239	496.2990	248.6532
H	594.2994	297.6534	425.2619	213.1346
L	707.3835	354.1954	288.2030	144.6051
R	863.4846	432.2459	175.1190	88.0631

3

Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	6	2	441.251	0.0007	QSLGAHLR	9	80.1	98.3

QSLGAHLRtgriffin_koore004_060611_P6C_6 #2424 RT: 19.82 AV: 1 NL: 1.07E4
T: ITMS + c NSI d Full ms2 441.25@cid35.00 [110.00-895.00]

Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	6	2	441.251	0.0007	QSLGAHLR	9	80.1	98.3

Protein ID
Spectra
Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
21.1.1.2204.1		812.4392	407.2268	2	27	LNVENPK		87.4	812.4392	2

Peptide ID Hypotheses - 21.1.1.2204.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
87.4	9	27	LNVENPK		812.4392	407.2269	2	-0.0001
<1	7	426, 673	NLHPNPK		812.4214	407.2180	2	0.0176
<1	8		LHVQPNK	Deamidated(O)@4	812.4392	407.2269	2	-0.0001
<1	7		ARVEPNK		812.4504	407.2325	2	-0.0114
<1	7		INLDNPK		812.4392	407.2269	2	-0.0001
<1	7		IVGEGNPK		812.4392	407.2269	2	-0.0001

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

LNVENPK

Residue	b	b+2	y	y+2
L	114.0913	57.5493	813.4485	407.2269
N	228.1343	114.5708	700.3624	350.6849
V	327.2027	164.1050	586.3195	293.6634
E	466.2453	228.6263	487.2511	244.1292
N	570.2882	285.6477	358.2085	179.6079
P	667.3410	334.1741	244.1656	122.5864
K	795.4359	398.2216	147.1128	74.0600

4

Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
1	3	2	407.226	-0.0001	LNVENPK	9	87.4	98.1

Protein ID
Spectra
Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
21.1.1.2204.1		812.4391	407.2268	2	29	LNVENPK		98.1	812.4392	2

Peptide ID Hypotheses - 21.1.1.2204.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
98.1	9	29	LNVENPK		812.4392	407.2269	2	-0.0001
<1	7	493, 629	NLHPNPK		812.4214	407.2180	2	0.0176
<1	5		DRNPFALR		812.4504	407.2325	2	-0.0114
<1	5		MEPVLPK		812.4466	407.2306	2	-0.0075
<1	5		NLNPTVR		812.4504	407.2325	2	-0.0114

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

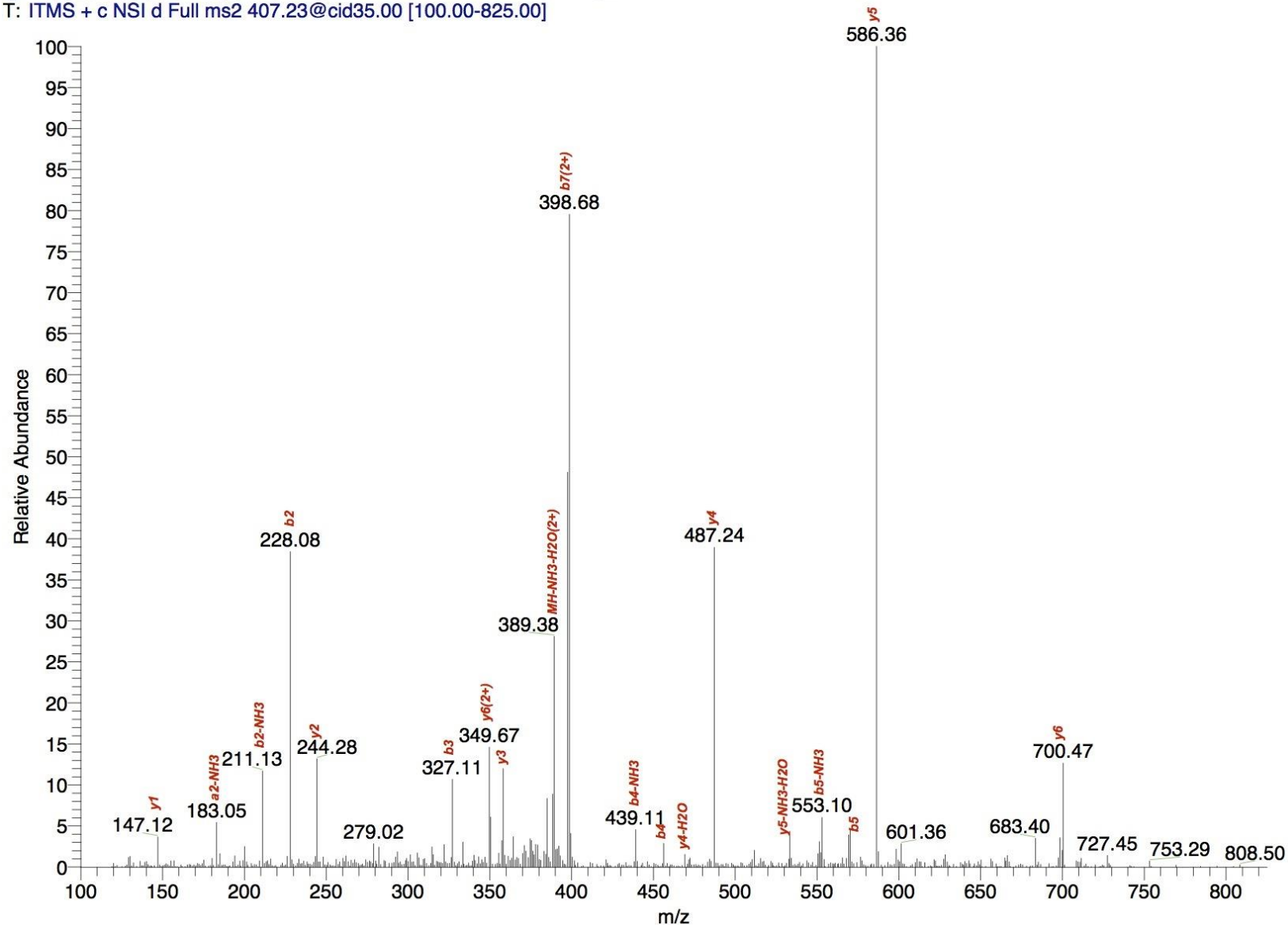
LNVENPK

Residue	b	b+2	y	y+2
L	114.0913	57.5493	813.4465	407.2269
N	228.1343	114.5708	700.3624	350.6849
V	327.2027	164.1050	586.3195	293.6634
E	456.2453	228.6263	487.2511	244.1292
N	570.2882	285.6477	358.2085	179.6079
P	667.3410	334.1741	244.1656	122.5864
K	795.4359	398.2216	147.1128	74.0600

4

Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
1	3	2	407.226	-0.0001	LNVENPK	9	87.4	98.1

tgriffin_koore004_051211_PIC3 #2204 RT: 20.11 AV: 1 NL: 1.76E4
 T: ITMS + c NSI d Full ms2 407.23@cid35.00 [100.00-825.00]



Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
1	3	2	407.226	-0.0001	LNVENPK	9	87.1	98.1

Protein ID
Spectra
Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
21.1.1.7802.1		1267.6927	634.8537	2	27	WLSLPGETRPL		88.1	1267.6925	2

Peptide ID Hypotheses - 21.1.1.7802.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
88.1	11	27	WLSLPGETRPL		1267.6925	634.8535	2	0.0003
<1	8		DALINGSGPGLR		1267.6885	634.8515	2	0.0043
<1	8		SVIISHGKSMAR		1267.6997	634.8571	2	-0.0069
<1	8		VQAPSGDLLAAR		1267.6885	634.8515	2	0.0043

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

WLSLPGETRPL

Residue	b	b+2	y	y+2
W	187.0866	94.0469	1268.6997	634.8535
L	300.1707	150.5890	1082.6204	541.8139
S	387.2027	194.1050	969.5364	485.2718
L	500.2867	250.6470	882.5043	441.7558
P	597.3395	299.1734	769.4203	385.2138
G	654.3610	327.6841	672.3675	336.6874
E	783.4036	392.2054	615.3461	306.1767
T	884.4512	442.7293	486.3035	243.6554
R	1040.5524	520.7798	385.2558	193.1315
P	1137.6051	569.3062	229.1547	115.0810
L	1250.6892	625.8482	132.1019	66.5546

Spectrum information					Identification			Peptide Conf	
Sample	Fraction	Scan	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
1	3	7802	2	634.853	0.0003	WLSLPGETRPL	11	88.1	96.6

Protein ID
Spectra
Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
21.1.1.7802.1		1267.6927	634.8537	2	29	WLSLPGETRPL		96.6	1267.6925	2

Peptide ID Hypotheses - 21.1.1.7802.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
96.6	11	29	WLSLPGETRPL		1267.6925	634.8535	2	0.0003
<1	6		HPALVIPEVGSR		1267.6958	634.8552	2	-0.0031
<1	5		DAYFRLTKVR		1267.7037	634.8591	2	-0.0109
<1	5		EGLSKAKHEAAK		1267.6885	634.8515	2	0.0043
<1	5		SCKEHIDNIKK		1267.6885	634.8515	2	0.0043

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

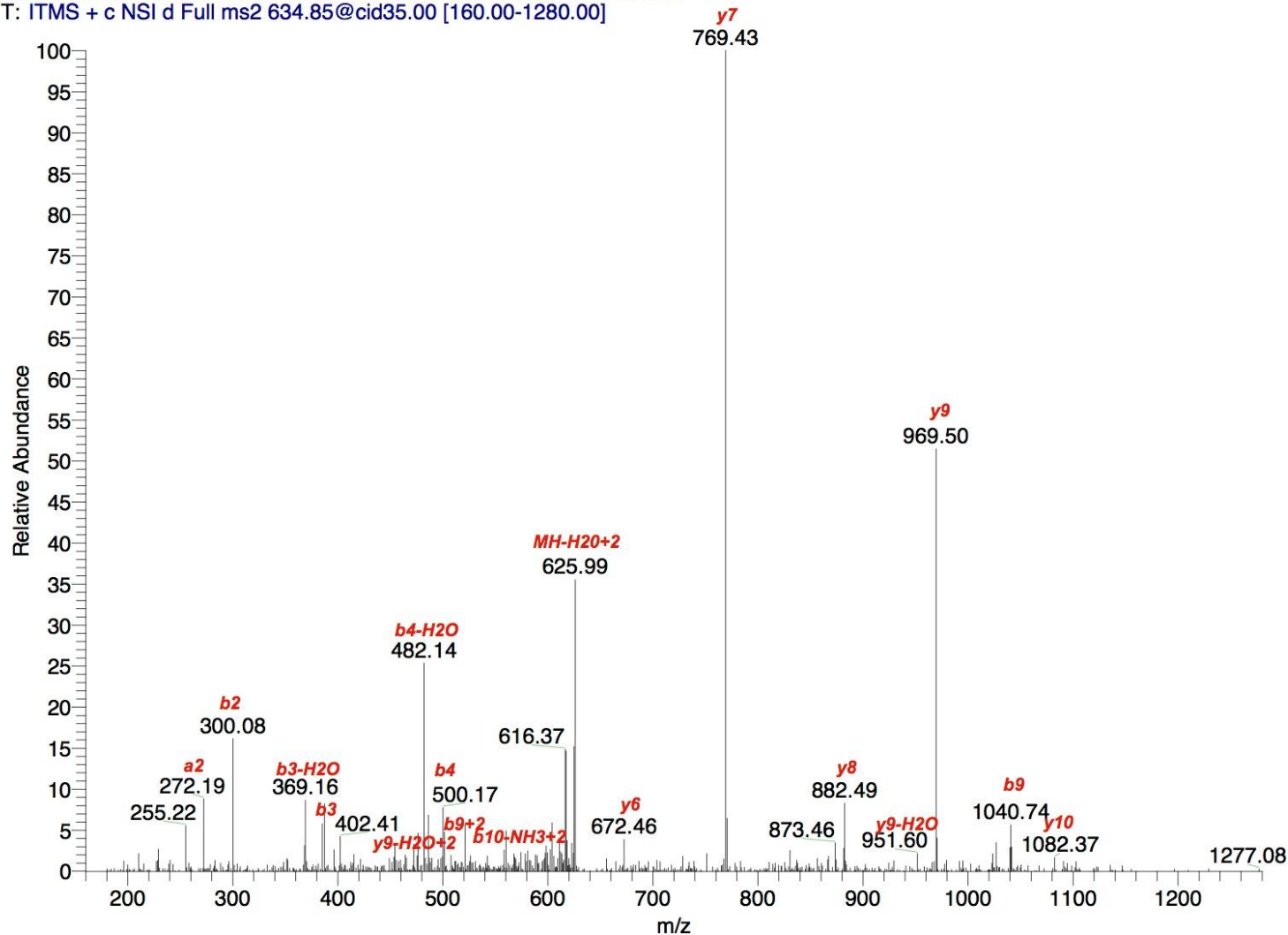
WLSLPGETRPL

Residue	b	b+2	y	y+2
W	187.0866	94.0469	1268.6997	634.8535
L	300.1707	150.5890	1082.6204	541.8139
S	387.2027	194.1050	969.5364	485.2718
L	600.2867	250.6470	882.5043	441.7558
P	597.3395	299.1734	769.4203	385.2138
G	654.3610	327.6841	672.3675	336.6874
E	783.4036	392.2054	615.3481	308.1767
T	684.4512	442.7293	406.3035	243.6554
R	1040.5524	520.7798	385.2558	193.1315
P	1137.6051	569.3062	229.1547	115.0810
L	1250.6892	625.8482	132.1019	66.5546

5

Spectrum information				Identification			Peptide Conf		
Sample	Fraction	Scan	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
1	3	7802	2	634.853	0.0003	WLSLPGETRPL	11	88.1	96.6

tgriffin_koore004_051211_PIC3 #7802 RT: 58.05 AV: 1 NL: 4.22E3
 T: ITMS + c NSI d Full ms2 634.85@cid35.00 [160.00-1280.00]



5

Spectrum information					Identification			Peptide Conf	
Sample	Fraction	Scan	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
1	3	7802	2	634.853	0.0003	WLSLPGETRPL	11	88.1	96.6

Workflow Tasks

- Identify Proteins
- LC...
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- Spot-Based (MS and MS/MS)...
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- Peptide Summary...
- Protein Summary...

Protein ID Spectra Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
41.1.1.4385.1		1021.4871	511.7508	2	873	EHFAIYKD		66.1	1021.4869	2

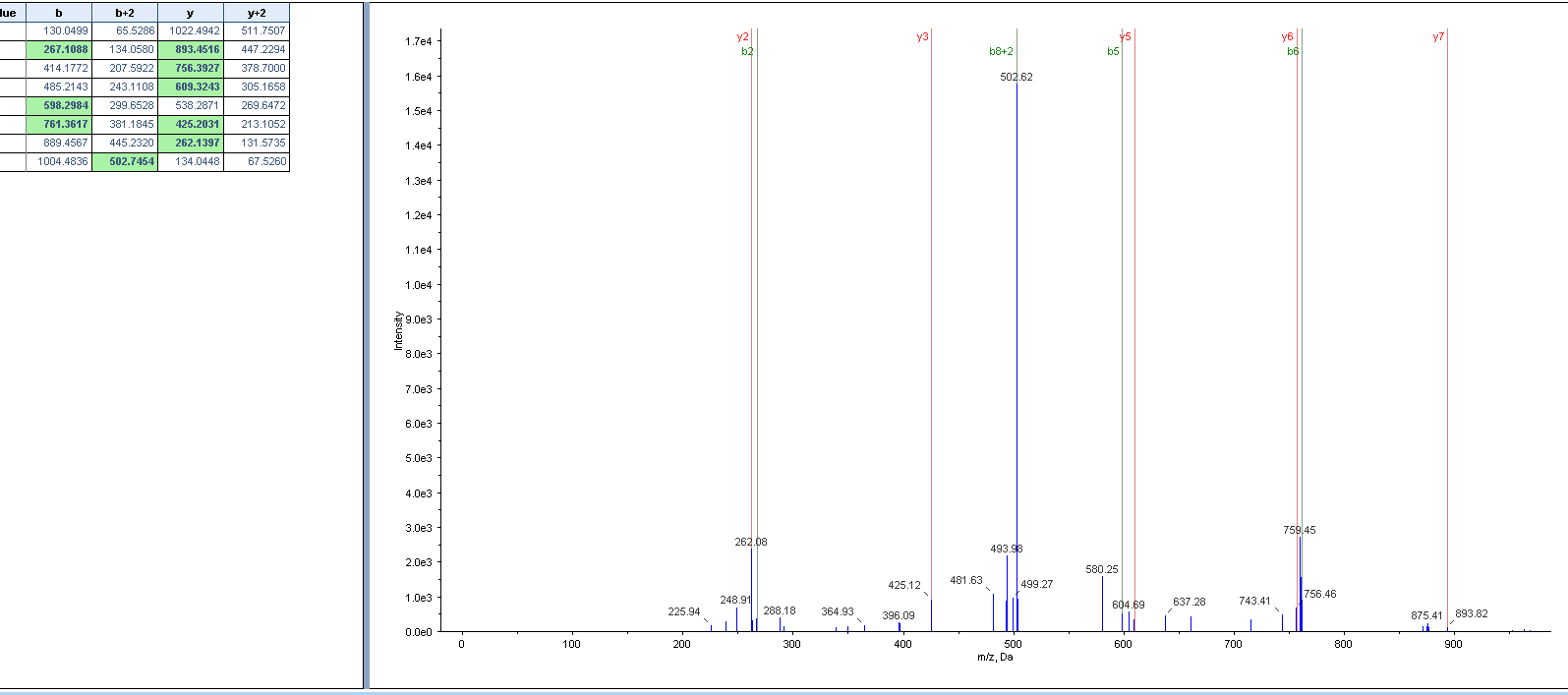
Peptide ID Hypotheses - 41.1.1.4385.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
66.1	8	873	EHFAIYKD		1021.4869	511.7507	2	0.0002
<1	7		HTWLERDK	Oxidation(M)@1	1021.4863	511.7504	2	0.0008
<1	6		EHEQKHSK		1021.4941	511.7543	2	-0.0070
<1	6		EHTTEHLR		1021.4941	511.7543	2	-0.0070
<1	6		KEQSGGSSSR		1021.4788	511.7467	2	0.0082

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide



6

Spectrum information				Identification			Peptide Conf		
Sample	Fraction	Scan	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	6	4385	2	511.751	0.0002	EHFAIYKD	8	66.1	95.5

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...

Protein ID Spectra Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
41.1.1.4385.1		1021.4871	511.7508	2	630	EHFAIYKD		95.5	1021.4869	2

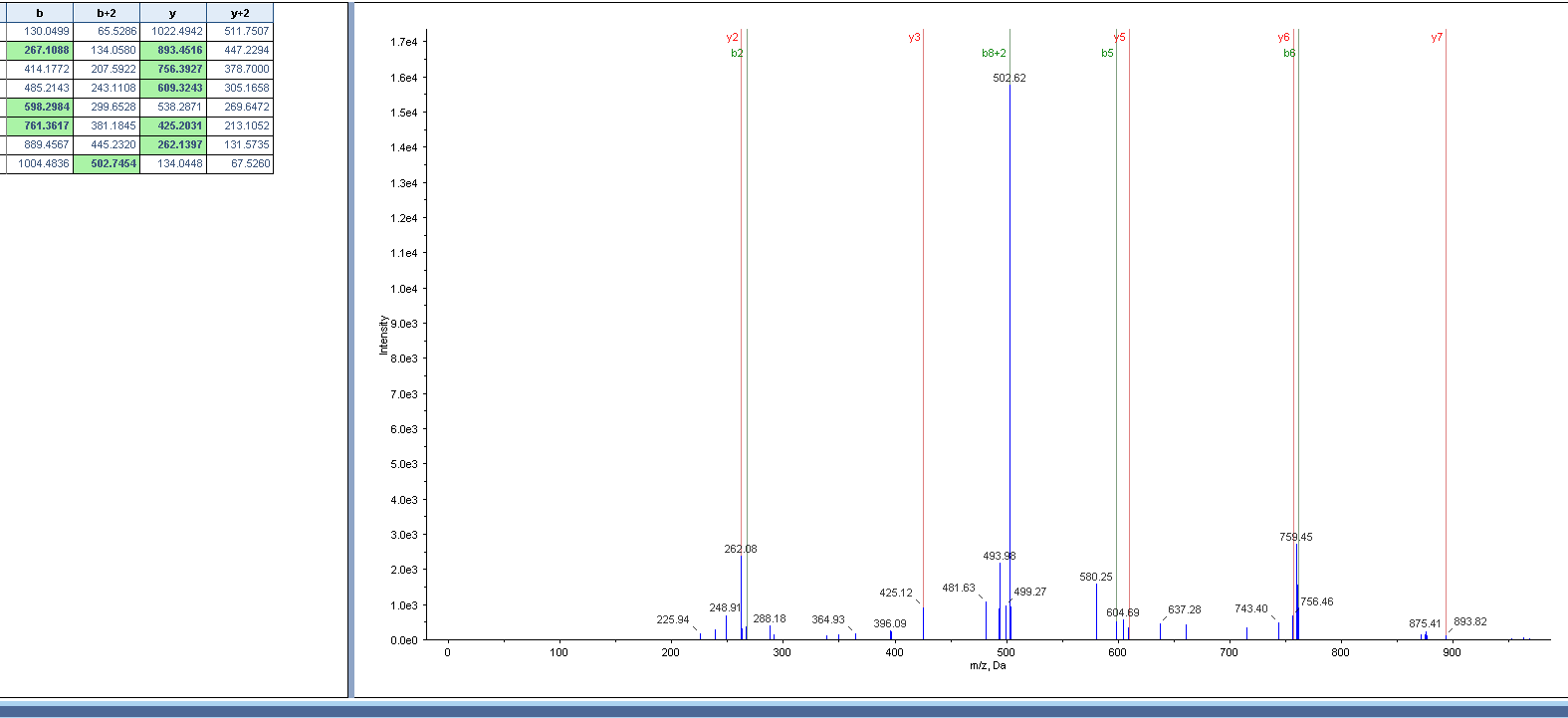
Peptide ID Hypotheses - 41.1.1.4385.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
95.5	8	630	EHFAIYKD		1021.4869	511.7507	2	0.0002
<1	6		DFRGQRDK	Deamidated(Q)@5	1021.4941	511.7543	2	-0.0070
<1	6		KEQSGGSSSR		1021.4788	511.7467	2	0.0082
<1	6		MTHVYLDK	Oxidation(M)@1	1021.4903	511.7524	2	-0.0032
<1	5		EFDRGRDK		1021.4941	511.7543	2	-0.0070

