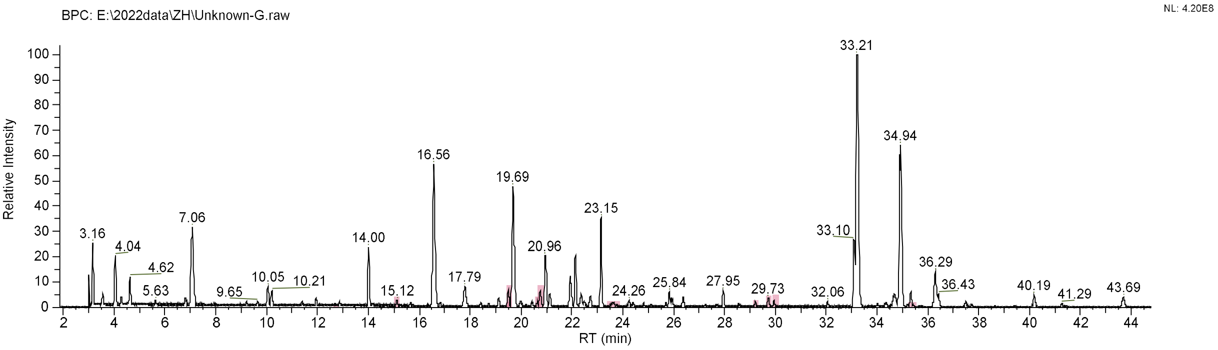
Chymotrypsin



No.	Identification	Positions	Peptide Sequence	Mod	Δ ppm	Conf. Score	Best ASR	ID Type	RT	M/Z	Charge St.	Mono Mass Exp.	Avg Mass Exp.	Mono Mass Theo.	Missed Cleavages	MS Area	Protein
103	1:L80-W81 = 317.1739m	80-81	LW	None	1.95	98.8	1	MS2	12.71	318.182	1	317.1746	317.33	317.1739	1	523699.78	translated protein
111	1:H21-F29 = 901.4658m	21-29	HAGVISTAF	None	1.35	100	1.1	MS2	15.12	451.741	2	901.467	901.85	901.4658	0	1436181	translated protein
122	1:V5-F8 = 514.2904m	5-8	VHLF	None	1.5	99.6	1	MS2	19.5	515.298	1	514.2911	514.52	514.2904	1	835549.5	translated protein
123	1:L4-F8 = 627.3744m	4-8	LVHLF	None	-0.46	98.6	1	MS2	19.5	314.694	2	627.3741	627.65	627.3744	2	3351740.25	translated protein
129	1:G17-F29 = 1286.6619m[non	17-29	GSQLHAGVISTAF	nonspecific	2.06	100	1.4	MS2	20.64	644.34	2	1286.6646	1287.3	1286.6619	1	1424578.5	translated protein
130	1:A72-L77 = 568.3584m	72-77	APVGLL	None	2.06	99.8	1	MS2	20.75	569.367	1	568.3596	568.64	568.3584	1	4015463.25	translated protein
161	1:L66-W71 = 701.3748m[non	66-71	LLPSSW	nonspecific	2.08	100	1	MS2	23.62	702.384	1	701.3763	701.71	701.3748	2	2553038	translated protein
181	1:F3-F8 = 774.4428m	3-8	FLVHLF	None	1.21	100	1	MS2	29.22	388.229	2	774.4438	774.77	774.4428	3	1096006	translated protein
182	1:A78-W81 = 535.2795m	78-81	AFLW	None	1.73	99.8	1.3	MS2	29.73	536.288	1	535.2804	535.53	535.2795	2	1832013.25	translated protein
183	1:S105-L116 = 1345.7341m	105-116	SDKLLETEVSLL	None	1.59	100	1.5	MS2	29.95	673.875	2	1345.7362	1346.38	1345.7341	3	1675398.5	translated protein
207	1:L84-L94 = 1079.5651m[non	84-94	LGASASFPAFL	nonspecific	1.73	100	1.2	MS2	35.41	540.791	2	1079.567	1080.14	1079.5651	3	1119591	translated protein

Sequence Coverage Map - User Defined

Created on 09/09/22
Minimum MS Signal = 0
Data File = Unknown-G.raw
Protease = Chymotrypsin

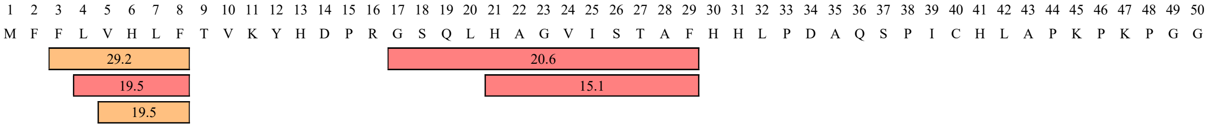
Proteins	Number of MS Peaks	MS Peak Area	Sequence Coverage	Abundance (mol)
1:translated protein	11	100.0%	33.9%	100.00%
Unidentified	0	0.0%		

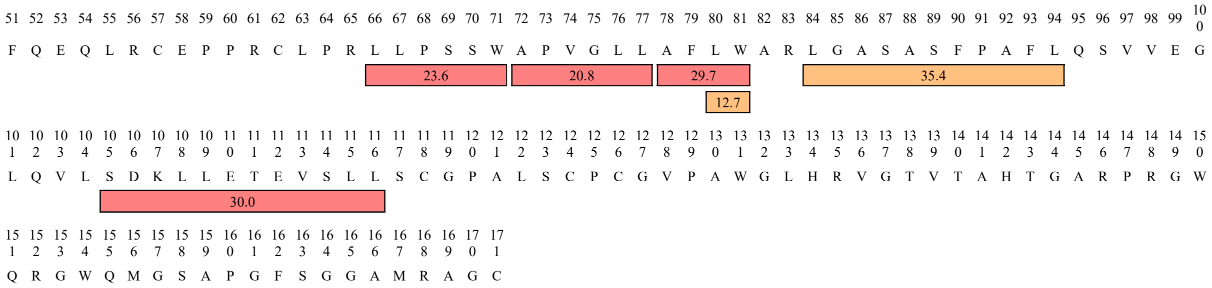
Minimum Recovery = 0%
Minimum Recovery of Overlapping Peptides = 0%
Minimum Confidence = 0
Maximum Mass = 11000

Color code for peptide recovery

>50.0%	>20.0%	>10.0%	>5.0%	>2.0%	>1.0%	>0.5%	>0.2%	>0.1%	>0.0%
good			fair			poor			

translated protein





51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

F Q E Q L R C E P P R C L P R L L P S S W A P V G L L A F L W A R L G A S A S F P A F L Q S V V E G

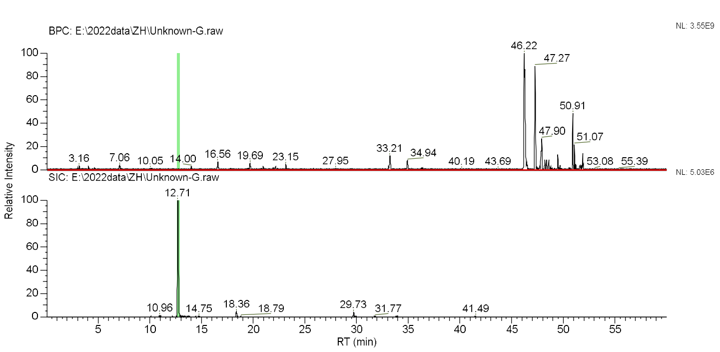
101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150

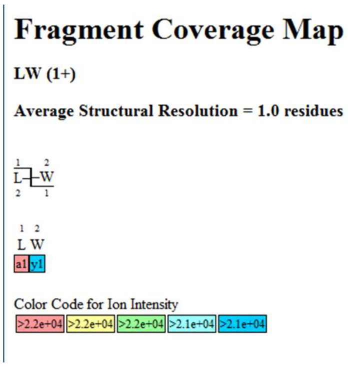
L Q V L S D K L L E T E V S L L S C G P A L S C P C G V P A W G L H R V G T V T A H T G A R P R G W

151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171

Q R G W Q M G S A P G F S G G A M R A G C

No.103 LW (1+)





Fragment Coverage Map

LW (1+)

Average Structural Resolution = 1.0 residues

>1:translated protein

```
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MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL

        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP

       170        180
GFSGGAMRAG C
```
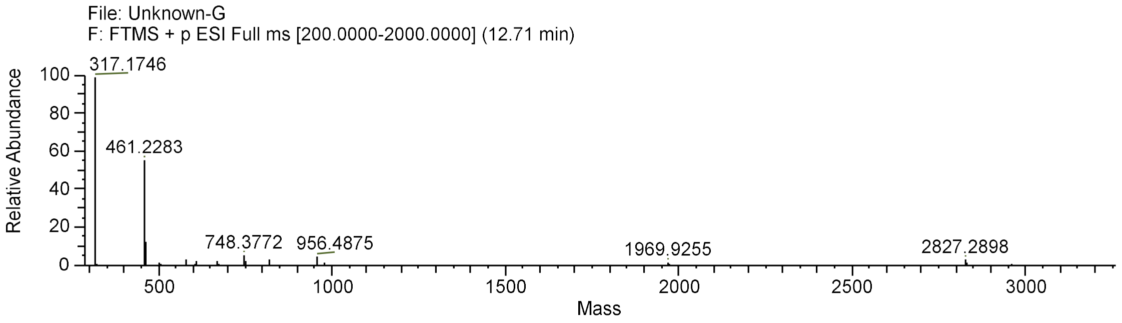
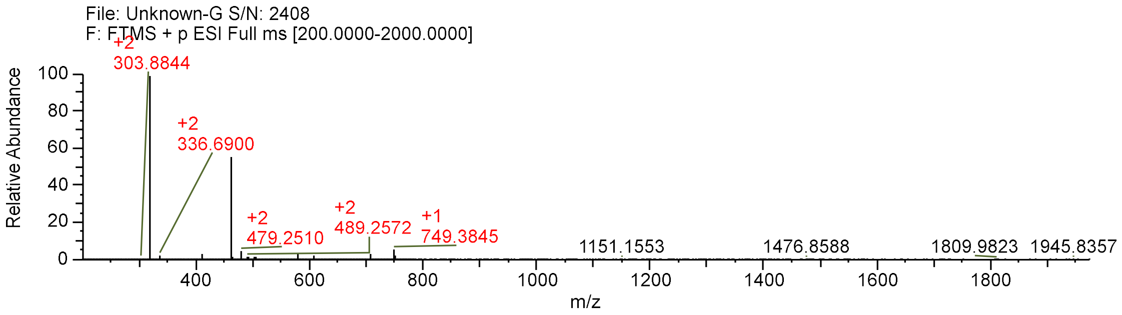
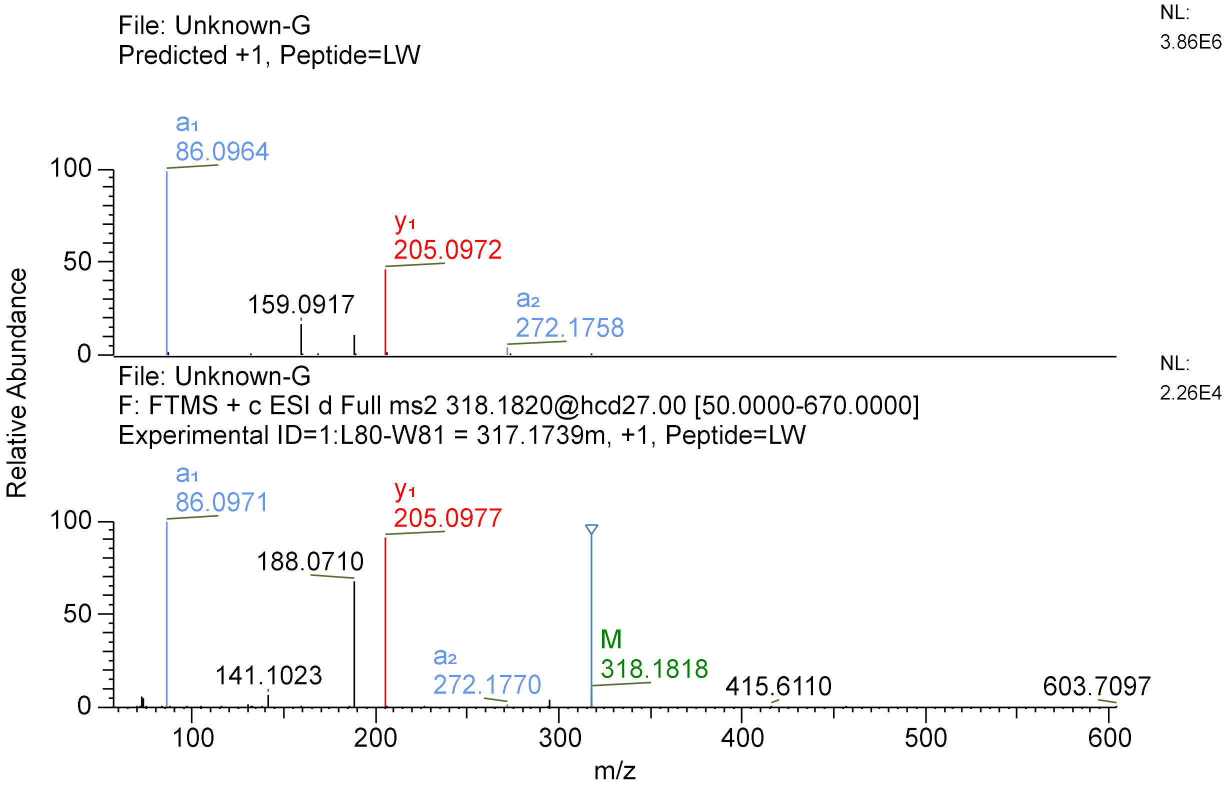



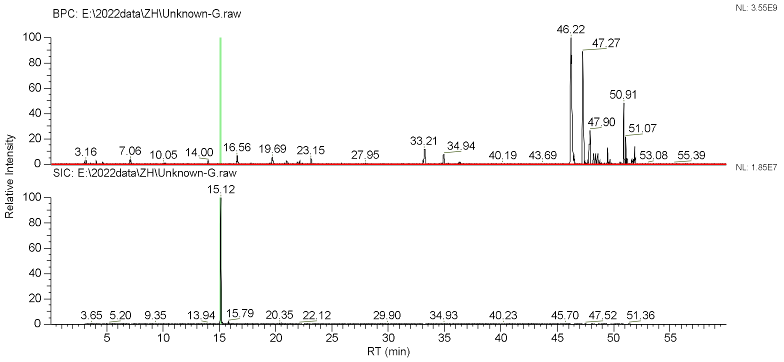
File: Unknown-G
F: FTMS + p ESI Full ms [200.0000-2000.0000] (12.71 min)



File: Unknown-G S/N: 2408
F: FTMS + p ESI Full ms [200.0000-2000.0000]


File: Unknown-G
Predicted +1, Peptide=LW
NL:
3.86E6
a₁
86.0964
y₁
205.0972
159.0917
a₂
272.1758
100
50
0
Relative Abundance
File: Unknown-G
F: FTMS + c ESI d Full ms2 318.1820@hcd27.00 [50.0000-670.0000]
Experimental ID=1:L80-W81 = 317.1739m, +1, Peptide=LW
NL:
2.26E4
a₁
86.0971
y₁
205.0977
188.0710
141.1023
a₂
272.1770
M
318.1818
415.6110
603.7097
100
50
0
100
200
300
400
500
600
m/z

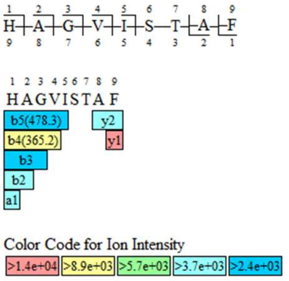
No.111 HAGVISTAF (2+)



Fragment Coverage Map

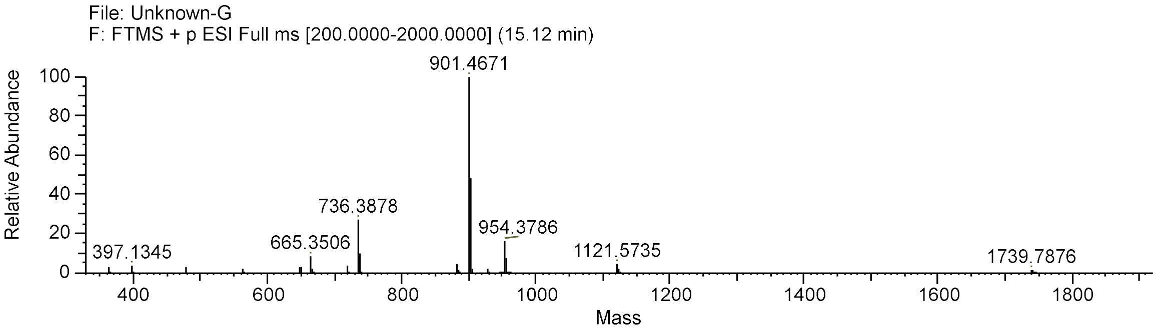
HAGVISTAF (2+)

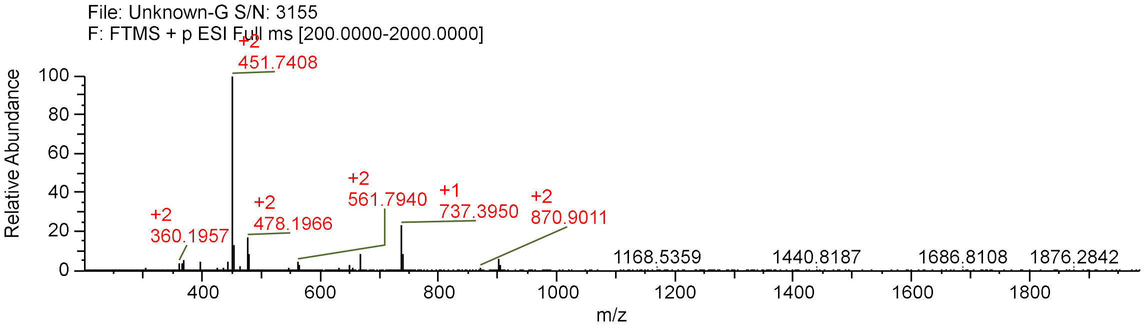
Average Structural Resolution = 1.1 residues

