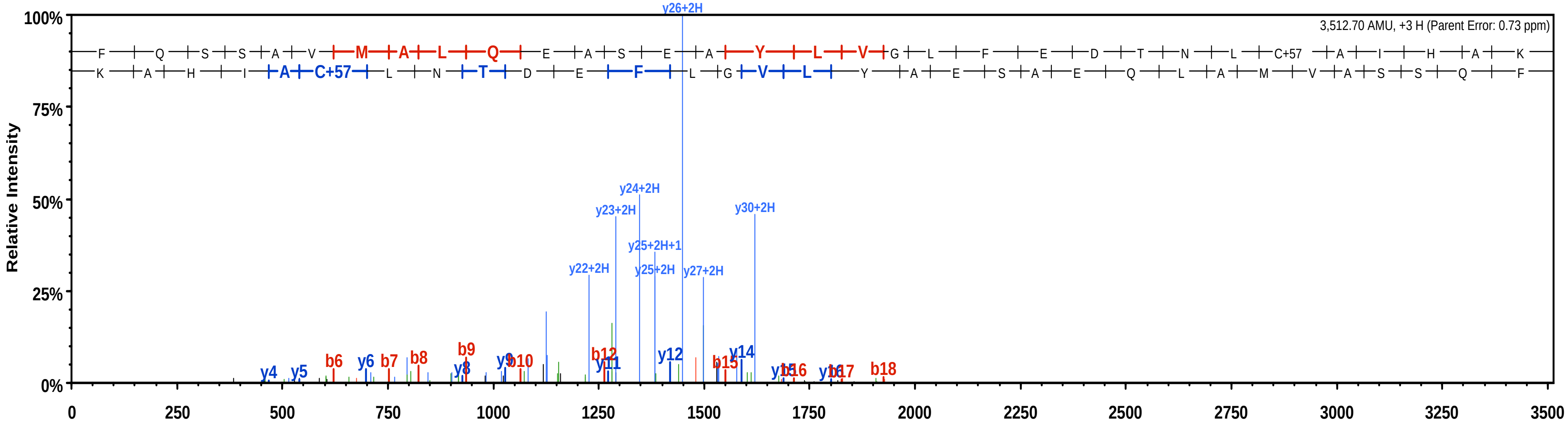
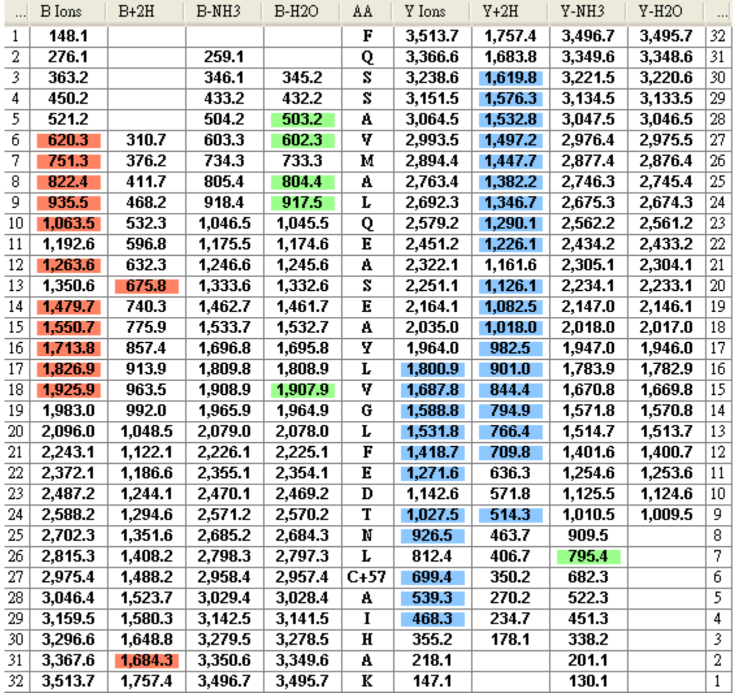
Supplementary Figure S1

Fig. S1. The annotated spectra represented quantified proteins with single peptide identifications, including 136 proteins identified in whole proteome and 137 proteins identified in nuclear proteome.

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-1	sp|Q71DI3|H32_HUMAN	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	135.45	Unmodified	Light	3	1171.9058

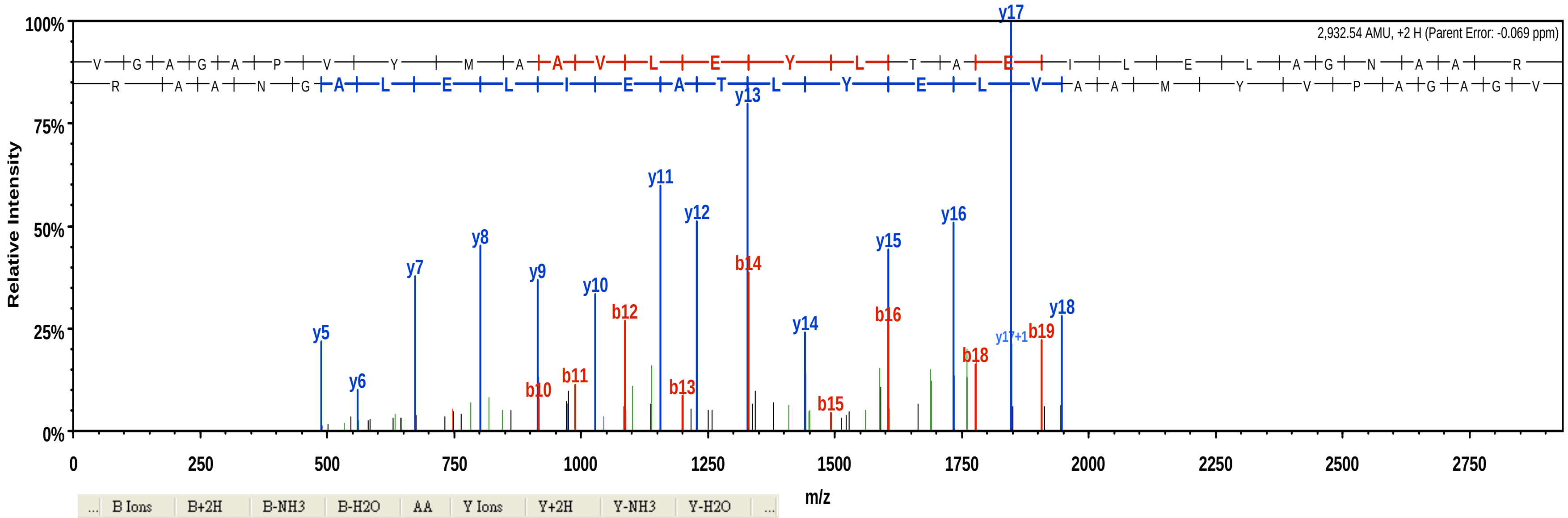


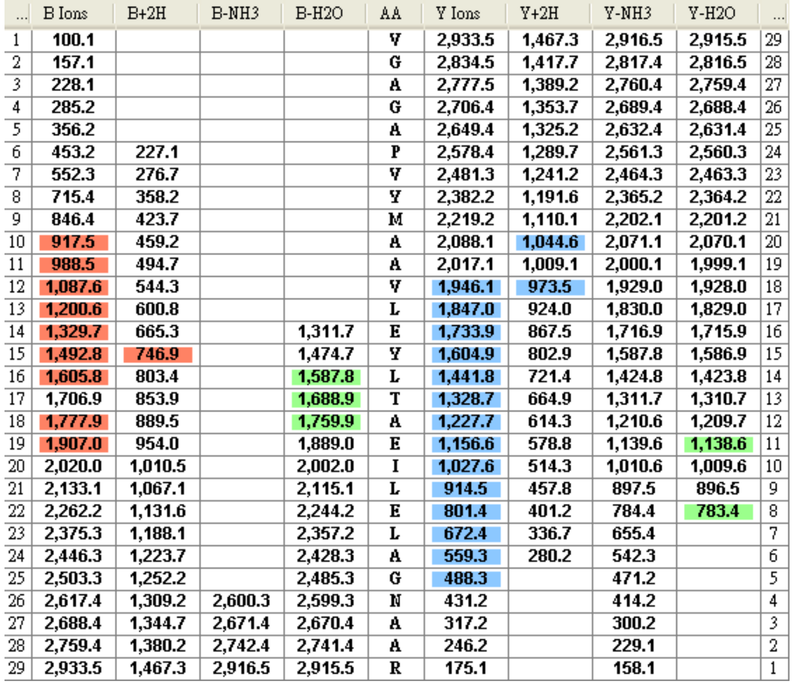


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.1				F	3,513.7	1,757.4	3,496.7	3,495.7	32
2	276.1		259.1		Q	3,366.6	1,683.8	3,349.6	3,348.6	31
3	363.2		346.1	345.2	S	3,238.6	1,619.8	3,221.5	3,220.6	30
4	450.2		433.2	432.2	S	3,151.5	1,576.3	3,134.5	3,133.5	29
5	521.2		504.2	503.2	A	3,064.5	1,532.8	3,047.5	3,046.5	28
6	620.3	310.7	603.3	602.3	V	2,993.5	1,497.2	2,976.4	2,975.5	27
7	751.3	376.2	734.3	733.3	M	2,894.4	1,447.7	2,877.4	2,876.4	26
8	822.4	411.7	805.4	804.4	A	2,763.4	1,382.2	2,746.3	2,745.4	25
9	935.5	468.2	918.4	917.5	L	2,692.3	1,346.7	2,675.3	2,674.3	24
10	1,063.5	532.3	1,046.5	1,045.5	Q	2,579.2	1,290.1	2,562.2	2,561.2	23
11	1,192.6	596.8	1,175.5	1,174.6	E	2,451.2	1,226.1	2,434.2	2,433.2	22
12	1,263.6	632.3	1,246.6	1,245.6	A	2,322.1	1,161.6	2,305.1	2,304.1	21
13	1,350.6	675.8	1,333.6	1,332.6	S	2,251.1	1,126.1	2,234.1	2,233.1	20
14	1,479.7	740.3	1,462.7	1,461.7	E	2,164.1	1,082.5	2,147.0	2,146.1	19
15	1,550.7	775.9	1,533.7	1,532.7	A	2,035.0	1,018.0	2,018.0	2,017.0	18
16	1,713.8	857.4	1,696.8	1,695.8	Y	1,964.0	982.5	1,947.0	1,946.0	17
17	1,826.9	913.9	1,809.8	1,808.9	L	1,800.9	901.0	1,783.9	1,782.9	16
18	1,925.9	963.5	1,908.9	1,907.9	V	1,687.8	844.4	1,670.8	1,669.8	15
19	1,983.0	992.0	1,965.9	1,964.9	G	1,588.8	794.9	1,571.8	1,570.8	14
20	2,096.0	1,048.5	2,079.0	2,078.0	L	1,531.8	766.4	1,514.7	1,513.7	13
21	2,243.1	1,122.1	2,226.1	2,225.1	F	1,418.7	709.8	1,401.6	1,400.7	12
22	2,372.1	1,186.6	2,355.1	2,354.1	E	1,271.6	636.3	1,254.6	1,253.6	11
23	2,487.2	1,244.1	2,470.1	2,469.2	D	1,142.6	571.8	1,125.5	1,124.6	10
24	2,588.2	1,294.6	2,571.2	2,570.2	T	1,027.5	514.3	1,010.5	1,009.5	9
25	2,702.3	1,351.6	2,685.2	2,684.3	N	926.5	463.7	909.5		8
26	2,815.3	1,408.2	2,798.3	2,797.3	L	812.4	406.7	795.4		7
27	2,975.4	1,488.2	2,958.4	2,957.4	C+57	699.4	350.2	682.3		6
28	3,046.4	1,523.7	3,029.4	3,028.4	A	539.3	270.2	522.3		5
29	3,159.5	1,580.3	3,142.5	3,141.5	I	468.3	234.7	451.3		4
30	3,296.6	1,648.8	3,279.5	3,278.5	H	355.2	178.1	338.2		3
31	3,367.6	1,684.3	3,350.6	3,349.6	A	218.1		201.1		2
32	3,513.7	1,757.4	3,496.7	3,495.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-2	sp|Q6FI13|H2A2A_HUMAN	VGAGAPVYMAAVLEYLTAEILELAGNAAR	127.84	Unmodified		2	1467.2757