Precursor MS Region

No Data Showing

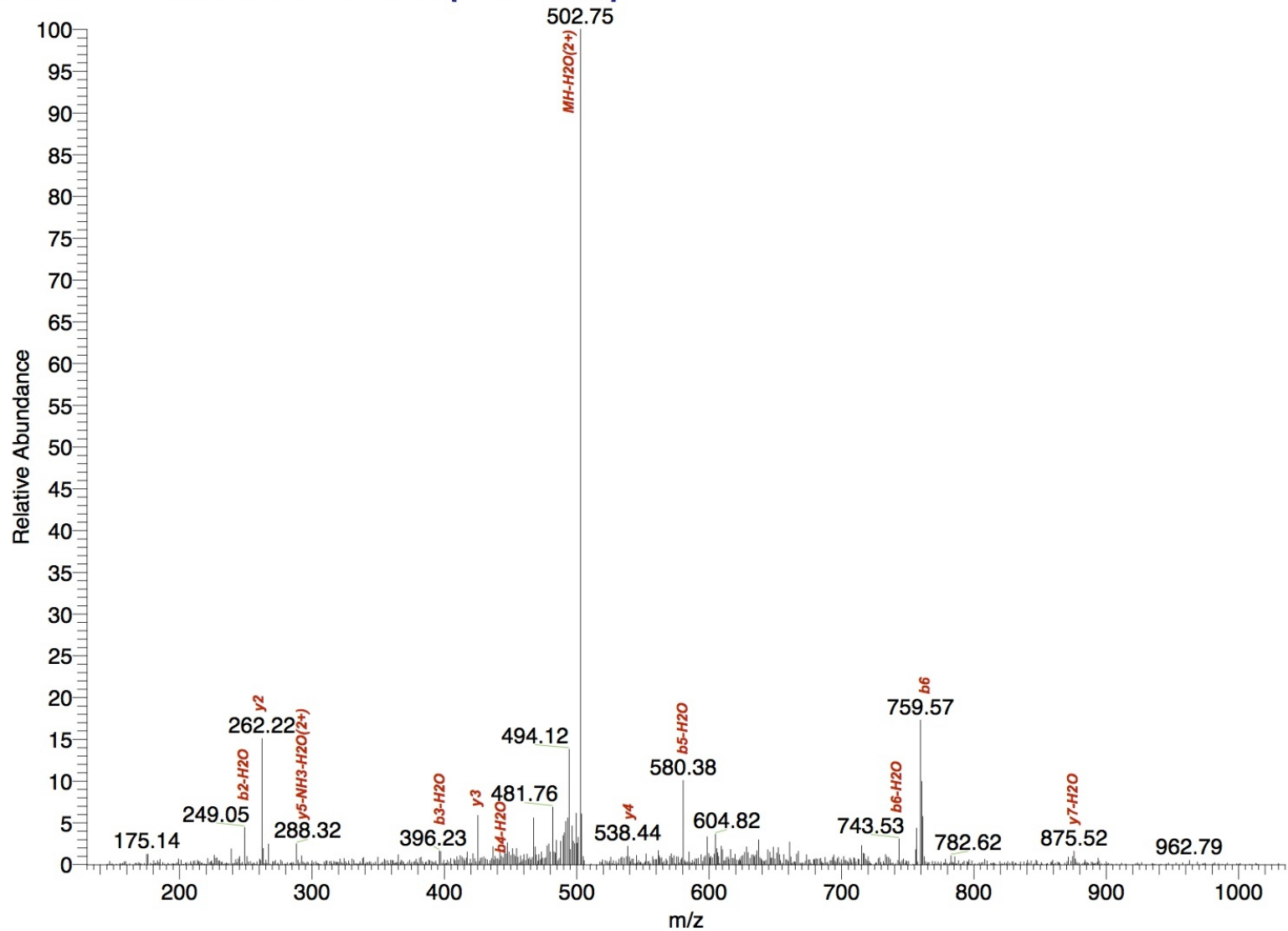
Fragmentation Evidence for Peptide



6

Spectrum information				Identification			Peptide Conf		
Sample	Fraction	Scan	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	6	4385	2	511.751	0.0002	EHFAIYKD	8	66.1	95.5

tgriffin_koore004_060611_P6C_6 #4385 RT: 34.54 AV: 1 NL: 1.58E4
T: ITMS + c NSI d Full ms2 511.75@cid35.00 [130.00-1035.00]



6

Spectrum information					Identification			Peptide Conf	
Sample	Fraction	Scan	Charge	Theor m/z	D Mass	Sequence	Sc	One Step Method	Two Step Method
6	6	4385	2	511.751	0.0002	EHFAIYKD	8	66.1	95.5

Identified in
two-step but
not in one-
step method.

PROTEOGENOMICS

Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
1 6	3	2	510.232	0.0061	MDNAIGDQR	9	66.1	96.7
2 4	3	2	498.774	-0.0005	MSPHLQRK	9	92.1	96.2
3 6	5	2	574.2341	0.0019	GEEEGEGGGGGR	9	84.8	97.5
4 6	5	2	679.8591	-0.0093	RTSVCPRTWPR	10	73.85	98.1

Protein ID
Spectra
Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
35.1.1.3655.1		1018.4564	510.2354	2	1352	MDNAIGDQR		66.1	1018.4502	2

Peptide ID Hypotheses - 35.1.1.3655.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
66.1	9	1352	MDNAIGDQR		1018.4502	510.2324	2	0.0061
23.6	9		HWLNANVR	Deamidated(N)@2	1018.4655	510.2400	2	-0.0091
<1	7		EAUSGGAMR		1018.4621	510.2383	2	-0.0058
<1	7		IEEESAGER		1018.4567	510.2366	2	-0.0004
<1	7		HWNNKQNR	Deamidated(N)@2	1018.4614	510.2380	2	-0.0051

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

MDNAIGDQR

Residue	b	b+2	y	y+2
M	132.0478	66.5275	1019.4575	510.2324
D	247.0747	124.0410	888.4170	444.7121
N	361.1176	181.0625	773.3900	387.1987
A	432.1547	216.5810	659.3471	330.1772
I	545.2388	273.1230	588.3100	294.6586
G	602.2603	301.6338	475.2259	238.1166
D	717.2872	359.1472	418.2045	209.6059
Q	845.3468	423.1765	303.1775	152.0924
R	1001.4469	501.2271	175.1190	88.0631

1

Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	6	2	510.232	0.0061	MDNAIGDQR	9	66.1	96.7

Protein ID
Spectra
Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
35.1.1.3655.1		1018.4564	510.2354	2	1032	MDNAIGDQR		96.7	1018.4502	2

Peptide ID Hypotheses - 35.1.1.3655.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
96.7	9	1032	MDNAIGDQR		1018.4502	510.2324	2	0.0061
<1	6		CLWAGGAGQR	Deamidated(Q)@9	1018.4655	510.2400	2	-0.0091
<1	6		DESQKAGER		1018.4680	510.2412	2	-0.0116
<1	6		GTDQVSAGEE		1018.4680	510.2412	2	-0.0116
<1	6		MILLDFHK	Deamidated(N)@2	1018.4542	510.2344	2	0.0021

Precursor MS Region

No Data Showing

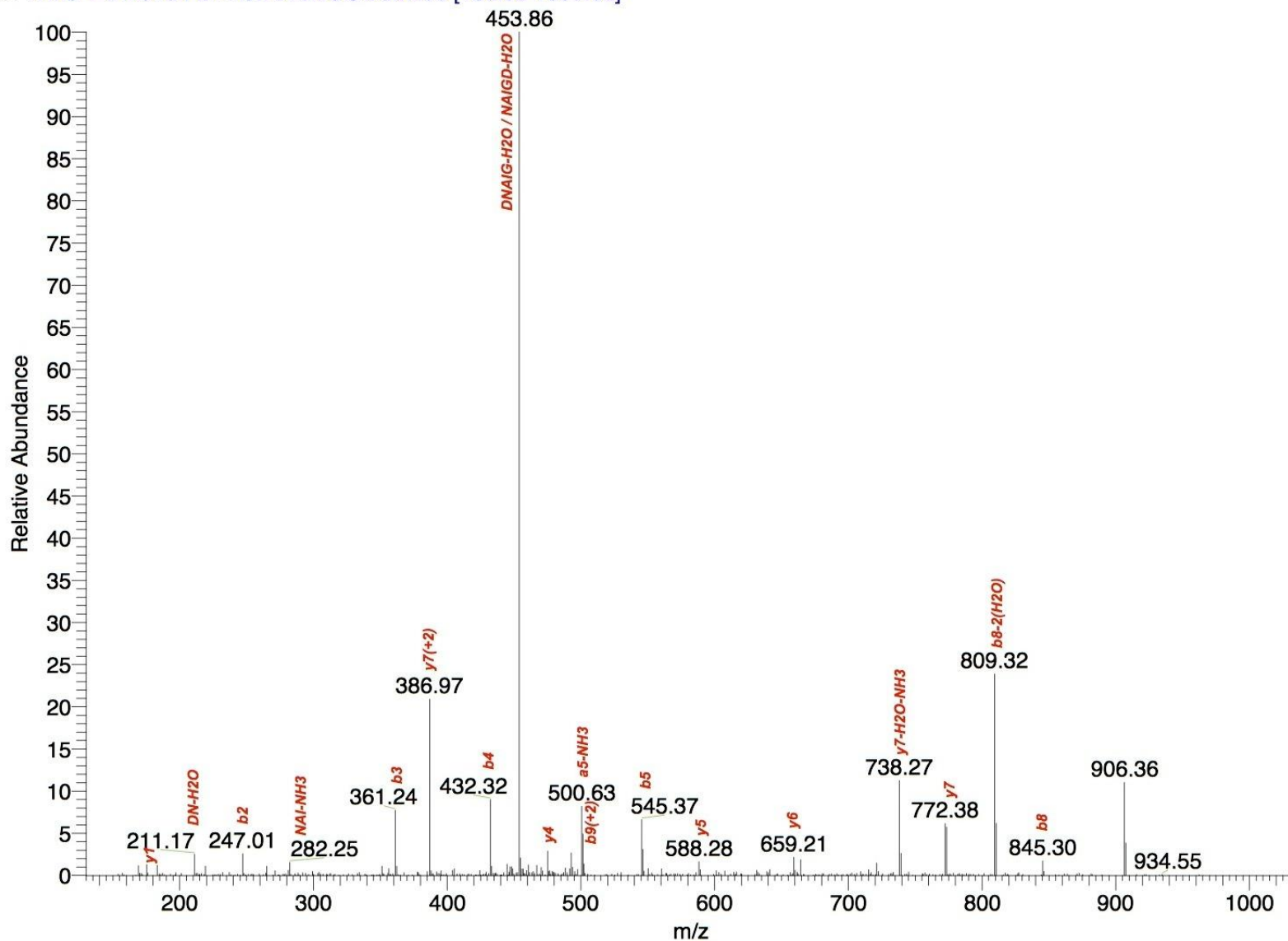
Fragmentation Evidence for Peptide

MDNAIGDQR

Residue	b	b+2	y	y+2
M	132.0478	66.5275	1018.4575	510.2324
D	247.0747	124.0410	888.4170	444.7121
N	361.1176	181.0625	773.3900	387.1987
A	432.1647	216.5810	659.3471	330.1772
I	545.2388	273.1230	588.3100	294.6586
G	602.2603	301.6338	475.2259	238.1166
D	717.2872	359.1472	418.2045	209.6059
Q	845.3458	423.1765	303.1775	152.0924
R	1001.4469	501.2271	175.1190	88.0631

1	Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
		6	3	2	510.232	0.0061	MDNAIGDQR	9	66.1

tgriffin_koore004_060611_P6C_3 #3655 RT: 33.44 AV: 1 NL: 6.66E4
 T: ITMS + c NSI d Full ms2 510.23@cid35.00 [130.00-1035.00]



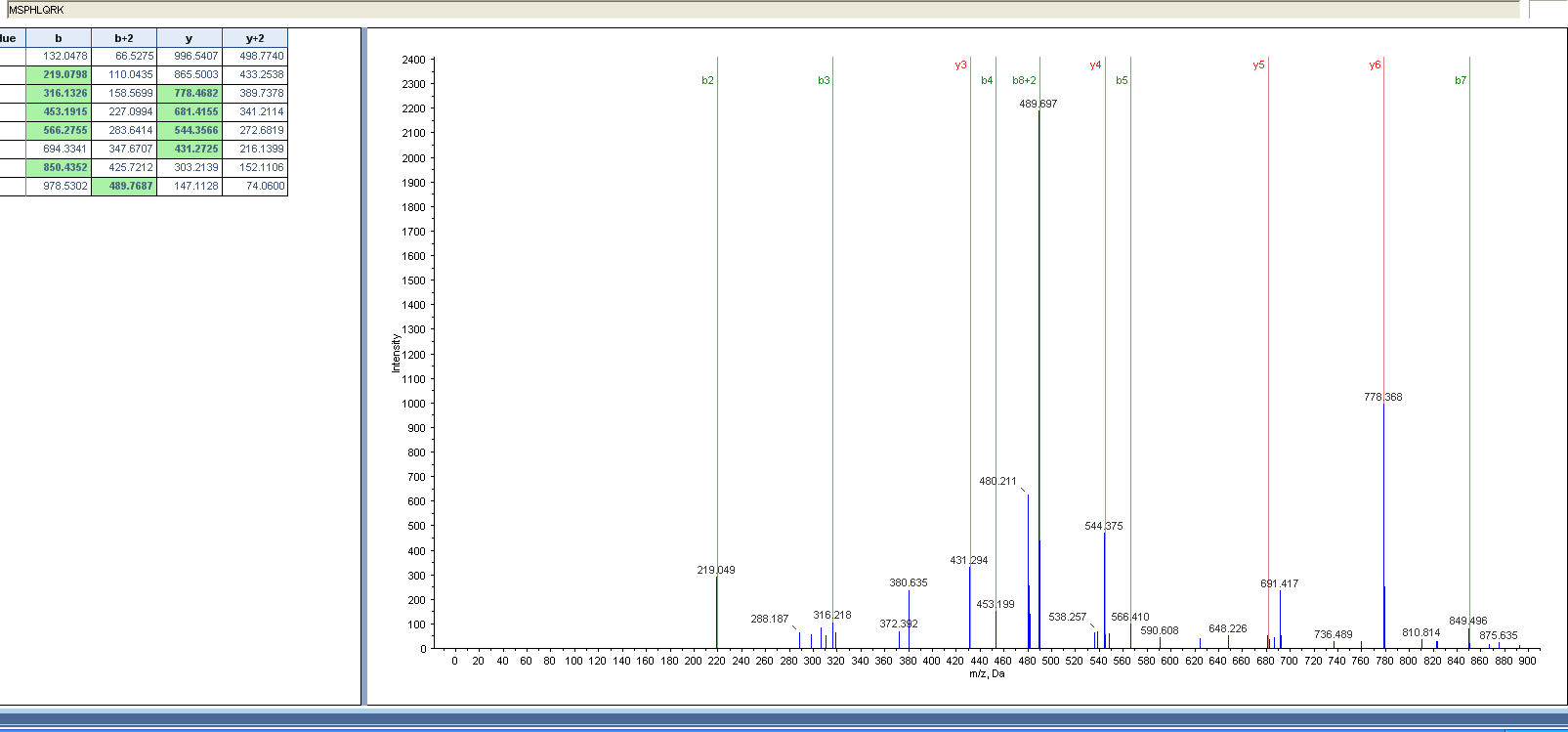
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	3	2	510.232	0.0061	MDNAIGDQR	9	66.1	96.7

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...

Protein ID							Spectra			Summary Statistics		
Spectrum List												
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications			Conf	Theor MW	z
7.1.1.6097.1		995.5330	498.7737	2	1000	MSPHLQRK				92.1	995.5334	2

Peptide ID Hypotheses - 7.1.1.6097.1										Precursor MS Region		
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass	No Data Showing			
92.1	9	1000	MSPHLQRK		995.5334	498.7740	2	-0.0005				
<1	4	1028	HILELFSK	Oxidation(M)@1	995.5361	498.7754	2	-0.0032				
<1	7		MAFPAPAGLR	Oxidation(M)@1	995.5222	498.7684	2	0.0107				
<1	7		SVPFIFVST		995.5328	498.7737	2	0.0001				
<1	6		CVHLLNAAR		995.5334	498.7740	2	-0.0005				
<1	6		EMISLLYK		995.5361	498.7754	2	-0.0032				



2

Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
4	3	2	498.774	-0.0005	MSPHLQRK	9	92.1	96.2

Protein ID
Spectra
Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
7.1.1.6097.1		995.5330	498.7737	2	1048	MSPHLQRK		96.2	995.5334	2

Peptide ID Hypotheses - 7.1.1.6097.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
96.2	9	1048	MSPHLQRK		995.5334	498.7740	2	-0.0006
<1	7		MAPPAPAGLR	Oxidation(M)@1	995.5222	498.7684	2	0.0107
<1	6		FALIQNYK		995.5440	498.7793	2	-0.0111
<1	5		ALIYSTSMK		995.5267	498.7717	2	0.0042
<1	5		EGQVTLPLR		995.5400	498.7773	2	-0.0071

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

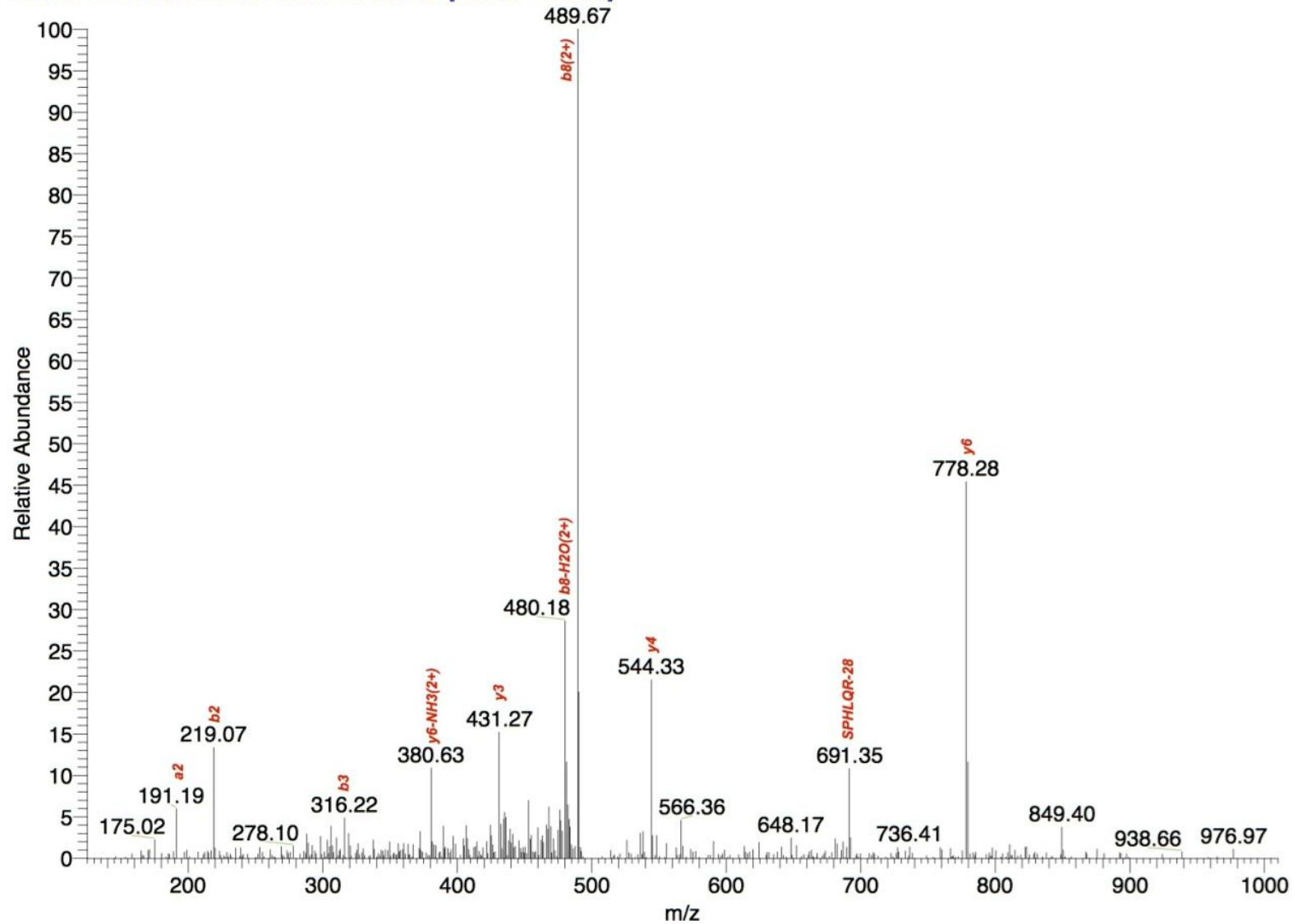
MSPHLQRK

Residue	b	b+2	y	y+2
M	132.0478	66.5275	998.5407	498.7740
S	219.0798	110.0435	865.5003	433.2538
P	316.1326	158.5699	778.4682	389.7378
H	453.1915	227.0994	681.4155	341.2114
L	566.2755	283.6414	544.3566	272.6819
Q	694.3341	347.6707	431.2725	216.1399
R	850.4352	425.7212	303.2139	152.1106
K	978.5302	489.7687	147.1128	74.0600

2

Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
4	3	2	498.774	-0.0005	MSPHLQRK	9	92.1	96.2

tgriffin_koore004_040511_patient4_control_CC_Fr3 #6097 RT: 45.97 AV: 1 NL: 2.19E3
 T: ITMS + c NSI d Full ms2 498.77@cid35.00 [125.00-1010.00]



Spectrum information				Identification			Peptide Conf	
Sample	Fraction	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
4	3	2	498.774	-0.0005	MSPHLQRK	9	92.1	96.2

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...