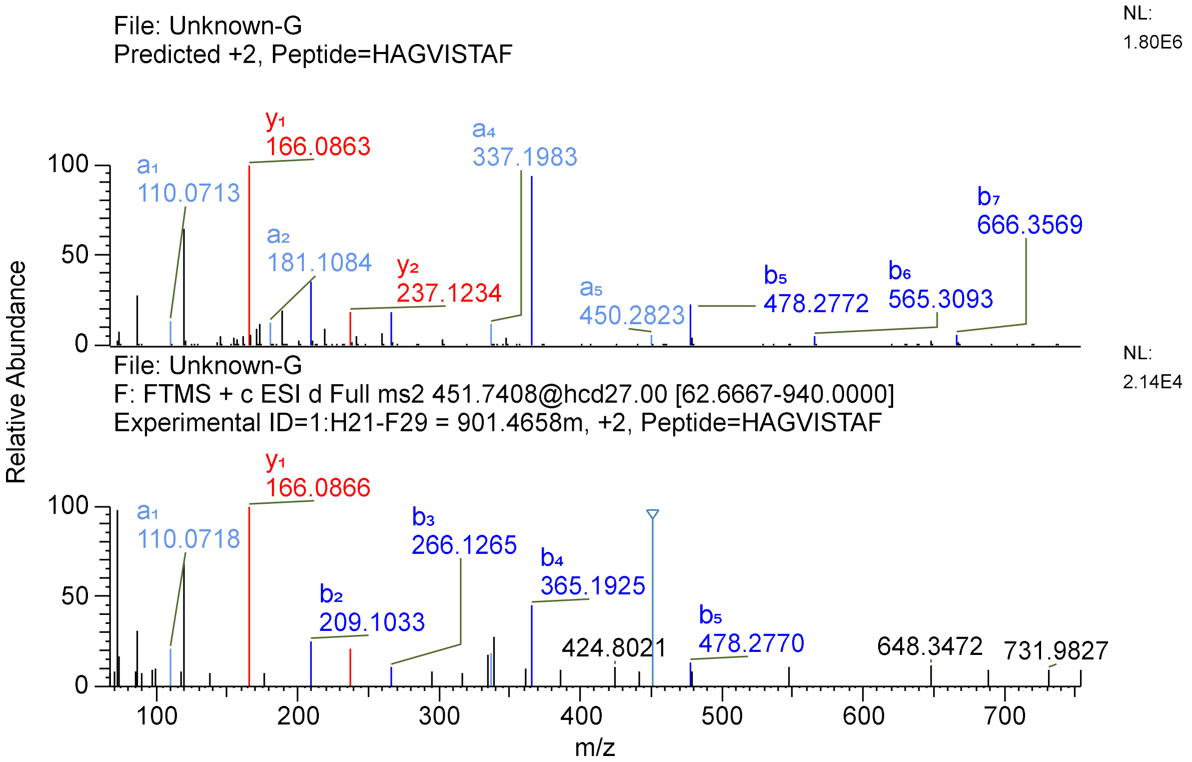


>1:translated protein

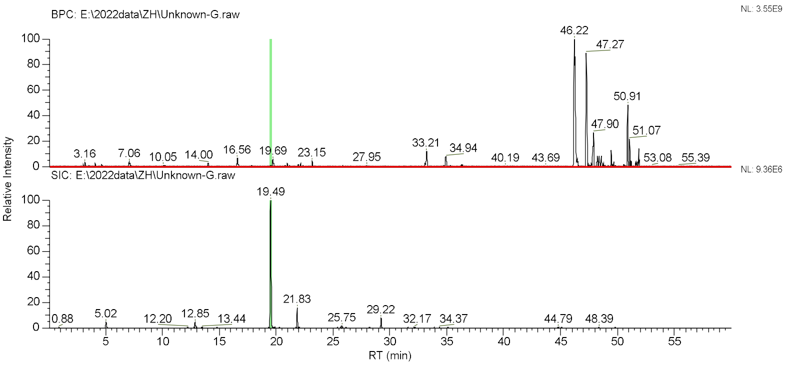
```
        10         20         30         40         50         60         70         80
MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL
        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP
       170        180
GFSGGAMRAG C
```






File: Unknown-G
Predicted +2, Peptide=HAGVISTAF
NL:
1.80E6
Relative Abundance
100
50
0
a1
110.0713
y1
166.0863
a2
181.1084
y2
237.1234
a4
337.1983
a5
450.2823
b5
478.2772
b6
565.3093
b7
666.3569
File: Unknown-G
F: FTMS + c ESI d Full ms2 451.7408@hcd27.00 [62.6667-940.0000]
Experimental ID=1:H21-F29 = 901.4658m, +2, Peptide=HAGVISTAF
NL:
2.14E4
100
50
0
a1
110.0718
y1
166.0866
b2
209.1033
b3
266.1265
b4
365.1925
424.8021
b5
478.2770
648.3472
731.9827
100
200
300
400
500
600
700
m/z

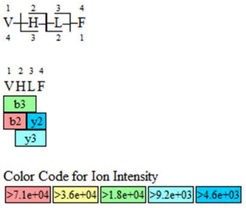
No.122 VHLF (1+)



Fragment Coverage Map

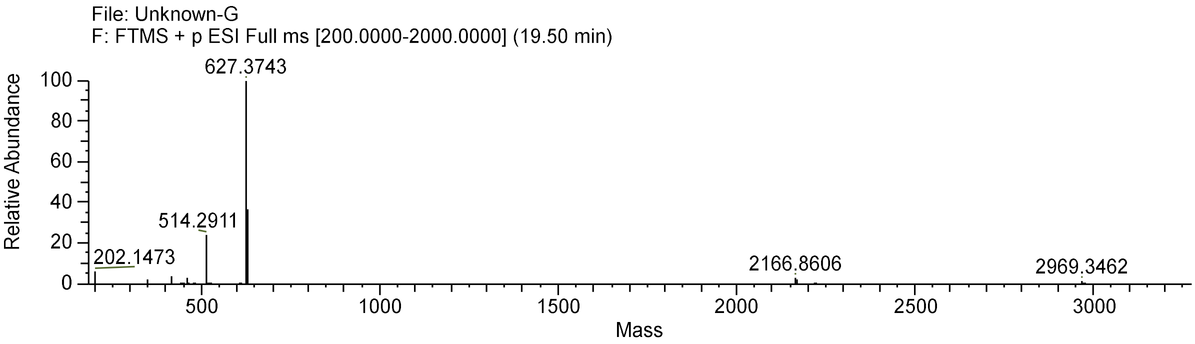
VHLF (1+)

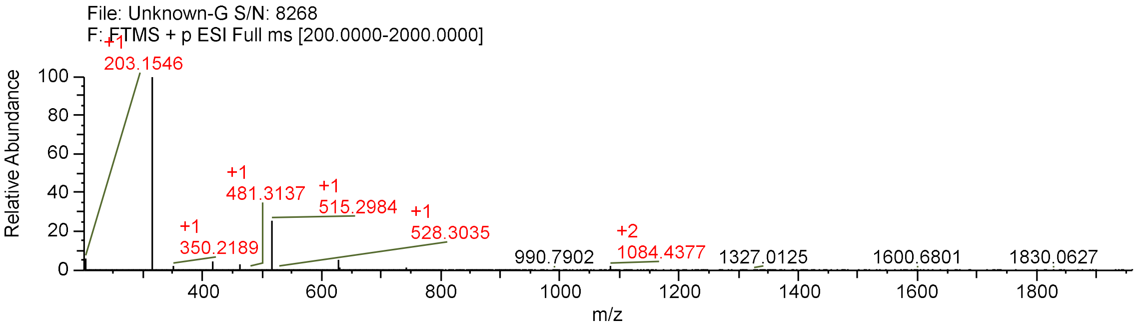
Average Structural Resolution = 1.0 residues

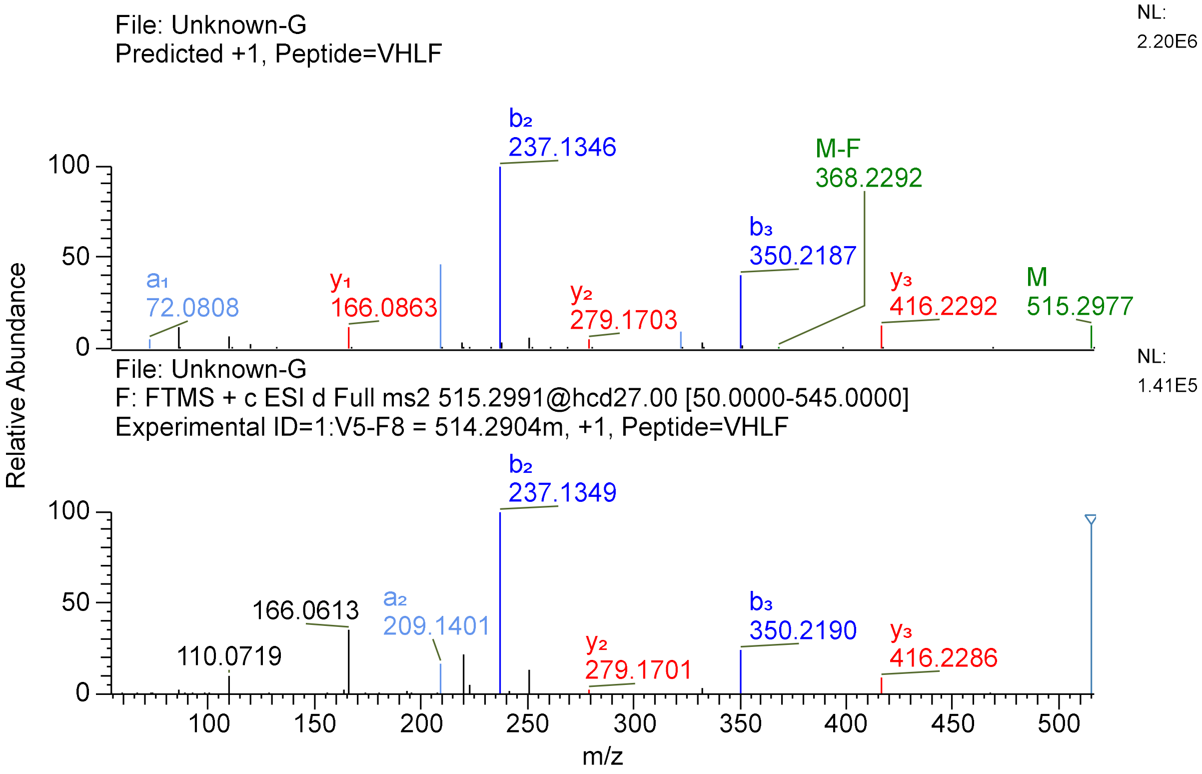


>1:translated protein

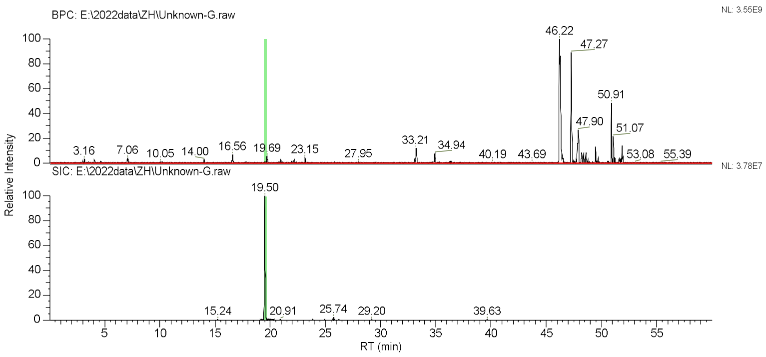
```
        10         20         30         40         50         60         70         80
MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL
        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP
       170        180
GFSGGAMRAG C
```






File: Unknown-G
Predicted +1, Peptide=VHLF
NL:
2.20E6
b₂
237.1346
M-F
368.2292
b₃
350.2187
a₁
72.0808
y₁
166.0863
y₂
279.1703
y₃
416.2292
M
515.2977
100
50
0
Relative Abundance
File: Unknown-G
F: FTMS + c ESI d Full ms2 515.2991@hcd27.00 [50.0000-545.0000]
Experimental ID=1:V5-F8 = 514.2904m, +1, Peptide=VHLF
NL:
1.41E5
b₂
237.1349
166.0613
a₂
209.1401
110.0719
y₂
279.1701
b₃
350.2190
y₃
416.2286
100
50
0
100
150
200
250
300
350
400
450
500
m/z

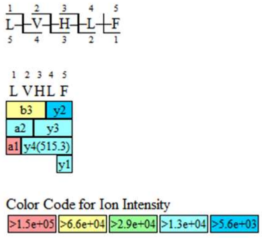
No.123 LVHLF (2+)



Fragment Coverage Map

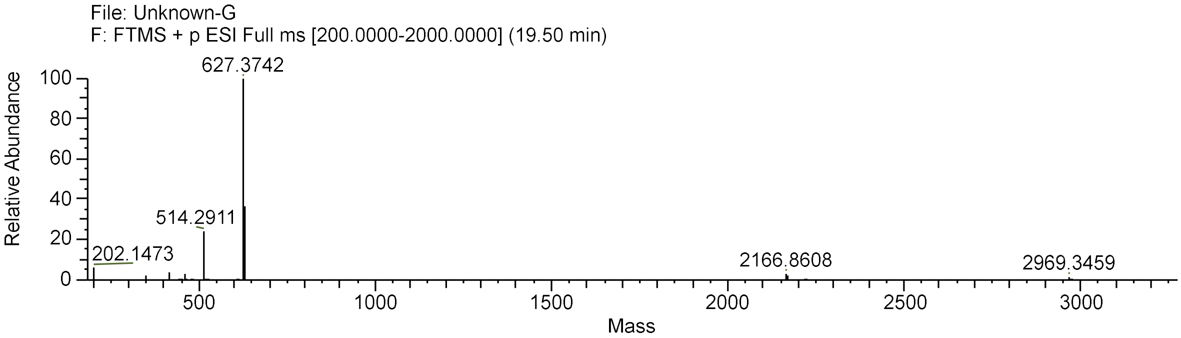
LVHLF (2+)

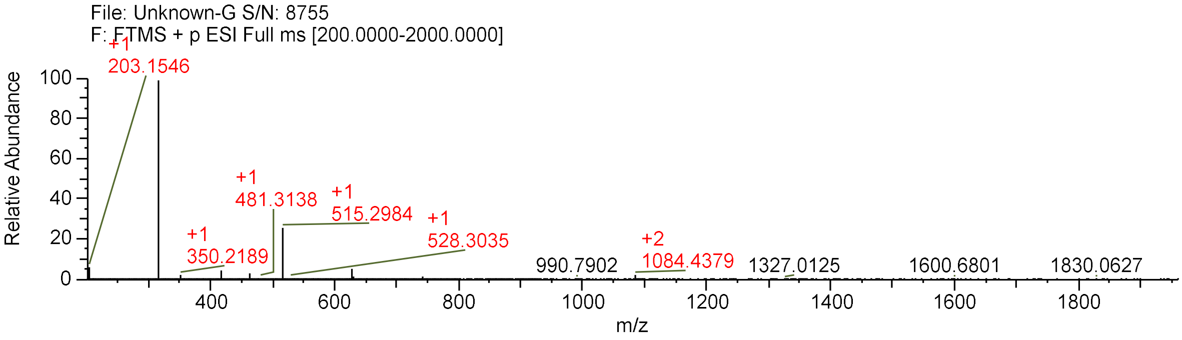
Average Structural Resolution = 1.0 residues

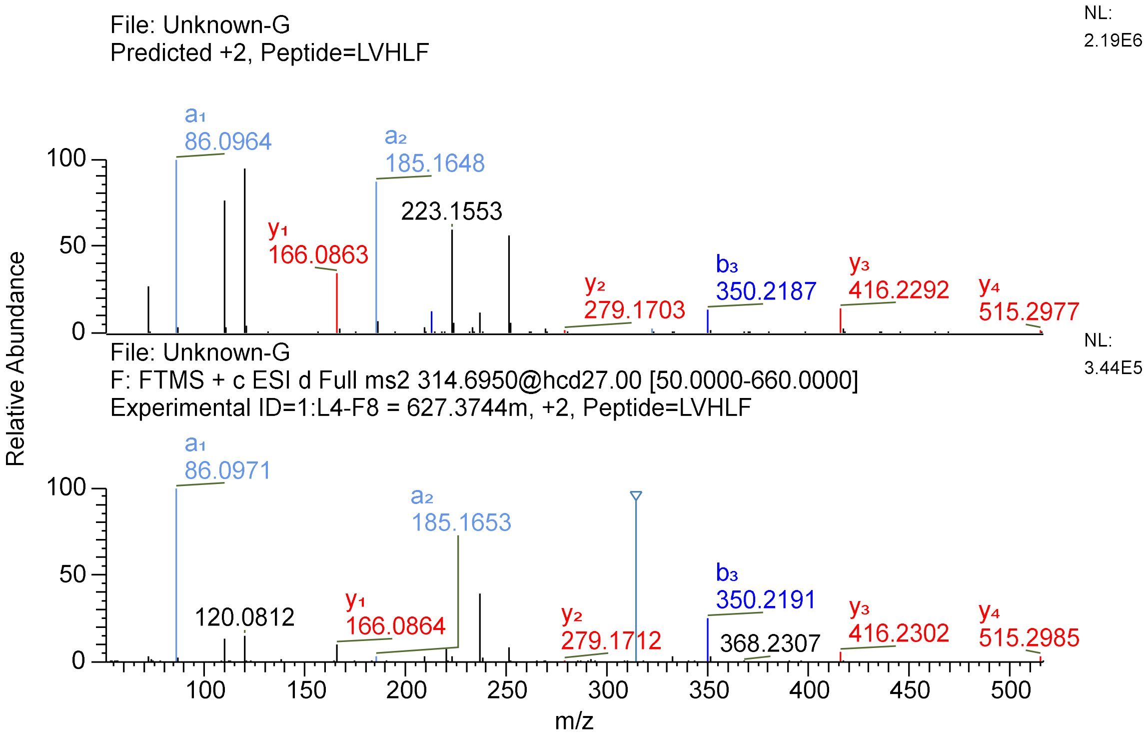


>1:translated protein

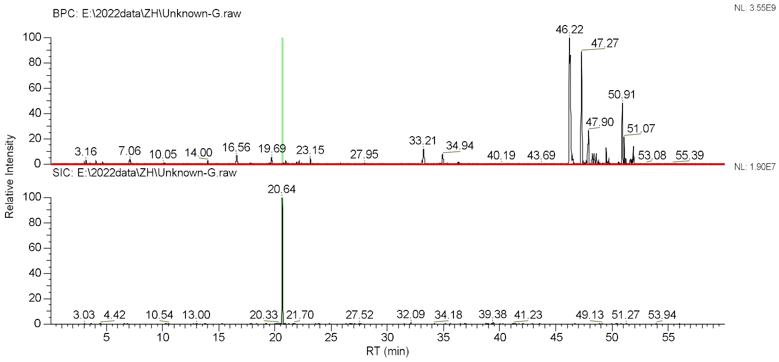
```
        10         20         30         40         50         60         70         80
MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL

        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP

       170        180
GFSGGAMRAG C
```