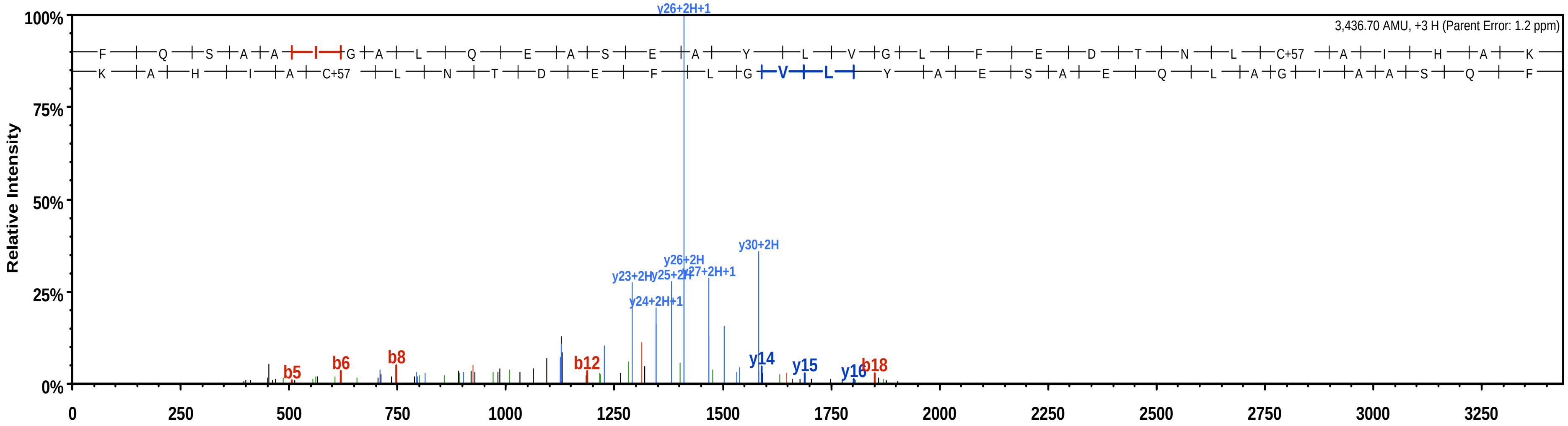


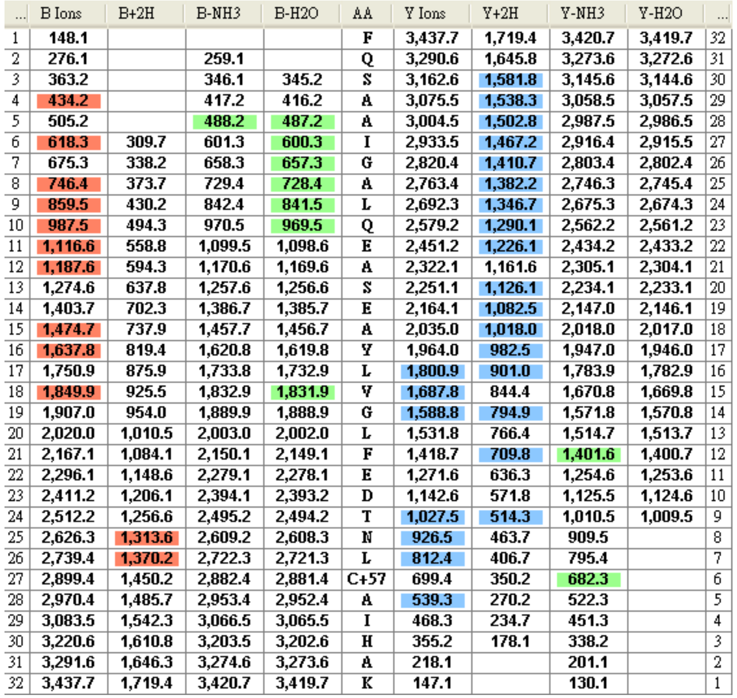


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	2,933.5	1,467.3	2,916.5	2,915.5	29
2	157.1				G	2,834.5	1,417.7	2,817.4	2,816.5	28
3	228.1				A	2,777.5	1,389.2	2,760.4	2,759.4	27
4	285.2				G	2,706.4	1,353.7	2,689.4	2,688.4	26
5	356.2				A	2,649.4	1,325.2	2,632.4	2,631.4	25
6	453.2	227.1			P	2,578.4	1,289.7	2,561.3	2,560.3	24
7	552.3	276.7			V	2,481.3	1,241.2	2,464.3	2,463.3	23
8	715.4	358.2			Y	2,382.2	1,191.6	2,365.2	2,364.2	22
9	846.4	423.7			M	2,219.2	1,110.1	2,202.1	2,201.2	21
10	917.5	459.2			A	2,088.1	1,044.6	2,071.1	2,070.1	20
11	988.5	494.7			A	2,017.1	1,009.1	2,000.1	1,999.1	19
12	1,087.6	544.3			V	1,946.1	973.5	1,929.0	1,928.0	18
13	1,200.6	600.8			L	1,847.0	924.0	1,830.0	1,829.0	17
14	1,329.7	665.3		1,311.7	E	1,733.9	867.5	1,716.9	1,715.9	16
15	1,492.8	746.9		1,474.7	Y	1,604.9	802.9	1,587.8	1,586.9	15
16	1,605.8	803.4		1,587.8	L	1,441.8	721.4	1,424.8	1,423.8	14
17	1,706.9	853.9		1,688.9	T	1,328.7	664.9	1,311.7	1,310.7	13
18	1,777.9	889.5		1,759.9	A	1,227.7	614.3	1,210.6	1,209.7	12
19	1,907.0	954.0		1,889.0	E	1,156.6	578.8	1,139.6	1,138.6	11
20	2,020.0	1,010.5		2,002.0	I	1,027.6	514.3	1,010.6	1,009.6	10
21	2,133.1	1,067.1		2,115.1	L	914.5	457.8	897.5	896.5	9
22	2,262.2	1,131.6		2,244.2	E	801.4	401.2	784.4	783.4	8
23	2,375.3	1,188.1		2,357.2	L	672.4	336.7	655.4		7
24	2,446.3	1,223.7		2,428.3	A	559.3	280.2	542.3		6
25	2,503.3	1,252.2		2,485.3	G	488.3		471.2		5
26	2,617.4	1,309.2	2,600.3	2,599.3	N	431.2		414.2		4
27	2,688.4	1,344.7	2,671.4	2,670.4	A	317.2		300.2		3
28	2,759.4	1,380.2	2,742.4	2,741.4	A	246.2		229.1		2
29	2,933.5	1,467.3	2,916.5	2,915.5	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-2	sp|P84243|H33_HUMAN	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	114.78	Unmodified	Light	3	1146.573