Protein ID Spectra Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
39.1.1.2617.1		1146.4733	574.2439	2	1131	GEEEGEGGGGGGR		84.8	1146.4537	2

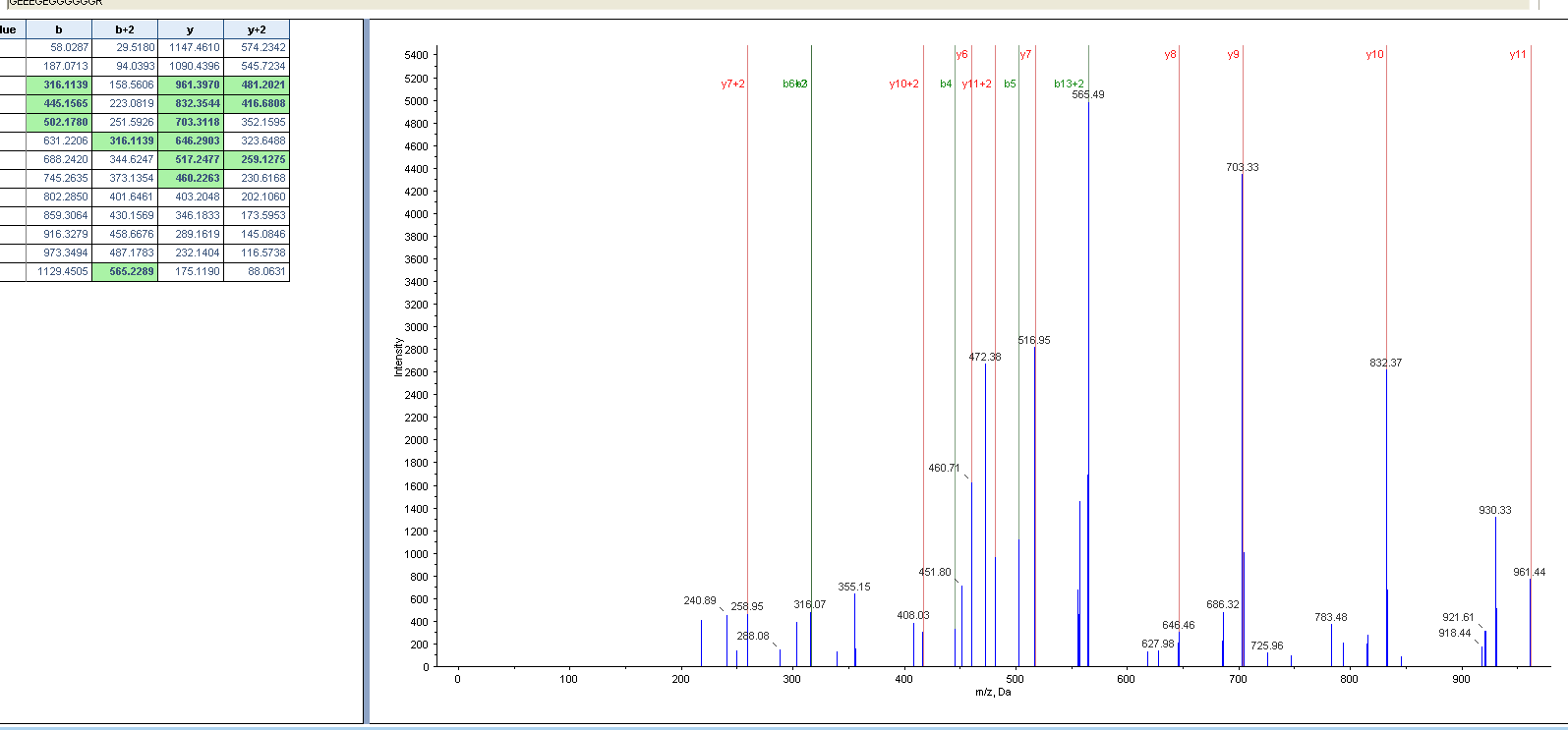
Peptide ID Hypotheses - 39.1.1.2617.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
84.8	9	1131	GEEEGEGGGGGGR		1146.4537	574.2341	2	0.0195
<1	7		DCPGADSAQAGR		1146.4724	574.2435	2	0.0008
<1	6		EWFGSPQEW	Glu->pyro-Glu@N-term	1146.4771	574.2458	2	-0.0038
<1	6		GCGNERNGP SR	Deamidated(N)@4	1146.4836	574.2491	2	-0.0104
<1	6		QEGEAGSGEGEK	Deamidated(Q)@1	1146.4789	574.2457	2	-0.0057

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide



3

Spectrum information					Identification		Peptide Conf		
Sample	Fraction	Scan	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	5	2617	2	574.2341	0.019598	GEEEGEGGGGGGR	9	84.84	97.48

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
39.1.1.2617.1		1146.4734	574.2440	2	1008	GEEEGEGGGGGGR		97.5	1146.4537	2

Peptide ID Hypotheses - 39.1.1.2617.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
97.5	9	1008	GEEEGEGGGGGGR		1146.4537	574.2341	2	0.0196
<1	4		CPNEPECVQK	Deamidated(N)@3	1146.4685	574.2416	2	0.0048
<1	4		CPSGAQECPGAK		1146.4797	574.2472	2	-0.0064
<1	4		QVCEPENPCK	Deamidated(N)@7	1146.4685	574.2416	2	0.0048
<1	3		AMEQPFQFSM		1146.4685	574.2416	2	0.0048

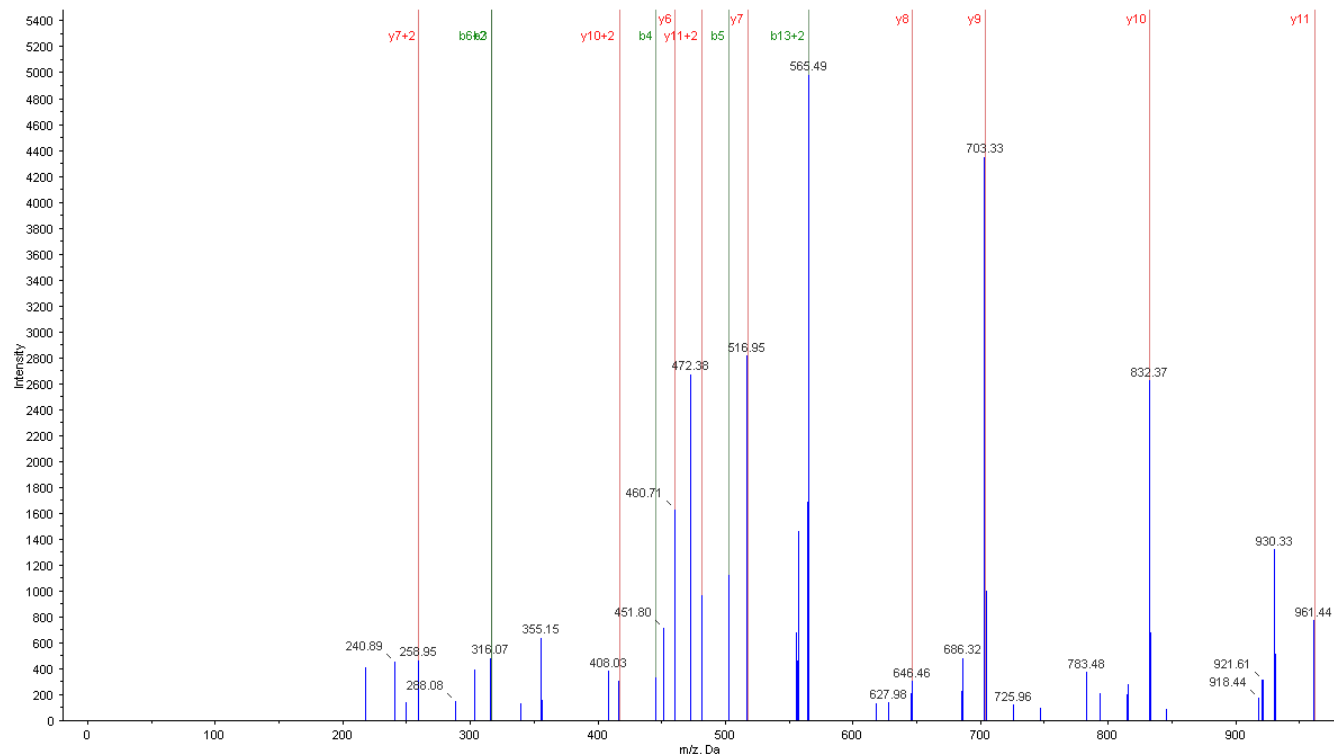
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

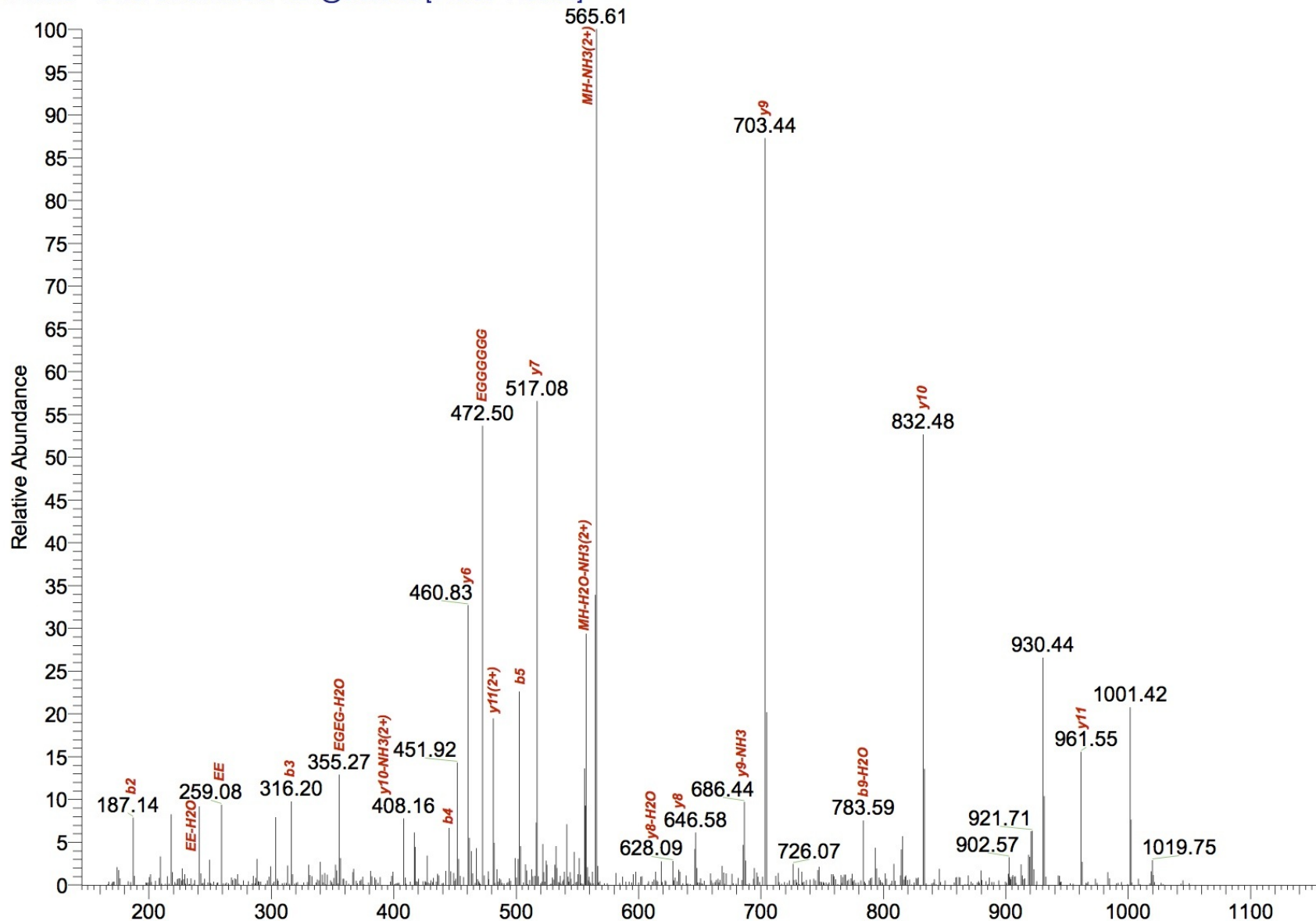
GEEEGEGGGGGGR

Residue	b	b+2	y	y+2
G	58.0287	29.5180	1147.4610	574.2342
E	167.0713	94.0393	1090.4396	545.7234
E	316.1139	158.5806	961.3970	481.2021
E	445.1565	223.0819	832.3544	416.6808
G	502.1780	251.5926	703.3118	352.1595
E	631.2206	316.1139	646.2903	323.6488
G	688.2420	344.6247	517.2477	259.1275
G	745.2635	373.1354	460.2263	230.6168
G	802.2850	401.6461	403.2048	202.1060
G	859.3064	430.1569	346.1833	173.5953
G	916.3279	458.6676	289.1619	145.0846
G	973.3494	487.1783	232.1404	116.5738
R	1129.4505	565.2289	175.1190	88.0631



3

Spectrum information					Identification			Peptide Conf	
Sample	Fraction	Scan	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	5	2617	2	574.2341	0.019598	GEEEGEGGGGGGR	9	84.84	97.48



3

Spectrum information					Identification			Peptide Conf	
Sample	Fraction	Scan	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	5	2617	2	574.2341	0.019598	GEEEGEGGGGGR	9	84.84	97.48

Workflow Tasks

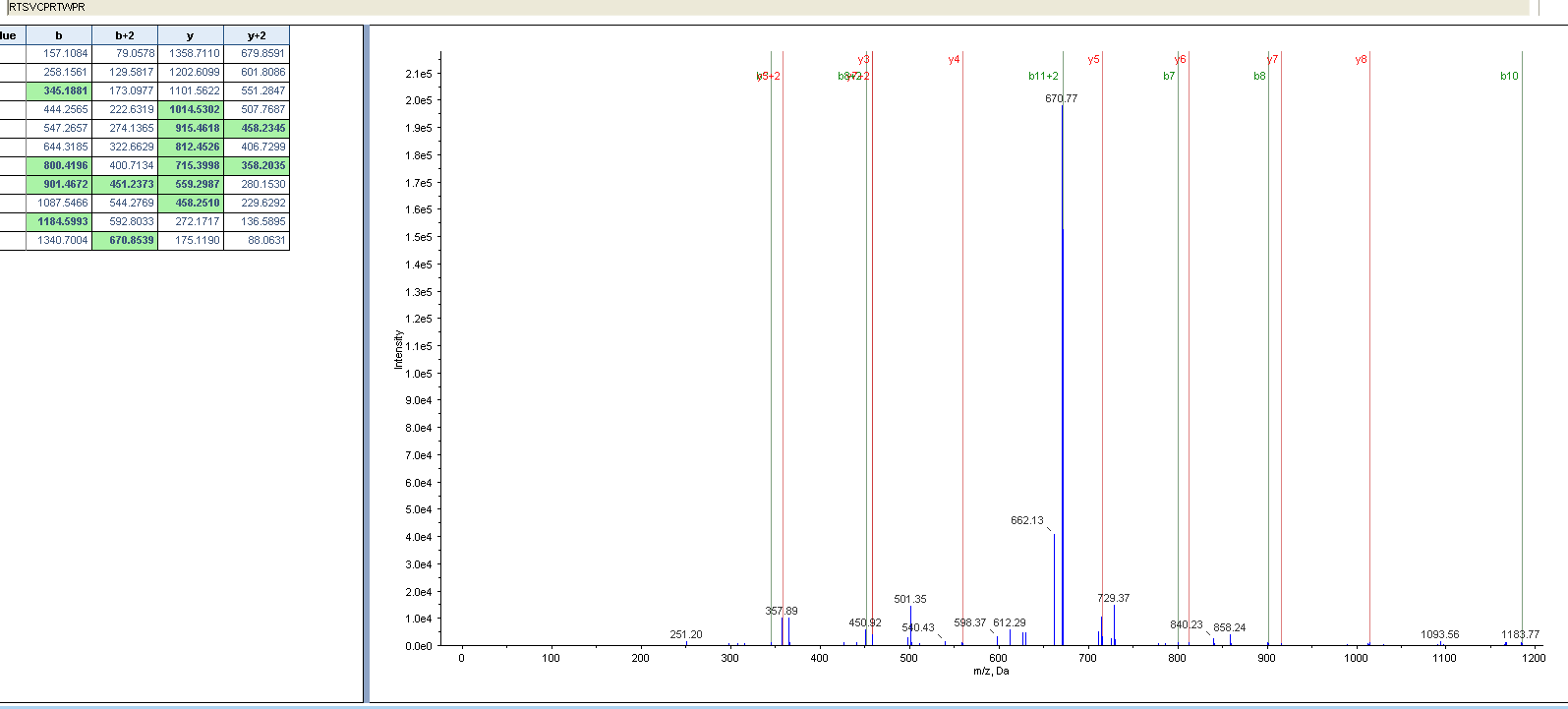
- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...

Protein ID						Spectra		Summary Statistics			
Spectrum List											
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications		Conf	Theor MW	z
39.1.1.3792.1		1357.6945	679.8545	2	1308	RTSVCPRTWPR			73.8	1357.7037	2

Peptide ID Hypotheses - 39.1.1.3792.1									
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass	
73.8	10	1308	RTSVCPRTWPR		1357.7037	679.8591	2	-0.0093	
<1	9	1630	CGGELVLVGEGLVGR		1357.7024	679.8565	2	-0.0080	
<1	8		EEVGQLSGVGGLR		1357.6990	679.8568	2	-0.0046	
<1	7		AWAETLSSPAVAR		1357.6990	679.8568	2	-0.0046	
<1	7		CLQLLASSAEPAR		1357.7024	679.8565	2	-0.0080	

Precursor MS Region

No Data Showing



4

Spectrum information					Identification			Peptide Conf	
Sample	Fraction	Scan	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	5	3792	2	679.8591	-0.00927	RTSVCPRTWPR	10	73.85	98.08

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
39.1.1.3792.1		1357.6945	679.8545	2	928	RTSVCPRTWPR		98.1	1357.7037	2

Peptide ID Hypotheses - 39.1.1.3792.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
98.1	10	928	RTSVCPRTWPR		1357.7037	679.8591	2	-0.0093
<1	7	7, 20, ...	QSVVEADINGLRR	Deamidated(N)@8	1357.6949	679.8548	2	-0.0005
<1	7	19	QTVEADVINGLRR	Deamidated(N)@8	1357.6949	679.8548	2	-0.0005
<1	6	1081	KLCLDQTPTSRPR		1357.7024	679.8585	2	-0.0079
<1	5	1196	ACRELGGLDLPTR		1357.6772	679.8459	2	0.0172
<1	7	1463	QLSEDRGLR	Deamidated(Q)@8	1357.7062	679.8604	2	-0.0118
<1	7	1524	GEKREVEERLGR		1357.6949	679.8548	2	-0.0005
<1	6	1752	GESLQPSDSLVAR		1357.6837	679.8492	2	0.0107

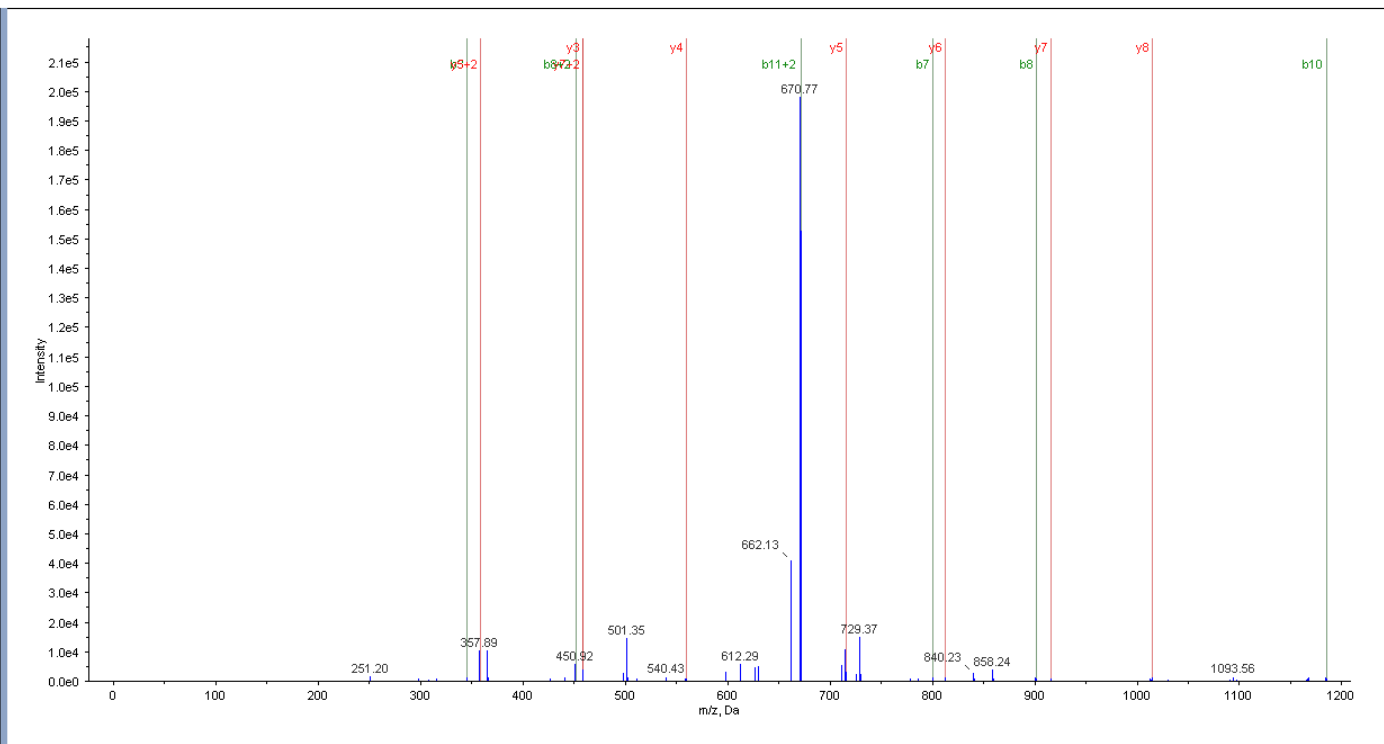
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