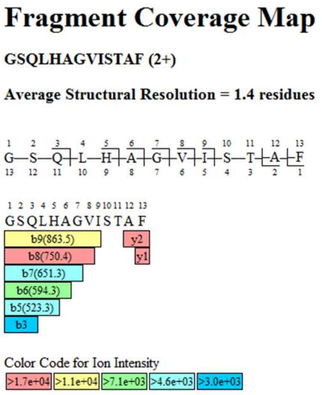


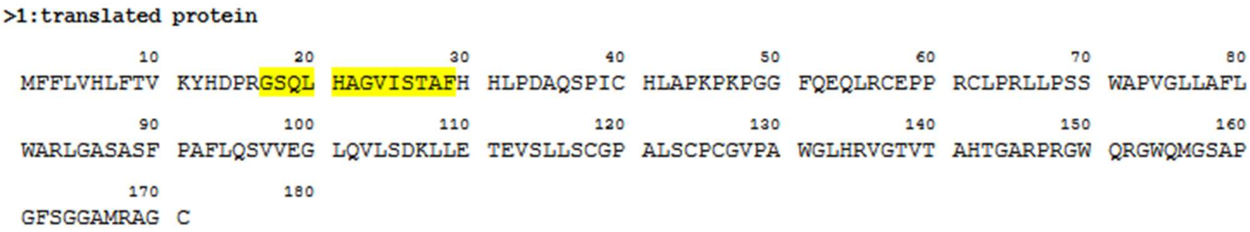



File: Unknown-G
Predicted +2, Peptide=LVHLF
NL:
2.19E6
a₁
86.0964
a₂
185.1648
223.1553
y₁
166.0863
y₂
279.1703
b₃
350.2187
y₃
416.2292
y₄
515.2977
File: Unknown-G
F: FTMS + c ESI d Full ms2 314.6950@hcd27.00 [50.0000-660.0000]
Experimental ID=1:L4-F8 = 627.3744m, +2, Peptide=LVHLF
NL:
3.44E5
a₁
86.0971
a₂
185.1653
120.0812
y₁
166.0864
y₂
279.1712
b₃
350.2191
368.2307
y₃
416.2302
y₄
515.2985
Relative Abundance
100
50
0
100
50
0
100
150
200
250
300
350
400
450
500
m/z

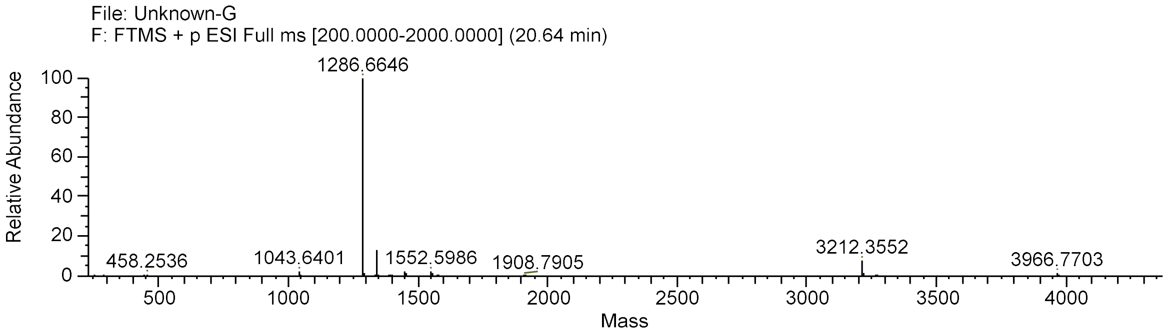
No.129 GSQLHAGVISTAF (2+)

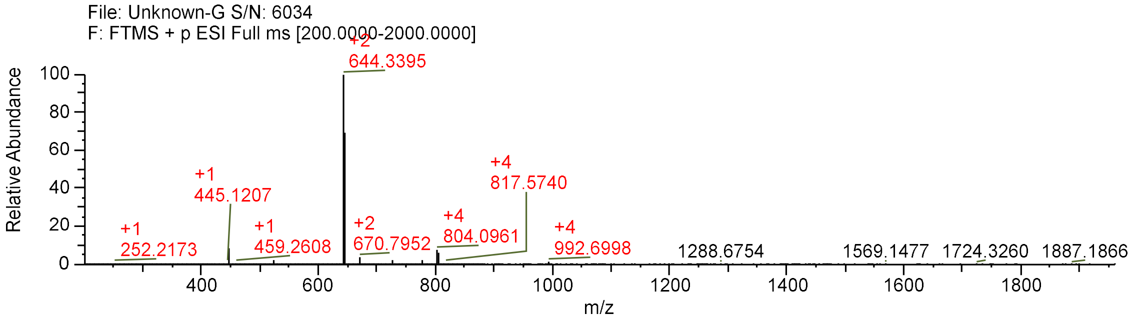


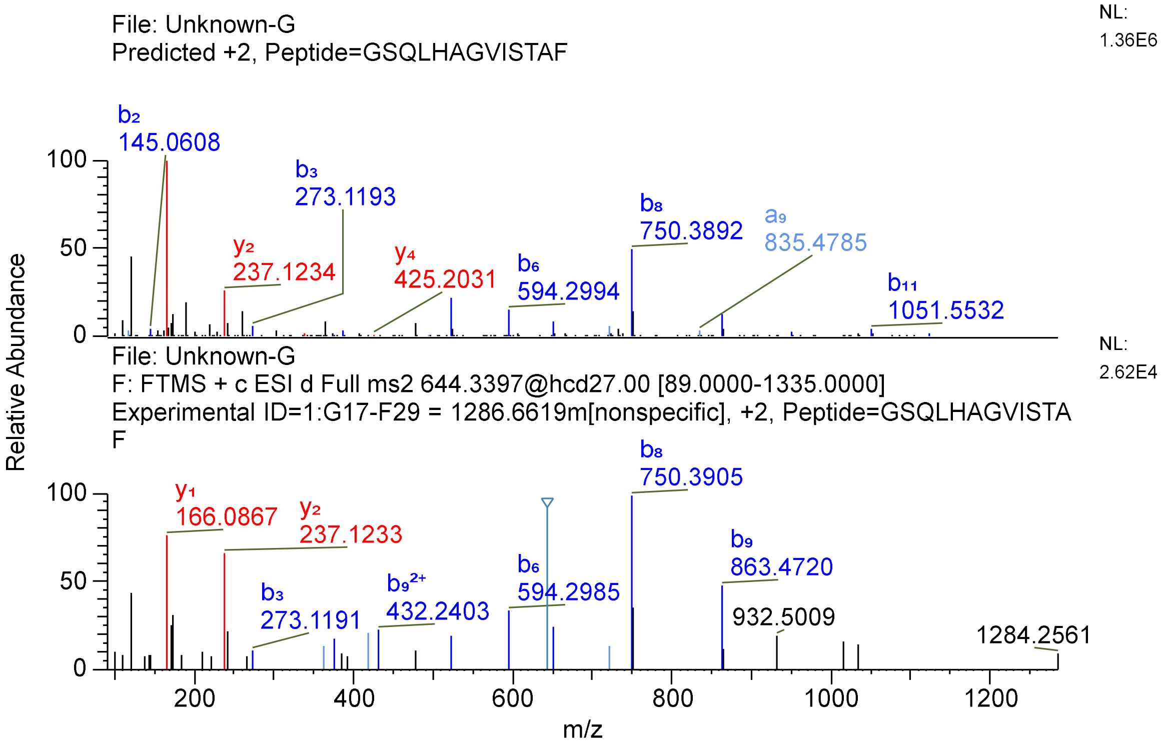




```
>1:translated protein
         10         20         30         40         50         60         70         80
MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL
         90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP
        170        180
GFSGGAMRAG C
```



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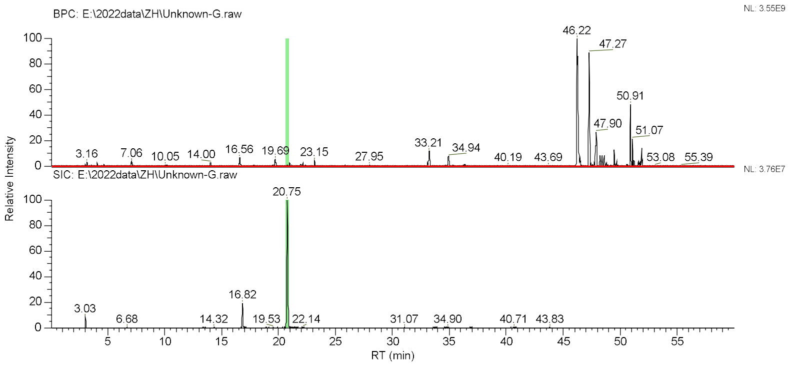
Predicted +2, Peptide=GSQLHAGVISTAF
NL:
1.36E6
b2
145.0608
b3
273.1193
y2
237.1234
y4
425.2031
b6
594.2994
b8
750.3892
a9
835.4785
b11
1051.5532
File: Unknown-G
F: FTMS + c ESI d Full ms2 644.3397@hcd27.00 [89.0000-1335.0000]
Experimental ID=1:G17-F29 = 1286.6619m[nonspecific], +2, Peptide=GSQLHAGVISTA
F
NL:
2.62E4
y1
166.0867
y2
237.1233
b3
273.1191
b9²⁺
432.2403
b6
594.2985
b8
750.3905
b9
863.4720
932.5009
1284.2561
Relative Abundance
100
50
0
100
50
0
200
400
600
800
1000
1200
m/z

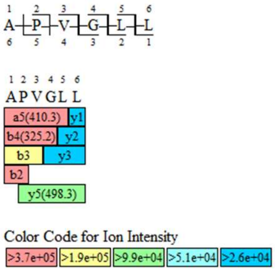
No.130 APVGLL (1+)



Fragment Coverage Map

APVGLL (1+)

Average Structural Resolution = 1.0 residues



>1:translated protein

```
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MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL
        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP
       170        180
GFSGGAMRAG C
```

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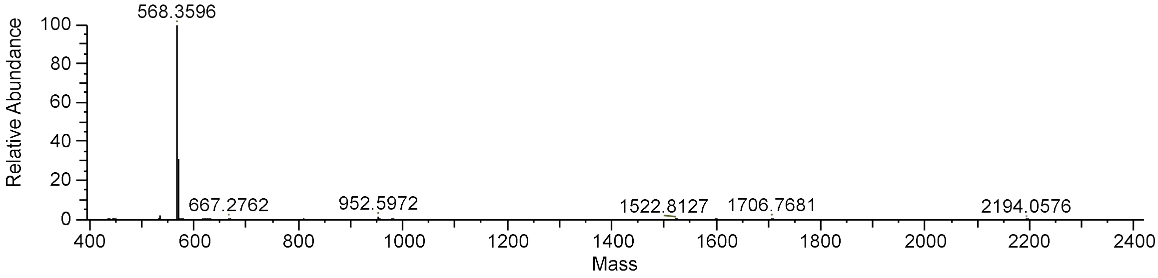
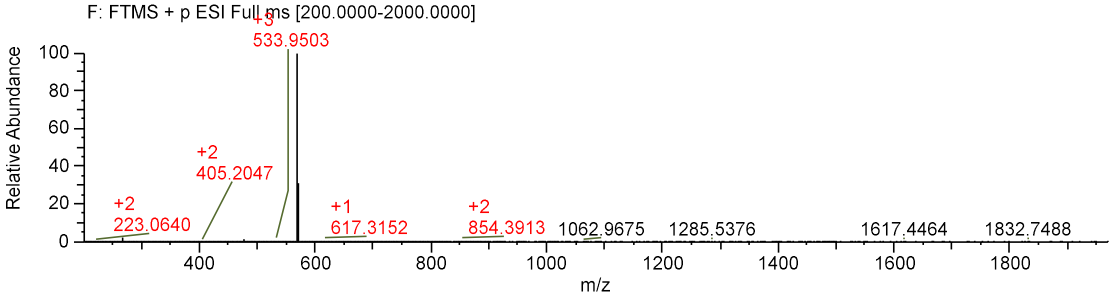
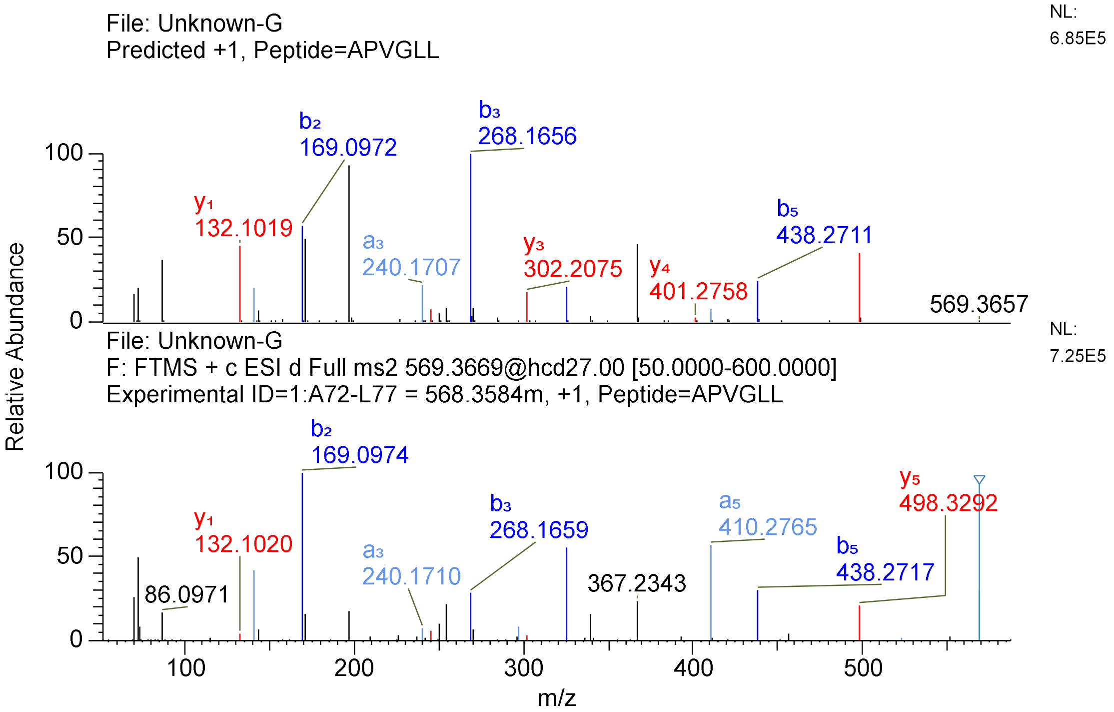
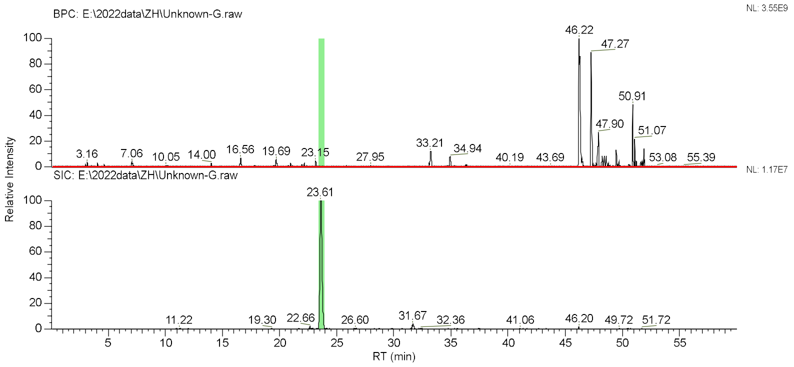


File: Unknown-G S/N: 13427
F: FTMS + p ESI Full ms [200.0000-2000.0000]




File: Unknown-G
Predicted +1, Peptide=APVGLL
NL:
6.85E5
b₂
169.0972
b₃
268.1656
y₁
132.1019
a₃
240.1707
y₃
302.2075
y₄
401.2758
b₅
438.2711
569.3657
File: Unknown-G
F: FTMS + c ESI d Full ms2 569.3669@hcd27.00 [50.0000-600.0000]
Experimental ID=1:A72-L77 = 568.3584m, +1, Peptide=APVGLL
NL:
7.25E5
b₂
169.0974
y₁
132.1020
86.0971
a₃
240.1710
b₃
268.1659
367.2343
a₅
410.2765
b₅
438.2717
y₅
498.3292
Relative Abundance
100
50
0
100
200
300
400
500
m/z

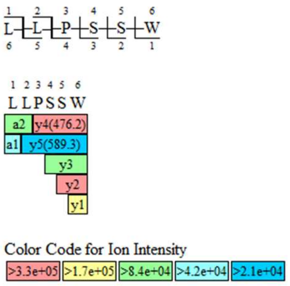
No.161 LLPSSW (1+)



Fragment Coverage Map

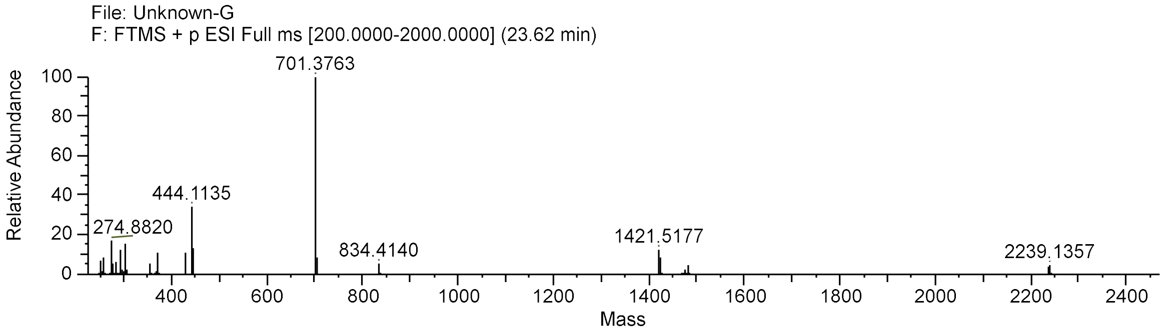
LLPSSW (1+)

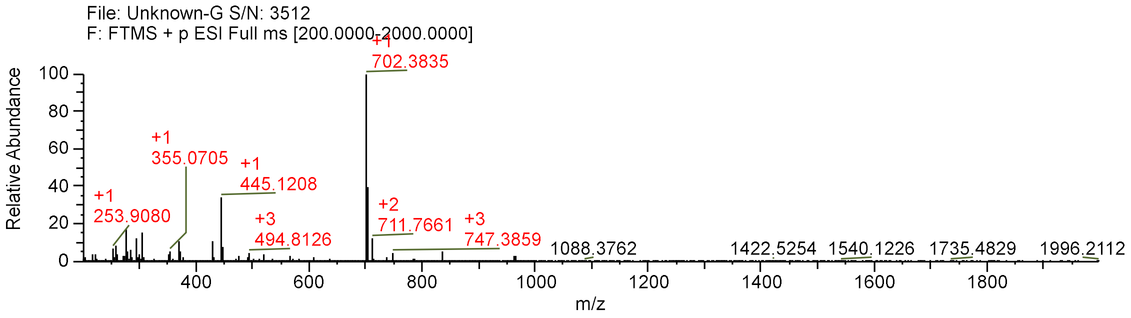
Average Structural Resolution = 1.0 residues