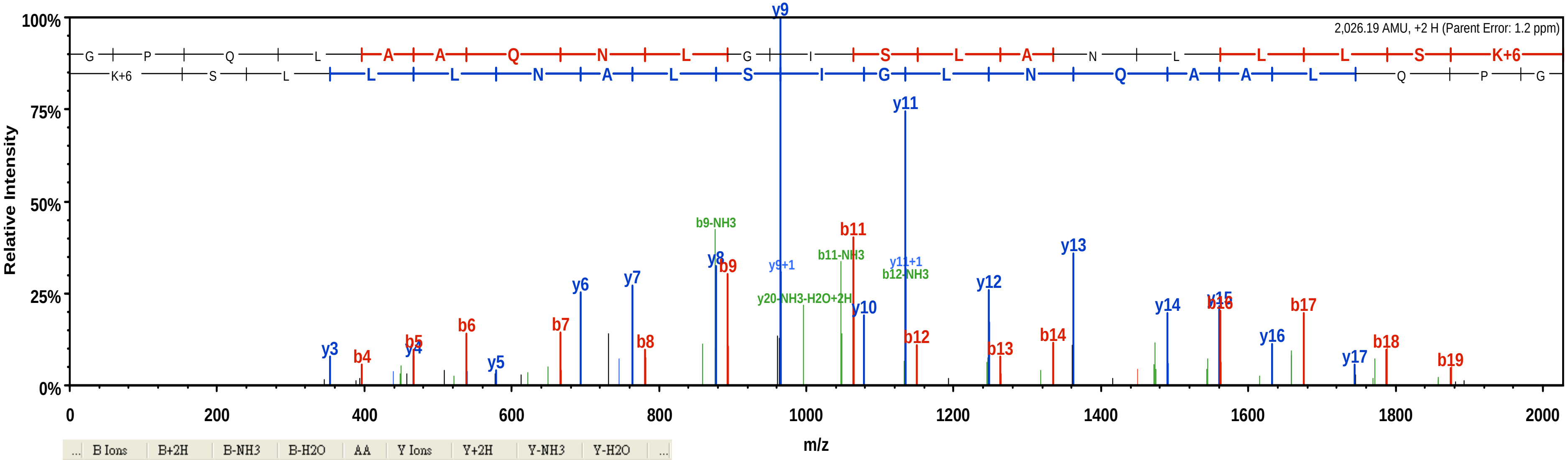


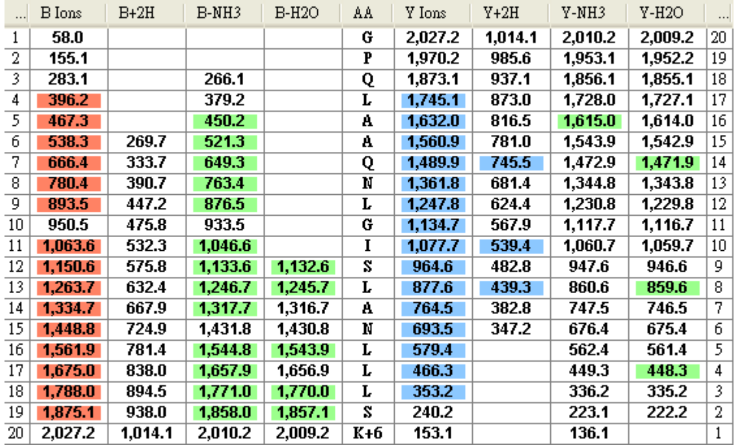


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.1				F	3,437.7	1,719.4	3,420.7	3,419.7	32
2	276.1		259.1		Q	3,290.6	1,645.8	3,273.6	3,272.6	31
3	363.2		346.1	345.2	S	3,162.6	1,581.8	3,145.6	3,144.6	30
4	434.2		417.2	416.2	A	3,075.5	1,538.3	3,058.5	3,057.5	29
5	505.2		488.2	487.2	A	3,004.5	1,502.8	2,987.5	2,986.5	28
6	618.3	309.7	601.3	600.3	I	2,933.5	1,467.2	2,916.4	2,915.5	27
7	675.3	338.2	658.3	657.3	G	2,820.4	1,410.7	2,803.4	2,802.4	26
8	746.4	373.7	729.4	728.4	A	2,763.4	1,382.2	2,746.3	2,745.4	25
9	859.5	430.2	842.4	841.5	L	2,692.3	1,346.7	2,675.3	2,674.3	24
10	987.5	494.3	970.5	969.5	Q	2,579.2	1,290.1	2,562.2	2,561.2	23
11	1,116.6	558.8	1,099.5	1,098.6	E	2,451.2	1,226.1	2,434.2	2,433.2	22
12	1,187.6	594.3	1,170.6	1,169.6	A	2,322.1	1,161.6	2,305.1	2,304.1	21
13	1,274.6	637.8	1,257.6	1,256.6	S	2,251.1	1,126.1	2,234.1	2,233.1	20
14	1,403.7	702.3	1,386.7	1,385.7	E	2,164.1	1,082.5	2,147.0	2,146.1	19
15	1,474.7	737.9	1,457.7	1,456.7	A	2,035.0	1,018.0	2,018.0	2,017.0	18
16	1,637.8	819.4	1,620.8	1,619.8	Y	1,964.0	982.5	1,947.0	1,946.0	17
17	1,750.9	875.9	1,733.8	1,732.9	L	1,800.9	901.0	1,783.9	1,782.9	16
18	1,849.9	925.5	1,832.9	1,831.9	V	1,687.8	844.4	1,670.8	1,669.8	15
19	1,907.0	954.0	1,889.9	1,888.9	G	1,588.8	794.9	1,571.8	1,570.8	14
20	2,020.0	1,010.5	2,003.0	2,002.0	L	1,531.8	766.4	1,514.7	1,513.7	13
21	2,167.1	1,084.1	2,150.1	2,149.1	F	1,418.7	709.8	1,401.6	1,400.7	12
22	2,296.1	1,148.6	2,279.1	2,278.1	E	1,271.6	636.3	1,254.6	1,253.6	11
23	2,411.2	1,206.1	2,394.1	2,393.2	D	1,142.6	571.8	1,125.5	1,124.6	10
24	2,512.2	1,256.6	2,495.2	2,494.2	T	1,027.5	514.3	1,010.5	1,009.5	9
25	2,626.3	1,313.6	2,609.2	2,608.3	N	926.5	463.7	909.5		8
26	2,739.4	1,370.2	2,722.3	2,721.3	L	812.4	406.7	795.4		7
27	2,899.4	1,450.2	2,882.4	2,881.4	C+57	699.4	350.2	682.3		6
28	2,970.4	1,485.7	2,953.4	2,952.4	A	539.3	270.2	522.3		5
29	3,083.5	1,542.3	3,066.5	3,065.5	I	468.3	234.7	451.3		4
30	3,220.6	1,610.8	3,203.5	3,202.6	H	355.2	178.1	338.2		3
31	3,291.6	1,646.3	3,274.6	3,273.6	A	218.1		201.1		2
32	3,437.7	1,719.4	3,420.7	3,419.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-3	sp|P08397|HEM3_HUMAN	GPQLAAQNLGISLANLLLSK	111.92	Unmodified	Heavy	2	1011.0913

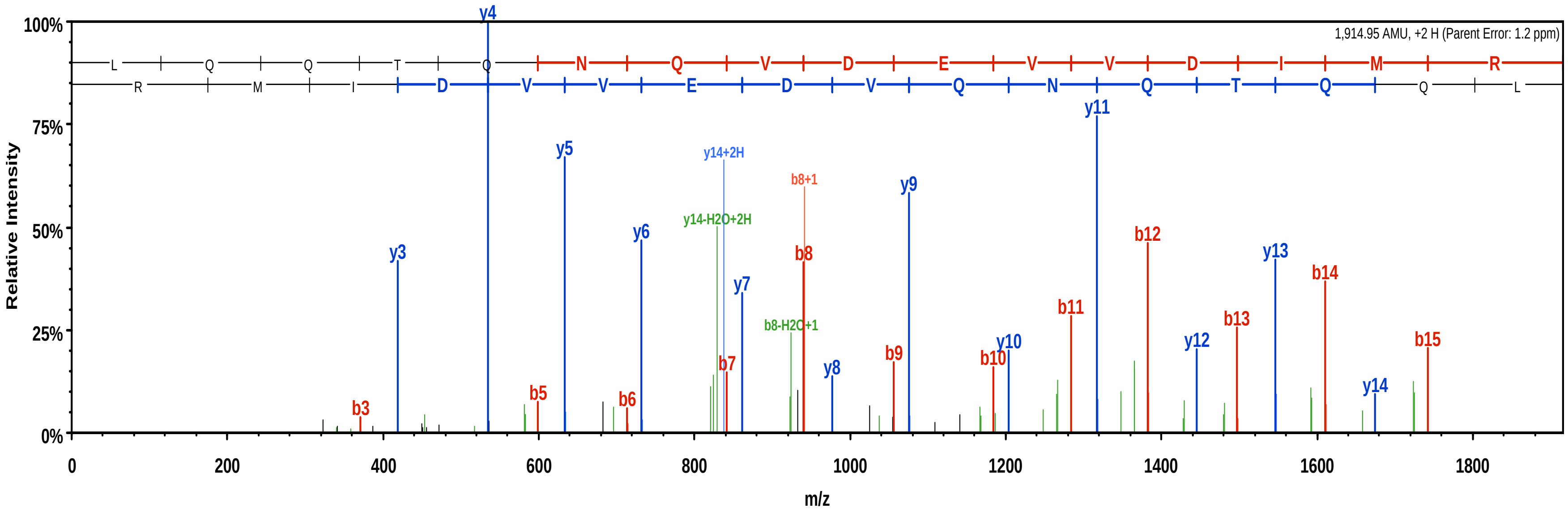


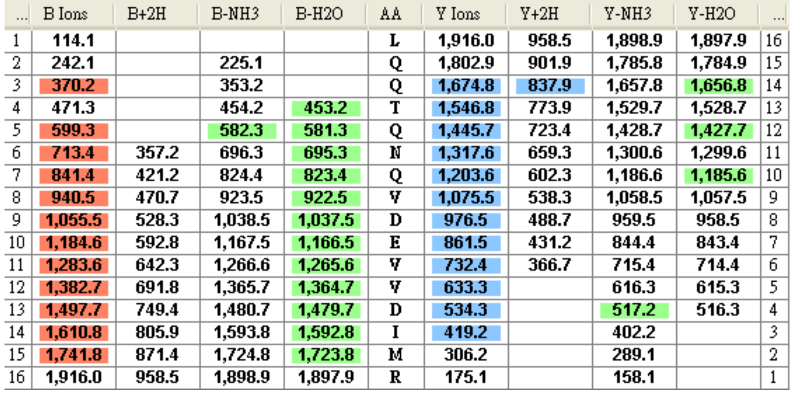


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	2,027.2	1,014.1	2,010.2	2,009.2	20
2	155.1				P	1,970.2	985.6	1,953.1	1,952.2	19
3	283.1		266.1		Q	1,873.1	937.1	1,856.1	1,855.1	18
4	396.2		379.2		L	1,745.1	873.0	1,728.0	1,727.1	17
5	467.3		450.2		A	1,632.0	816.5	1,615.0	1,614.0	16
6	538.3	269.7	521.3		A	1,560.9	781.0	1,543.9	1,542.9	15
7	666.4	333.7	649.3		Q	1,489.9	745.5	1,472.9	1,471.9	14
8	780.4	390.7	763.4		N	1,361.8	681.4	1,344.8	1,343.8	13
9	893.5	447.2	876.5		L	1,247.8	624.4	1,230.8	1,229.8	12
10	950.5	475.8	933.5		G	1,134.7	567.9	1,117.7	1,116.7	11
11	1,063.6	532.3	1,046.6		I	1,077.7	539.4	1,060.7	1,059.7	10
12	1,150.6	575.8	1,133.6	1,132.6	S	964.6	482.8	947.6	946.6	9
13	1,263.7	632.4	1,246.7	1,245.7	L	877.6	439.3	860.6	859.6	8
14	1,334.7	667.9	1,317.7	1,316.7	A	764.5	382.8	747.5	746.5	7
15	1,448.8	724.9	1,431.8	1,430.8	N	693.5	347.2	676.4	675.4	6
16	1,561.9	781.4	1,544.8	1,543.9	L	579.4		562.4	561.4	5
17	1,675.0	838.0	1,657.9	1,656.9	L	466.3		449.3	448.3	4
18	1,788.0	894.5	1,771.0	1,770.0	L	353.2		336.2	335.2	3
19	1,875.1	938.0	1,858.0	1,857.1	S	240.2		223.1	222.2	2
20	2,027.2	1,014.1	2,010.2	2,009.2	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-5	sp|Q15836|VAMP3_HUMAN	LQQTQNQVDEVVDIMR	111.61	Unmodified		2	958.48074