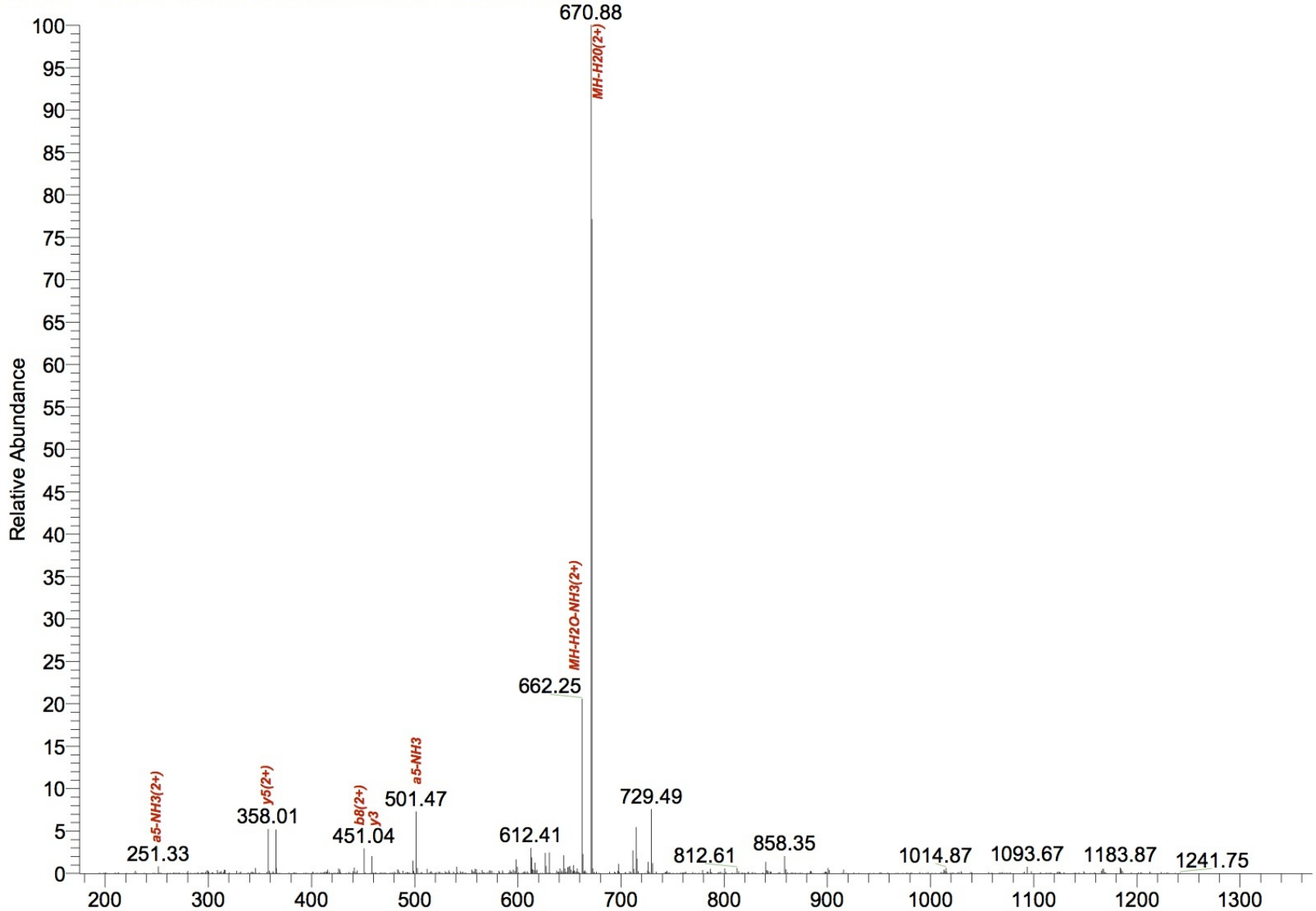
RTSVCPRTWPR

Residue	b	b+2	y	y+2
R	157.1084	79.0578	1358.7110	679.8591
T	258.1561	129.5817	1202.6099	601.8086
S	345.1884	173.0977	1101.5622	551.2847
V	444.2565	222.6319	1014.5302	507.7687
C	547.2657	274.1365	915.4618	458.2345
P	644.3185	322.6629	812.4526	406.7299
R	806.4196	400.7134	715.3998	358.2035
T	901.4672	451.2373	559.2987	280.1530
WV	1067.5466	544.2769	458.2510	229.6292
P	1184.5993	592.8033	272.1717	136.5895
R	1340.7004	670.8539	175.1190	88.0631



4

Spectrum information					Identification			Peptide Conf	
Sample	Fraction	Scan	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	5	3792	2	679.8591	-0.00927	RTSVCPRTWPR	10	73.85	98.08



4

Spectrum information					Identification			Peptide Conf	
Sample	Fraction	Scan	Charge	Theor m/z	Δ Mass	Sequence	Sc	One Step Method	Two Step Method
6	5	3792	2	679.8591	-0.00927	RTSVCPTWPR	10	73.85	98.08

Metaproteomics (Identified in one-step but not by two-step method)

Spectrum	One Step Method	Conf	Sc	Two Step Method	Conf	Sc	Reason why it was not identified in two step method
18.1.1.3933.1	NNEDEIAGK	97.6	11	DLTEQQQK	17.3	8	Protein present in second step database. Reason unknown.
19.1.1.2087.1	AEAPAAPAQEAPK	99	13	HPFQPWVNPk	6.0	1	Protein present in second step database. Reason unknown.
19.1.1.6769.1	IALTPVAIAAGR	99	13	ALLTPVAIAAGR	99.0	13	Not detected in the first step.
19.1.1.7363.1	VQIVGDDLfVTNPER	97.4	13	VQLVGDDLfVTNPER	99.0	13	Not detected in the first step.
19.1.1.7502.1	GDMGIEVPFEMVPVYQK	99	16	QT ANLHAEPDYLEVLEQ	8.0	1	Protein present in second step database. Reason unknown.
19.1.1.8053.1	VAQEEIFGPVATVIK	96.4	12	VQLYGPTNVAPIISK	12.4	8	Protein present in second step database. Reason unknown.
33.1.1.4545.1	ASGEVPLDVAPQK	99	15	AKDNAVMSTRFK	76.5	9	Protein present in second step database. Reason unknown.

- Workflow Tasks
- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...
- MGF Peaklist(s)...

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
18.1.1.3933.1		0.0000	495.2484	0	924	NNEDEIAGK		97.6	986.4462	2

Peptide ID Hypotheses - 18.1.1.3933.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
97.6	11	924	NNEDEIAGK		986.4462	495.2303	2	0.0361
<1	10		DIEDELKK		988.5077	495.2611	2	-0.0254
<1	10		DLEDEIQK		988.4713	495.2429	2	0.0110
<1	10		DLEDEIQK		988.4713	495.2429	2	0.0110
<1	10		DLEEDIAGK		988.4713	495.2429	2	0.0110

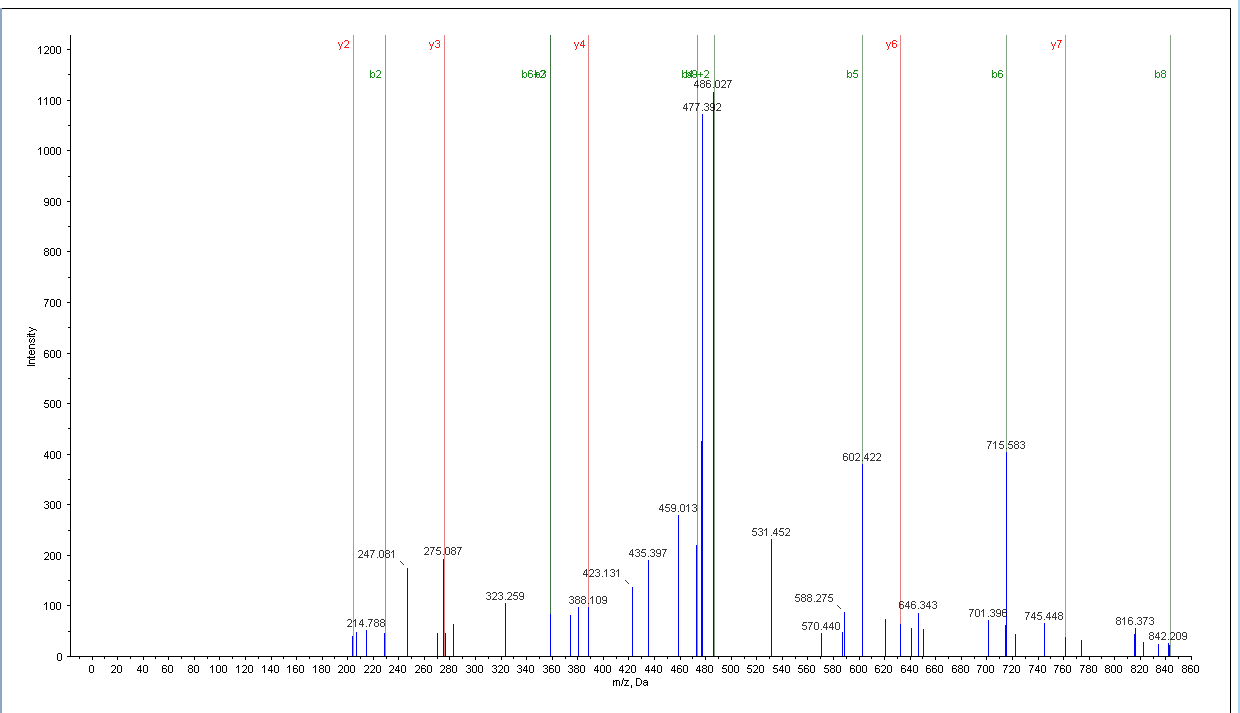
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

NNEDEIAGK

Residue	b	b+2	y	y+2
N	115.0502	58.0287	989.4534	495.2304
N	229.0931	115.0502	875.4105	438.2089
E	358.1357	179.5715	761.3676	381.1874
D	473.1627	237.0850	632.3259	316.6661
E	602.2053	301.6063	517.2980	259.1527
I	715.2893	358.1483	388.2554	194.6314
A	786.3264	393.6669	275.1714	138.0893
G	843.3479	422.1776	204.1343	102.5708
K	971.4429	486.2251	147.1128	74.0600



Spectrum	One Step Method	Conf	Sc
18.1.1.3933.1	NNEDEIAGK	97.6	11

Protein ID										Spectra										Summary Statistics									
Workflow Tasks																													
Identify Proteins																													
LC...																													
Spot-Based (MS only)...																													
Spot-Based (MS and MS/MS)...																													
View																													
Analysis Log...																													
Result...																													
Export																													
Peptide Summary...																													
Protein Summary...																													
MGF Peaklist(s)...																													

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
18.1.1.3933.1		0.0000	495.2485	0		DLTEQQQK		17.3	988.4825	2

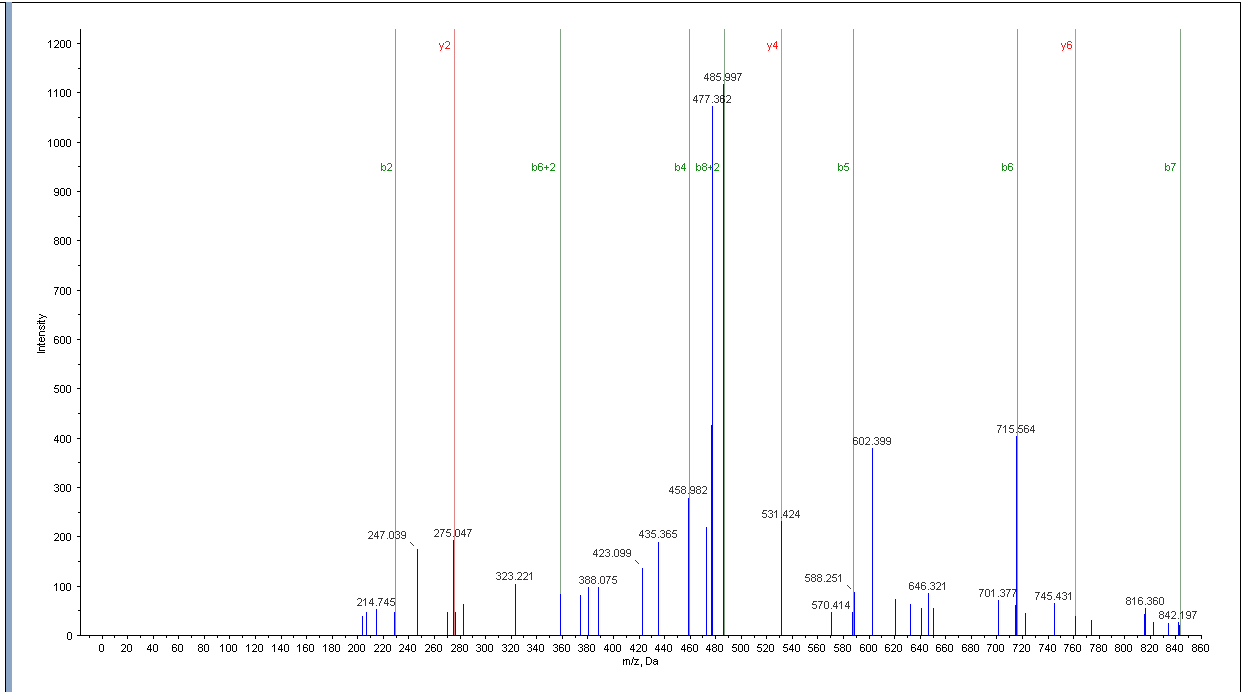
Peptide ID Hypotheses - 18.1.1.3933.1									
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass	
17.3	8		DLTEQQQK		988.4825	495.2485	2	0.0022	
14.2	8	842	ENSAEAIQK		988.4825	495.2485	2	0.0022	
14.2	8		VDELAATR		988.4825	495.2485	2	0.0022	
5	8		NLENIEEK	Deamidated(N)@1	988.4713	495.2429	2	0.0134	
4.9	7		ETLQDQK		988.4825	495.2485	2	0.0022	
<1	7	156	MEINELTR	Deamidated(N)@1	988.4825	495.2485	2	0.0022	

Precursor MS Region				
No Data Showing				

Fragmentation Evidence for Peptide

DLTEQQQK

Residue	b	b+2	y	y+2
D	116.0342	58.5207	989.4898	495.2485
L	229.1183	115.0628	874.4629	437.7351
T	330.1660	165.5866	761.3788	381.1930
E	459.2086	230.1079	660.3311	330.6692
Q	587.2671	294.1372	531.2885	266.1479
Q	715.3257	358.1665	403.2300	202.1186
Q	843.3843	422.1958	275.1714	138.0893
K	971.4793	486.2433	147.1128	74.0600



Spectrum	Two Step Method	Conf	Sc
18.1.1.3933.1	DLTEQQQK	17.3	8

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...
- MGF Peaklist(s)...

Protein ID						Spectra				Summary Statistics	
Spectrum List											
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z	
19.1.1.2087.1		1249.6300	625.8223	2	810	AEAPAAPAQEAPK		99	1249.6302	2	

Peptide ID Hypotheses - 19.1.1.2087.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	13	810	AEAPAAPAQEAPK		1249.6302	625.8224	2	-0.0002
<1	7		QD IYDQ IKAR	Deamidated(O)@5	1249.6302	625.8224	2	-0.0002
<1	7		QD QP IRHEVK	Deamidated(O)@3	1249.6415	625.8280	2	-0.0115
<1	6		AEHRFLQAR		1249.6238	625.8192	2	0.0063
<1	6		AGDEGRYIKMK		1249.6415	625.8280	2	-0.0115

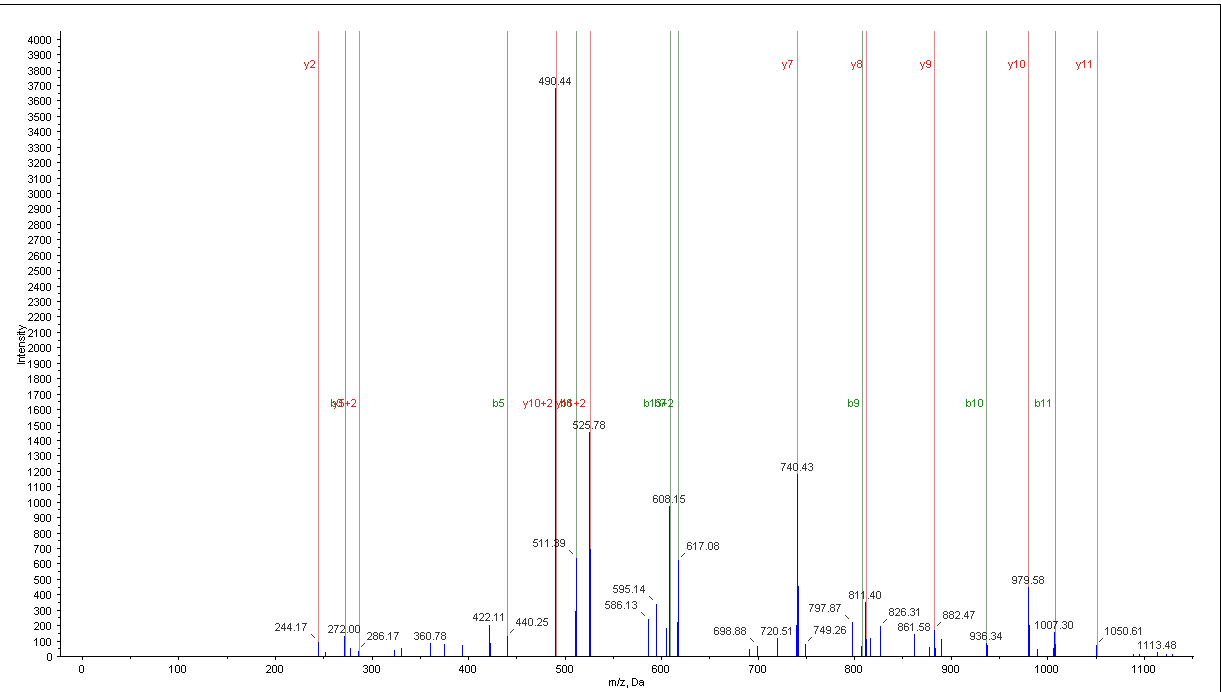
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

AEAPAAPAQEAPK

Residue	b	b+2	y	y+2
A	72.0444	36.5258	1250.6375	625.8224
E	201.0870	101.0471	1179.6004	590.3039
A	272.1241	136.5657	1050.5578	525.7826
P	369.1769	185.0921	979.5207	490.2640
A	440.2140	220.6106	882.4680	441.7376
A	511.2511	256.1292	811.4308	406.2191
P	608.3039	304.6556	740.3937	370.7005
A	679.3410	340.1741	643.3410	322.1741
Q	807.3995	404.2034	572.3039	286.6556
E	936.4421	468.2247	444.2453	222.6263
A	1007.4793	504.2433	315.2027	158.1050
P	1104.5320	552.7696	244.1656	122.5864
K	1232.6270	616.8171	147.1128	74.0600



Spectrum	One Step Method	Conf	Sc
19.1.1.2087.1	AEAPAAPAQEAPK	99	13

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...
- MGF Peaklist(s)...

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
19.1.1.2087.1		1249.6300	625.8223	2		HPFQPWVNP	Deamidated(O)@4	<1	1249.6244	2

Peptide ID Hypotheses - 19.1.1.2087.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
<1	6		HPFQPWVNP	Deamidated(O)@4	1249.6244	625.8195	2	0.0056
<1	6		KSPANEFAFPR		1249.6415	625.8280	2	-0.0115
<1	5		HRETLDPSAFK		1249.6415	625.8280	2	-0.0115
<1	5		KGECLSRSGAAR		1249.6198	625.8171	2	0.0103
<1	4		EFNYVSHAKR		1249.6204	625.8174	2	0.0096

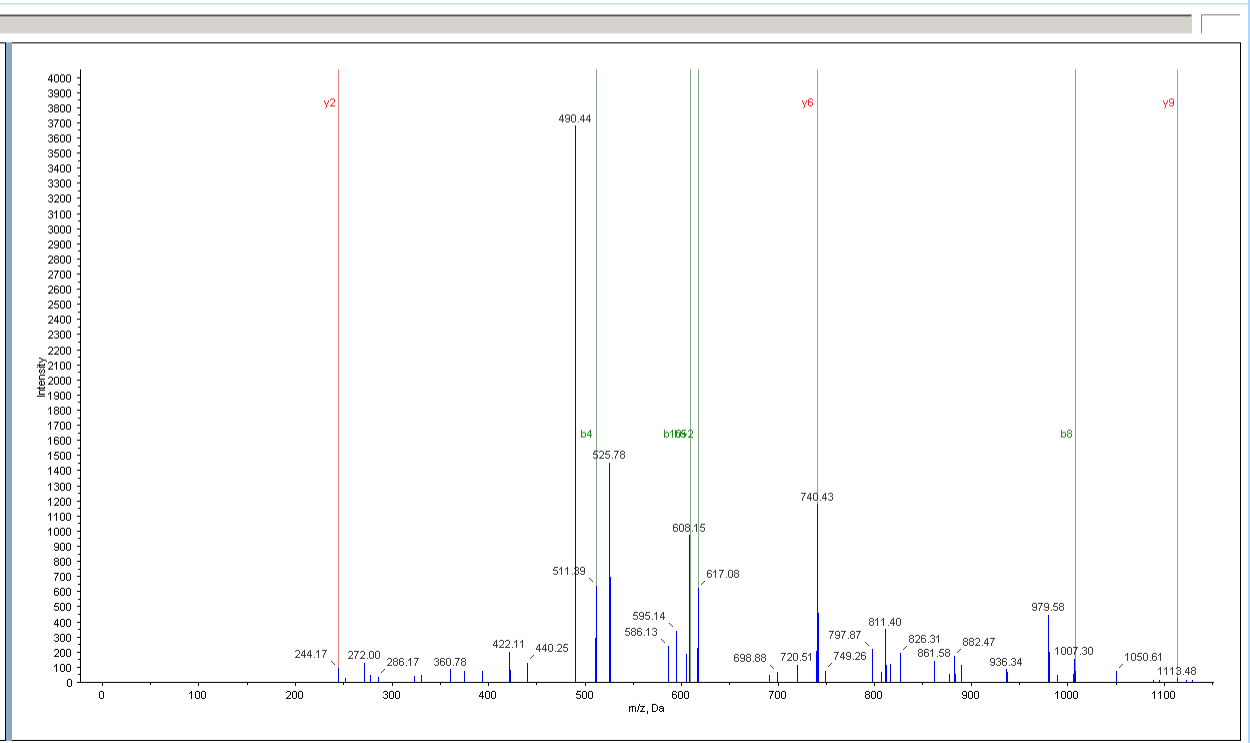
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

HPFQ[Dea]PWWNP

Residue	b	b+2	y	y+2
H	138.0662	69.5367	1250.6317	625.8195
P	235.1190	118.0631	1113.5728	557.2900
F	382.1874	191.5973	1016.5200	508.7636
Q[Dea]	511.2300	256.1186	869.4516	435.2294
P	608.2827	304.6450	740.4090	370.7081
W	794.3620	397.6847	643.3562	322.1817
V	893.4304	447.2189	457.2769	229.1421
N	1007.4734	504.2403	358.2085	179.6079
P	1104.5261	552.7667	244.1656	122.5864
K	1232.6211	616.8142	147.1128	74.0600



Spectrum	Two Step Method	Conf	Sc
19.1.1.2087.1	HPFQPWVNP	6.0	1

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...
- MGF Peaklist(s)...