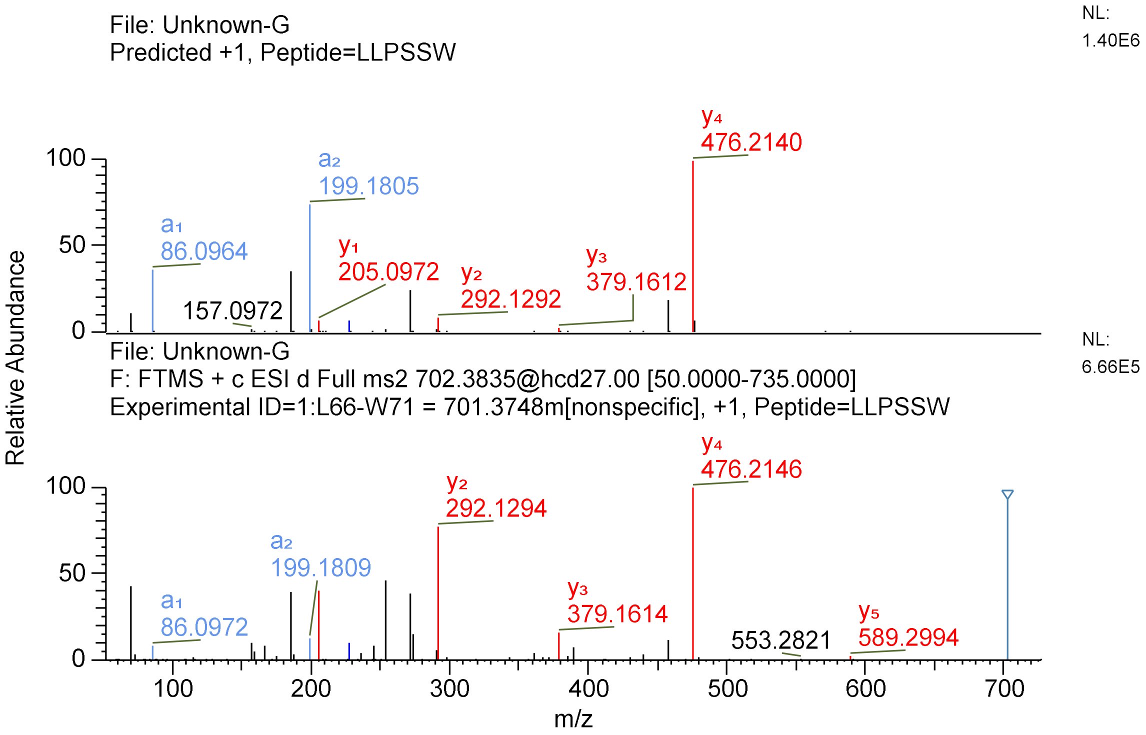


>1:translated protein

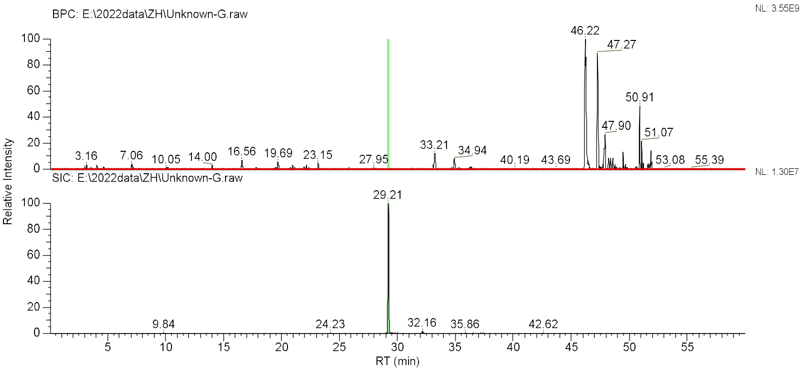
```
        10         20         30         40         50         60         70         80
MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL

        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP

       170        180
GFSGGAMRAG C
```






File: Unknown-G
Predicted +1, Peptide=LLPSSW
NL:
1.40E6
Relative Abundance
100
50
0
a₁
86.0964
157.0972
a₂
199.1805
y₁
205.0972
y₂
292.1292
y₃
379.1612
y₄
476.2140
File: Unknown-G
F: FTMS + c ESI d Full ms2 702.3835@hcd27.00 [50.0000-735.0000]
Experimental ID=1:L66-W71 = 701.3748m[nonspecific], +1, Peptide=LLPSSW
NL:
6.66E5
100
50
0
a₁
86.0972
a₂
199.1809
y₂
292.1294
y₃
379.1614
y₄
476.2146
553.2821
y₅
589.2994
100
200
300
400
500
600
700
m/z

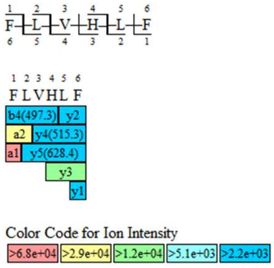
No.181 FLVHLF (2+)



Fragment Coverage Map

FLVHLF (2+)

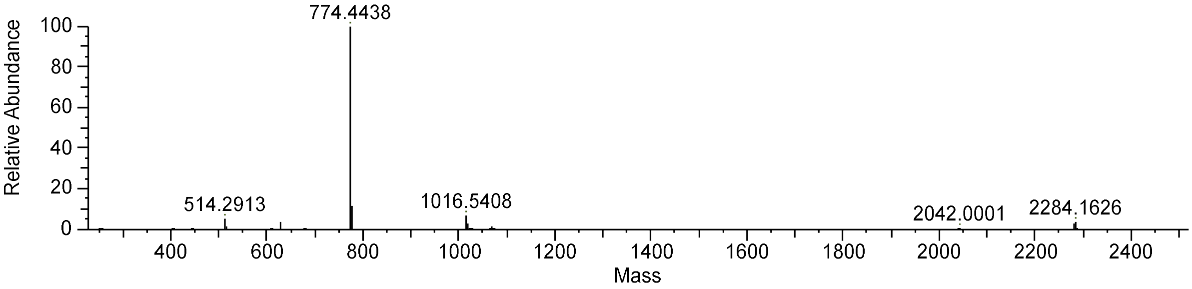
Average Structural Resolution = 1.0 residues



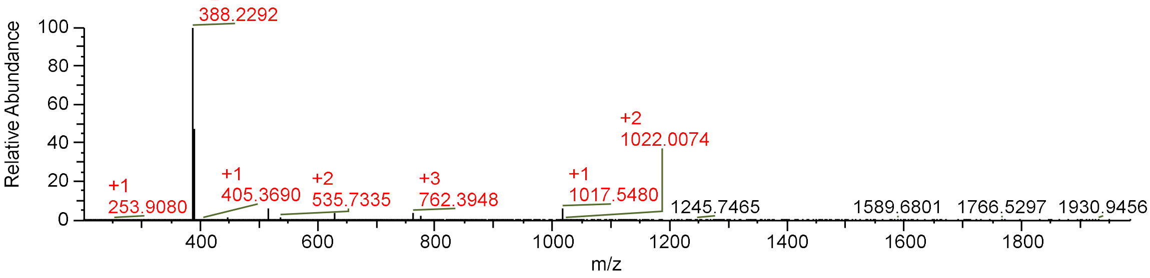
>1:translated protein

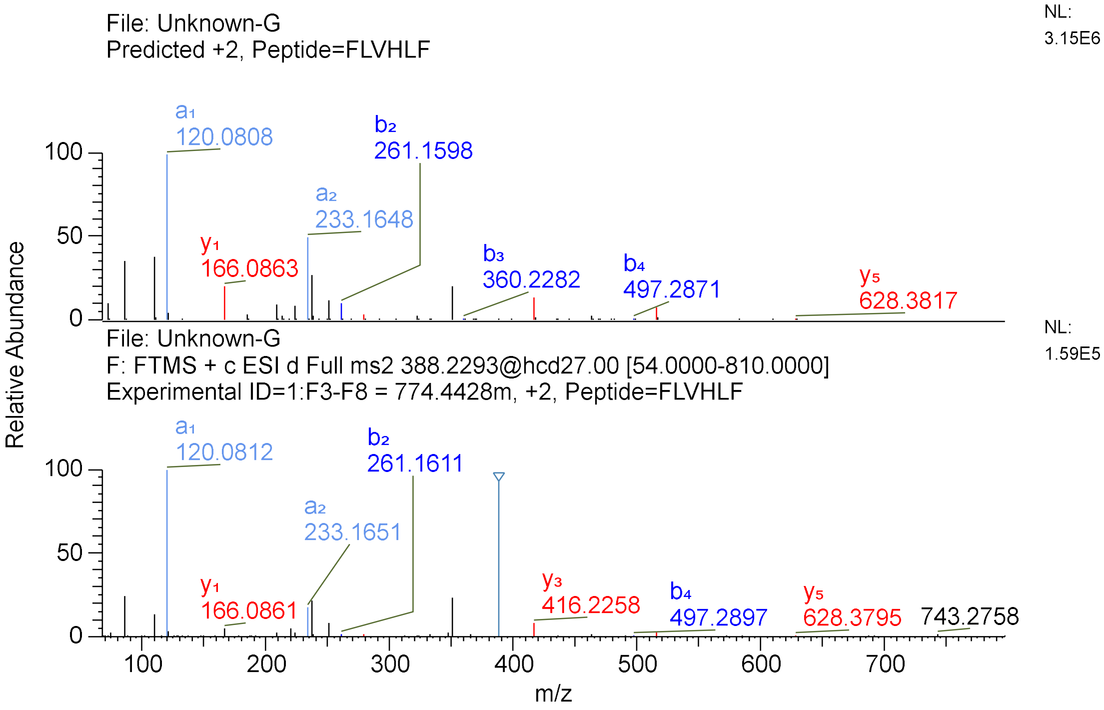
```
        10         20         30         40         50         60         70         80
MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL
        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP
       170        180
GFSGGAMRAG C
```

File: Unknown-G
F: FTMS + p ESI Full ms [200.0000-2000.0000] (29.22 min)

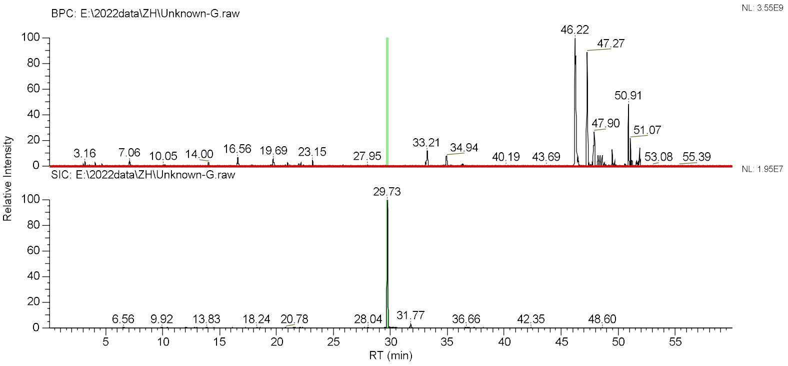


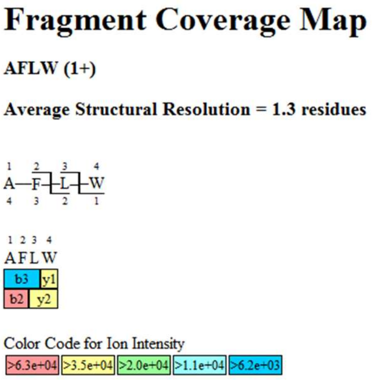
File: Unknown-G S/N: 3130
F: FTMS + p ESI Full ms [200.0000-2000.0000]




File: Unknown-G
Predicted +2, Peptide=FLVHLF
NL:
3.15E6
a₁
120.0808
b₂
261.1598
a₂
233.1648
y₁
166.0863
b₃
360.2282
b₄
497.2871
y₅
628.3817
100
50
0
Relative Abundance
File: Unknown-G
F: FTMS + c ESI d Full ms2 388.2293@hcd27.00 [54.0000-810.0000]
Experimental ID=1:F3-F8 = 774.4428m, +2, Peptide=FLVHLF
NL:
1.59E5
a₁
120.0812
b₂
261.1611
a₂
233.1651
y₁
166.0861
y₃
416.2258
b₄
497.2897
y₅
628.3795
743.2758
100
50
0
100
200
300
400
500
600
700
m/z

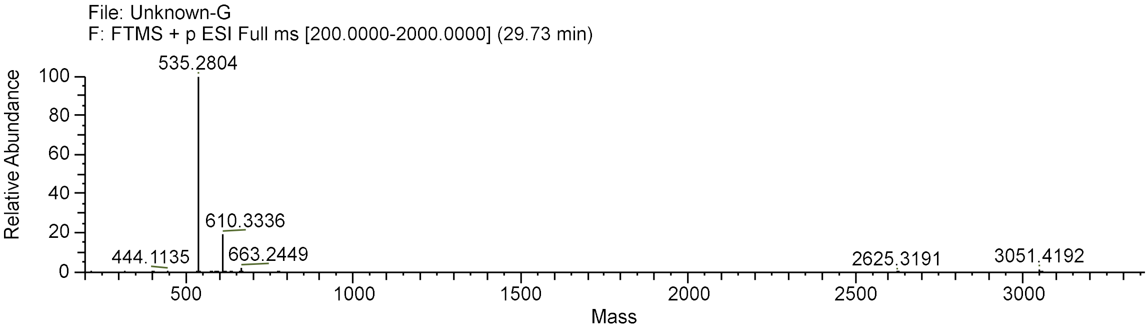
No.182 AFLW (1+)

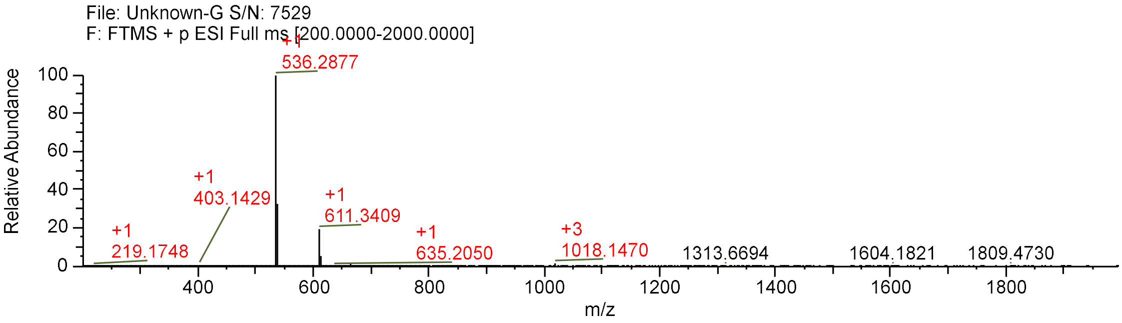


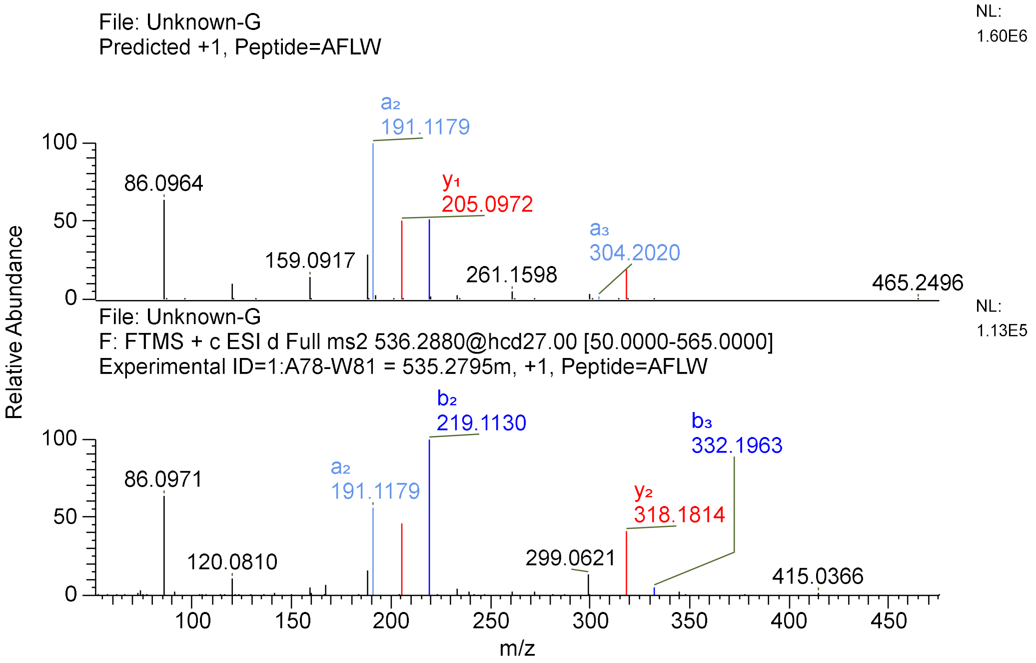


>1:translated protein

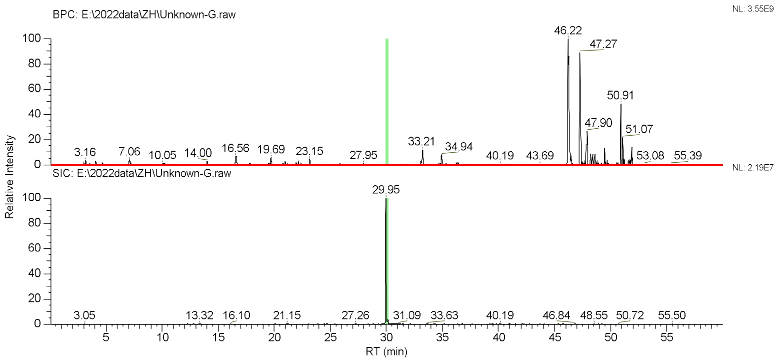
```
        10         20         30         40         50         60         70         80
MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL

        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP

       170        180
GFSGGAMRAG C
```






File: Unknown-G
Predicted +1, Peptide=AFLW
NL:
1.60E6
a₂
191.1179
y₁
205.0972
a₃
304.2020
86.0964
159.0917
261.1598
465.2496
100
50
0
File: Unknown-G
F: FTMS + c ESI d Full ms2 536.2880@hcd27.00 [50.0000-565.0000]
Experimental ID=1:A78-W81 = 535.2795m, +1, Peptide=AFLW
NL:
1.13E5
b₂
219.1130
b₃
332.1963
a₂
191.1179
y₂
318.1814
86.0971
120.0810
299.0621
415.0366
100
50
0
Relative Abundance
100
150
200
250
300
350
400
450
m/z