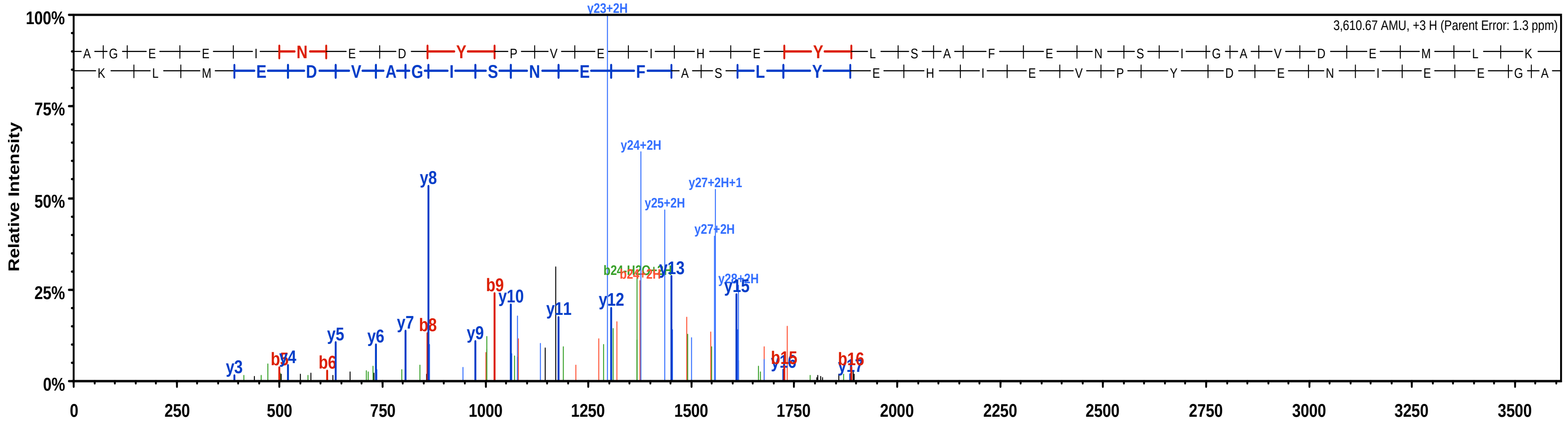


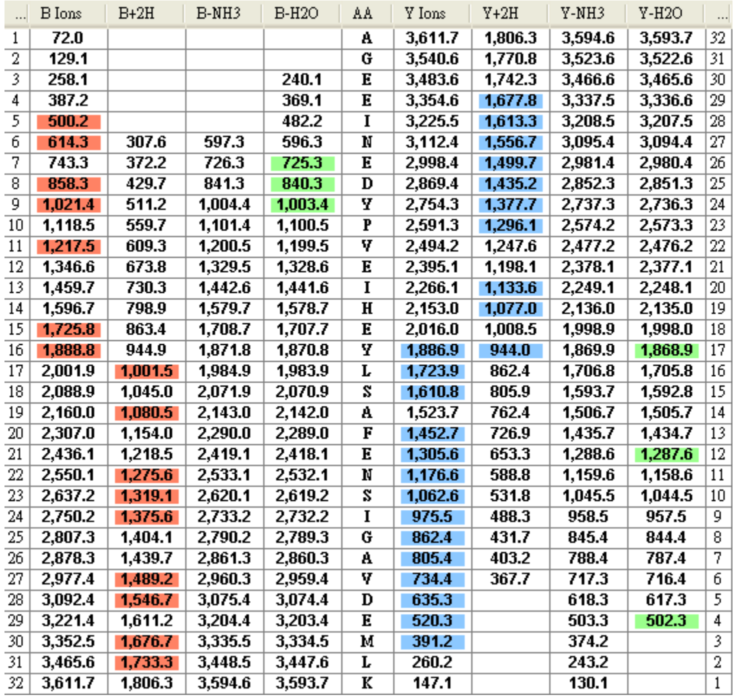


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	1,916.0	958.5	1,898.9	1,897.9	16
2	242.1		225.1		Q	1,802.9	901.9	1,785.8	1,784.9	15
3	370.2		353.2		Q	1,674.8	837.9	1,657.8	1,656.8	14
4	471.3		454.2	453.2	T	1,546.8	773.9	1,529.7	1,528.7	13
5	599.3		582.3	581.3	Q	1,445.7	723.4	1,428.7	1,427.7	12
6	713.4	357.2	696.3	695.3	N	1,317.6	659.3	1,300.6	1,299.6	11
7	841.4	421.2	824.4	823.4	Q	1,203.6	602.3	1,186.6	1,185.6	10
8	940.5	470.7	923.5	922.5	V	1,075.5	538.3	1,058.5	1,057.5	9
9	1,055.5	528.3	1,038.5	1,037.5	D	976.5	488.7	959.5	958.5	8
10	1,184.6	592.8	1,167.5	1,166.5	E	861.5	431.2	844.4	843.4	7
11	1,283.6	642.3	1,266.6	1,265.6	V	732.4	366.7	715.4	714.4	6
12	1,382.7	691.8	1,365.7	1,364.7	V	633.3		616.3	615.3	5
13	1,497.7	749.4	1,480.7	1,479.7	D	534.3		517.2	516.3	4
14	1,610.8	805.9	1,593.8	1,592.8	I	419.2		402.2		3
15	1,741.8	871.4	1,724.8	1,723.8	M	306.2		289.1		2
16	1,916.0	958.5	1,898.9	1,897.9	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-4	sp|Q13901|C1D_HUMAN	AGEEINEDYPVEIHEYLSAFENSIGAVDEMLK	109.12	Unmodified	Light	3	1204.5627

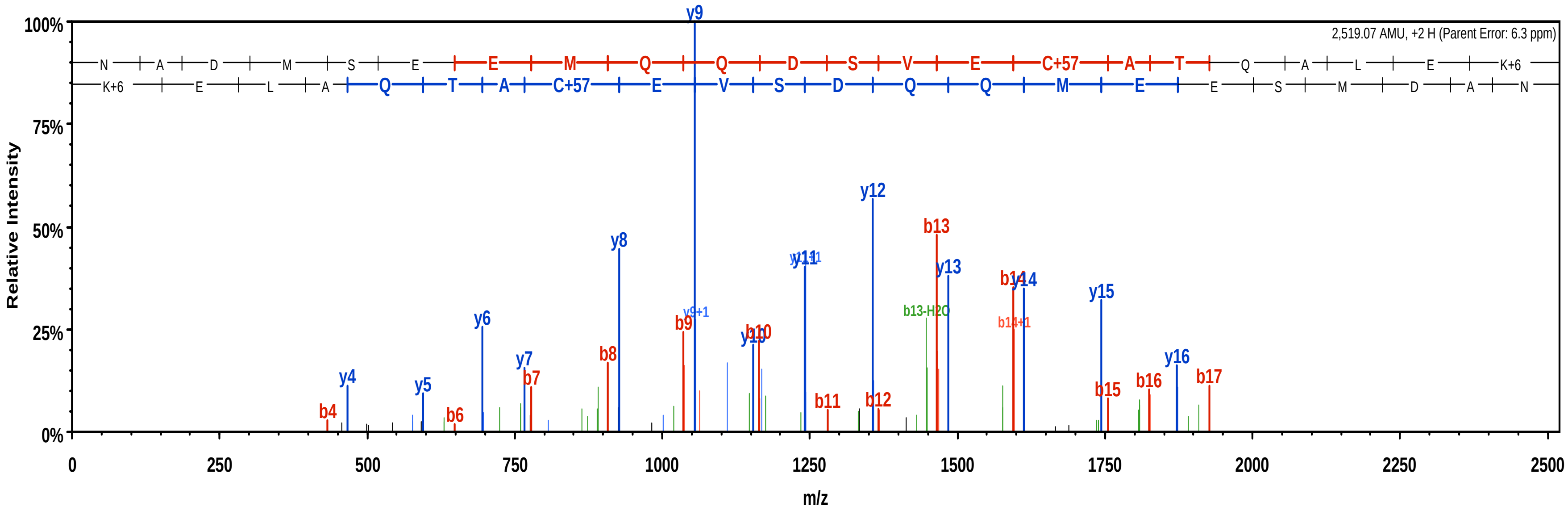


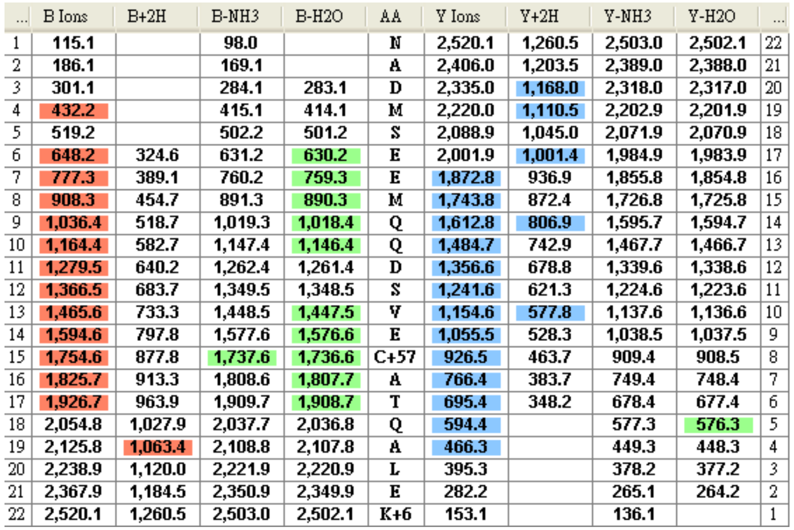


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	3,611.7	1,806.3	3,594.6	3,593.7	32
2	129.1				G	3,540.6	1,770.8	3,523.6	3,522.6	31
3	258.1			240.1	E	3,483.6	1,742.3	3,466.6	3,465.6	30
4	387.2			369.1	E	3,354.6	1,677.8	3,337.5	3,336.6	29
5	500.2			482.2	I	3,225.5	1,613.3	3,208.5	3,207.5	28
6	614.3	307.6	597.3	596.3	N	3,112.4	1,556.7	3,095.4	3,094.4	27
7	743.3	372.2	726.3	725.3	E	2,998.4	1,499.7	2,981.4	2,980.4	26
8	858.3	429.7	841.3	840.3	D	2,869.4	1,435.2	2,852.3	2,851.3	25
9	1,021.4	511.2	1,004.4	1,003.4	Y	2,754.3	1,377.7	2,737.3	2,736.3	24
10	1,118.5	559.7	1,101.4	1,100.5	P	2,591.3	1,296.1	2,574.2	2,573.3	23
11	1,217.5	609.3	1,200.5	1,199.5	V	2,494.2	1,247.6	2,477.2	2,476.2	22
12	1,346.6	673.8	1,329.5	1,328.6	E	2,395.1	1,198.1	2,378.1	2,377.1	21
13	1,459.7	730.3	1,442.6	1,441.6	I	2,266.1	1,133.6	2,249.1	2,248.1	20
14	1,596.7	798.9	1,579.7	1,578.7	H	2,153.0	1,077.0	2,136.0	2,135.0	19
15	1,725.8	863.4	1,708.7	1,707.7	E	2,016.0	1,008.5	1,998.9	1,998.0	18
16	1,888.8	944.9	1,871.8	1,870.8	Y	1,886.9	944.0	1,869.9	1,868.9	17
17	2,001.9	1,001.5	1,984.9	1,983.9	L	1,723.9	862.4	1,706.8	1,705.8	16
18	2,088.9	1,045.0	2,071.9	2,070.9	S	1,610.8	805.9	1,593.7	1,592.8	15
19	2,160.0	1,080.5	2,143.0	2,142.0	A	1,523.7	762.4	1,506.7	1,505.7	14
20	2,307.0	1,154.0	2,290.0	2,289.0	F	1,452.7	726.9	1,435.7	1,434.7	13
21	2,436.1	1,218.5	2,419.1	2,418.1	E	1,305.6	653.3	1,288.6	1,287.6	12
22	2,550.1	1,275.6	2,533.1	2,532.1	N	1,176.6	588.8	1,159.6	1,158.6	11
23	2,637.2	1,319.1	2,620.1	2,619.2	S	1,062.6	531.8	1,045.5	1,044.5	10
24	2,750.2	1,375.6	2,733.2	2,732.2	I	975.5	488.3	958.5	957.5	9
25	2,807.3	1,404.1	2,790.2	2,789.3	G	862.4	431.7	845.4	844.4	8
26	2,878.3	1,439.7	2,861.3	2,860.3	A	805.4	403.2	788.4	787.4	7
27	2,977.4	1,489.2	2,960.3	2,959.4	V	734.4	367.7	717.3	716.4	6
28	3,092.4	1,546.7	3,075.4	3,074.4	D	635.3		618.3	617.3	5
29	3,221.4	1,611.2	3,204.4	3,203.4	E	520.3		503.3	502.3	4
30	3,352.5	1,676.7	3,335.5	3,334.5	M	391.2		374.2		3
31	3,465.6	1,733.3	3,448.5	3,447.6	L	260.2		243.2		2
32	3,611.7	1,806.3	3,594.6	3,593.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-7	sp|P63167|DYL1_HUMAN	NADMSEEMQQDSVECATQALEK	108.94	Unmodified	Heavy	2	1257.5251