Protein ID

Spectra

Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
19.1.1.6769.1		1151.7028	576.8587	2	774	IALTPVAIAAGR		99	1151.7026	2

Peptide ID Hypotheses - 19.1.1.6769.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	13	774	IALTPVAIAAGR		1151.7026	576.8586	2	0.0001
99	13		ALLTPVAIAAGR		1151.7026	576.8586	2	0.0001
<1	7		ALIRLDPAK		1151.7139	576.8642	2	-0.0111
<1	7		LRQFPAAGR		1151.7000	576.8572	2	0.0028
<1	6		ALIVGGTRPIR		1151.7139	576.8642	2	-0.0111

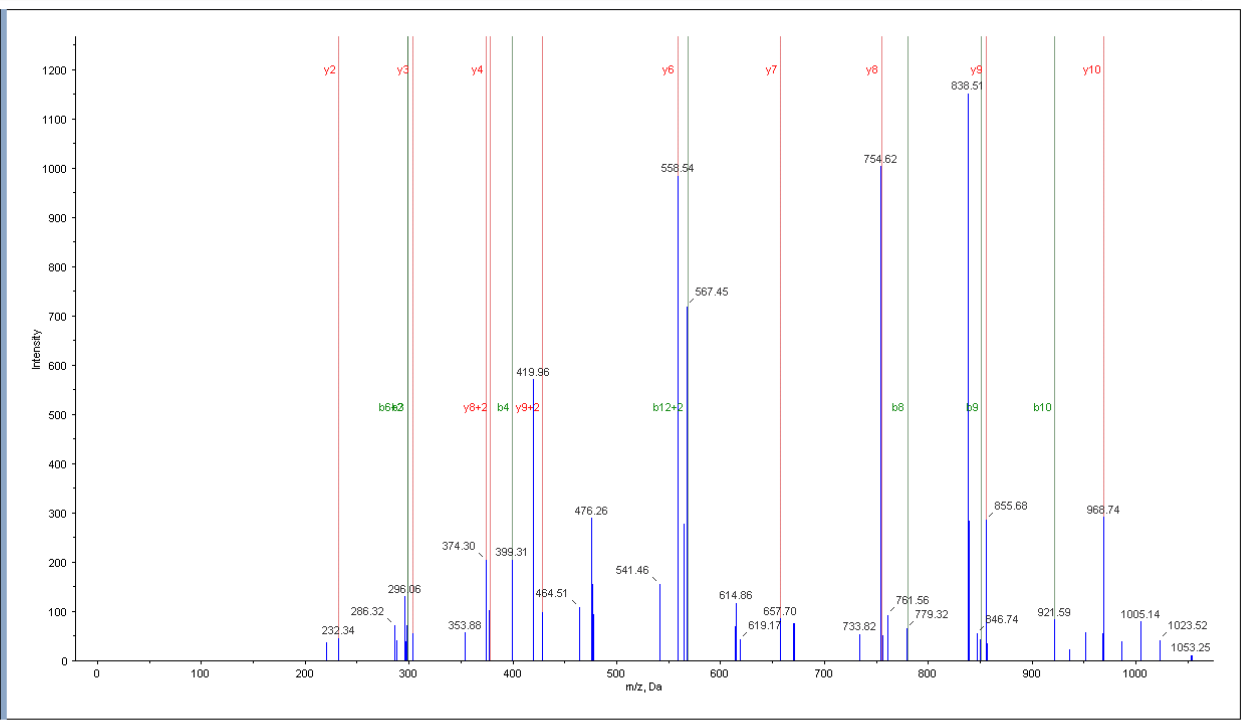
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

IALTPVAIAAGR

Residue	b	b+2	y	y+2
I	114.0913	57.5493	1152.7099	576.8586
A	185.1265	93.0679	1039.6259	520.3166
L	298.2125	149.6099	968.5887	484.7990
T	399.2682	200.1337	855.5047	428.2560
P	496.3130	248.6601	754.4570	377.7321
V	595.3814	298.1943	657.4042	329.2058
A	686.4185	333.7129	568.3358	279.6715
I	779.5026	390.2549	487.2967	244.1530
A	858.5397	425.7735	374.2146	187.6110
A	921.5768	461.2920	303.1775	152.0924
G	978.5982	489.8028	232.1404	116.5738
R	1134.6994	567.8533	175.1190	88.0631



Spectrum	One Step Method	Conf	Sc
19.1.1.6769.1	IALTPVAIAAGR	99	13

Workflow Tasks

Identify Proteins

LC...

Spot-Based (MS only)...

Spot-Based (MS and MS/MS)...

View

Analysis Log...

Result...

Export

Peptide Summary...

Protein Summary...

MGF Peaklist(s)...

Protein ID		Spectra				Summary Statistics				
Spectrum List										
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
19.1.1.6769.1		1151.7028	576.8537	2	875	ALLTPVAIAAGR		99	1151.7026	2

Peptide ID Hypotheses - 19.1.1.6769.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	13	875	ALLTPVAIAAGR		1151.7026	576.8536	2	0.0001
<1	5		KRPRLQAQR		1151.7000	576.8572	2	0.0028
<1	5		QAPKIAQIKR		1151.7139	576.8642	2	-0.0111
<1	4		ALIGNILATGLP		1151.6914	576.8530	2	0.0113
<1	4		LKAVNGPVAKR		1151.7139	576.8642	2	-0.0111

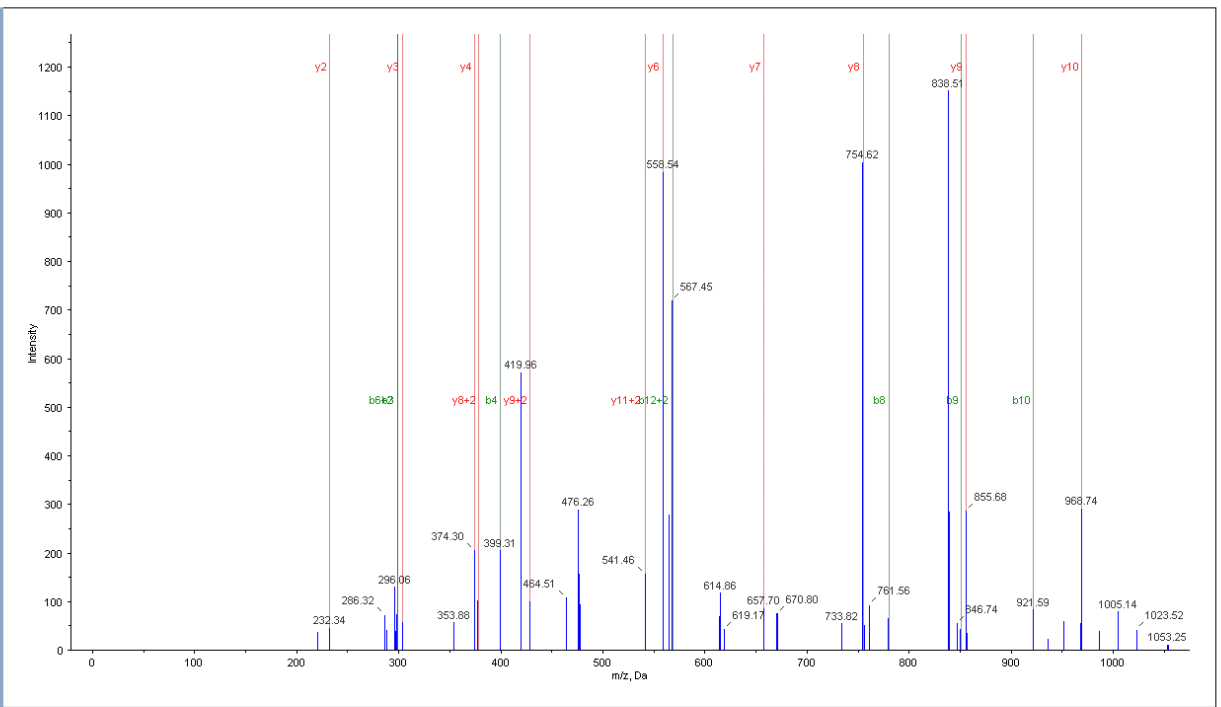
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

ALLTPVAIAAGR

Residue	b	b+2	y	y+2
A	72.0444	96.5258	1152.7099	576.8596
L	185.1285	93.0679	1081.6728	541.3488
L	298.2125	149.6099	968.5887	484.7960
T	399.2602	200.1337	855.5047	428.2568
P	496.3130	248.6801	754.4678	377.7321
V	595.3814	298.1943	657.4042	329.2058
A	666.4185	333.7129	558.3358	279.6715
I	779.5026	390.2549	487.2987	244.1530
A	850.5397	425.7735	374.2146	187.6110
A	921.5768	461.2920	303.1775	152.0924
G	978.5982	489.8028	232.1404	116.5738
R	1134.6994	567.8533	175.1190	88.0631



Spectrum	Two Step Method	Conf	Sc
19.1.1.6769.1	ALLTPVAIAAGR	99.0	13

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...
- MGF Peaklist(s)...

Protein ID Spectra Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
19.1.1.7363.1		1700.8761	851.4453	2	929	VQIVGDDLFVTNPER		97.4	1700.8733	2

Peptide ID Hypotheses - 19.1.1.7363.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
97.4	13	929	VQIVGDDLFVTNPER		1700.8733	851.4440	2	0.0027
97.4	13		VQIVGDDIFVTNPER		1700.8733	851.4440	2	0.0027
97.4	13		VQIVGDDLFVTNPER		1700.8733	851.4440	2	0.0027
<1	9	1596	ALNTNGHLDNKAAVTYK	Deamidated(N)@3	1700.8694	851.4420	2	0.0067
<1	7	1765	CLLKSI GA E V P D E A E K		1700.8655	851.4400	2	0.0105
<1	10		GENYDVAMTLIRLAR	Deamidated(N)@3	1700.8846	851.4496	2	-0.0086
<1	9		EASLPSTVEEVGDIKK		1700.8833	851.4469	2	-0.0072

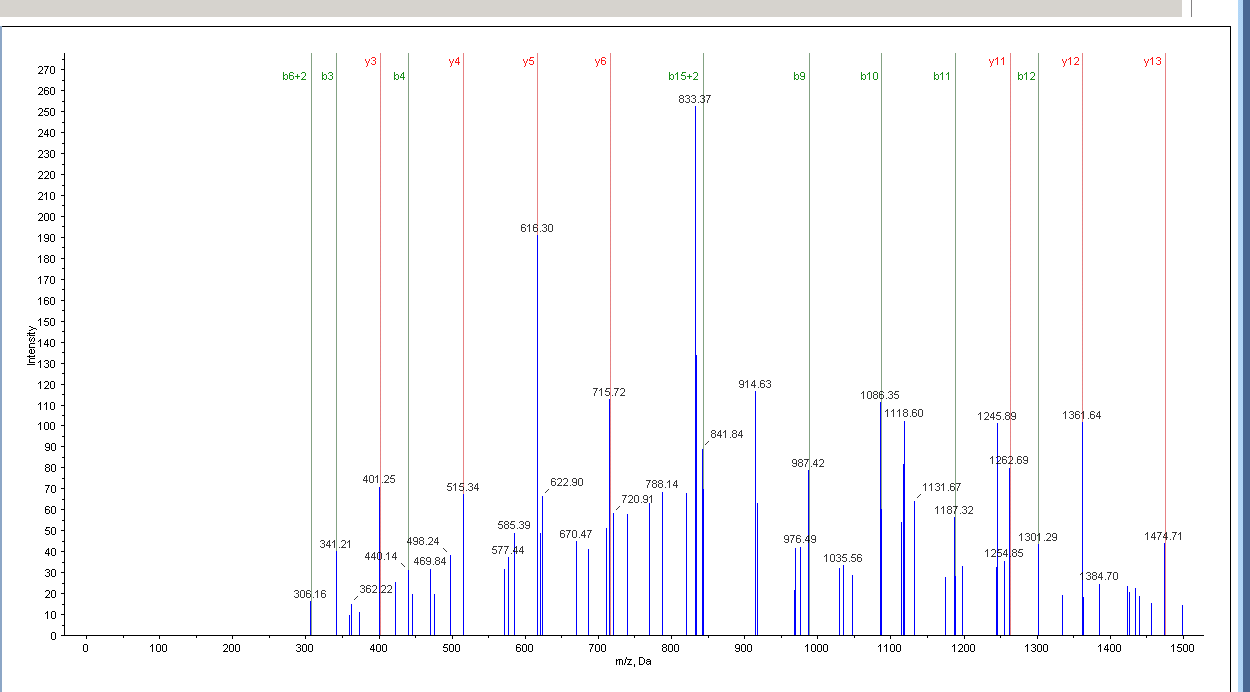
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

VQIVGDDLFVTNPER

Residue	b	b+2	y	y+2
V	100.0757	50.5415	1701.8906	851.4440
Q	228.1343	114.5708	1602.8122	801.9097
I	341.2183	171.1128	1474.7536	737.8805
V	440.2867	220.6470	1361.6696	681.3384
G	497.3082	249.1577	1262.6012	631.8042
D	612.3352	306.6712	1205.5797	603.2935
D	727.3621	364.1847	1090.5527	545.7800
L	840.4462	420.7267	975.5258	488.2665
F	987.6146	494.2609	862.4417	431.7245
V	1086.6830	543.7951	715.3733	358.1903
T	1187.6307	594.3190	616.3049	308.6561
N	1301.6738	651.3404	516.2572	258.1323
P	1398.7264	699.8668	401.2143	201.1108
E	1527.7690	764.3881	304.1815	152.5844
R	1683.8701	842.4387	175.1190	88.0631



Spectrum	One Step Method	Conf	Sc
19.1.1.7363.1	VQIVGDDLFVTNPER	97.4	13

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...
- MGF Peaklist(s)...

Protein ID										Spectra										Summary Statistics									
Spectrum List																													
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence										Modifications										Conf	Theor MW	z	
19.1.1.7363.1		1700.8761	851.4453	2	1007	VQLVGDDLFTNPER																				98	1700.8733	2	

Peptide ID Hypotheses - 19.1.1.7363.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
98	13	1007	VQLVGDDLFTNPER		1700.8733	851.4440	2	0.0027
<1	7		KGLPSSCLESRGPAAEK		1700.8767	851.4456	2	-0.0007
<1	7		WTLNSGKAREWTPR		1700.8746	851.4446	2	-0.0013
<1	6		ERDRIDPSAASILMK		1700.8879	851.4512	2	-0.0119
<1	6		IESGQLSLEPAAFSPR		1700.8733	851.4440	2	0.0027

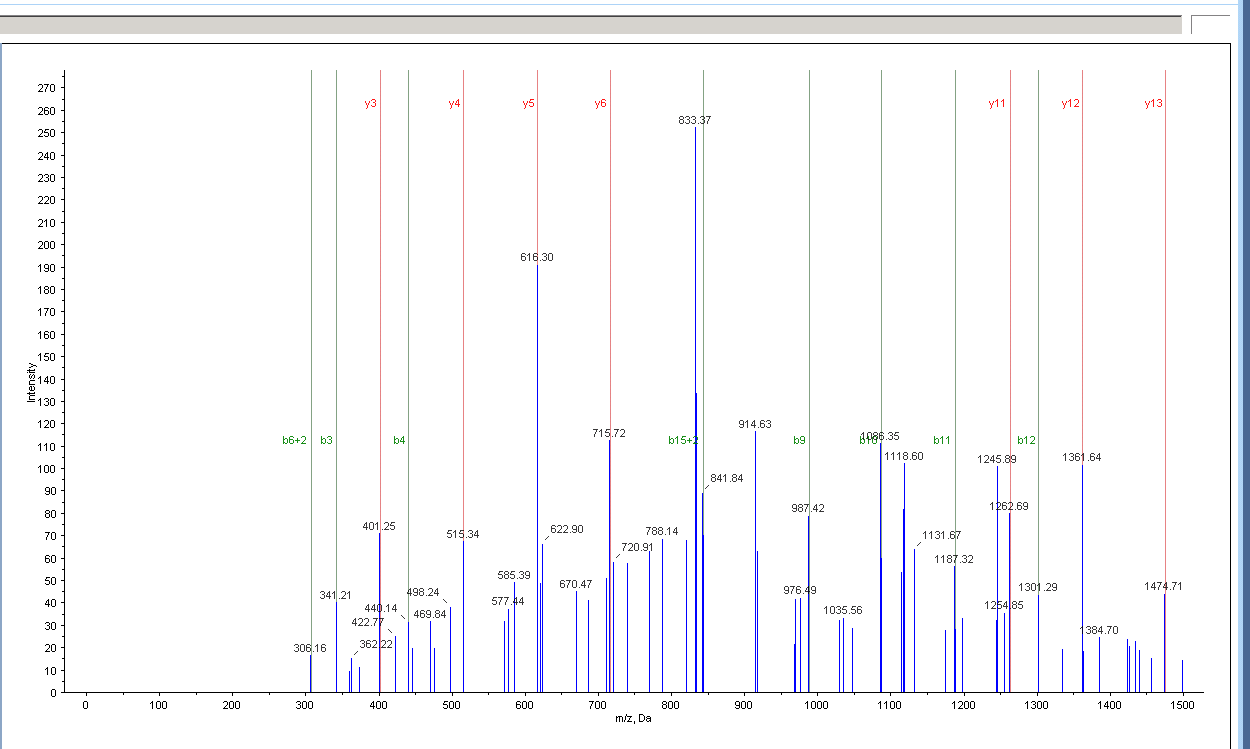
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

VQLVGDDLFTNPER

Residue	b	b+2	y	y+2
V	100.0757	50.5415	1701.8806	851.4440
Q	228.1343	114.5708	1602.8122	801.9097
L	341.2183	171.1128	1474.7536	737.8805
V	440.2867	220.6470	1361.6696	681.3384
G	497.3082	249.1577	1262.6012	631.8042
D	612.3352	306.6712	1205.5797	603.2935
D	727.3621	364.1847	1090.5527	545.7800
L	840.4462	420.7267	975.5258	488.2665
F	987.5146	494.2609	862.4417	431.7245
V	1086.5830	543.7951	715.3733	358.1903
T	1187.6307	594.3190	616.3049	308.6561
N	1301.6736	651.3404	515.2572	258.1323
P	1398.7264	699.8668	401.2143	201.1108
E	1527.7690	764.3881	304.1815	152.5844
R	1683.8701	842.4387	175.1190	88.0631



Spectrum	Two Step Method	Conf	Sc
19.1.1.7363.1	VQLVGDDLFTNPER	99.0	13

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
19.1.1.7502.1		1969.9125	985.9635	2	911	GDMGIEVVPFEMVPPVYQK	Oxidation(M)@3, Oxidation(...)	99	1969.9165	2

Peptide ID Hypotheses - 19.1.1.7502.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	16	911	GDMGIEVVPFEMVPPVYQK	Oxidation(M)@3, Oxidation(...)	1969.9165	985.9655	2	-0.0041
<1	16		GDMGIEVVPFEMVPPVYQK	Oxidation(M)@3, Oxidation(...)	1969.9165	985.9655	2	-0.0041
<1	8		ANLHAEFDYLVLEQQT	Deamidated(O)@16	1969.9269	985.9707	2	-0.0145
<1	8		DTCLVDAAAGFNQISNMKK	Oxidation(M)@16	1969.9237	985.9692	2	-0.0113
<1	8		FDIHSLLDRETMMDYR	Oxidation(M)@4	1969.9237	985.9692	2	-0.0113