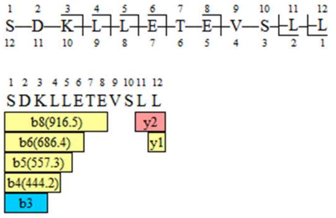
No.183 SDKLLETEVSLL (2+)



Fragment Coverage Map

SDKLLETEVSLL (2+)

Average Structural Resolution = 1.5 residues

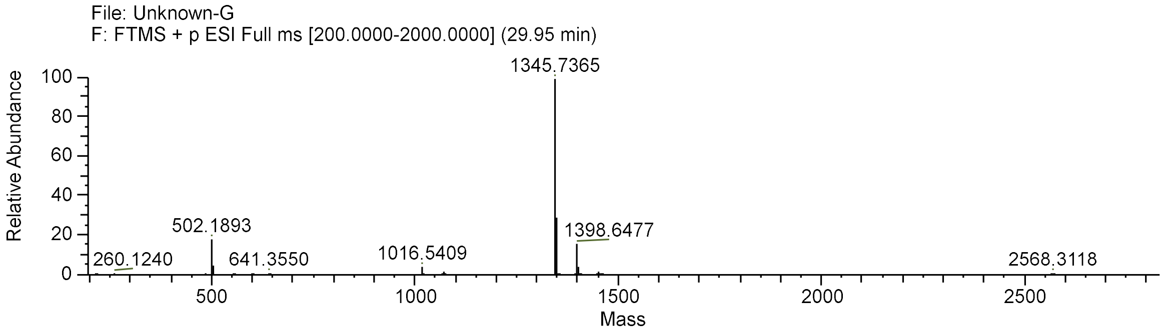


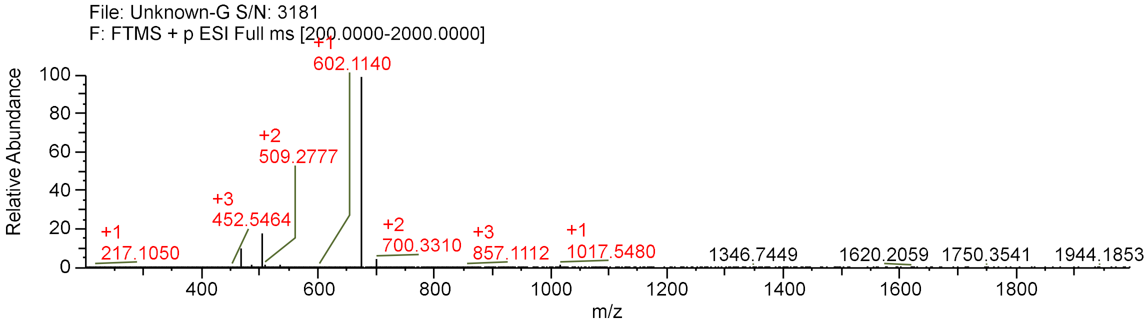
Color Code for Ion Intensity

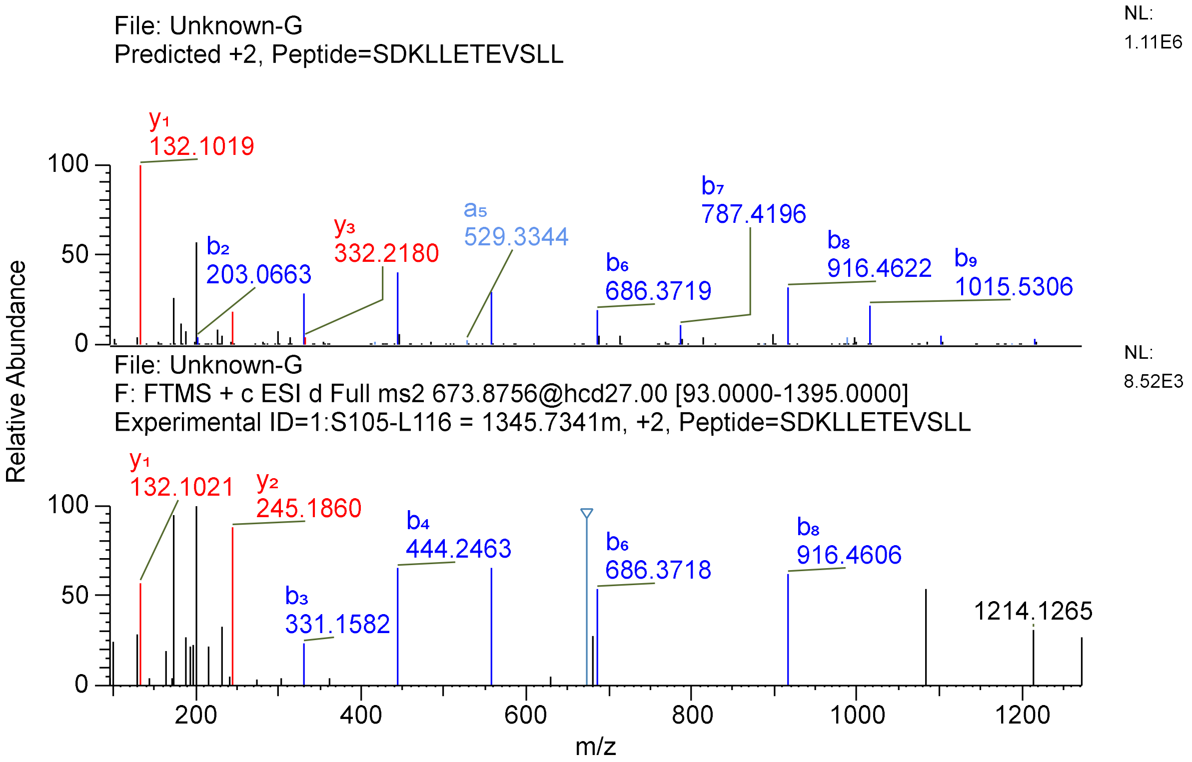
🟥 >5.8e+03 🟨 >4.5e+03 🟩 >3.4e+03 🟦 >2.6e+03 🟦 >2.0e+03

>1:translated protein

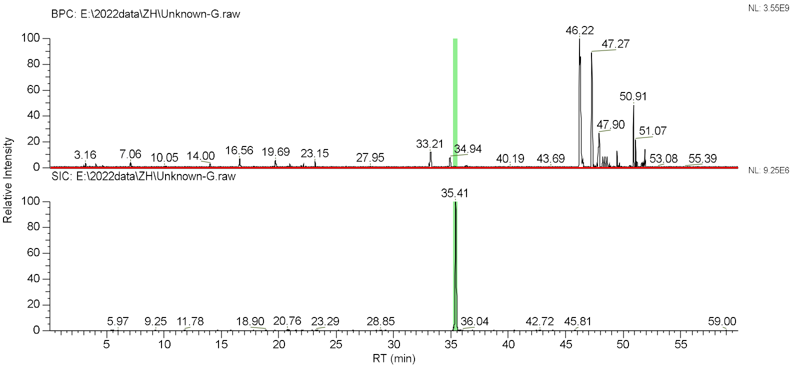
```
        10         20         30         40         50         60         70         80
MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL

        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP

       170        180
GFSGGAMRAG C
```






File: Unknown-G
Predicted +2, Peptide=SDKLLETEVSLL
NL:
1.11E6
y₁
132.1019
b₂
203.0663
y₃
332.2180
a₅
529.3344
b₆
686.3719
b₇
787.4196
b₈
916.4622
b₉
1015.5306
File: Unknown-G
F: FTMS + c ESI d Full ms2 673.8756@hcd27.00 [93.0000-1395.0000]
Experimental ID=1:S105-L116 = 1345.7341m, +2, Peptide=SDKLLETEVSLL
NL:
8.52E3
y₁
132.1021
y₂
245.1860
b₃
331.1582
b₄
444.2463
b₆
686.3718
b₈
916.4606
1214.1265
Relative Abundance
100
50
0
100
50
0
200
400
600
800
1000
1200
m/z

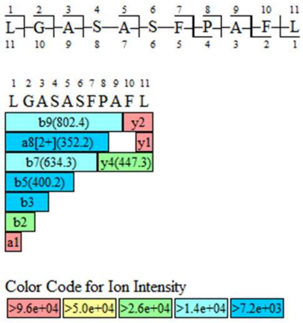
No.207 LGASASFPAFL (2+)



Fragment Coverage Map

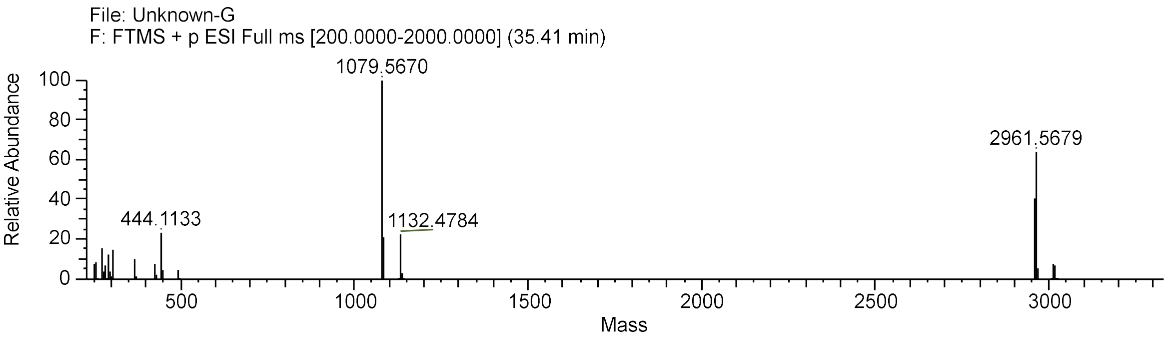
LGASASFPAFL (2+)

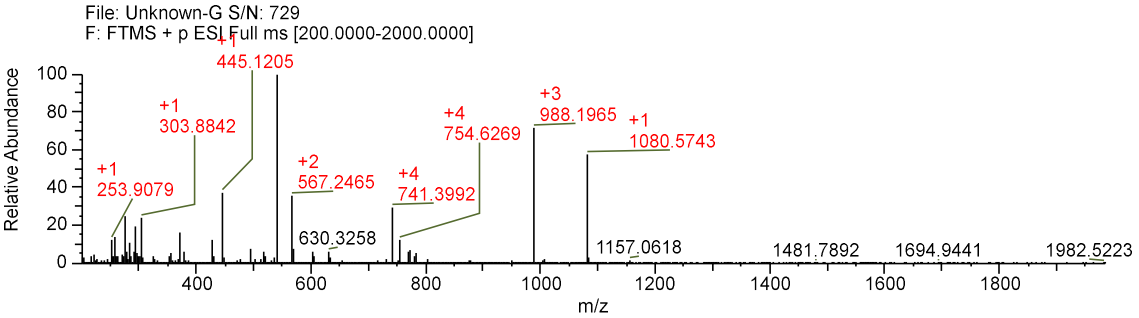
Average Structural Resolution = 1.2 residues

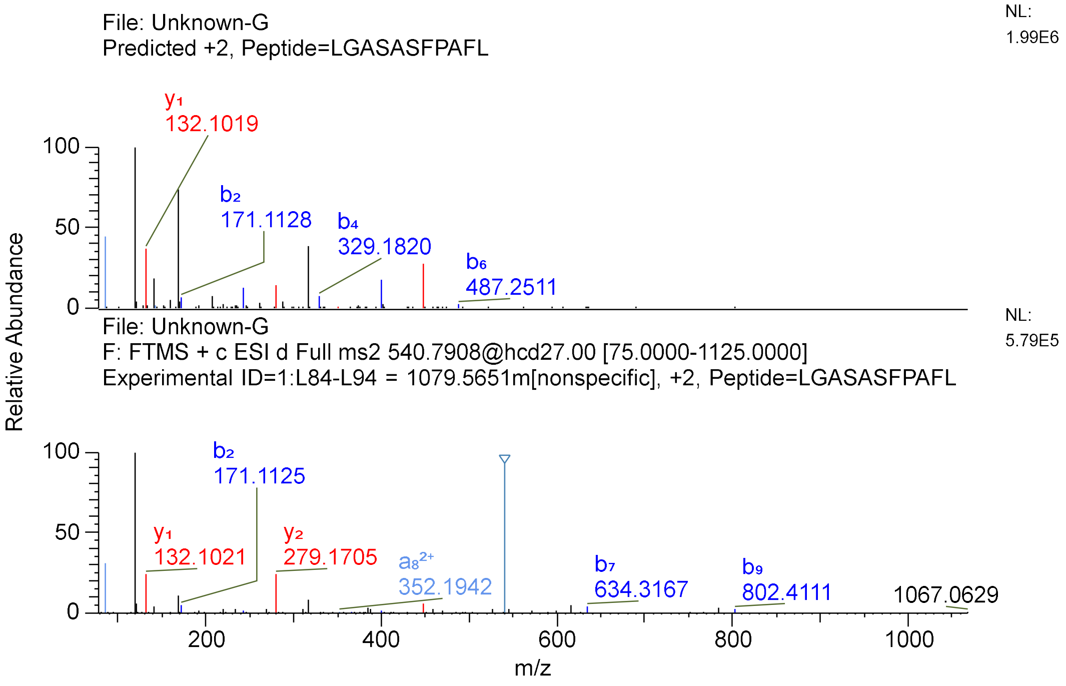


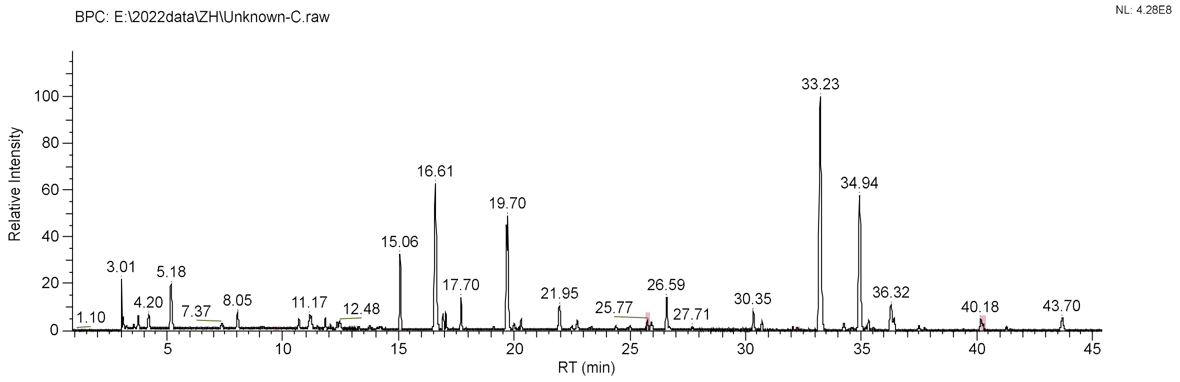
>1:translated protein

```
        10         20         30         40         50         60         70         80
MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL

        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP

       170        180
GFSGGAMRAG C
```






File: Unknown-G
Predicted +2, Peptide=LGASASFPAFL
NL:
1.99E6
y₁
132.1019
b₂
171.1128
b₄
329.1820
b₆
487.2511
100
50
0
Relative Abundance
File: Unknown-G
F: FTMS + c ESI d Full ms2 540.7908@hcd27.00 [75.0000-1125.0000]
Experimental ID=1:L84-L94 = 1079.5651m[nonspecific], +2, Peptide=LGASASFPAFL
NL:
5.79E5
100
50
0
b₂
171.1125
y₁
132.1021
y₂
279.1705
a₈²⁺
352.1942
b₇
634.3167
b₉
802.4111
1067.0629
200
400
600
800
1000
m/z



No.	Identification	Positions	Peptide Sequence	Mod	Site	Δ ppm	Conf. Score	Best ASR	ID Type	RT	M/Z	Charge St.	Mono Mass Exp.	Avg Mass Exp.	Mono Mass Theo.	Missed Cleavages	MS Area
101	1:G100-K107 = 858.4811m[nc	100-107	GLQVLSDK	nonspecific		1.92	100	1.1	MS2	9.72	430.249	2	858.4827	858.8	858.4811	1	809016.06
131	1:V113-S117 = 517.3112m[no	113-117	VSLLS	nonspecific		1.29	89.5	1	MS2	15.12	518.319	1	517.3118	517.53	517.3112	0	379157.94
178	1:G100-E110 = 1213.6918m	100-110	GLQVLSDKLLE	None		1.08	100	1.6	MS2	25.77	607.854	2	1213.6931	1214.29	1213.6918	1	2608572.25
193	1:G100-E110 = 1213.6918m(K	100-110	GLQVLSDKLLE	43.0072	K107	1.05	100	1.8	MS2	32.25	629.357	2	1256.7003	1257.31	1256.699	1	737955.12
217	1:L84-E99 = 1621.8352m[non	84-99	LGASASFPAFLQSVVE	nonspecific		1.15	100	1.2	MS2	40.26	811.926	2	1621.837	1622.75	1621.8352	0	3005006.5

Sequence Coverage Map - User Defined

Created on 09/09/22
Minimum MS Signal = 0
Data File = Unknown-C.raw
Protease = Glu-C

Proteins	Number of MS Peaks	MS Peak Area	Sequence Coverage	Abundance (mol)
1:translated protein	5	100.0%	18.7%	100.00%
Unidentified	0	0.0%		

Minimum Recovery = 0%
Minimum Recovery of Overlapping Peptides = 0%
Minimum Confidence = 0
Maximum Mass = 11000

Color code for peptide recovery

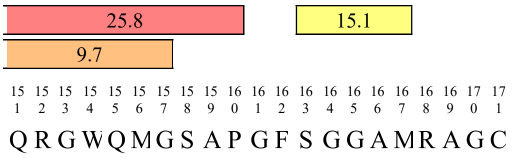
>50.0%	>20.0%	>10.0%	>5.0%	>2.0%	>1.0%	>0.5%	>0.2%	>0.1%	>0.0%
good			fair		poor				

translated protein

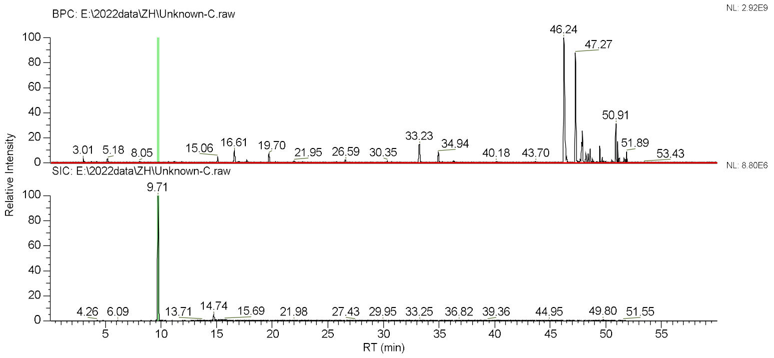
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50
M F F L V H L F T V K Y H D P R G S Q L H A G V I S T A F H H L P D A Q S P I C H L A P K P K P G G