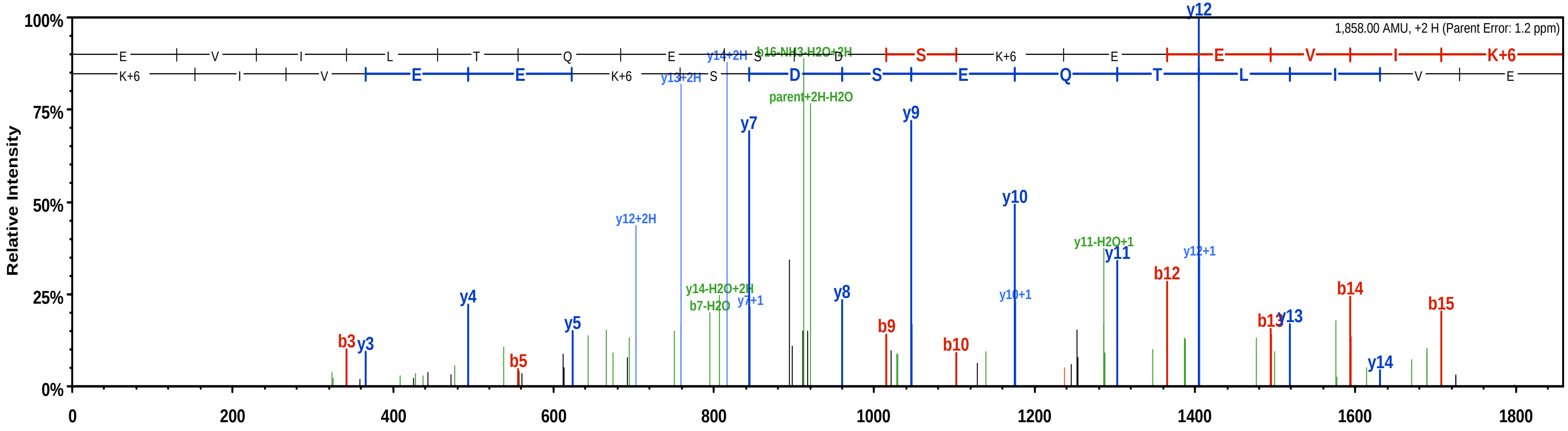


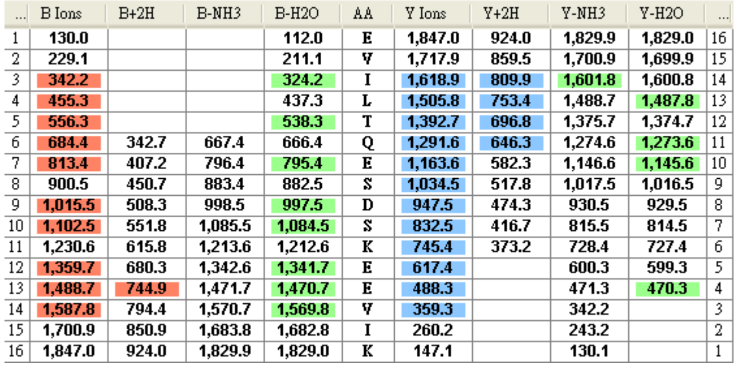


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	115.1		98.0		N	2,520.1	1,260.5	2,503.0	2,502.1	22
2	186.1		169.1		A	2,406.0	1,203.5	2,389.0	2,388.0	21
3	301.1		284.1	283.1	D	2,335.0	1,168.0	2,318.0	2,317.0	20
4	432.2		415.1	414.1	M	2,220.0	1,110.5	2,202.9	2,201.9	19
5	519.2		502.2	501.2	S	2,088.9	1,045.0	2,071.9	2,070.9	18
6	648.2	324.6	631.2	630.2	E	2,001.9	1,001.4	1,984.9	1,983.9	17
7	777.3	389.1	760.2	759.3	E	1,872.8	936.9	1,855.8	1,854.8	16
8	908.3	454.7	891.3	890.3	M	1,743.8	872.4	1,726.8	1,725.8	15
9	1,036.4	518.7	1,019.3	1,018.4	Q	1,612.8	806.9	1,595.7	1,594.7	14
10	1,164.4	582.7	1,147.4	1,146.4	Q	1,484.7	742.9	1,467.7	1,466.7	13
11	1,279.5	640.2	1,262.4	1,261.4	D	1,356.6	678.8	1,339.6	1,338.6	12
12	1,366.5	683.7	1,349.5	1,348.5	S	1,241.6	621.3	1,224.6	1,223.6	11
13	1,465.6	733.3	1,448.5	1,447.5	V	1,154.6	577.8	1,137.6	1,136.6	10
14	1,594.6	797.8	1,577.6	1,576.6	E	1,055.5	528.3	1,038.5	1,037.5	9
15	1,754.6	877.8	1,737.6	1,736.6	C+57	926.5	463.7	909.4	908.5	8
16	1,825.7	913.3	1,808.6	1,807.7	A	766.4	383.7	749.4	748.4	7
17	1,926.7	963.9	1,909.7	1,908.7	T	695.4	348.2	678.4	677.4	6
18	2,054.8	1,027.9	2,037.7	2,036.8	Q	594.4		577.3	576.3	5
19	2,125.8	1,063.4	2,108.8	2,107.8	A	466.3		449.3	448.3	4
20	2,238.9	1,120.0	2,221.9	2,220.9	L	395.3		378.2	377.2	3
21	2,367.9	1,184.5	2,350.9	2,349.9	E	282.2		265.1	264.2	2
22	2,520.1	1,260.5	2,503.0	2,502.1	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-5	sp|Q9NUY8|TBC23_HUMAN	EVILTQESDSKEEVIK	107.85	Unmodified	Light	2	923.98585

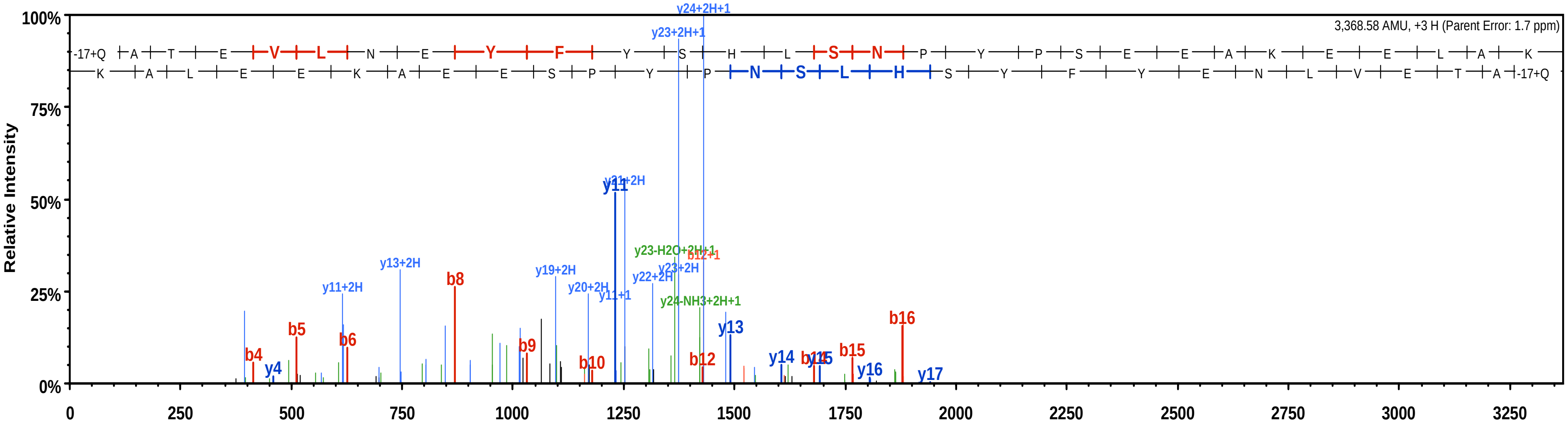


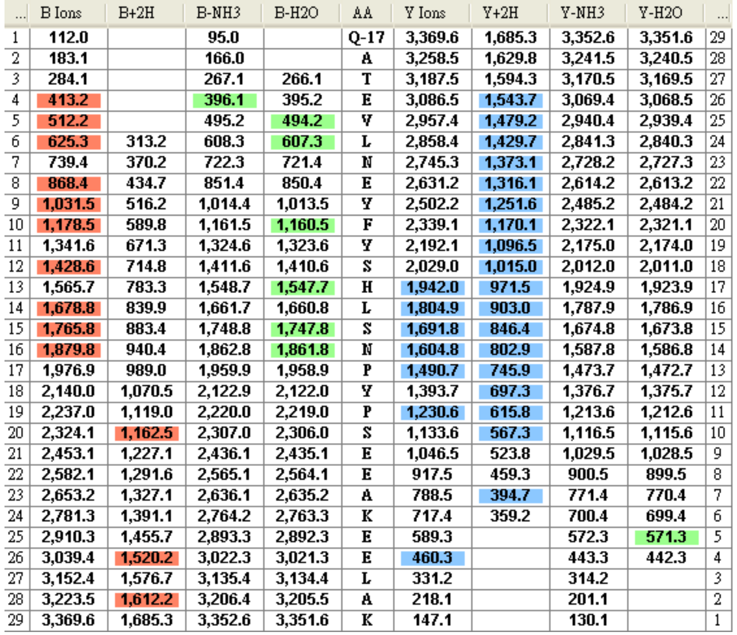


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	1,847.0	924.0	1,829.9	1,829.0	16
2	229.1			211.1	V	1,717.9	859.5	1,700.9	1,699.9	15
3	342.2			324.2	I	1,618.9	809.9	1,601.8	1,600.8	14
4	455.3			437.3	L	1,505.8	753.4	1,488.7	1,487.8	13
5	556.3			538.3	T	1,392.7	696.8	1,375.7	1,374.7	12
6	684.4	342.7	667.4	666.4	Q	1,291.6	646.3	1,274.6	1,273.6	11
7	813.4	407.2	796.4	795.4	E	1,163.6	582.3	1,146.6	1,145.6	10
8	900.5	450.7	883.4	882.5	S	1,034.5	517.8	1,017.5	1,016.5	9
9	1,015.5	508.3	998.5	997.5	D	947.5	474.3	930.5	929.5	8
10	1,102.5	551.8	1,085.5	1,084.5	S	832.5	416.7	815.5	814.5	7
11	1,230.6	615.8	1,213.6	1,212.6	K	745.4	373.2	728.4	727.4	6
12	1,359.7	680.3	1,342.6	1,341.7	E	617.4		600.3	599.3	5
13	1,488.7	744.9	1,471.7	1,470.7	E	488.3		471.3	470.3	4
14	1,587.8	794.4	1,570.7	1,569.8	V	359.3		342.2		3
15	1,700.9	850.9	1,683.8	1,682.8	I	260.2		243.2		2
16	1,847.0	924.0	1,829.9	1,829.0	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-6	sp|P40425|PBX2_HUMAN	QATEVLNEYFYSHLSNPYPSEEAKEELAK	106.71	Gln->pyro-Glu (N-term Q)	Light	3	1123.8648