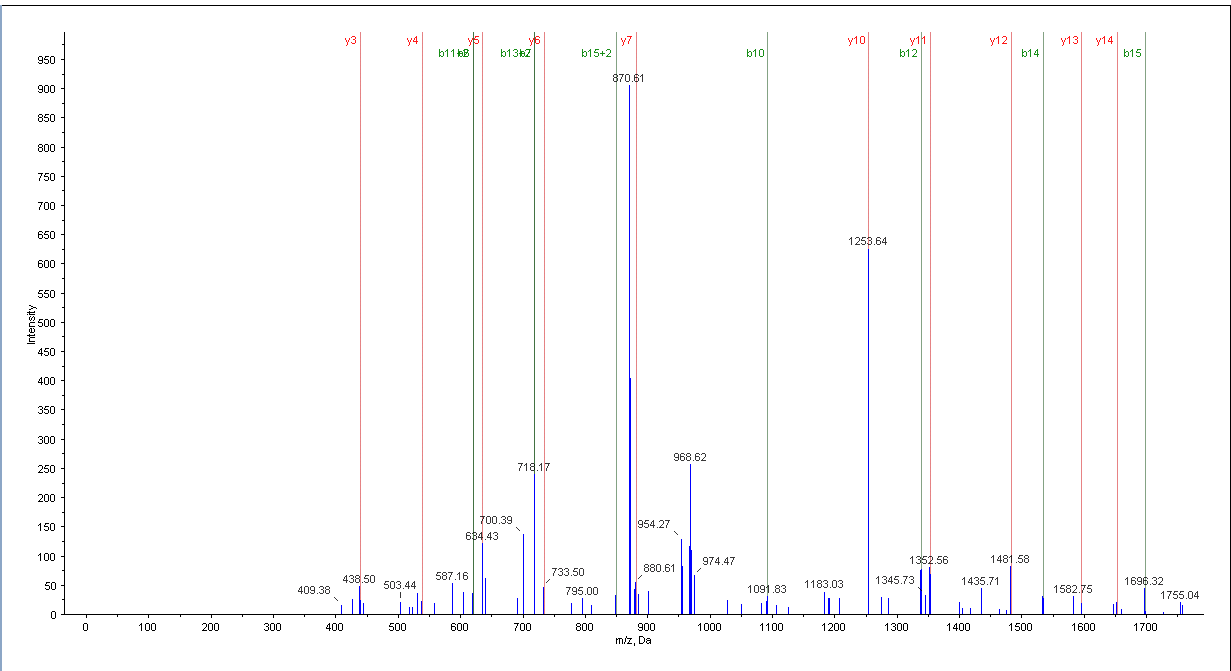
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

[GDM(Ox)]GIEVVPFEM(Ox)VPVYQK

Residue	b	b+2	y	y+2
G	58.0287	29.5180	1970.9236	985.9655
D	173.0557	87.0315	1913.9023	957.4548
M(Ox)	320.0911	160.5452	1798.8754	899.9413
G	377.1125	189.0599	1651.8400	826.4236
I	490.1966	245.6019	1594.8185	797.9129
E	619.2392	310.1232	1481.7345	741.3709
V	718.3076	359.8574	1352.6919	676.8496
P	815.3604	408.1838	1253.6235	627.3154
F	962.4288	481.7180	1156.5707	578.7890
E	1091.4714	546.2393	1009.5023	505.2548
M(Ox)	1238.5068	619.7570	880.4597	440.7335
V	1337.5752	669.2912	733.4243	367.2158
P	1434.6280	717.8176	634.3559	317.6816
V	1533.6964	767.3518	537.3031	269.1552
Y	1696.7597	848.8835	438.2347	219.6210
Q	1824.8183	912.9128	275.1714	138.0893
K	1952.9132	976.9603	147.1128	74.0600



Spectrum 19.1.1.7502.1 **One Step Method** GDMGIEVVPFEMVPPVYQK **Conf** 99 **Sc** 16

Protein ID	Spectra	Summary Statistics
Spectrum List		
Spectrum ▾	Time	Prec MW Prec m/z Prec z Prot N Best Sequence Modifications Conf Theor MW z
19.1.1.7502.1		1969.9125 985.9635 2 ANLHAE PDYLEVLEQQT Deamidated(Q)@16 <1 1969.9268 2
Peptide ID Hypotheses - 19.1.1.7502.1		
Conf ▾	Sc	Prot N Sequence Modifications Theor MW Theor m/z z ΔMass ▾
<1	8	ANLHAE PDYLEVLEQQT Deamidated(Q)@16 1969.9268 985.9707 2 -0.0145
<1	6	SFKKNIDSI SSEEQSDR Deamidated(Q)@14 1969.9228 985.9687 2 -0.0104
<1	6	SSHNF PFIIG LLEDINAM Deamidated(N)@16 1969.9092 985.9619 2 0.0033
<1	4	DCMHFCHEVTR LHSYK 1969.9073 985.9609 2 0.0051
<1	4	GELQPD SRAAE SPPRETY 1969.9164 985.9655 2 -0.0039
Precursor MS Region		
No Data Showing		

Fragmentation Evidence for Peptide				
ANLHAE PDYLEVLEQQT[Dea]T				
Residue	b	b+2	y	y+2
A	72.0444	36.5258	1970.9342	985.9707
N	186.0873	93.5473	1899.8971	950.4522
L	299.1714	150.0893	1785.8541	893.4307
H	436.2303	218.6188	1672.7701	836.8887
A	507.2674	254.1373	1535.7112	768.3592
E	636.3100	318.6586	1464.6740	732.8407
P	733.3628	367.1850	1335.6315	668.3194
D	848.3897	424.6985	1238.5797	619.7930
Y	1011.4530	506.2302	1123.5517	562.2795
L	1124.5371	562.7722	960.4884	480.7478
E	1253.5797	627.2935	847.4044	424.2058
V	1352.6481	676.8277	718.3618	359.6845
L	1485.7322	733.3697	619.2933	310.1503
E	1594.7748	797.8910	506.2093	253.6083
Q	1722.8333	861.9203	377.1667	189.0870
Q[Dea]	1851.8759	926.4416	249.1081	125.0577
T	1952.9236	976.9654	120.0655	60.5364

Spectrum	Two Step Method	Conf	Sc
19.1.1.7502.1	ANLHAE PDYLEVLEQQT	8.0	1

Workflow Tasks

Identify Proteins

LC...

Spot-Based (MS only)...

Spot-Based (MS and MS/MS)...

View

Analysis Log...

Result...

Export

Peptide Summary...

Protein Summary...

MGF Peaklist(s)...

Protein ID						Spectra				Summary Statistics	
Spectrum List											
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z	
19.1.1.8053.1		1599.8872	800.9509	2	962	VAQEEIFGPVATVIK		96.4	1599.8872	2	

Peptide ID Hypotheses - 19.1.1.8053.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
96.4	12	962	VAQEEIFGPVATVIK		1599.8872	800.9509	2	0.0000
<1	8		DLVVKD SRN ID VVK	Deamidated(N)@9	1599.8832	800.9489	2	0.0041
<1	8		LINSKI IIDNGSADK		1599.8832	800.9489	2	0.0041
<1	8		VQLYGFTRVAP IISK	Deamidated(N)@8	1599.8872	800.9509	2	0.0000
<1	7		AREVIDTMLETVLK		1599.8832	800.9489	2	0.0041

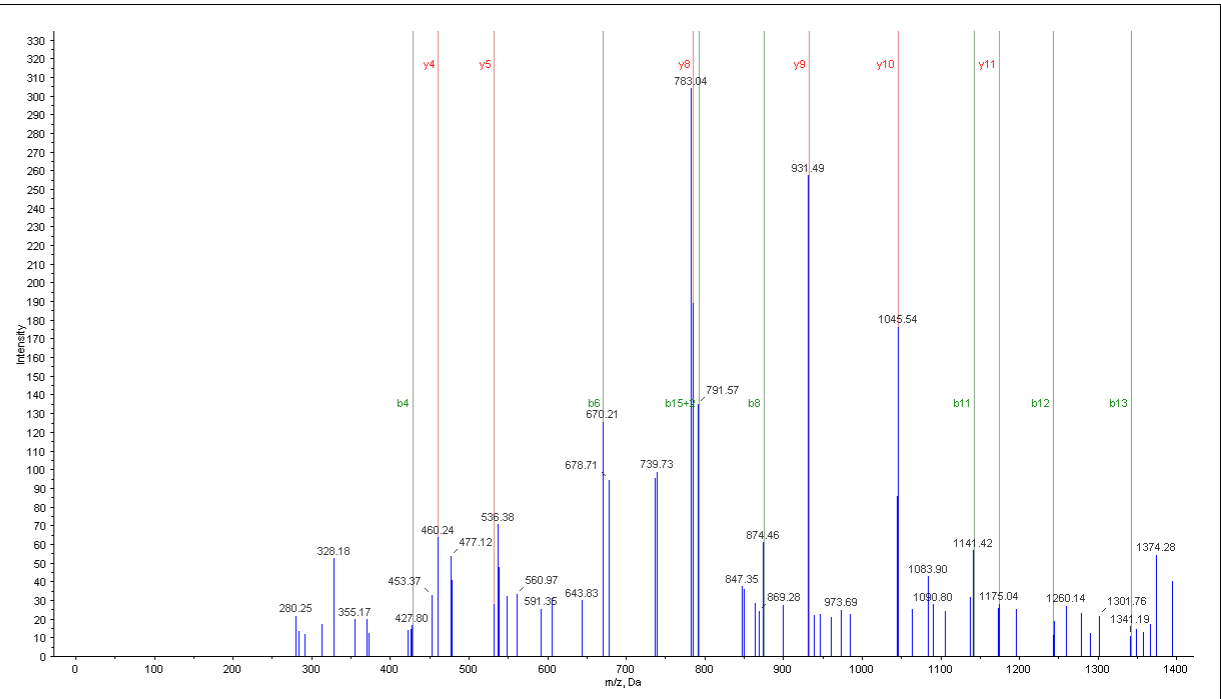
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

VAQEEIFGPVATVIK

Residue	b	b+2	y	y+2
V	100.0757	50.5415	1600.8945	800.9509
A	171.1128	86.0600	1501.8261	751.4167
Q	299.1714	150.0893	1430.7890	715.8981
E	428.2140	214.6106	1302.7304	651.8688
E	557.2566	279.1319	1173.6678	587.3475
I	670.3406	335.6740	1044.6452	522.8262
F	817.4090	409.2082	931.5611	466.2842
G	874.4305	437.7189	784.4927	392.7500
P	971.4833	486.2453	727.4713	364.2393
V	1070.5517	535.7795	630.4185	315.7129
A	1141.5888	571.2980	531.3501	266.1787
T	1242.6365	621.8219	460.3130	230.6601
V	1341.7049	671.3561	359.2653	180.1363
I	1454.7890	727.8981	260.1969	130.6021
K	1582.8839	791.9456	147.1128	74.0600



Spectrum	One Step Method	Conf	Sc
19.1.1.8053.1	VAQEEIFGPVATVIK	96.4	12

- Workflow Tasks
- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...
- MGF Peaklist(s)...

Protein ID		Spectra					Summary Statistics			
Spectrum List										
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot H	Best Sequence	Modifications	Conf	Theor MW	z
19.1.1.8053.1		1599.8873	800.9509	2		VQLYGPTNVAPIISK	Deamidated(N)@6	12.4	1599.8872	2

Peptide ID Hypotheses - 19.1.1.8053.1									
Conf	Sc	Prot H	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass	
12.4	8		VQLYGPTNVAPIISK	Deamidated(N)@6	1599.8872	800.9509	2	0.0000	
<1	6		LNELQLNQSIVTLK		1599.8832	800.9489	2	0.0041	
<1	6		NQKLEIALTLDTK		1599.8832	800.9489	2	0.0041	
<1	6		TVVQIUSIVGTTIR	Deamidated(O)@5	1599.8984	800.9565	2	-0.0112	
<1	6		VIRESIERNKQA		1599.8733	800.9439	2	0.0140	

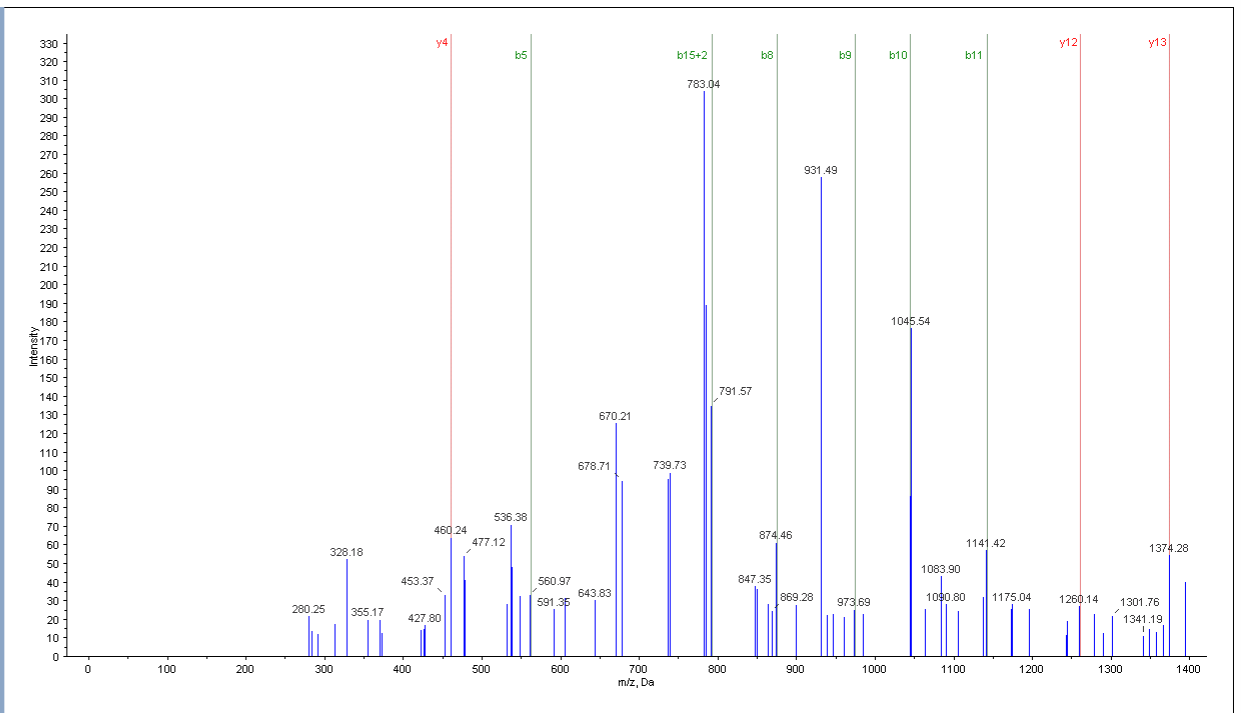
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

VQLYGPTN[Dea]VAPIISK

Residue	b	b+2	y	y+2
V	100.0757	50.5415	1800.8945	800.9509
Q	228.1343	114.5708	1501.8261	751.4167
L	341.2183	171.1128	1373.7675	687.3874
Y	504.2817	252.6445	1260.6834	630.8454
G	561.3031	281.1552	1097.6201	549.3137
P	658.3559	329.6816	1040.5986	520.8030
T	759.4036	380.2054	943.5459	472.2766
N[Dea]	874.4305	437.7189	842.4982	421.7527
V	873.4989	437.2531	727.4713	364.2393
A	1044.5360	522.7717	628.4028	314.7051
P	1141.5888	571.2980	557.3657	279.1865
I	1254.6729	627.8401	460.3130	230.6601
I	1367.7569	684.3821	347.2289	174.1181
S	1454.7890	727.8981	234.1448	117.5761
K	1582.8839	791.9456	147.1128	74.0600



Spectrum	Two Step Method	Conf	Sc
19.1.1.8053.1	VQLYGPTNVAPIISK	12.4	8

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...
- MGF Peaklist(s)...

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
33.1.1.4545.1		1366.7087	684.3616	2	27	ASGEVPLDVAPQGK		99	1366.7092	2

Peptide ID Hypotheses - 33.1.1.4545.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	15	27	ASGEVPLDVAPQGK		1366.7092	684.3619	2	-0.0006
<1	4	97	AHSSHWGVNLPQK		1366.7028	684.3586	2	0.0059
<1	4	528	SVTGTVDIVVFSK		1366.6980	684.3563	2	0.0106
<1	9		AKDNAVHSTRFK		1366.7028	684.3586	2	0.0059
<1	9		QASGVVYFLPLGK	Deamidated(O)@1	1366.7133	684.3639	2	-0.0046
<1	8		ESKTAHDFLMKK		1366.7205	684.3675	2	-0.0118
<1	8		QIFGAHDSALAVR	Gln->pyro-Glu@N-term	1366.6993	684.3569	2	0.0093

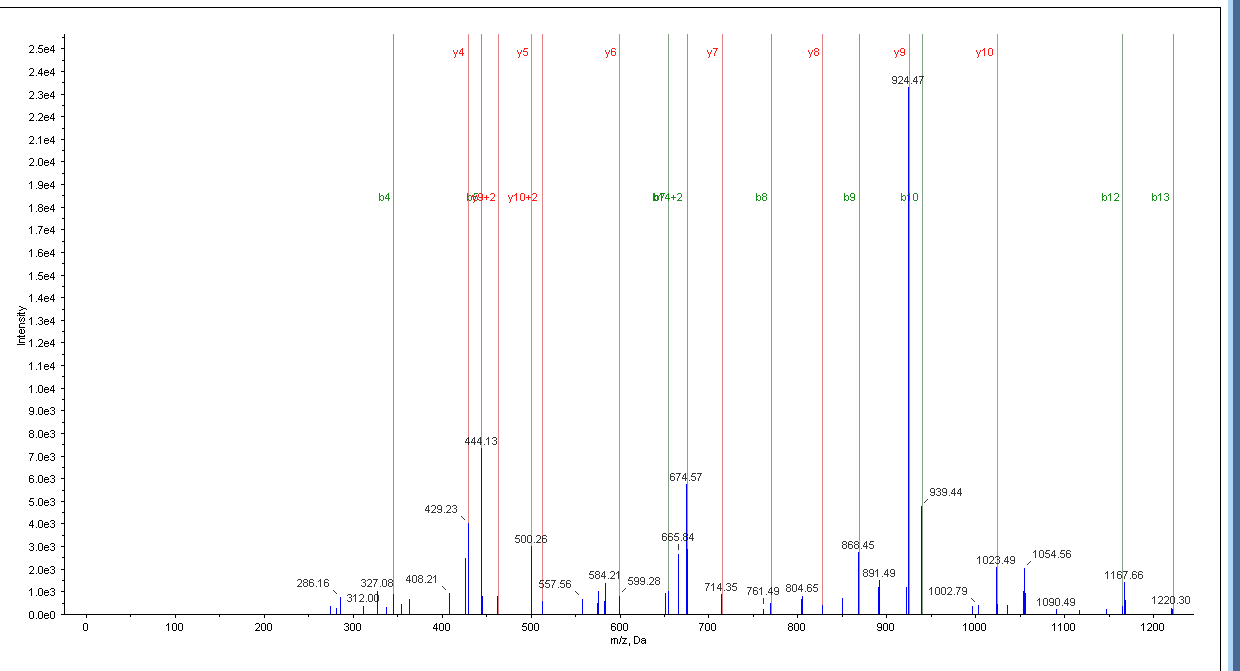
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

ASGEVPLDVAPQGK

Residue	b	b+2	y	y+2
A	72.0444	36.5258	1367.7185	684.3619
S	159.0764	80.0418	1296.6794	648.8433
G	216.0979	108.5526	1209.6474	605.3273
E	345.1405	173.0739	1152.6259	576.8166
V	444.2089	222.6081	1023.5833	512.2953
P	541.2617	271.1345	924.5149	462.7611
L	654.3457	327.6785	827.4621	414.2347
D	769.3727	385.1900	714.3781	357.6927
V	868.4411	434.7242	599.3511	300.1792
A	939.4782	470.2427	500.2827	250.6450
P	1036.5310	518.7691	429.2456	215.1264
Q	1164.5895	582.7984	332.1928	166.6001
G	1221.6110	611.3091	204.1343	102.5708
K	1349.7060	675.3566	147.1128	74.0600



Spectrum	One Step Method	Conf	Sc
33.1.1.4545.1	ASGEVPLDVAPQGK	99	15

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...
- MGF Peaklist(s)...