51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
F Q E Q L R C E P P R C L P R L L P S S W A P V G L L A F L W A R L G A S A S F P A F L Q S V V E G

101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
L Q V L S D K L L E T E V S L L S C G P A L S C P C G V P A W G L H R V G T V T A H T G A R P R G W


25.8
15.1
9.7
151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171
Q R G W Q M G S A P G F S G G A M R A G C

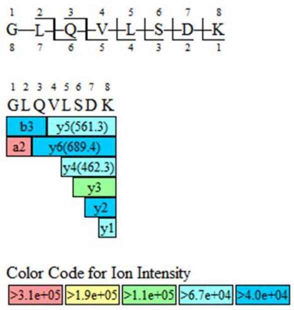
No.101 GLQVLSDK (2+)



Fragment Coverage Map

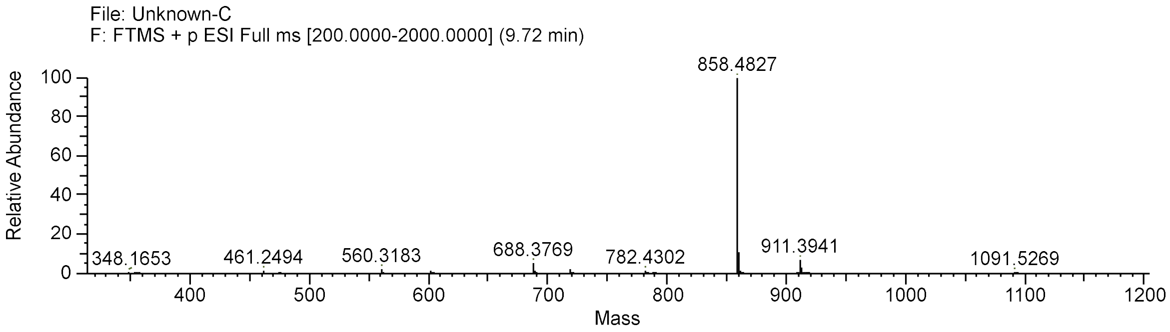
GLQVLSDK (2+)

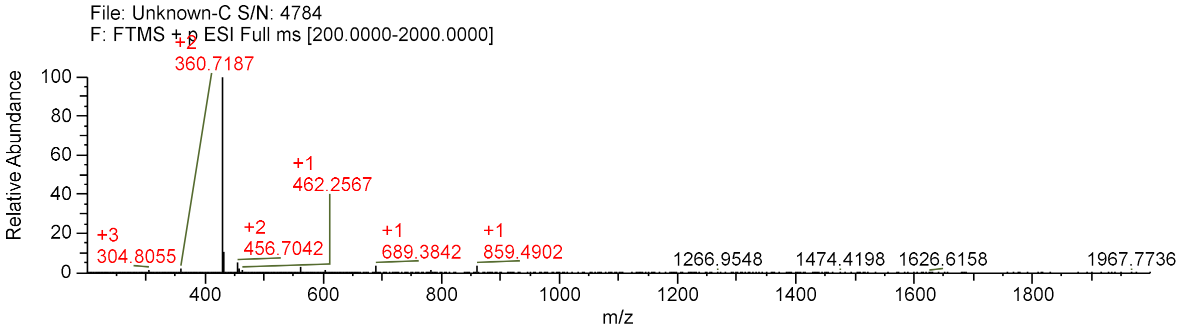
Average Structural Resolution = 1.1 residues

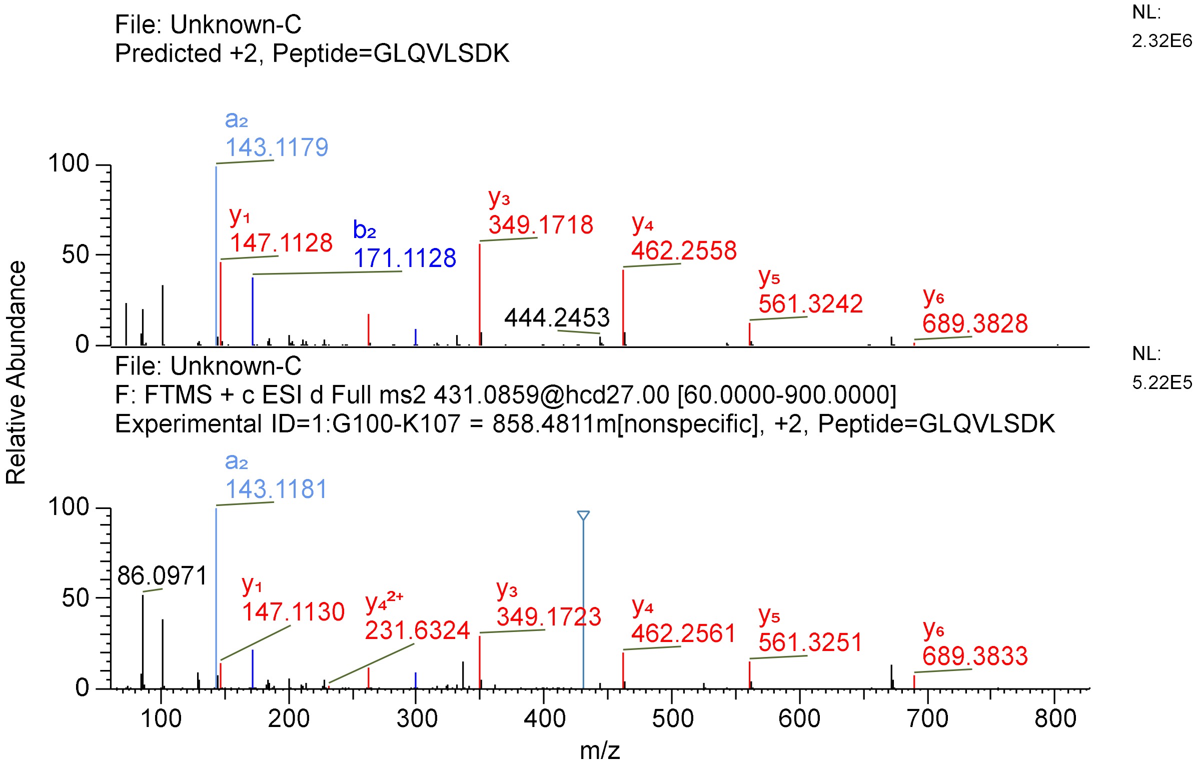


>1:translated protein

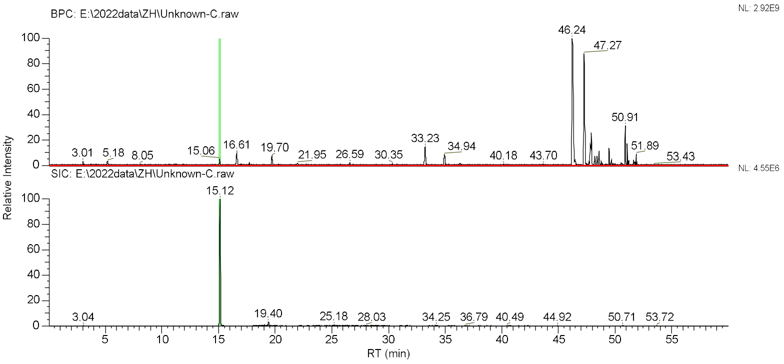
```
        10         20         30         40         50         60         70         80
MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL

        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP

       170        180
GFSGGAMRAG C
```






File: Unknown-C
Predicted +2, Peptide=GLQVLSDK
NL:
2.32E6
a₂
143.1179
y₁
147.1128
b₂
171.1128
y₃
349.1718
444.2453
y₄
462.2558
y₅
561.3242
y₆
689.3828
100
50
0
File: Unknown-C
F: FTMS + c ESI d Full ms2 431.0859@hcd27.00 [60.0000-900.0000]
Experimental ID=1:G100-K107 = 858.4811m[nonspecific], +2, Peptide=GLQVLSDK
NL:
5.22E5
a₂
143.1181
86.0971
y₁
147.1130
y₄²⁺
231.6324
y₃
349.1723
y₄
462.2561
y₅
561.3251
y₆
689.3833
100
50
0
Relative Abundance
100
200
300
400
500
600
700
800
m/z

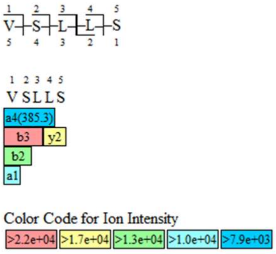
No.131 VSLLS (1+)



Fragment Coverage Map

VSLLS (1+)

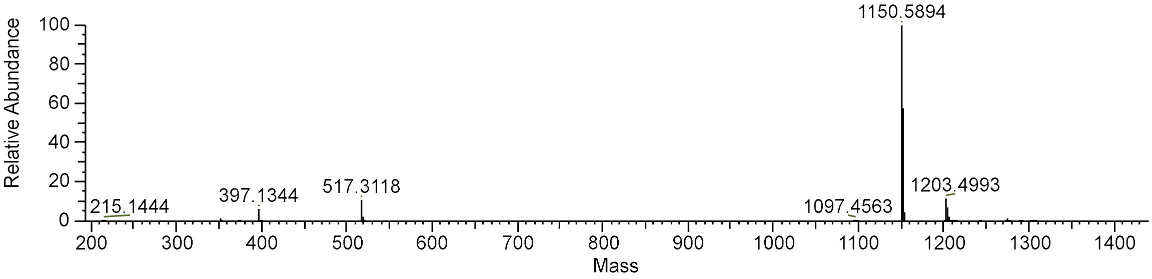
Average Structural Resolution = 1.0 residues



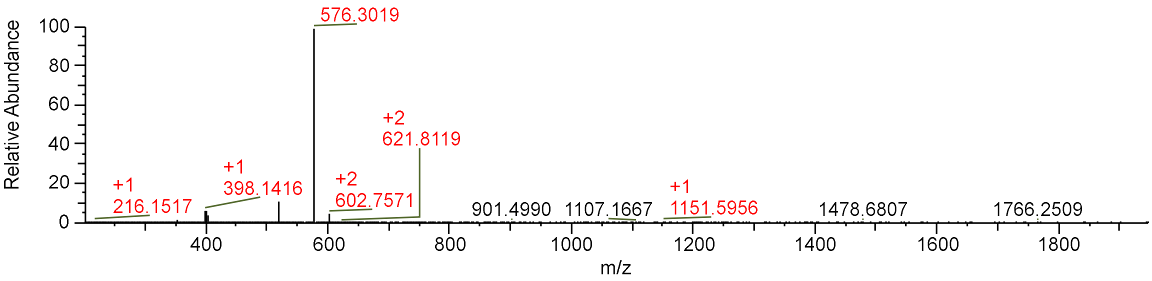
>1:translated protein

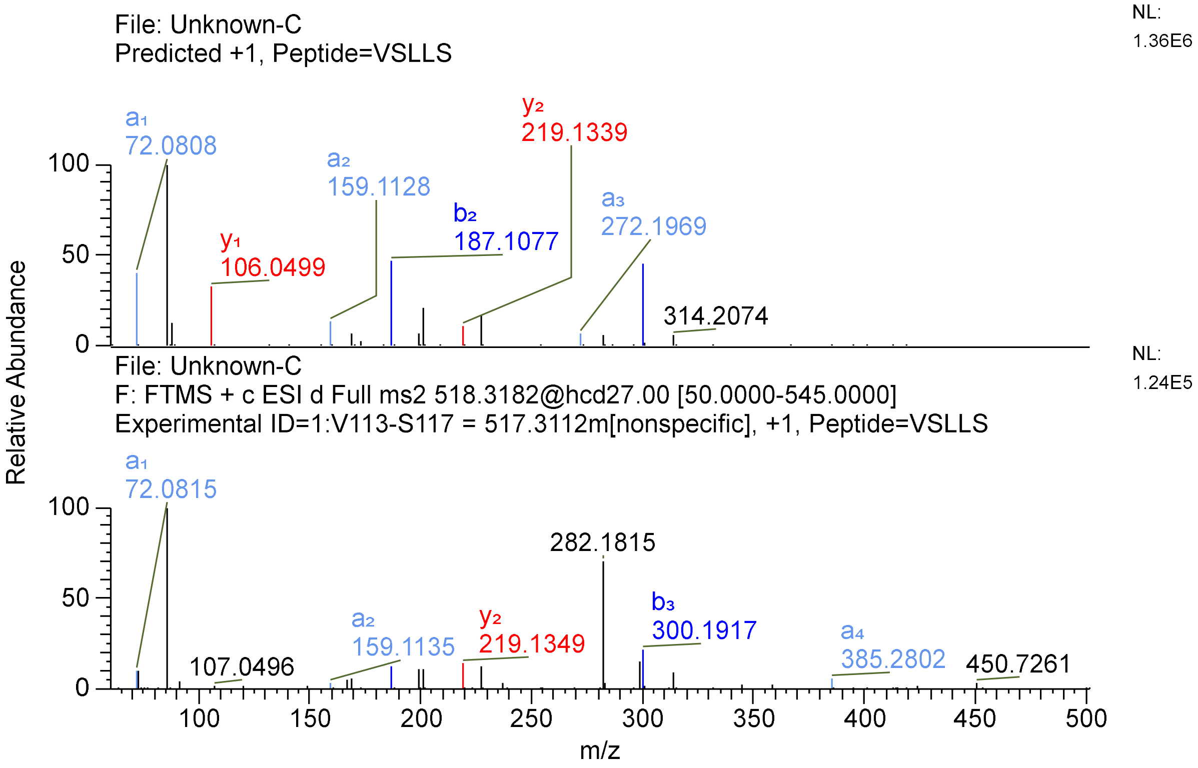
```
        10         20         30         40         50         60         70         80
MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL

        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP

       170        180
GFSGGAMRAG C
```

File: Unknown-C
F: FTMS + p ESI Full ms [200.0000-2000.0000] (15.12 min)

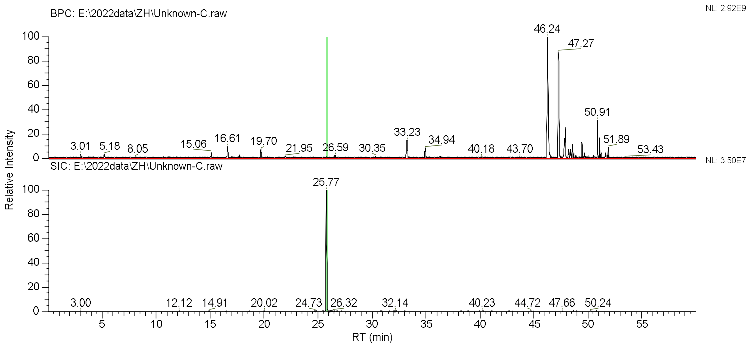


File: Unknown-C S/N: 4848
F: FTMS + p ESI Full ms [200.0000-2000.0000]




File: Unknown-C
Predicted +1, Peptide=VSLLS
NL:
1.36E6
a1
72.0808
y1
106.0499
a2
159.1128
b2
187.1077
y2
219.1339
a3
272.1969
314.2074
File: Unknown-C
F: FTMS + c ESI d Full ms2 518.3182@hcd27.00 [50.0000-545.0000]
Experimental ID=1:V113-S117 = 517.3112m[nonspecific], +1, Peptide=VSLLS
NL:
1.24E5
a1
72.0815
107.0496
a2
159.1135
y2
219.1349
282.1815
b3
300.1917
a4
385.2802
450.7261
Relative Abundance
100
50
0
100
150
200
250
300
350
400
450
500
m/z

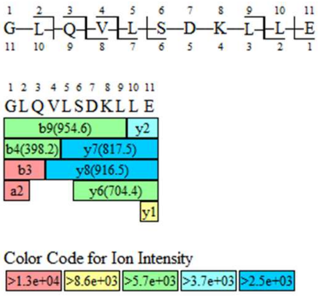
No.178 GLQVLSDKLLE (2+)



Fragment Coverage Map

GLQVLSDKLLE (2+)

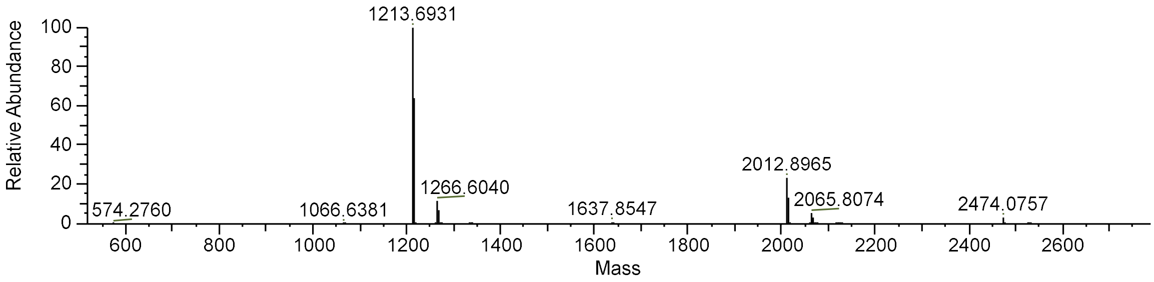
Average Structural Resolution = 1.6 residues