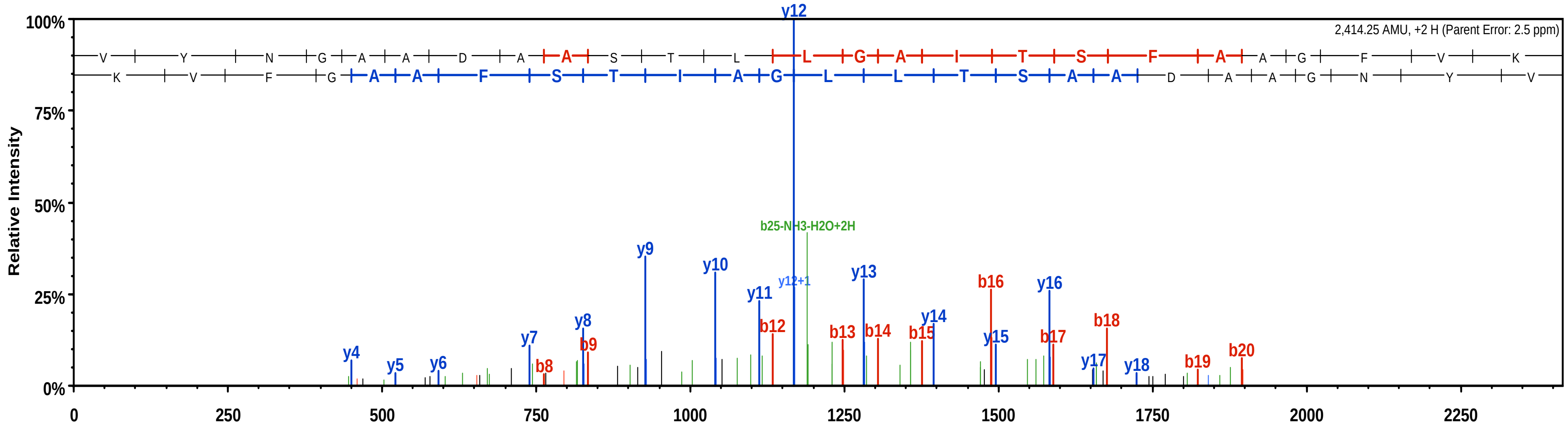


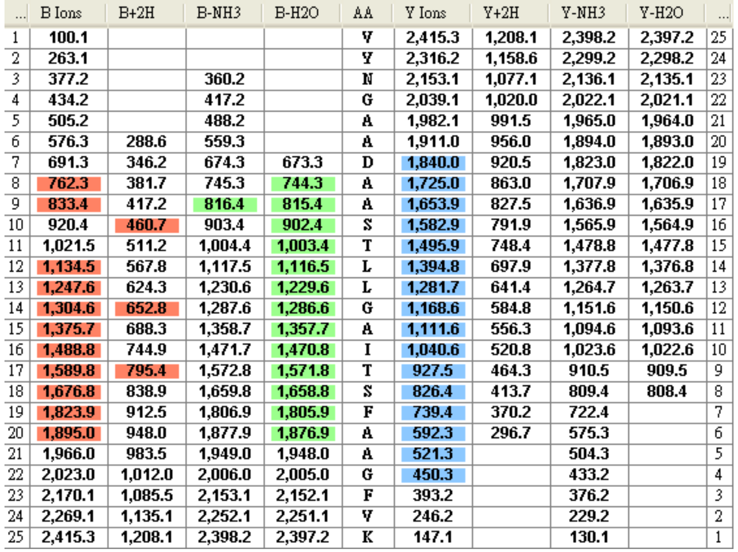


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	3,369.6	1,685.3	3,352.6	3,351.6	29
2	183.1		166.0		A	3,258.5	1,629.8	3,241.5	3,240.5	28
3	284.1		267.1	266.1	T	3,187.5	1,594.3	3,170.5	3,169.5	27
4	413.2		396.1	395.2	E	3,086.5	1,543.7	3,069.4	3,068.5	26
5	512.2		495.2	494.2	V	2,957.4	1,479.2	2,940.4	2,939.4	25
6	625.3	313.2	608.3	607.3	L	2,858.4	1,429.7	2,841.3	2,840.3	24
7	739.4	370.2	722.3	721.4	N	2,745.3	1,373.1	2,728.2	2,727.3	23
8	868.4	434.7	851.4	850.4	E	2,631.2	1,316.1	2,614.2	2,613.2	22
9	1,031.5	516.2	1,014.4	1,013.5	Y	2,502.2	1,251.6	2,485.2	2,484.2	21
10	1,178.5	589.8	1,161.5	1,160.5	F	2,339.1	1,170.1	2,322.1	2,321.1	20
11	1,341.6	671.3	1,324.6	1,323.6	Y	2,192.1	1,096.5	2,175.0	2,174.0	19
12	1,428.6	714.8	1,411.6	1,410.6	S	2,029.0	1,015.0	2,012.0	2,011.0	18
13	1,565.7	783.3	1,548.7	1,547.7	H	1,942.0	971.5	1,924.9	1,923.9	17
14	1,678.8	839.9	1,661.7	1,660.8	L	1,804.9	903.0	1,787.9	1,786.9	16
15	1,765.8	883.4	1,748.8	1,747.8	S	1,691.8	846.4	1,674.8	1,673.8	15
16	1,879.8	940.4	1,862.8	1,861.8	N	1,604.8	802.9	1,587.8	1,586.8	14
17	1,976.9	989.0	1,959.9	1,958.9	P	1,490.7	745.9	1,473.7	1,472.7	13
18	2,140.0	1,070.5	2,122.9	2,122.0	Y	1,393.7	697.3	1,376.7	1,375.7	12
19	2,237.0	1,119.0	2,220.0	2,219.0	P	1,230.6	615.8	1,213.6	1,212.6	11
20	2,324.1	1,162.5	2,307.0	2,306.0	S	1,133.6	567.3	1,116.5	1,115.6	10
21	2,453.1	1,227.1	2,436.1	2,435.1	E	1,046.5	523.8	1,029.5	1,028.5	9
22	2,582.1	1,291.6	2,565.1	2,564.1	E	917.5	459.3	900.5	899.5	8
23	2,653.2	1,327.1	2,636.1	2,635.2	A	788.5	394.7	771.4	770.4	7
24	2,781.3	1,391.1	2,764.2	2,763.3	K	717.4	359.2	700.4	699.4	6
25	2,910.3	1,455.7	2,893.3	2,892.3	E	589.3		572.3	571.3	5
26	3,039.4	1,520.2	3,022.3	3,021.3	E	460.3		443.3	442.3	4
27	3,152.4	1,576.7	3,135.4	3,134.4	L	331.2		314.2		3
28	3,223.5	1,612.2	3,206.4	3,205.5	A	218.1		201.1		2
29	3,369.6	1,685.3	3,352.6	3,351.6	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-7	sp|P41440|S19A1_HUMAN	VYNGAADAASTLLGAITSFAAGFVK	106.7	Unmodified	Light	2	1208.1314

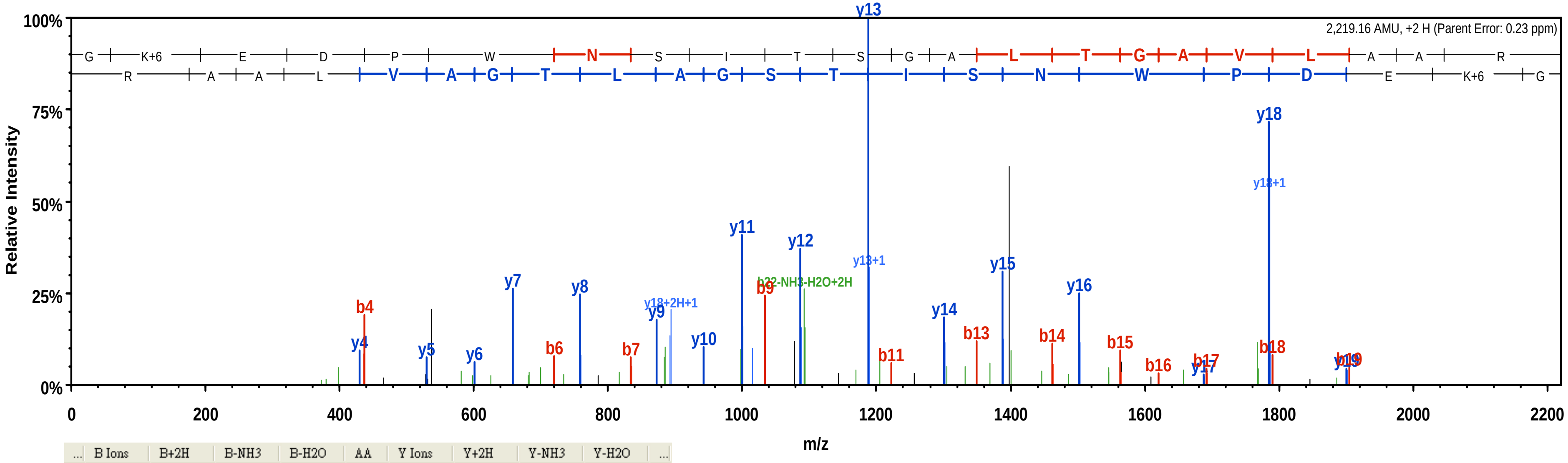


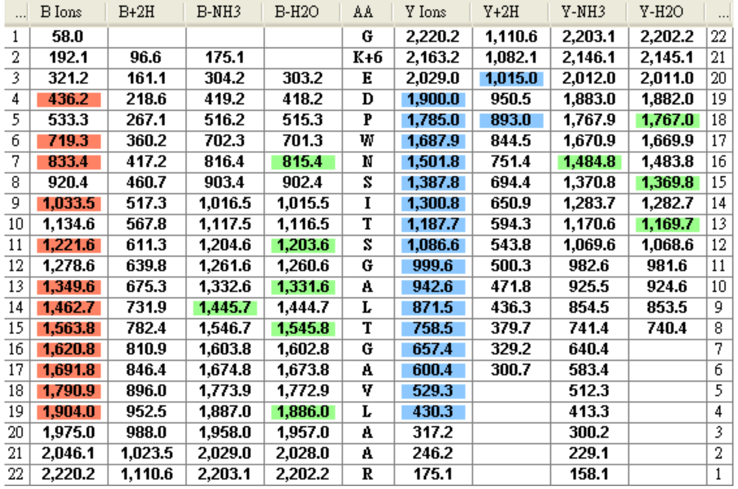


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	2,415.3	1,208.1	2,398.2	2,397.2	25
2	263.1				Y	2,316.2	1,158.6	2,299.2	2,298.2	24
3	377.2		360.2		N	2,153.1	1,077.1	2,136.1	2,135.1	23
4	434.2		417.2		G	2,039.1	1,020.0	2,022.1	2,021.1	22
5	505.2		488.2		A	1,982.1	991.5	1,965.0	1,964.0	21
6	576.3	288.6	559.3		A	1,911.0	956.0	1,894.0	1,893.0	20
7	691.3	346.2	674.3	673.3	D	1,840.0	920.5	1,823.0	1,822.0	19
8	762.3	381.7	745.3	744.3	A	1,725.0	863.0	1,707.9	1,706.9	18
9	833.4	417.2	816.4	815.4	A	1,653.9	827.5	1,636.9	1,635.9	17
10	920.4	460.7	903.4	902.4	S	1,582.9	791.9	1,565.9	1,564.9	16
11	1,021.5	511.2	1,004.4	1,003.4	T	1,495.9	748.4	1,478.8	1,477.8	15
12	1,134.5	567.8	1,117.5	1,116.5	L	1,394.8	697.9	1,377.8	1,376.8	14
13	1,247.6	624.3	1,230.6	1,229.6	L	1,281.7	641.4	1,264.7	1,263.7	13
14	1,304.6	652.8	1,287.6	1,286.6	G	1,168.6	584.8	1,151.6	1,150.6	12
15	1,375.7	688.3	1,358.7	1,357.7	A	1,111.6	556.3	1,094.6	1,093.6	11
16	1,488.8	744.9	1,471.7	1,470.8	I	1,040.6	520.8	1,023.6	1,022.6	10
17	1,589.8	795.4	1,572.8	1,571.8	T	927.5	464.3	910.5	909.5	9
18	1,676.8	838.9	1,659.8	1,658.8	S	826.4	413.7	809.4	808.4	8
19	1,823.9	912.5	1,806.9	1,805.9	F	739.4	370.2	722.4		7
20	1,895.0	948.0	1,877.9	1,876.9	A	592.3	296.7	575.3		6
21	1,966.0	983.5	1,949.0	1,948.0	A	521.3		504.3		5
22	2,023.0	1,012.0	2,006.0	2,005.0	G	450.3		433.2		4
23	2,170.1	1,085.5	2,153.1	2,152.1	F	393.2		376.2		3
24	2,269.1	1,135.1	2,252.1	2,251.1	V	246.2		229.2		2
25	2,415.3	1,208.1	2,398.2	2,397.2	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-8	sp|O60830|TI17B_HUMAN	GKEDPWNSITSGALTGAVLAAR	103.67	Unmodified	Heavy	2	1107.5793