Protein ID		Spectra				Summary Statistics						
Spectrum List												
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications			Conf	Theor MW	z
33.1.1.4545.1		1366.7086	684.3616	2	2038	AKDNAVMSTRFK				76.5	1366.7028	2

Peptide ID Hypotheses - 33.1.1.4545.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
76.5	9	2038	AKDNAVMSTRFK		1366.7028	684.3586	2	0.0059
<1	4	90	AHSSMVGWMLPQK		1366.7028	684.3586	2	0.0059
<1	4	353	SVTGTVDVIVFSK		1366.6980	684.3563	2	0.0106
<1	6		FSQNSHLIKHR	Deamidated(N)@4	1366.7106	684.3625	2	-0.0019
<1	6		HRPQVLSMKFK	Oxidation(M)@6	1366.7180	684.3663	2	-0.0093
<1	6		RNVVDLDAASHR	Deamidated(N)@2	1366.6953	684.3549	2	0.0133
<1	6		TNKVYDITERK	Deamidated(N)@2	1366.7092	684.3619	2	-0.0006

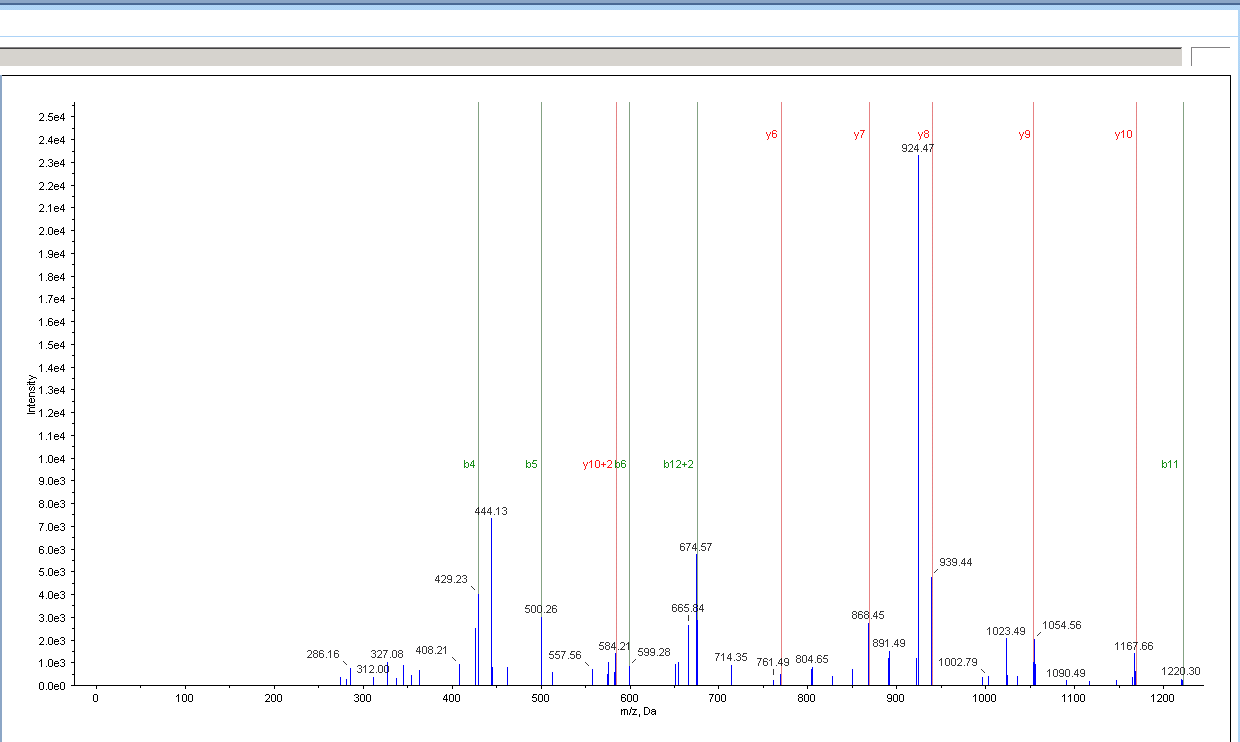
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

AKDNAVMSTRFK

Residue	b	b+2	y	y+2
A	72.0444	36.5258	1367.7100	684.3586
K	200.1394	100.5733	1296.6729	648.8401
D	315.1663	158.0868	1168.5779	584.7926
N	429.2092	215.1083	1053.5510	527.2791
A	500.2463	250.6268	938.5080	470.2577
V	599.3148	300.1610	868.4709	434.7391
M	730.3552	365.6813	769.4025	385.2049
S	817.3873	409.1973	638.3620	319.6847
T	918.4349	459.7211	551.3300	276.1686
R	1074.5361	537.7717	450.2823	225.6448
F	1221.6045	611.3059	294.1812	147.5942
K	1349.6994	676.3534	147.1128	74.0600



Spectrum	Two Step Method	Conf	Sc
33.1.1.4545.1	AKDNAVMSTRFK	76.5	9

ProteoGenomics (Identified in one-step method but not by two-step method)						
Spectrum	One Step Method	Conf Sc	Two Step Method	Conf Sc	Reason why it was not identified in two step method	
17.1.1.1993.1	FRFPSAFFSSVFPAAIEPGERASAR	99.0	13 LLNYNAQPLNSVQK ALELTGEGEDK	1	7	Protein present in second step database. Reason unknown.
26.1.1.484.1	GLSHAAASPGGASAGGR	99.0	11 GLSHAAASPGGASAG GR	24.1	11	Peptide identified at a lower Conf Sc.
33.1.1.7390.1	FNIHAPLCNTKK	99.0	13 NFLYAWCGKRK	61.9	9	Similar accession numbers. Peptide identified when correct accession numbers were restored.
35.1.1.3120.1	EAMSSKVSR	94.3	9 SISMSVAGSR	44.9	7	Similar accession numbers. Peptide identified when correct accession numbers were restored.
42.1.1.365.1	MNVGGAGVAGK	97.5	9 MNVGGAGVAGK	81.7	9	Peptide identified at a lower Conf Sc.

File Configure Window Help

Workflow Tasks

Identify Proteins

LC...

Spot-Based (MS only)...

Spot-Based (MS and MS/MS)...

View

Analysis Log...

Result...

Export

Peptide Summary...

Protein Summary...

MGF Peaklist(s)...

Protein ID										Spectra										Summary Statistics									
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Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
17.1.1.1993.1		2743.3850	915.4690	3	697	FRFPSAFFSSVFPAAIEPGERAS		99	2743.3870	3

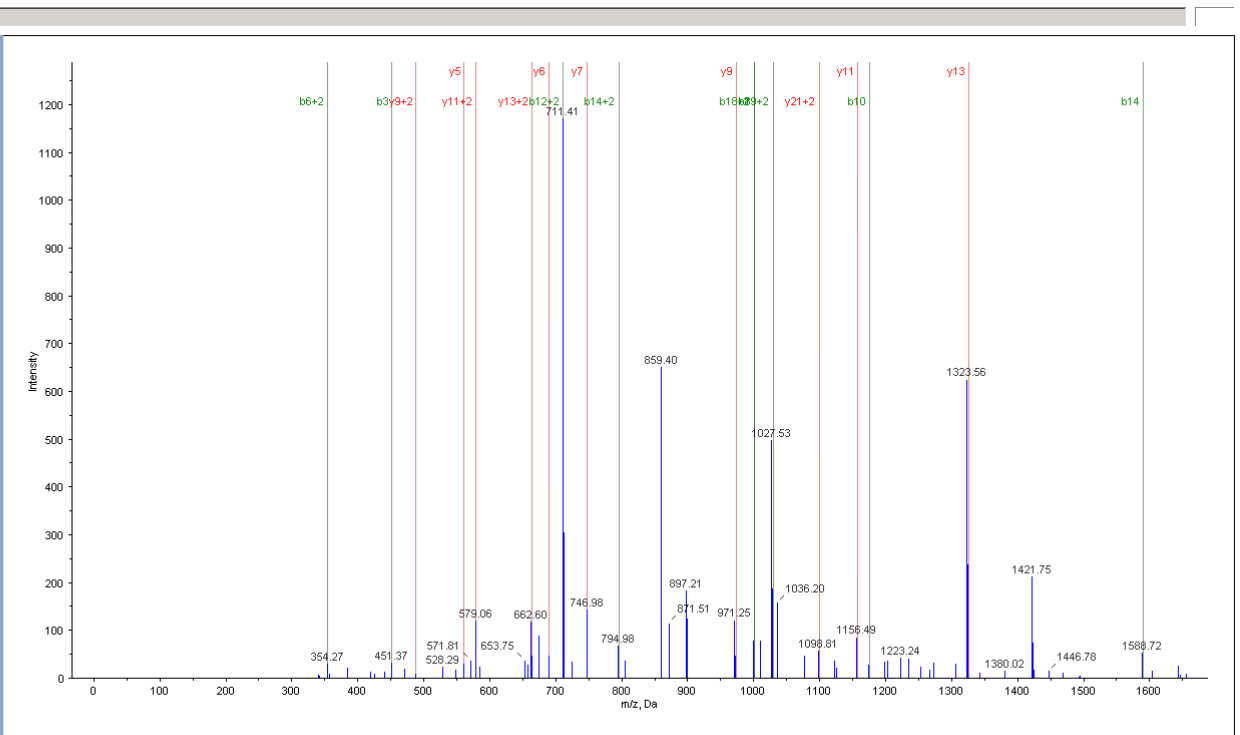
Peptide ID Hypotheses - 17.1.1.1993.1									
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass	
99	13	697	FRFPSAFFSSVFPAAIEPGERASAR		2743.3870	915.4696	3	-0.0020	
<1	9		NVPAASNATAQIPSTIVTATRTTSMGGR		2743.3850	915.4689	3	0.0002	
<1	9		TLPLQVCSRAQTQAVSGGAADLGEDRK	Deamidated(O)@5	2743.3811	915.4677	3	0.0040	
<1	8		AVQLHSKAGGQANSLRVGFGCSESLR		2743.3977	915.4731	3	-0.0126	
<1	8		GCKSTTRYLLLSVAHSLMQLSTFGH		2743.3860	915.4692	3	-0.0009	

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

Residue	b	b+2	y	y+2
F	148.0757	74.5415	2744.3943	1372.7008
R	304.1768	152.5920	2597.3259	1299.1666
F	451.2452	226.1262	2441.2248	1221.1160
P	548.2960	274.6526	2294.1564	1147.5818
S	635.3300	318.1686	2197.1036	1099.0555
A	706.3671	353.6872	2110.0716	1055.5394
F	853.4355	427.2214	2039.0345	1020.0209
F	1000.5039	500.7556	1891.9661	946.4867
S	1087.5360	544.2716	1744.8977	872.9525
S	1174.5680	587.7876	1657.8656	829.4365
V	1273.6364	637.3218	1570.8336	785.9204
F	1420.7048	710.8561	1471.7652	736.3862
P	1517.7576	759.3824	1324.6968	662.8520
A	1588.7947	794.9010	1227.6440	614.3257
A	1659.8318	830.4196	1156.6069	578.8071
I	1772.9159	886.9616	1085.5698	543.2885
E	1901.9585	951.4829	972.4857	486.7465
P	1939.0112	1000.0093	843.4431	422.2252
G	2056.0327	1028.5200	746.3904	373.6988
E	2185.0753	1093.0413	689.3689	345.1881
R	2341.1764	1171.0918	560.3263	280.6668
A	2412.2135	1206.6104	404.2252	202.6162
S	2499.2456	1250.1264	333.1881	167.0977
A	2570.2827	1285.6450	246.1561	123.5817
R	2726.3638	1363.6955	175.1190	88.0631



Spectrum	One Step Method	Conf	Sc
17.1.1.1993.1	FRFPSAFFSSVFPAAIEPGERASAR	99.0	13

Protein ID	Spectra	Summary Statistics						
Spectrum List								
Spectrum /	Time	Prec MW Prec m/z Prec z Prot H Best Sequence Modifications Conf Theor MW z						
17.1.1.1993.1		2743.3850 915.4690 3 LLNYYNAQPLNSVQKALELTGEGEDK Deamidated(O)@11 =1 2743.4028 3						
Peptide ID Hypotheses - 17.1.1.1993.1								
Conf /	Sc /	Prot H /	Sequence /	Modifications /	Theor MW	Theor m/z	z	ΔMass
<1	7		LLNYYNAQPLNSVQKALELTGEGEDK		2743.4028	915.4749	3	-0.0178
<1	7		VKISGLDHPHQYYIAMDIVPVDNK	Deamidated(O)@11	2743.3892	915.4703	3	-0.0041
<1	6		CADLHLKLDKDDANIAYVLASAGTR		2743.3962	915.4727	3	-0.0113
<1	6		TFTVPIASADLIHDVAETFOOQDK		2743.3816	915.4678	3	0.0033
<1	6		VAAEIVQCAIINSVLPFGSSDTGEEK		2743.3699	915.4639	3	0.0152
Precursor MS Region								
No Data Showing								

Fragmentation Evidence for Peptide				
Residue	b	b+2	y	y+2
L	114.0913	57.5493	2744.4101	1372.7087
L	227.1754	114.0913	2631.3261	1316.1667
N	341.2183	171.1128	2518.2420	1259.6246
Y	504.2817	252.6445	2404.1991	1202.6032
N	618.3246	309.6659	2241.1357	1121.0715
A	689.3617	345.1845	2127.0928	1064.0500
Q	817.4203	409.2138	2056.0557	1028.5315
P	914.4730	457.7402	1927.9971	964.5022
L	1027.6571	514.2822	1830.9443	915.9758
N	1141.6000	571.3037	1717.8603	859.4338
S	1228.6321	614.8197	1603.8174	802.4123
V	1327.7005	664.3539	1516.7853	758.8963
Q	1455.7591	728.3832	1417.7169	709.3621
K	1583.8540	792.4306	1289.6583	645.3328
A	1654.8911	827.9492	1161.5634	581.2853
L	1767.9752	884.4912	1090.5263	545.7668
E	1897.0178	949.0125	977.4422	489.2247
L	2010.1019	1005.5546	848.3996	424.7034
T	2111.1495	1056.0784	735.3155	368.1614
G	2168.1710	1084.5891	634.2679	317.6376
E	2297.2136	1149.1104	577.2464	289.1268
G	2354.2351	1177.6212	448.2038	224.6055
E	2483.2776	1242.1425	391.1623	196.0948
D	2598.3046	1299.6559	262.1397	131.5735
K	2726.3996	1363.7034	147.1128	74.0600

Spectrum	Two Step Method	Conf	Sc
17.1.1.1993.1	LLNYYNAQPLNSVQKALELTGEGEDK	1	7

Workflow Tasks

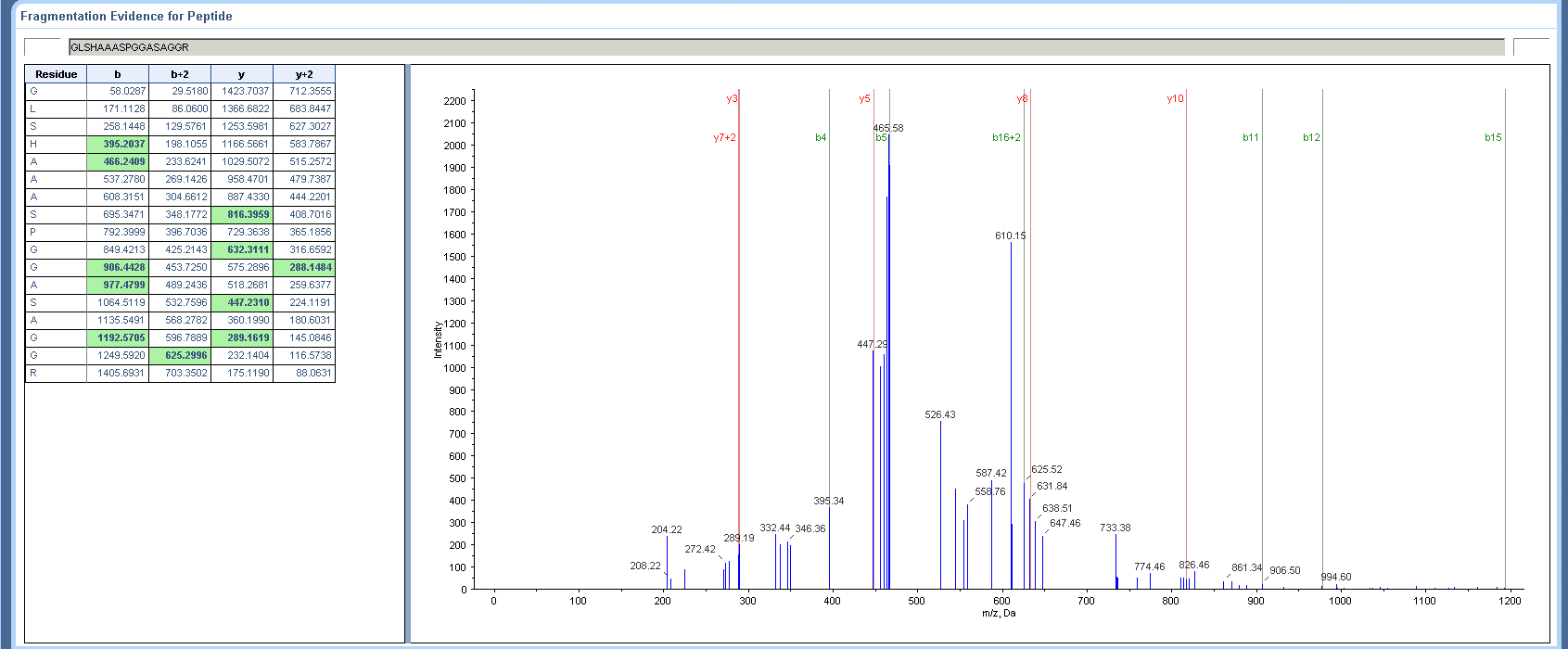
- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...
- MGF Peaklist(s)...

Protein ID				Spectra				Summary Statistics			
Spectrum List											
Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z	
26.1.1.484.1		0.0000	475.2354	0	695	GLSHAAASPGGASAGGR		99	1422.6964	3	
26.1.1.486.1		0.0000	393.5059	0		EMQFHCGLIK		<1	1177.5009	3	
26.1.1.493.1		0.0000	376.8001	0		KVTITLIIVK		<1	1126.7689	3	

Peptide ID Hypotheses - 26.1.1.484.1											
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass			
99	11	695	GLSHAAASPGGASAGGR		1422.6964	475.2394	3	-0.0120			
<1	9		MCVGTFFPRSGK		1422.6866	475.2362	3	-0.0023			
<1	8		MRQATAVVEIASGK		1422.6847	475.2355	3	-0.0003			
<1	7		DSEGAGPLPDPNVR		1422.6740	475.2319	3	0.0105			
<1	7		EFCRGRDLQCK		1422.6674	475.2297	3	0.0170			

Precursor MS Region

No Data Showing



Protein ID
Spectra
Summary Statistics

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
26.1.1.484.1		0.0000	475.2394	0		GLSHAAASPPGGASAGGR		24.1	1422.6964	3

Peptide ID Hypotheses - 26.1.1.484.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
24.1	11		GLSHAAASPPGGASAGGR		1422.6964	475.2394	3	-0.0120
<1	8		CVGS LCQGS SVRR	Deamidated(O)@8	1422.6708	475.2309	3	0.0136
<1	7		EYEMELAKA SNR		1422.6740	475.2319	3	0.0105
<1	6		CLDPTKAPDP PGR		1422.6925	475.2381	3	-0.0081
<1	6		CVSCTKTFPNA PR		1422.6748	475.2322	3	0.0096

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

GLSHAAASPPGGASAGGR

Residue	b	b+2	y	y+2
G	58.0287	29.5180	1423.7037	712.3555
L	171.1128	86.0600	1366.6822	683.8447
S	258.1448	129.5761	1253.5981	627.3027
H	395.2037	198.1055	1166.5661	583.7867
A	466.2409	233.6241	1029.5072	515.2572
A	537.2760	269.1426	958.4701	479.7387
A	608.3151	304.6612	867.4330	444.2201
S	695.3471	348.1772	816.3959	408.7016
P	792.3999	396.7036	729.3638	365.1856
G	849.4213	425.2143	632.3111	316.6592
G	906.4428	453.7250	575.2896	288.1484
A	977.4799	489.2436	518.2681	259.6377
S	1064.5119	532.7596	447.2310	224.1191
A	1135.5491	568.2782	360.1990	180.6031
G	1192.5705	596.7889	289.1619	145.0846
G	1249.5920	625.2986	232.1404	116.5738
R	1405.6931	703.3502	175.1190	88.0631

Spectrum	Two Step Method	Conf	Sc
26.1.1.484.1	GLSHAAASPPGGASAGGR	24.1	11

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
- View
- Analysis Log...
- Result...
- Export
- Peptide Summary...
- Protein Summary...
- MGF Peaklist(s)...

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
33.1.1.7390.1		1384.7192	693.3669	2	791	FNIHAPLCNTKK		99	1384.7285	2

Peptide ID Hypotheses - 33.1.1.7390.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	13	791	FNIHAPLCNTKK		1384.7285	693.3715	2	-0.0094
<1	9	864	NFLYAMCGKPK		1384.7074	693.3610	2	0.0118
<1	9		FCLMGLELSTKK	Oxidation(M)@4	1384.7095	693.3620	2	0.0097
<1	9		FLDHALGALNRS		1384.7252	693.3699	2	-0.0060

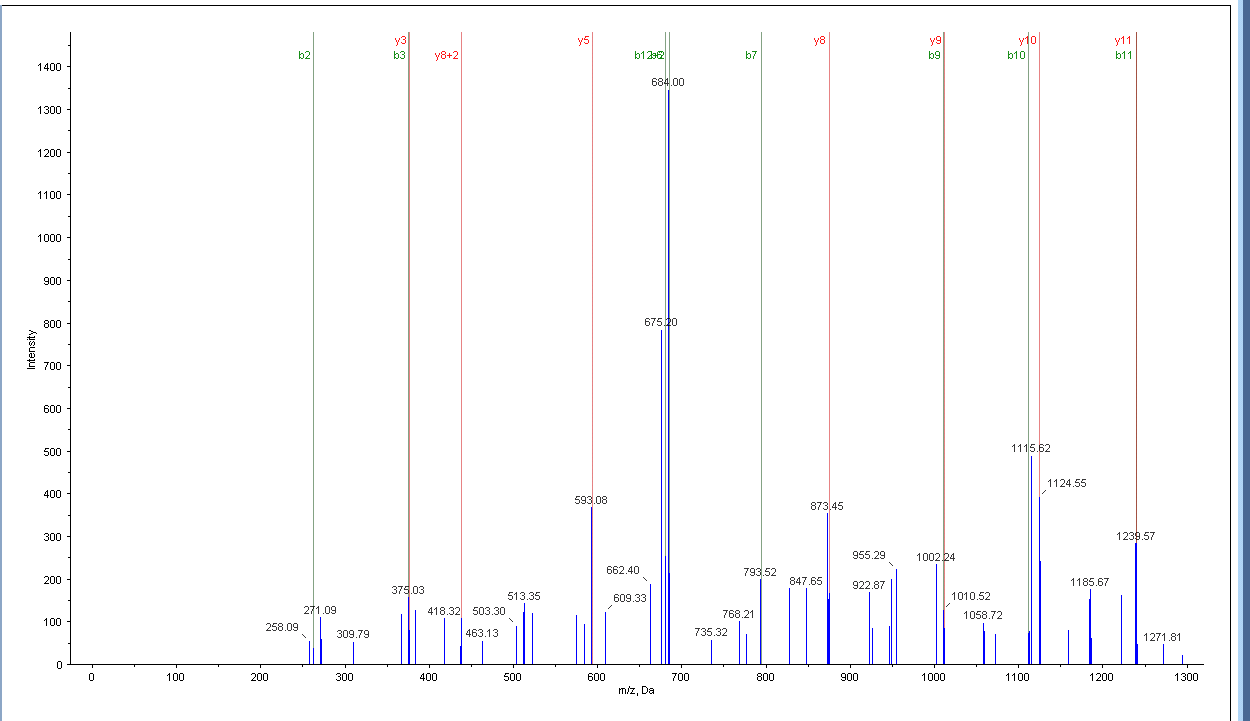
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

FNIHAPLCNTKK

Residue	b	b+2	y	y+2
F	148.0757	74.5415	1385.7358	693.3715
N	262.1188	131.5629	1238.6674	619.8373
I	375.2027	188.1050	1124.6246	562.8159
H	512.2616	256.6344	1011.5404	506.2738
A	583.2987	292.1530	874.4815	437.7444
P	680.3515	340.6794	803.4444	402.2258
L	793.4355	397.2214	706.3916	353.6994
C	896.4447	448.7260	693.3876	297.1574
N	1010.4876	505.7475	490.2984	245.6528
T	1111.5363	556.2713	376.2564	188.6314
K	1239.6303	620.3188	275.2078	138.1075
K	1367.7253	684.3663	147.1128	74.0600



Workflow Tasks

- Identify Proteins
- LC...
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- Protein Summary...
- MGF Peaklist(s)...