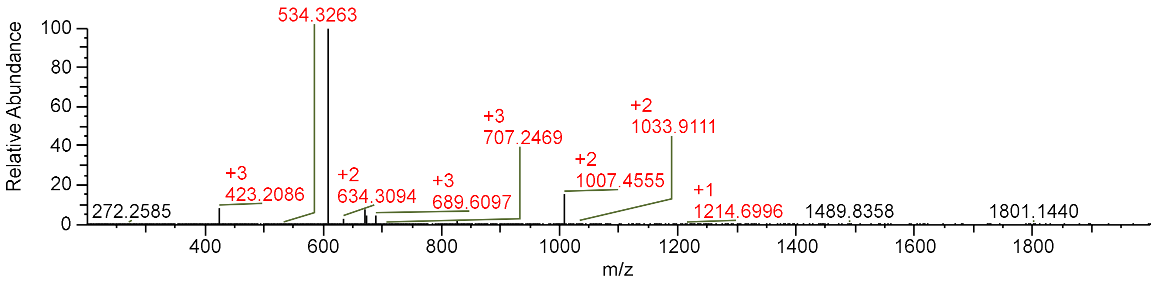
>1:translated protein

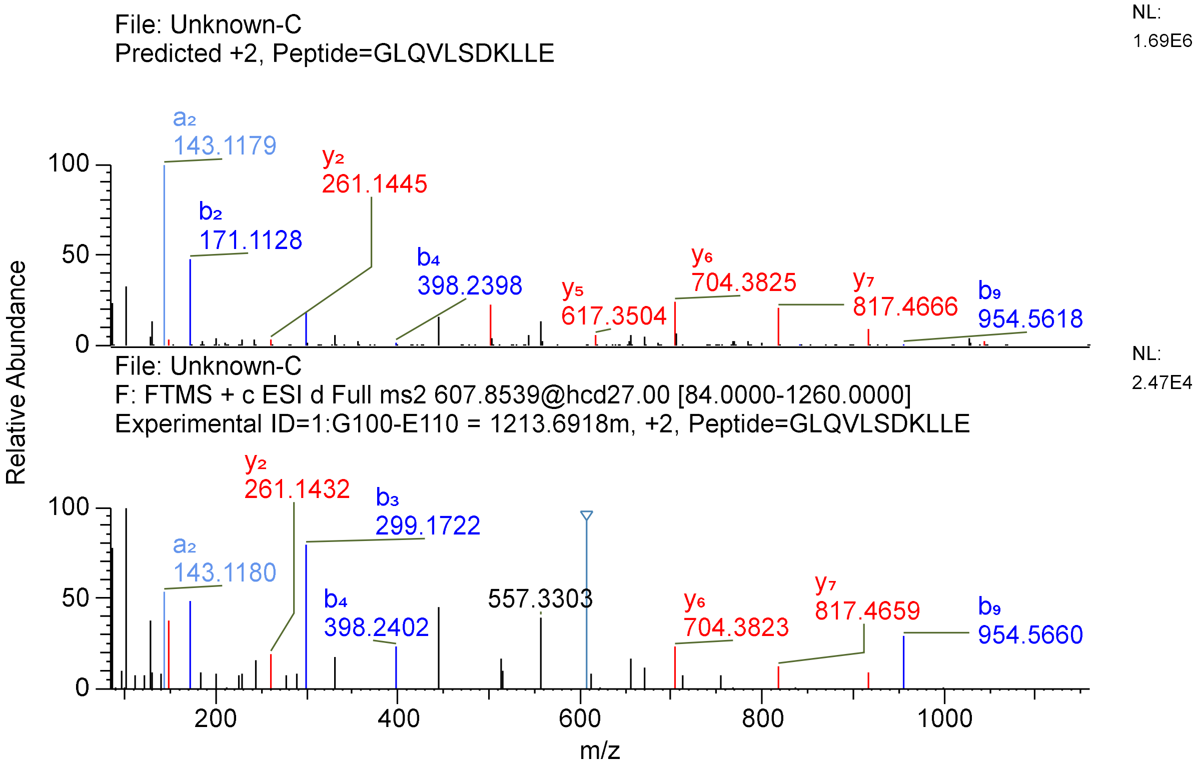
```
        10         20         30         40         50         60         70         80
MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL
        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP
       170        180
GFSGGAMRAG C
```

File: Unknown-C
F: FTMS + p ESI Full ms [200.0000-2000.0000] (25.77 min)

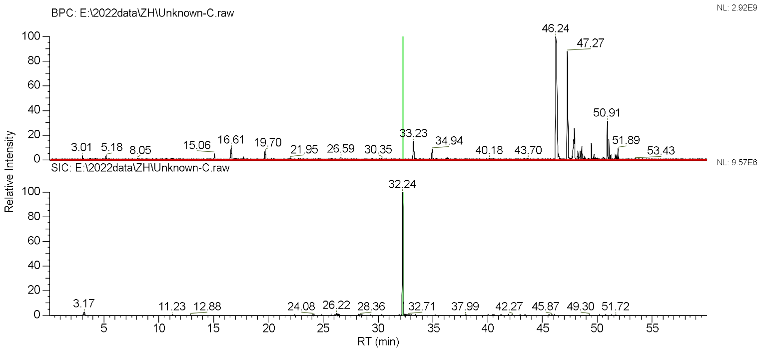


File: Unknown-C S/N: 9225
F: FTMS + p ESI Full ms [200.0000-2000.0000]




File: Unknown-C
Predicted +2, Peptide=GLQVLSDKLLE
NL:
1.69E6
a2
143.1179
b2
171.1128
y2
261.1445
b4
398.2398
y5
617.3504
y6
704.3825
y7
817.4666
b9
954.5618
File: Unknown-C
F: FTMS + c ESI d Full ms2 607.8539@hcd27.00 [84.0000-1260.0000]
Experimental ID=1:G100-E110 = 1213.6918m, +2, Peptide=GLQVLSDKLLE
NL:
2.47E4
y2
261.1432
b3
299.1722
a2
143.1180
b4
398.2402
557.3303
y6
704.3823
y7
817.4659
b9
954.5660
Relative Abundance
100
50
0
100
50
0
200
400
600
800
1000
m/z

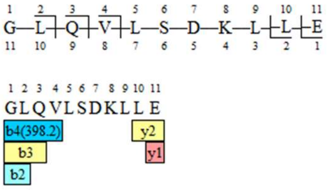
No.193 GLQVLSDKLLE(K8+43.00720) (2+)



Fragment Coverage Map

GLQVLSDKLLE(K8+43.00720) (2+)

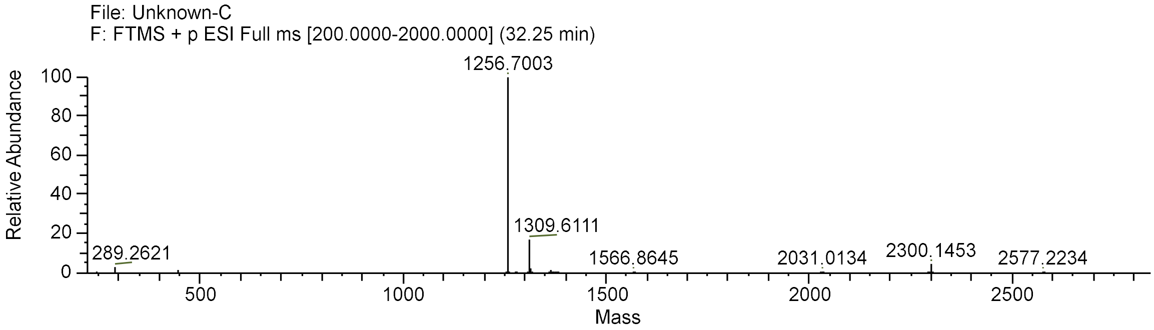
Average Structural Resolution = 1.8 residues

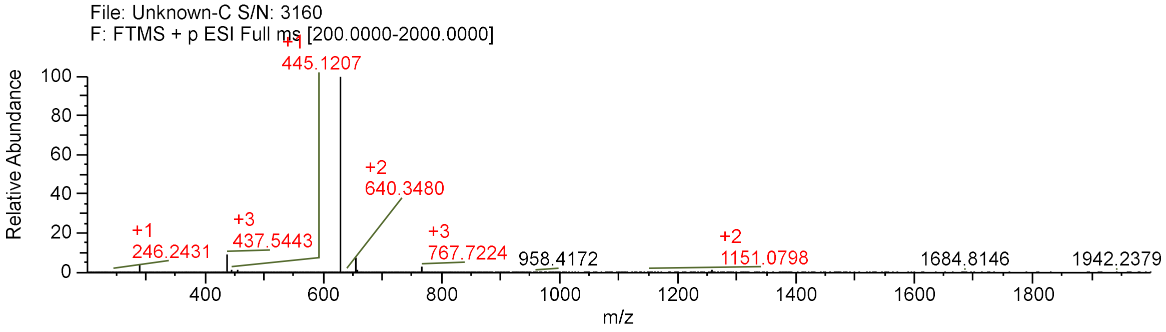


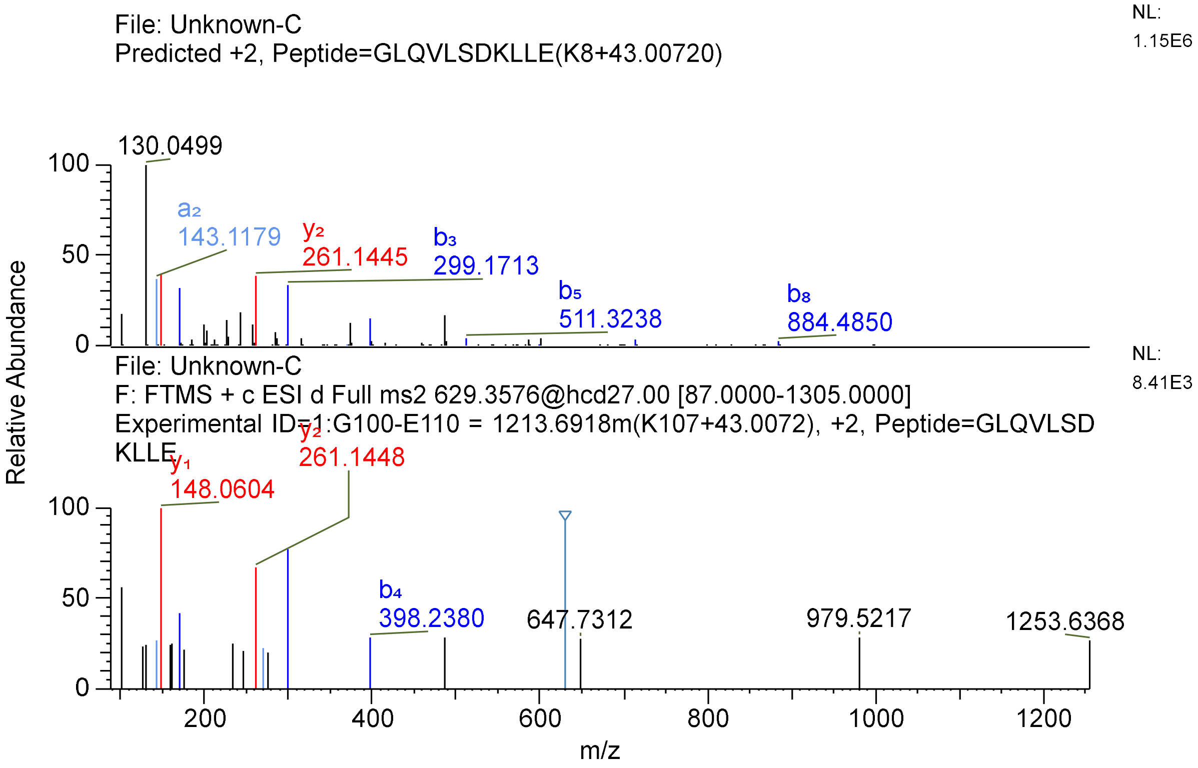
Color Code for Ion Intensity

🟥 >6.6e+03 🟨 >5.1e+03 🟩 >4.0e+03 >3.1e+03 >2.5e+03

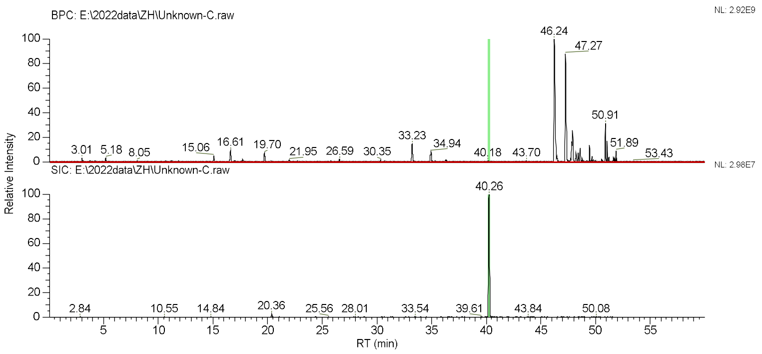
```
>1:translated protein
           10         20         30         40         50         60         70         80
 MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL
           90        100        110        120        130        140        150        160
 WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP
          170        180
 GFSGGAMRAG C
```

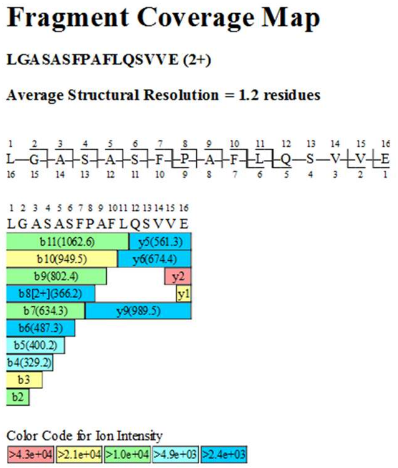





File: Unknown-C
Predicted +2, Peptide=GLQVLSDKLLE(K8+43.00720)
NL:
1.15E6
130.0499
a₂
143.1179
y₂
261.1445
b₃
299.1713
b₅
511.3238
b₈
884.4850
100
50
0
Relative Abundance
File: Unknown-C
F: FTMS + c ESI d Full ms2 629.3576@hcd27.00 [87.0000-1305.0000]
Experimental ID=1:G100-E110 = 1213.6918m(K107+43.0072), +2, Peptide=GLQVLSD
KLLE
NL:
8.41E3
y₁
148.0604
y₂
261.1448
b₄
398.2380
647.7312
979.5217
1253.6368
100
50
0
200
400
600
800
1000
1200
m/z

No.217 LGASASFPAFLQSVVE (2+)

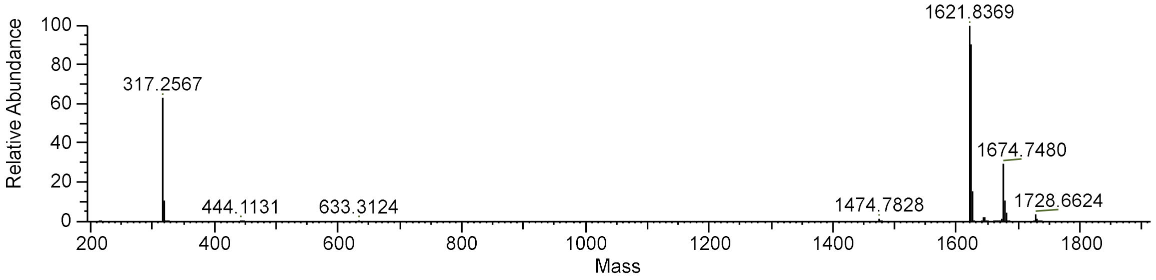




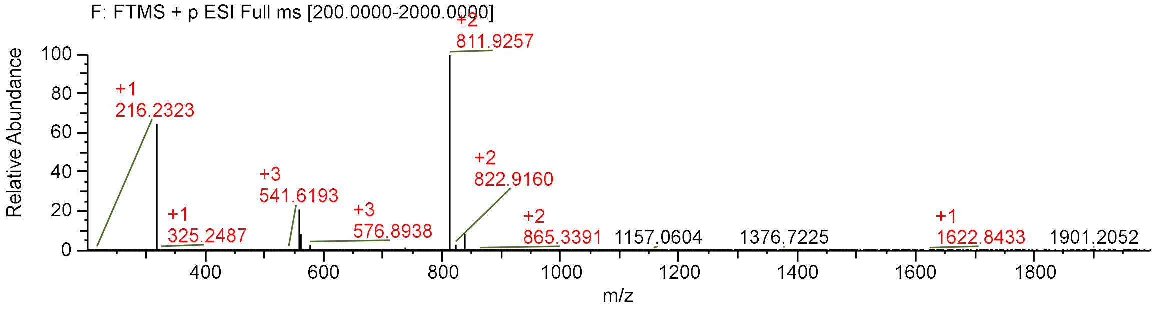
>1:translated protein

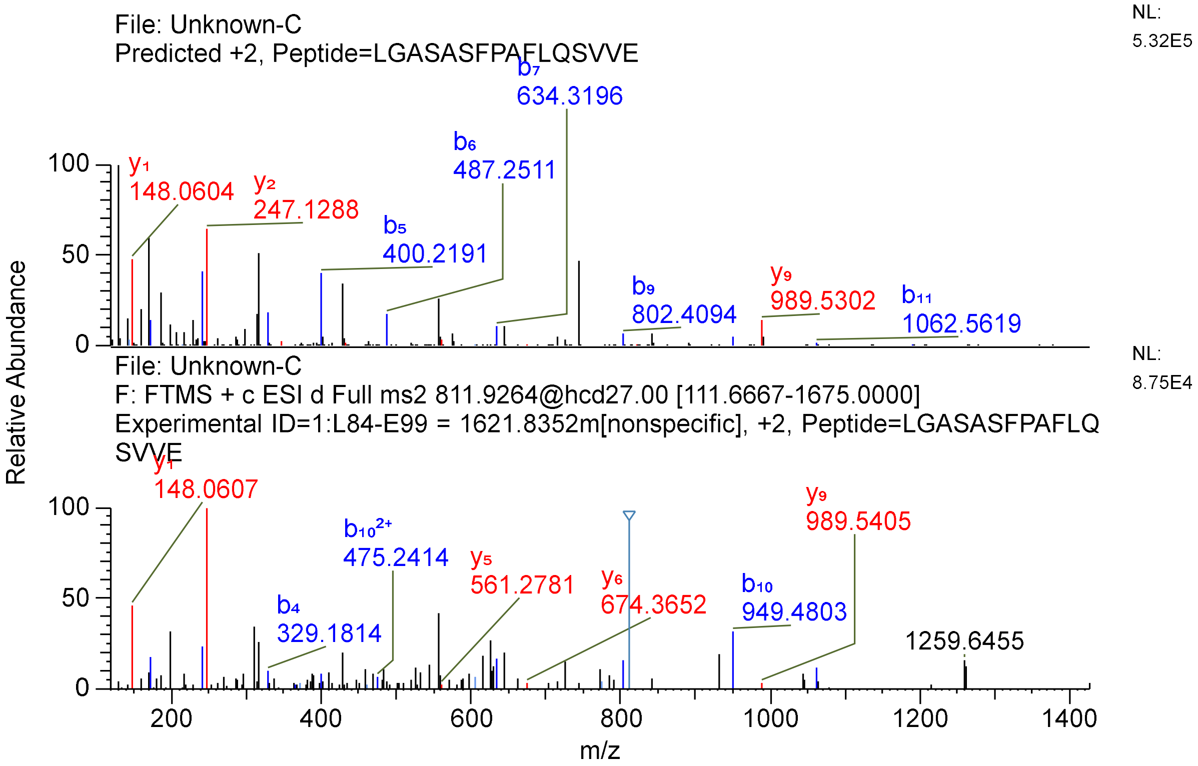
```
        10         20         30         40         50         60         70         80
MFFLVHLFTV KYHDPRGSQL HAGVISTAFH HLPDAQSPIC HLAPKPKPGG FQEQLRCEPP RCLPRLLPSS WAPVGLLAFL
        90        100        110        120        130        140        150        160
WARLGASASF PAFLQSVVEG LQVLSDKLLE TEVSLLSCGP ALSCPCGVPA WGLHRVGTVT AHTGARPRGW QRGWQMGSAP
       170        180
GFSGGAMRAG C
```