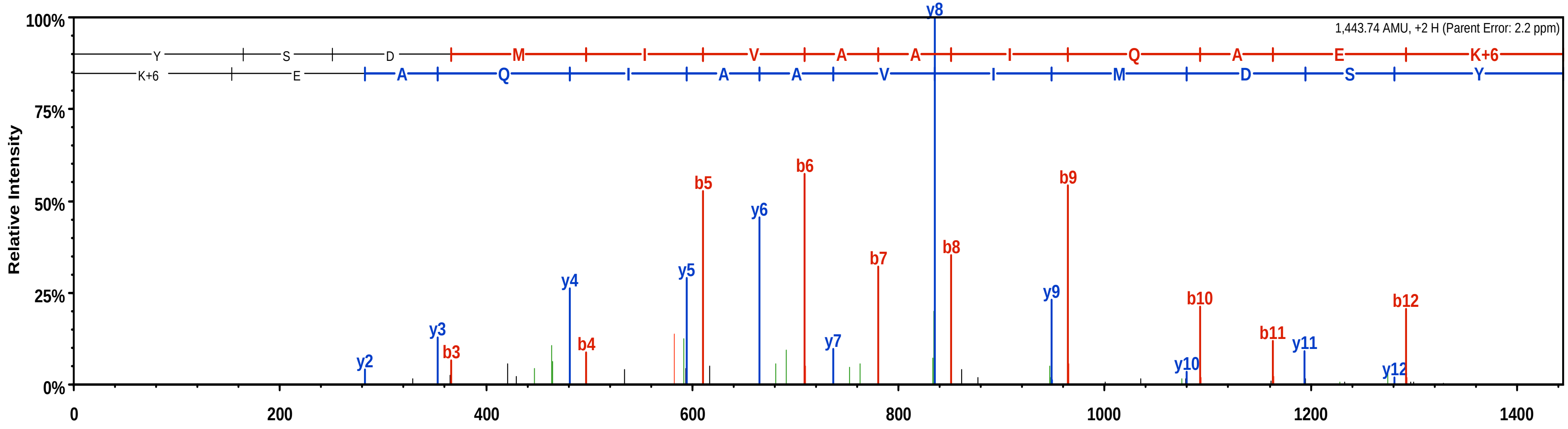


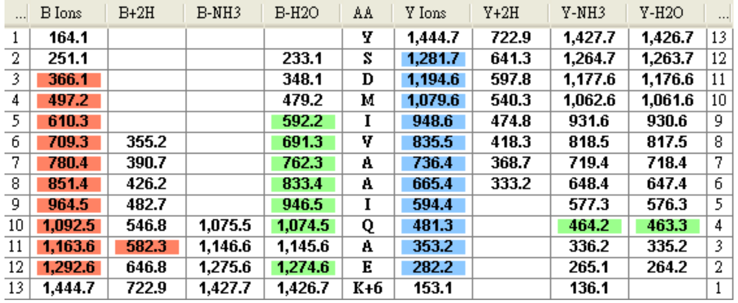


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	2,220.2	1,110.6	2,203.1	2,202.2	22
2	192.1	96.6	175.1		K+6	2,163.2	1,082.1	2,146.1	2,145.1	21
3	321.2	161.1	304.2	303.2	E	2,029.0	1,015.0	2,012.0	2,011.0	20
4	436.2	218.6	419.2	418.2	D	1,900.0	950.5	1,883.0	1,882.0	19
5	533.3	267.1	516.2	515.3	P	1,785.0	893.0	1,767.9	1,767.0	18
6	719.3	360.2	702.3	701.3	W	1,687.9	844.5	1,670.9	1,669.9	17
7	833.4	417.2	816.4	815.4	N	1,501.8	751.4	1,484.8	1,483.8	16
8	920.4	460.7	903.4	902.4	S	1,387.8	694.4	1,370.8	1,369.8	15
9	1,033.5	517.3	1,016.5	1,015.5	I	1,300.8	650.9	1,283.7	1,282.7	14
10	1,134.6	567.8	1,117.5	1,116.5	T	1,187.7	594.3	1,170.6	1,169.7	13
11	1,221.6	611.3	1,204.6	1,203.6	S	1,086.6	543.8	1,069.6	1,068.6	12
12	1,278.6	639.8	1,261.6	1,260.6	G	999.6	500.3	982.6	981.6	11
13	1,349.6	675.3	1,332.6	1,331.6	A	942.6	471.8	925.5	924.6	10
14	1,462.7	731.9	1,445.7	1,444.7	L	871.5	436.3	854.5	853.5	9
15	1,563.8	782.4	1,546.7	1,545.8	T	758.5	379.7	741.4	740.4	8
16	1,620.8	810.9	1,603.8	1,602.8	G	657.4	329.2	640.4		7
17	1,691.8	846.4	1,674.8	1,673.8	A	600.4	300.7	583.4		6
18	1,790.9	896.0	1,773.9	1,772.9	V	529.3		512.3		5
19	1,904.0	952.5	1,887.0	1,886.0	L	430.3		413.3		4
20	1,975.0	988.0	1,958.0	1,957.0	A	317.2		300.2		3
21	2,046.1	1,023.5	2,029.0	2,028.0	A	246.2		229.1		2
22	2,220.2	1,110.6	2,203.1	2,202.2	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-9	sp|P07305|H10_HUMAN	YSDMIVAAIQAEK	102.69	Unmodified	Heavy	2	719.86596

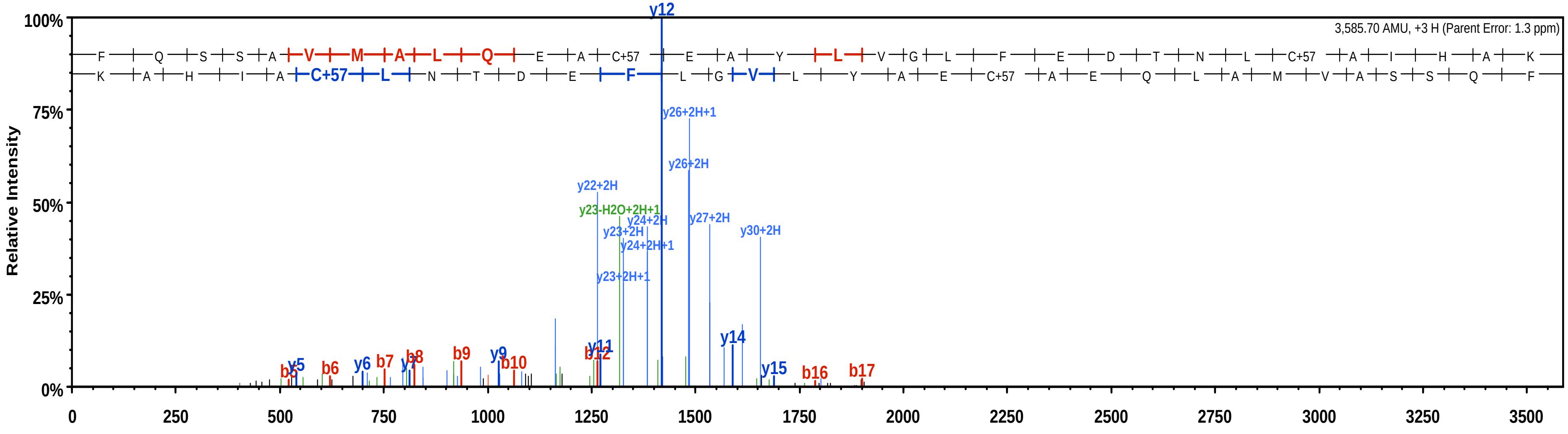


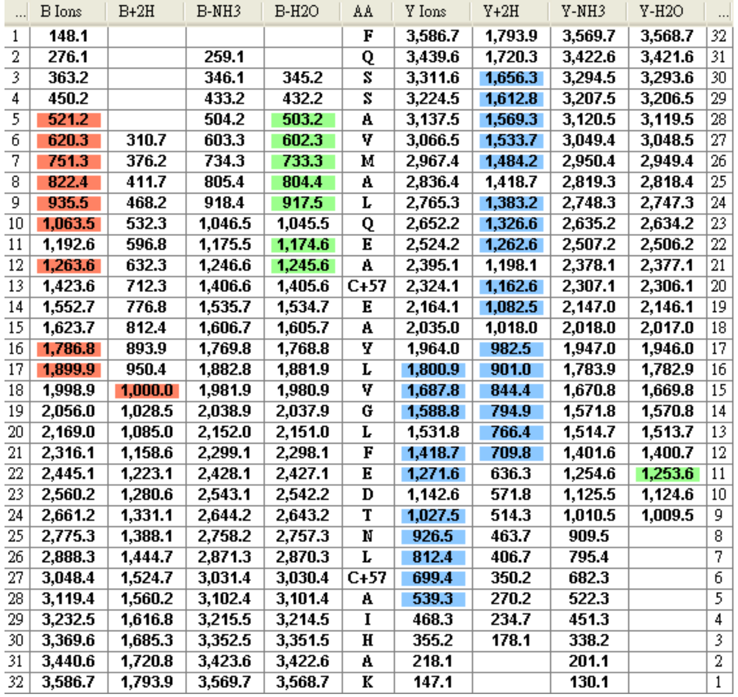


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	164.1				Y	1,444.7	722.9	1,427.7	1,426.7	13
2	251.1			233.1	S	1,281.7	641.3	1,264.7	1,263.7	12
3	366.1			348.1	D	1,194.6	597.8	1,177.6	1,176.6	11
4	497.2			479.2	M	1,079.6	540.3	1,062.6	1,061.6	10
5	610.3			592.2	I	948.6	474.8	931.6	930.6	9
6	709.3	355.2		691.3	V	835.5	418.3	818.5	817.5	8
7	780.4	390.7		762.3	A	736.4	368.7	719.4	718.4	7
8	851.4	426.2		833.4	A	665.4	333.2	648.4	647.4	6
9	964.5	482.7		946.5	I	594.4		577.3	576.3	5
10	1,092.5	546.8	1,075.5	1,074.5	Q	481.3		464.2	463.3	4
11	1,163.6	582.3	1,146.6	1,145.6	A	353.2		336.2	335.2	3
12	1,292.6	646.8	1,275.6	1,274.6	E	282.2		265.1	264.2	2
13	1,444.7	722.9	1,427.7	1,426.7	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-10	sp|P68431|H31_HUMAN	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	102.32	Unmodified	Light	3	1196.2387