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot H	Best Sequence	Modifications	Conf	Theor MW	z
33.1.1.7390.1		1384.7192	693.3669	2	894	NFLYAWCGKRK		61.9	1384.7074	2

Peptide ID Hypotheses - 33.1.1.7390.1

Conf	Sc	Prot H	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
61.9	9	894	NFLYAWCGKRK		1384.7074	693.3610	2	-0.0117
19.9	8		QAALLEEQARLK		1384.7311	693.3728	2	-0.0119
9.4	8		ESIAEHKPHIDK	Glu->pyro-Glu@N-term	1384.7100	693.3622	2	-0.0092
1.6	7		QRVELQEQVEK		1384.7311	693.3728	2	-0.0119
1.2	7		MHDELKSSVKTGK		1384.7311	693.3728	2	-0.0119

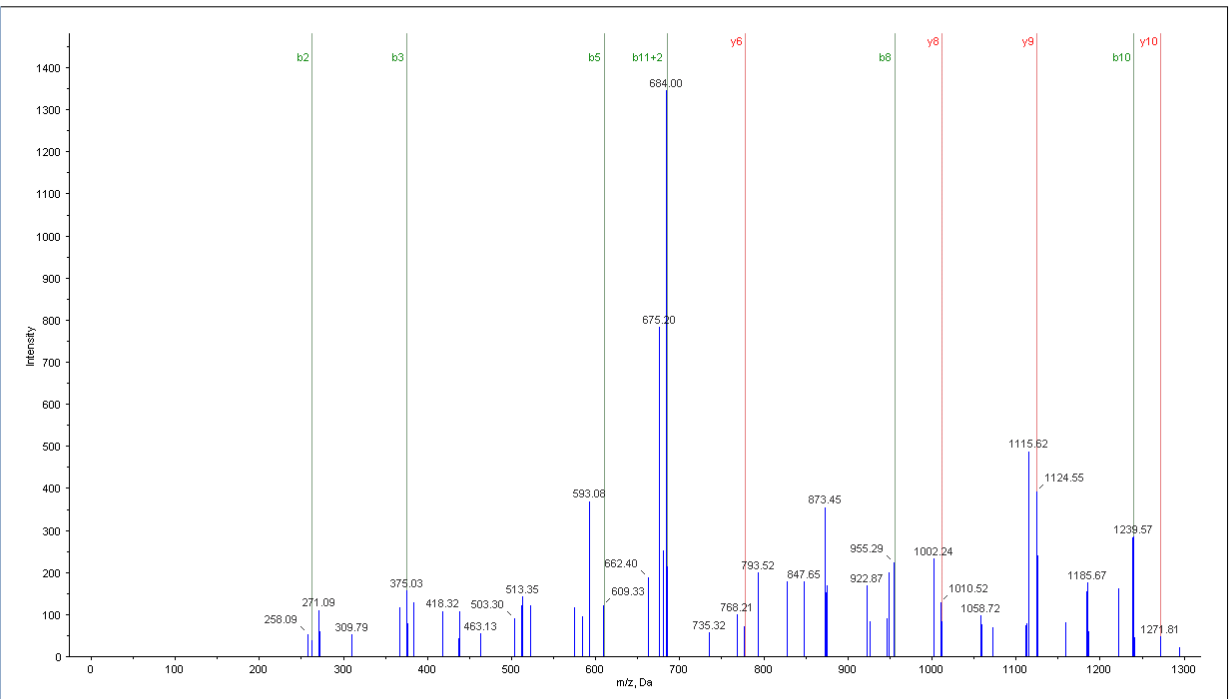
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

NFLYAWCGKRK

Residue	b	b+2	y	y+2
N	115.0502	58.0287	1385.7147	693.3610
F	262.1186	131.5629	1271.6718	636.3395
L	375.2027	188.1050	1124.6033	562.8053
Y	538.2660	269.6366	1011.5193	506.2633
A	609.3031	305.1552	848.4560	424.7316
W	795.3824	398.1949	777.4188	389.2131
C	898.3916	449.6994	591.3395	296.1734
G	955.4131	478.2102	488.3303	244.6888
K	1083.5090	542.2577	431.3089	216.1581
R	1239.6092	620.3082	303.2139	152.1106
K	1367.7041	684.3557	147.1128	74.0600



Spectrum	Two Step Method	Conf Sc
33.1.1.7390.1	NFLYAWCGKRK	61.9 9

Workflow Tasks

- Identify Proteins
- LC...
- Spot-Based (MS only)...
- Spot-Based (MS and MS/MS)...
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Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
35.1.1.3120.1		993.4904	497.7524	2	386	EAMSSKYSR		94.3	993.4913	2

Peptide ID Hypotheses - 35.1.1.3120.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
94.3	9	386	EAMSSKYSR		993.4913	497.7529	2	-0.0010
<1	7	6	SISMSVAGSR		993.4913	497.7529	2	-0.0010
<1	7		ISNSKVSQSR	Deamidated(N)@3	993.4913	497.7529	2	-0.0010
<1	6		FLASQSDR		993.4880	497.7513	2	0.0024
<1	6		FNDGTTGMR		993.4954	497.7548	2	-0.0050

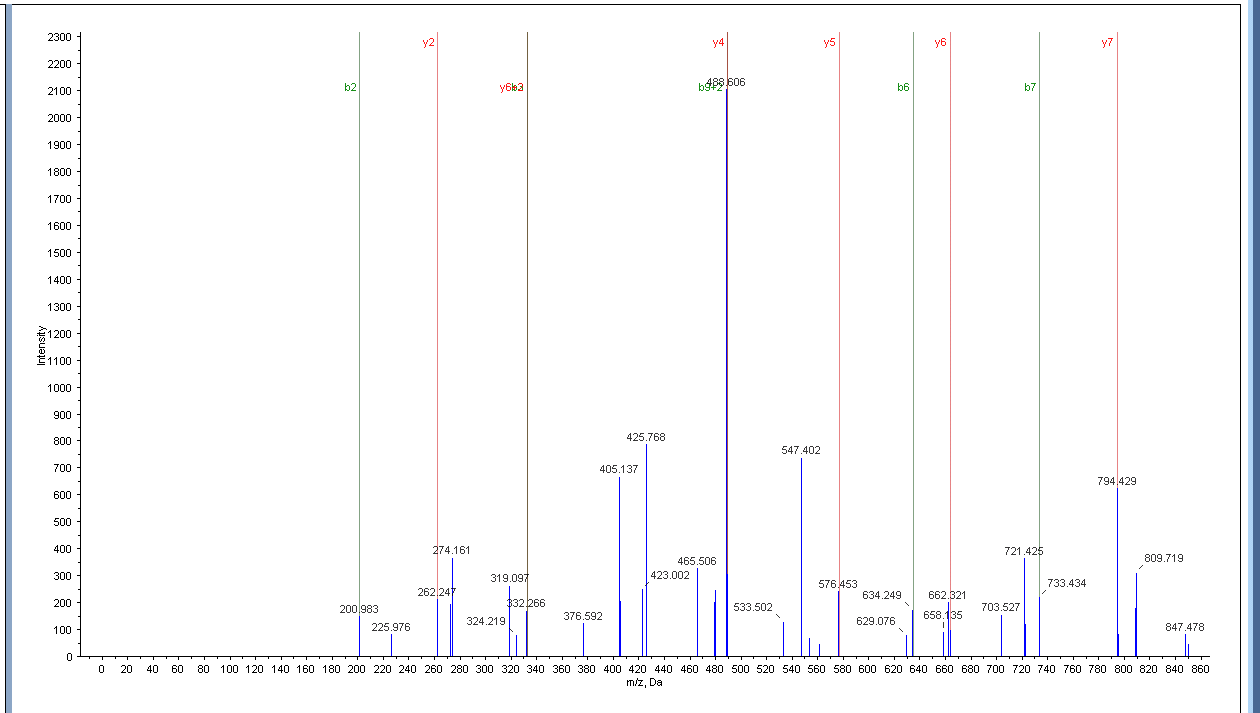
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

EAMSSKYSR

Residue	b	b+2	y	y+2
E	130.0499	65.5286	994.4986	497.7529
A	201.0870	101.0471	865.4560	433.2316
M	332.1275	166.5674	794.4189	397.7131
S	419.1595	210.0834	663.3784	332.1928
S	506.1915	253.5994	576.3464	288.6768
K	634.2065	317.6469	409.3144	245.1608
V	733.3549	367.1811	361.2194	181.1133
R	820.3869	410.6971	262.1510	131.5791
R	976.4880	488.7477	175.1190	88.0631



Workflow Tasks

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Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
35.1.1.3120.1		993.4904	497.7524	2	6,1861	SISMSVAGSR		45	993.4913	2

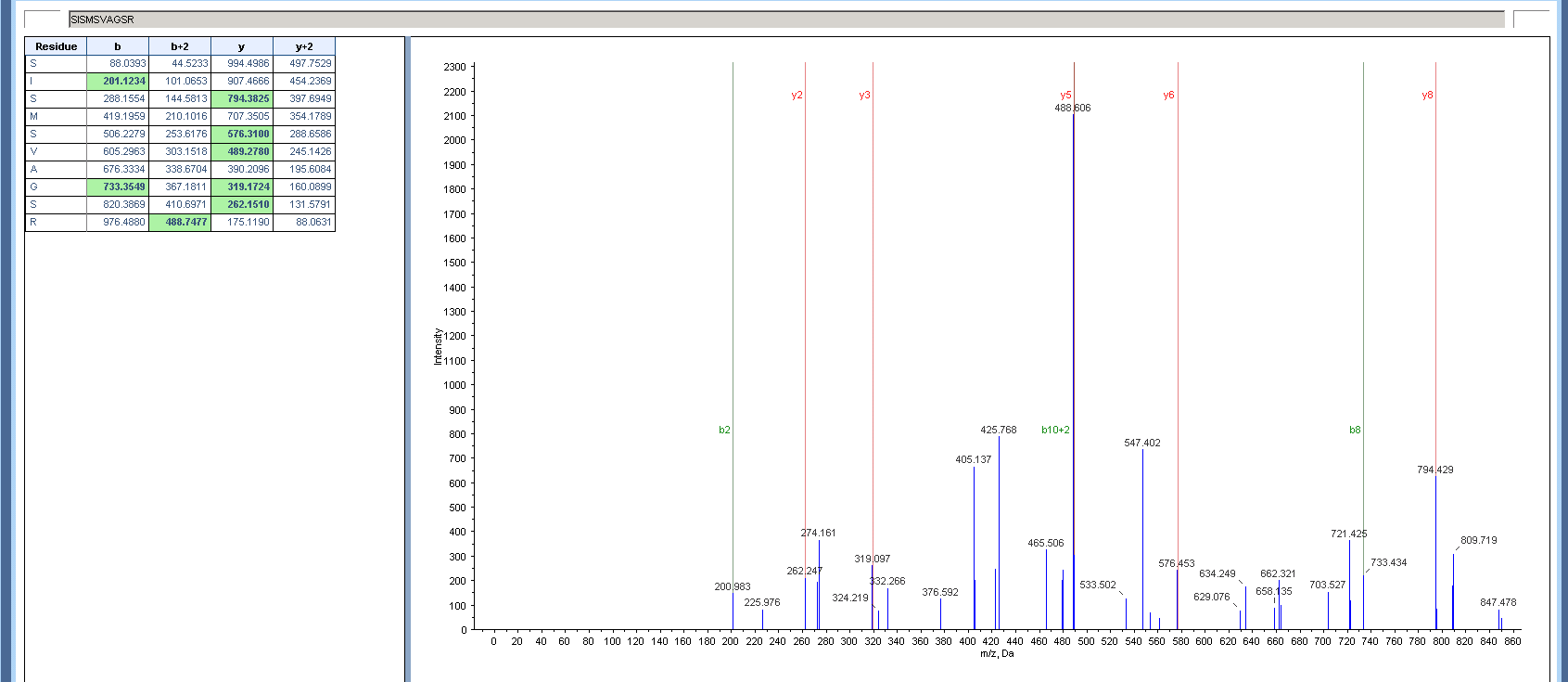
Peptide ID Hypotheses - 35.1.1.3120.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
45	7	6,1861	SISMSVAGSR		993.4913	497.7529	2	-0.0010
13.2	6		FLASQSADR		993.4880	497.7513	2	0.0024
13.2	6		SLNMTSVSR		993.4913	497.7529	2	-0.0010
<1	6		SLQSVHADK	Oxidation(M)@6	993.4801	497.7473	2	0.0102
<1	5		LSPPHGSSR		993.4992	497.7568	2	-0.0089

Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide



Spectrum	Two Step Method	Conf Sc
35.1.1.3120.1	SISMSVAGSR	44.9 7

Workflow Tasks

- Identify Proteins
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- Spot-Based (MS and MS/MS)...
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- MGF Peaklist(s)...

Spectrum List

Spectrum /	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
42.1.1.365.1		0.0000	480.7436	0	883	MNVGGAGVAGK		97.5	959.4858	2

Peptide ID Hypotheses - 42.1.1.365.1

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
97.5	9	883	MNVGGAGVAGK		959.4858	480.7502	2	-0.0132
<1	7		ATVEGGQAR	Deamidated(G)@6	959.4672	480.7409	2	0.0054
<1	6		AELSGGAEVK		959.4924	480.7535	2	-0.0197
<1	6		GHGQCTPKGK		959.4858	480.7502	2	-0.0132
<1	6		GTGCTRANQV		959.4785	480.7465	2	-0.0058
<1	6		...		959.4760	480.7452	2	-0.0032

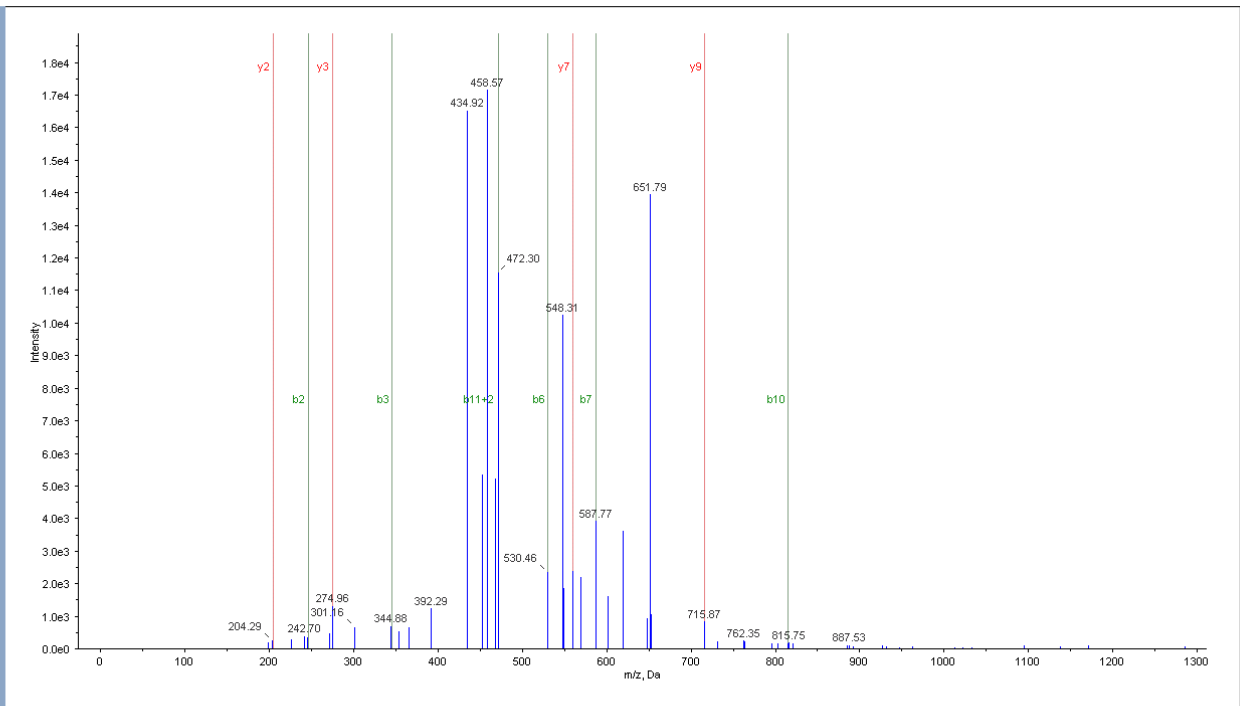
Precursor MS Region

No Data Showing

Fragmentation Evidence for Peptide

MNVGGAGVAGK

Residue	b	b+2	y	y+2
M	132.0478	66.5275	960.4931	480.7502
N	246.0907	123.5490	829.4526	415.2300
V	346.1591	173.0832	715.4097	358.2085
G	402.1806	201.5939	616.3413	308.6743
G	459.2020	230.1047	559.3198	280.1636
A	530.2391	265.6232	502.2984	251.6528
G	587.2606	294.1339	431.2813	216.1343
V	686.3290	343.6681	374.2390	187.6235
A	757.3661	379.1867	275.1714	138.0893
G	814.3876	407.6974	204.1343	102.5708
K	942.4826	471.7449	147.1128	74.0600



Spectrum	One Step Method	Conf Sc
42.1.1.365.1	MNVGGAGVAGK	97.5 9

File Configure Window Help

Workflow Tasks

- Identify Proteins
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- Protein Summary...
- MGF Peaklist(s)...

Spectrum List

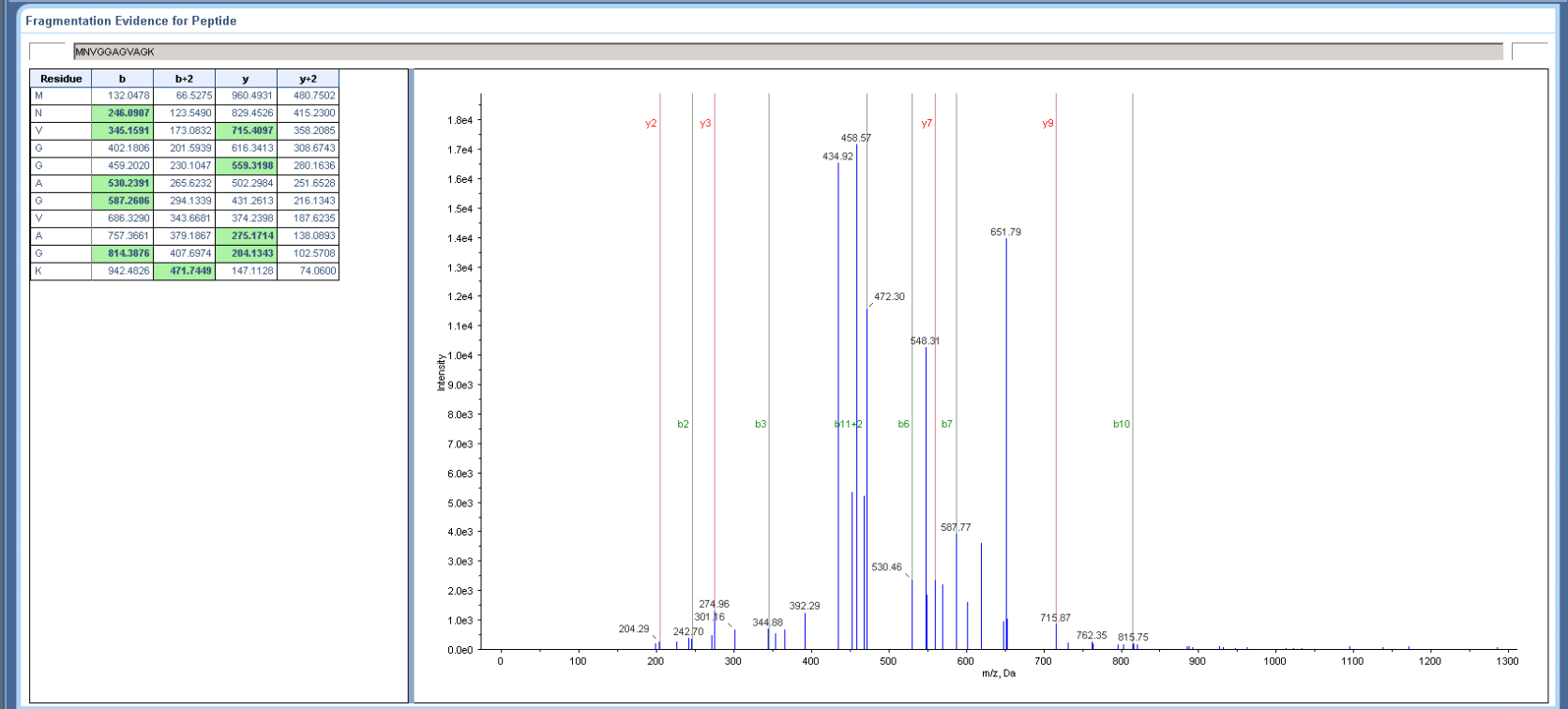
Spectrum /	Time	Pre MW	Pre m/z	Prec z	Prot #	Best Sequence	Modifications	Conf	Theor MW	z
42.1.1.365.1		0.0000	480.7436	0	1398	MNVGGAGVAGK		81.8	959.4858	2

Peptide ID Hypotheses - 42.1.1.365.1

Conf	Sc	Prot #	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
81.8	9	1398	MNVGGAGVAGK		959.4858	480.7502	2	-0.0132
<1	4	353	QNVETE LK	Gln->pyro-Glu@N-term	959.4634	480.7390	2	0.0092
<1	6		ENTQPKVAG		959.4746	480.7446	2	-0.0020
<1	6		MNRTWPR		959.4760	480.7452	2	-0.0033
<1	5		EDDQAGVYK		959.4560	480.7353	2	0.0166
<1	5		EDNIDAVYK		959.4560	480.7353	2	0.0166

Precursor MS Region

No Data Showing



Spectrum	Two Step Method	Conf Sc
42.1.1.365.1	MNVGGAGVAGK	81.7 9