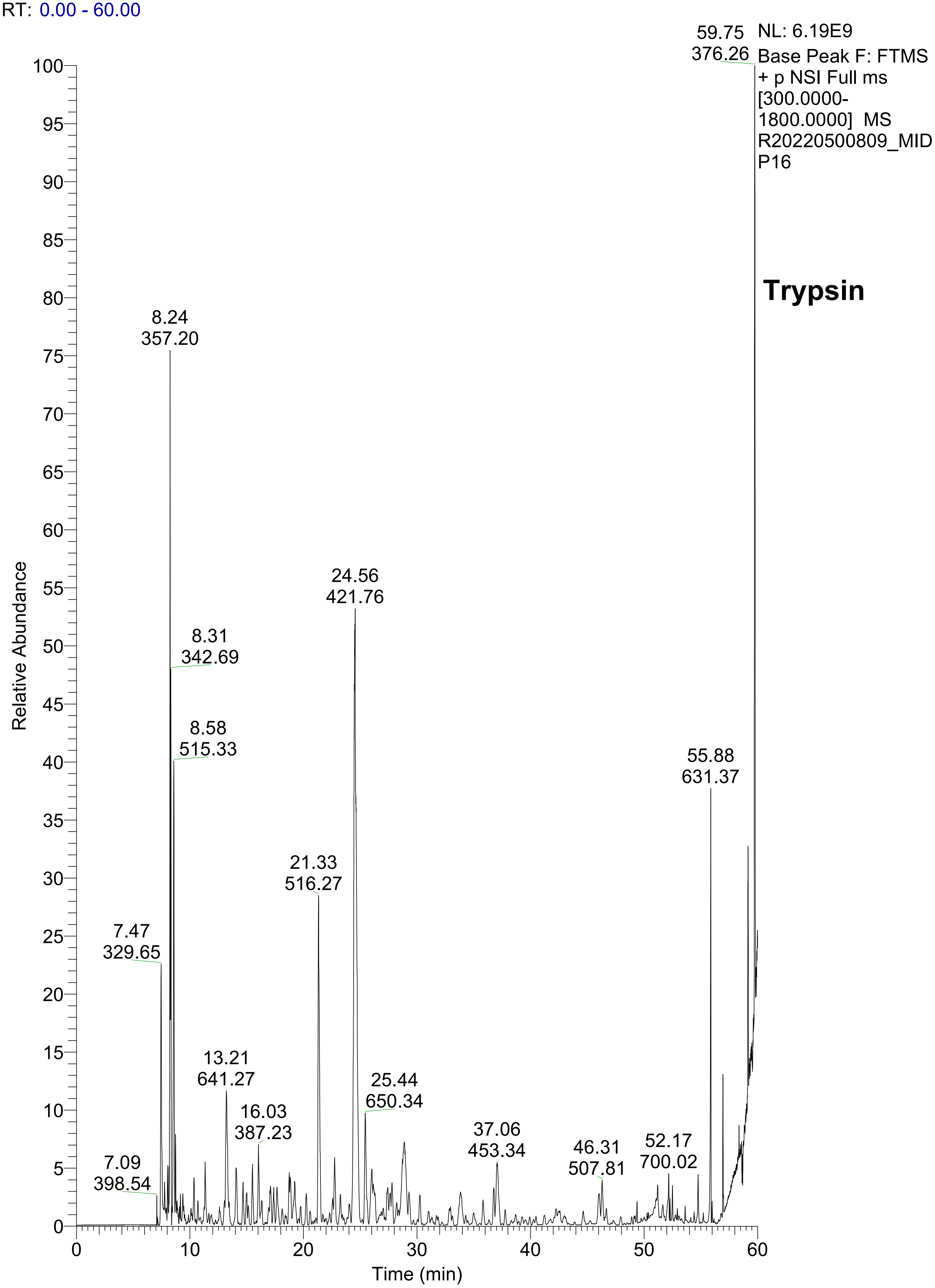
File: Unknown-C
F: FTMS + p ESI Full ms [200.0000-2000.0000] (40.26 min)

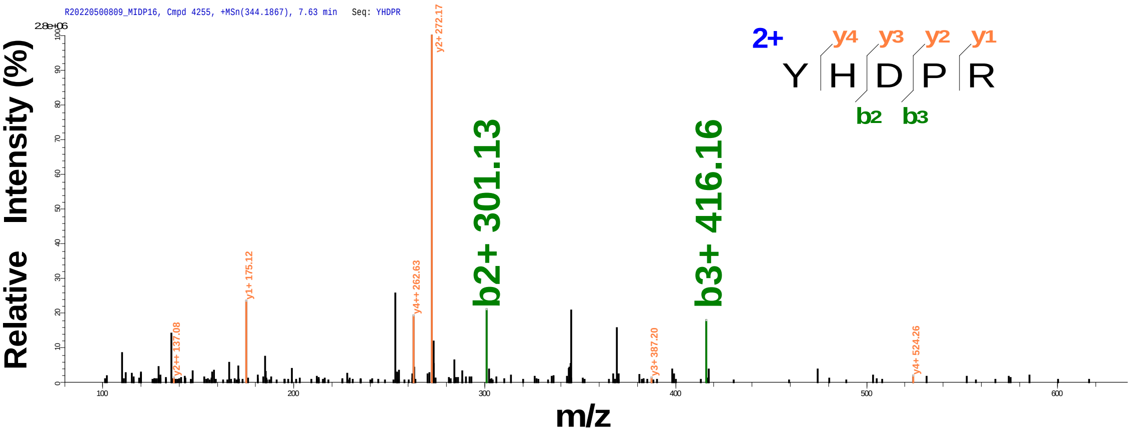


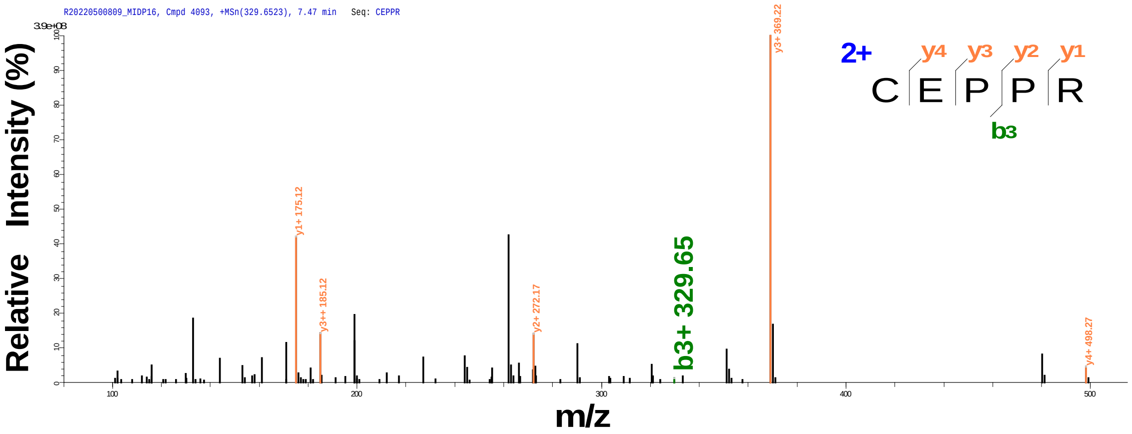
File: Unknown-C S/N: 11432
F: FTMS + p ESI Full ms [200.0000-2000.0000]

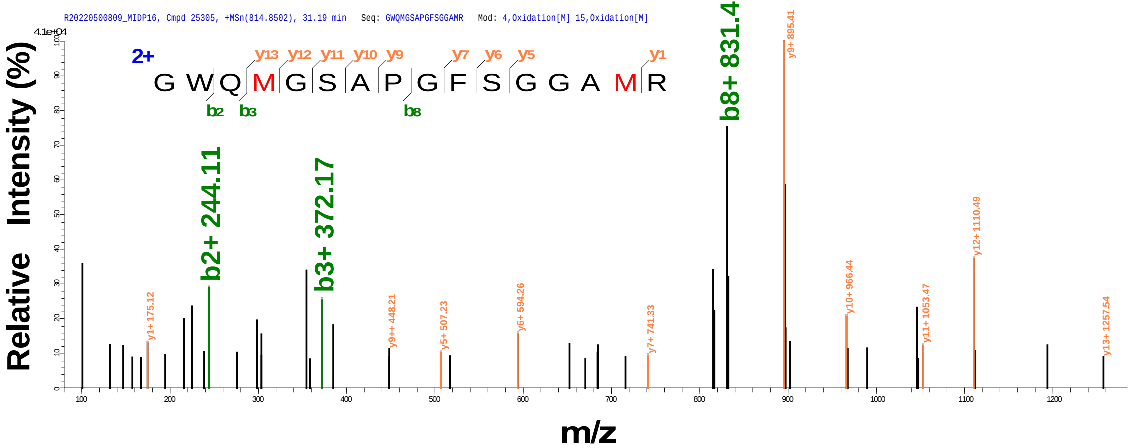


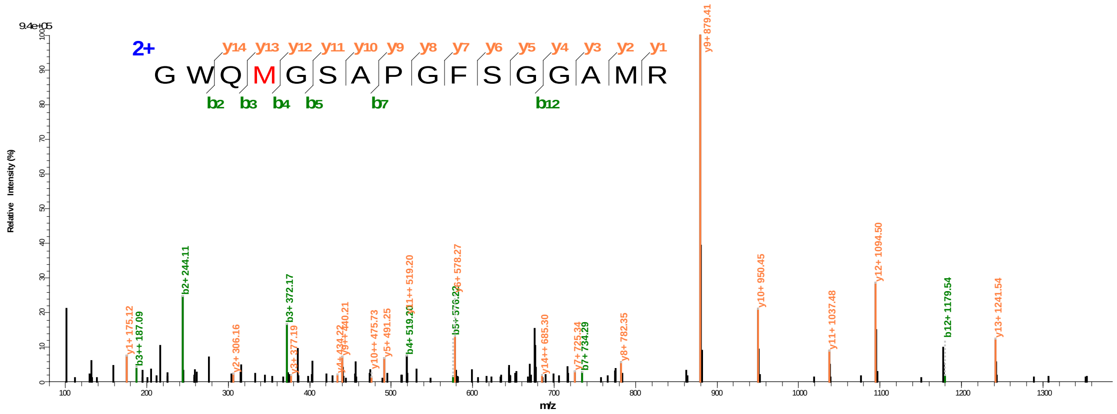

File: Unknown-C
Predicted +2, Peptide=LGASASFPAFLQSVVE
NL:
5.32E5
b₇
634.3196
b₆
487.2511
b₅
400.2191
y₁
148.0604
y₂
247.1288
b₉
802.4094
y₉
989.5302
b₁₁
1062.5619
100
50
0
Relative Abundance
File: Unknown-C
F: FTMS + c ESI d Full ms2 811.9264@hcd27.00 [111.6667-1675.0000]
Experimental ID=1:L84-E99 = 1621.8352m[nonspecific], +2, Peptide=LGASASFPAFLQSVVE
NL:
8.75E4
y₁
148.0607
b₁₀²⁺
475.2414
b₄
329.1814
y₅
561.2781
y₆
674.3652
b₁₀
949.4803
y₉
989.5405
1259.6455
100
50
0
200
400
600
800
1000
1200
1400
m/z

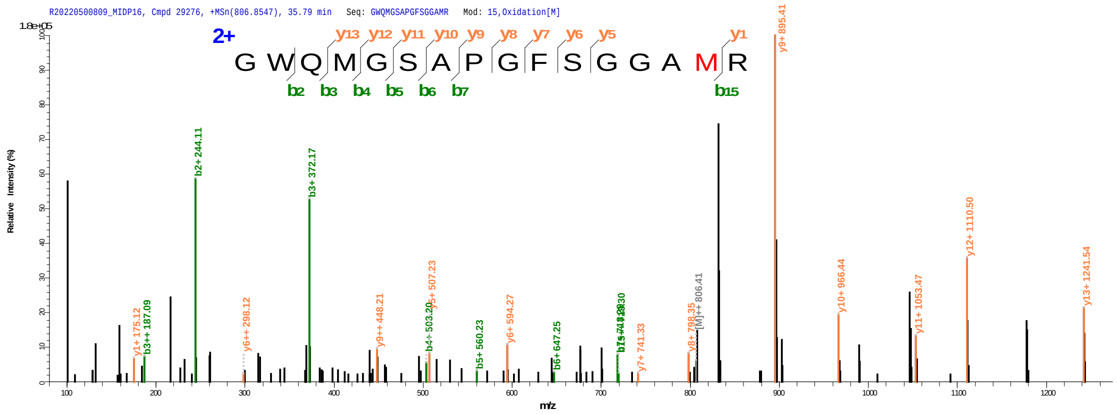

RT: 0.00 - 60.00
NL: 6.19E9
Base Peak F: FTMS + p NSI Full ms [300.0000-1800.0000] MS R20220500809_MIDP16
Trypsin
59.75 376.26
8.24 357.20
24.56 421.76
8.31 342.69
8.58 515.33
55.88 631.37
21.33 516.27
7.47 329.65
13.21 641.27
25.44 650.34
16.03 387.23
37.06 453.34
46.31 507.81
52.17 700.02
7.09 398.54
Relative Abundance
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
Time (min)
0
10
20
30
40
50
60

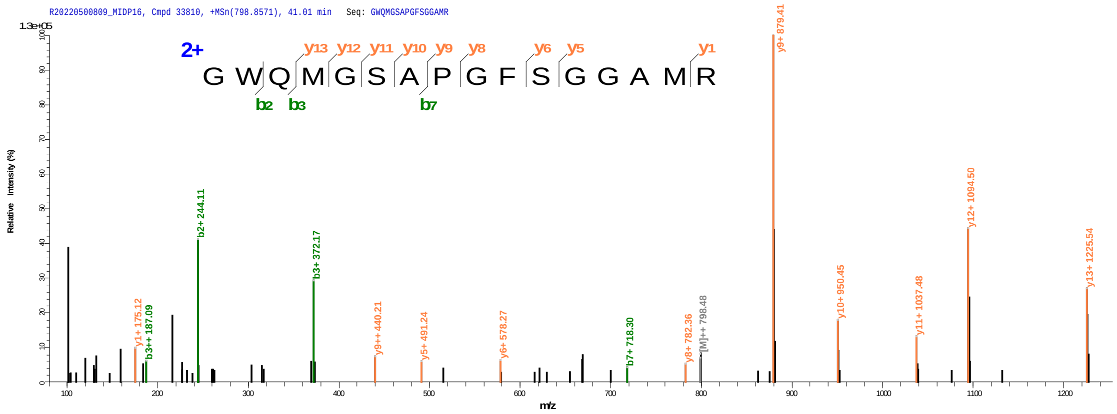

R20220500809_MIDP16, Cmpd 4255, +MSn(344.1867), 7.63 min Seq: YHDPR
2.8e+06
2+
y4 y3 y2 y1
Y H D P R
b2 b3
Relative Intensity (%)
y2+ 272.17
b2+ 301.13
b3+ 416.16
y1+ 175.12
y4++ 262.63
y2++ 137.08
y3+ 387.20
y4+ 524.26
m/z


R20220500809_MIDP16, Cmpd 4093, +MSn(329.6523), 7.47 min Seq: CEPPR
3.9e+08
2+
y4 y3 y2 y1
C E P P R
b3
Relative Intensity (%)
y3+ 369.22
y1+ 175.12
y3++ 185.12
y2+ 272.17
b3+ 329.65
y4+ 498.27
m/z


R20220500809_MIDP16, Cmpd 25305, +MSn(814.8502), 31.19 min Seq: GWQMGSAPGFSGGAMR Mod: 4,Oxidation[M] 15,Oxidation[M]
4.1e+04
2+
y13 y12 y11 y10 y9 y7 y6 y5 y1
G W Q M G S A P G F S G G A M R
b2 b3 b8
Relative Intensity (%)
b8+ 831.41
y9+ 895.41
b2+ 244.11
b3+ 372.17
y1+ 175.12
y9++ 448.21
y5+ 507.23
y6+ 594.26
y7+ 741.33
y10+ 966.44
y11+ 1053.47
y12+ 1110.49
y13+ 1257.54
m/z


9.4e+05
2+
y14 y13 y12 y11 y10 y9 y8 y7 y6 y5 y4 y3 y2 y1
G W Q M G S A P G F S G G A M R
b2 b3 b4 b5 b7 b12
Relative Intensity (%)
y9+ 879.41
y1+ 175.12
b3++ 187.09
b2+ 244.11
y2+ 306.16
b3+ 372.17
y3+ 377.19
b4+ 434.22
y9++ 440.21
y10++ 475.73
y5+ 491.25
b4+ 519.20
y11++ 519.20
b5+ 576.22
y6+ 578.27
y14++ 685.30
y7+ 725.34
b7+ 734.29
y8+ 782.35
y10+ 950.45
y11+ 1037.48
y12+ 1094.50
b12+ 1179.54
y13+ 1241.54
m/z


R20220500809_MIDP16, Cmpd 29276, +MSn(806.8547), 35.79 min Seq: GWQMGSAPGFSGGAMR Mod: 15,Oxidation[M]
1.8e+05
2+
y13 y12 y11 y10 y9 y8 y7 y6 y5 y1
G W Q M G S A P G F S G G A M R
b2 b3 b4 b5 b6 b7 b15
Relative Intensity (%)
y1+ 175.12
b3++ 187.09
b2+ 244.11
y6++ 298.12
b3+ 372.17
y9++ 448.21
b4+ 503.20
y5+ 507.23
b5+ 560.23
y6+ 594.27
b6+ 647.25
y7+ 741.33
y8+ 798.35
[M]++ 806.41
y9+ 895.41
y10+ 966.44
y11+ 1053.47
y12+ 1110.50
y13+ 1241.54
m/z


R20220500809_MIDP16, Cmpd 33810, +MSn(798.8571), 41.01 min Seq: GWQMGSAPGFSGGAMR
1.3e+05
2+
y13 y12 y11 y10 y9 y8 y6 y5 y1
G W Q M G S A P G F S G G A M R
b2 b3 b7
Relative Intensity (%)
y1+ 175.12
b3++ 187.09
b2+ 244.11
b3+ 372.17
y9++ 440.21
y5+ 491.24
y6+ 578.27
b7+ 718.30
y8+ 782.36
[M]++ 798.48
y9+ 879.41
y10+ 950.45
y11+ 1037.48
y12+ 1094.50
y13+ 1225.54
m/z