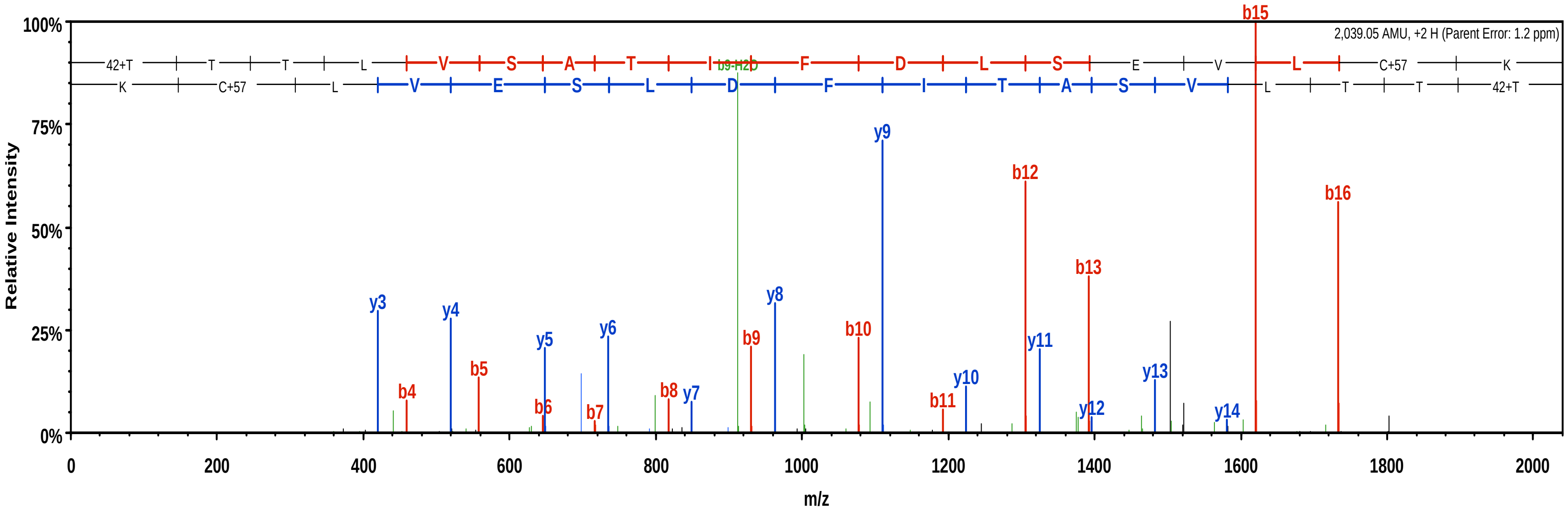


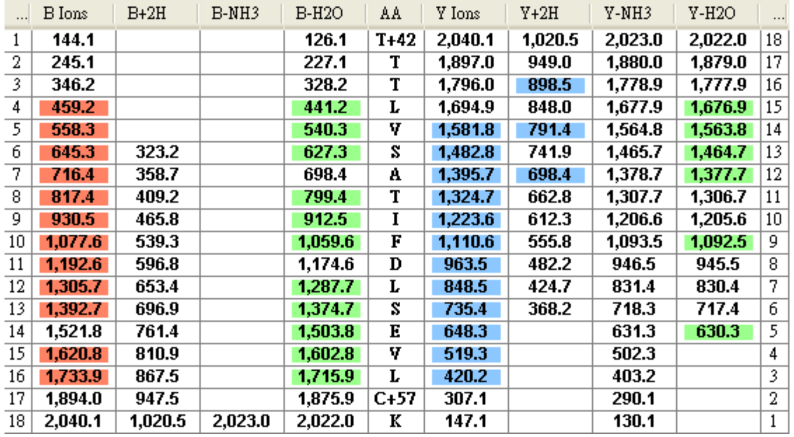


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.1				F	3,586.7	1,793.9	3,569.7	3,568.7	32
2	276.1		259.1		Q	3,439.6	1,720.3	3,422.6	3,421.6	31
3	363.2		346.1	345.2	S	3,311.6	1,656.3	3,294.5	3,293.6	30
4	450.2		433.2	432.2	S	3,224.5	1,612.8	3,207.5	3,206.5	29
5	521.2		504.2	503.2	A	3,137.5	1,569.3	3,120.5	3,119.5	28
6	620.3	310.7	603.3	602.3	V	3,066.5	1,533.7	3,049.4	3,048.5	27
7	751.3	376.2	734.3	733.3	M	2,967.4	1,484.2	2,950.4	2,949.4	26
8	822.4	411.7	805.4	804.4	A	2,836.4	1,418.7	2,819.3	2,818.4	25
9	935.5	468.2	918.4	917.5	L	2,765.3	1,383.2	2,748.3	2,747.3	24
10	1,063.5	532.3	1,046.5	1,045.5	Q	2,652.2	1,326.6	2,635.2	2,634.2	23
11	1,192.6	596.8	1,175.5	1,174.6	E	2,524.2	1,262.6	2,507.2	2,506.2	22
12	1,263.6	632.3	1,246.6	1,245.6	A	2,395.1	1,198.1	2,378.1	2,377.1	21
13	1,423.6	712.3	1,406.6	1,405.6	C+57	2,324.1	1,162.6	2,307.1	2,306.1	20
14	1,552.7	776.8	1,535.7	1,534.7	E	2,164.1	1,082.5	2,147.0	2,146.1	19
15	1,623.7	812.4	1,606.7	1,605.7	A	2,035.0	1,018.0	2,018.0	2,017.0	18
16	1,786.8	893.9	1,769.8	1,768.8	Y	1,964.0	982.5	1,947.0	1,946.0	17
17	1,899.9	950.4	1,882.8	1,881.9	L	1,800.9	901.0	1,783.9	1,782.9	16
18	1,998.9	1,000.0	1,981.9	1,980.9	V	1,687.8	844.4	1,670.8	1,669.8	15
19	2,056.0	1,028.5	2,038.9	2,037.9	G	1,588.8	794.9	1,571.8	1,570.8	14
20	2,169.0	1,085.0	2,152.0	2,151.0	L	1,531.8	766.4	1,514.7	1,513.7	13
21	2,316.1	1,158.6	2,299.1	2,298.1	F	1,418.7	709.8	1,401.6	1,400.7	12
22	2,445.1	1,223.1	2,428.1	2,427.1	E	1,271.6	636.3	1,254.6	1,253.6	11
23	2,560.2	1,280.6	2,543.1	2,542.2	D	1,142.6	571.8	1,125.5	1,124.6	10
24	2,661.2	1,331.1	2,644.2	2,643.2	T	1,027.5	514.3	1,010.5	1,009.5	9
25	2,775.3	1,388.1	2,758.2	2,757.3	N	926.5	463.7	909.5		8
26	2,888.3	1,444.7	2,871.3	2,870.3	L	812.4	406.7	795.4		7
27	3,048.4	1,524.7	3,031.4	3,030.4	C+57	699.4	350.2	682.3		6
28	3,119.4	1,560.2	3,102.4	3,101.4	A	539.3	270.2	522.3		5
29	3,232.5	1,616.8	3,215.5	3,214.5	I	468.3	234.7	451.3		4
30	3,369.6	1,685.3	3,352.5	3,351.5	H	355.2	178.1	338.2		3
31	3,440.6	1,720.8	3,423.6	3,422.6	A	218.1		201.1		2
32	3,586.7	1,793.9	3,569.7	3,568.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-14	sp|Q07352|TISB_HUMAN	TTTLVSATIFDLSEVLCK	101.4	Acetyl (Protein N-term)	Light	2	1020.5321

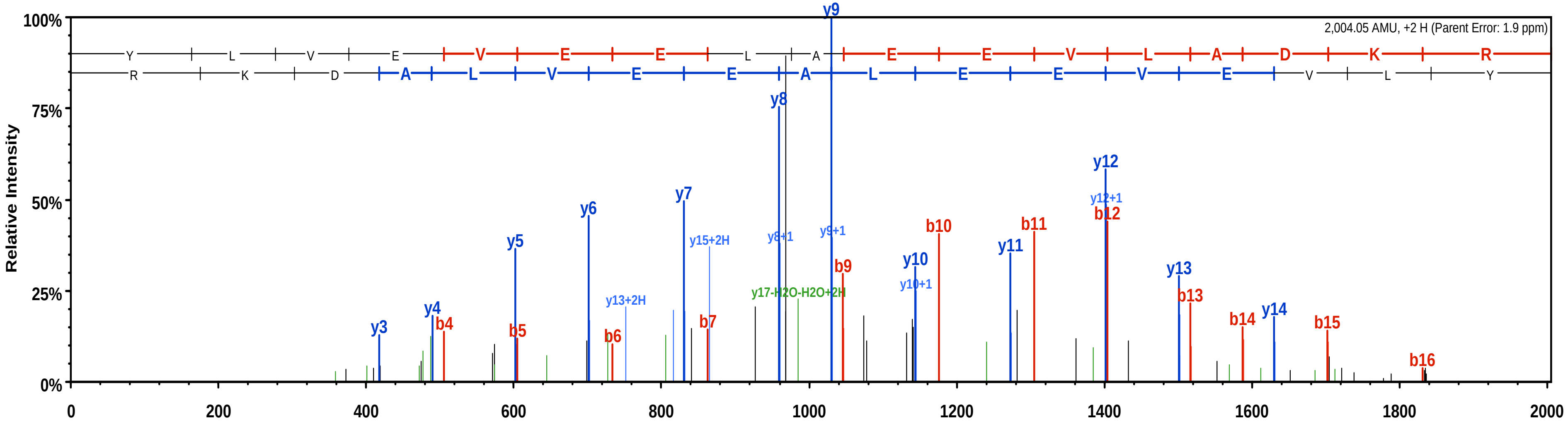


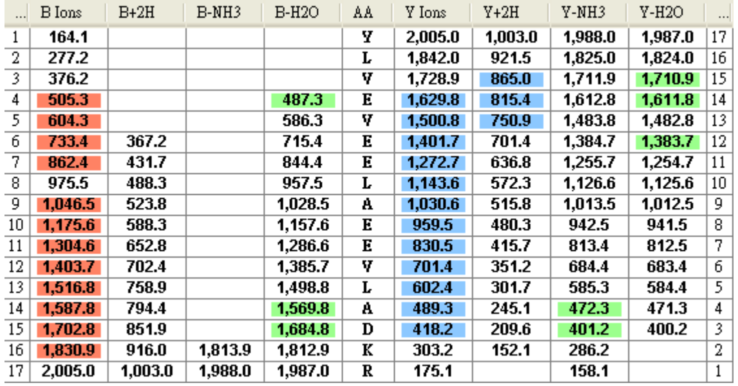


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	144.1			126.1	T+42	2,040.1	1,020.5	2,023.0	2,022.0	18
2	245.1			227.1	T	1,897.0	949.0	1,880.0	1,879.0	17
3	346.2			328.2	T	1,796.0	898.5	1,778.9	1,777.9	16
4	459.2			441.2	L	1,694.9	848.0	1,677.9	1,676.9	15
5	558.3			540.3	V	1,581.8	791.4	1,564.8	1,563.8	14
6	645.3	323.2		627.3	S	1,482.8	741.9	1,465.7	1,464.7	13
7	716.4	358.7		698.4	A	1,395.7	698.4	1,378.7	1,377.7	12
8	817.4	409.2		799.4	T	1,324.7	662.8	1,307.7	1,306.7	11
9	930.5	465.8		912.5	I	1,223.6	612.3	1,206.6	1,205.6	10
10	1,077.6	539.3		1,059.6	F	1,110.6	555.8	1,093.5	1,092.5	9
11	1,192.6	596.8		1,174.6	D	963.5	482.2	946.5	945.5	8
12	1,305.7	653.4		1,287.7	L	848.5	424.7	831.4	830.4	7
13	1,392.7	696.9		1,374.7	S	735.4	368.2	718.3	717.4	6
14	1,521.8	761.4		1,503.8	E	648.3		631.3	630.3	5
15	1,620.8	810.9		1,602.8	V	519.3		502.3		4
16	1,733.9	867.5		1,715.9	L	420.2		403.2		3
17	1,894.0	947.5		1,875.9	C+57	307.1		290.1		2
18	2,040.1	1,020.5	2,023.0	2,022.0	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-11	sp|Q9NUG6|PDRG1_HUMAN	YLVEVEELAEEVLADKR	100.77	Unmodified	Light	2	1003.028

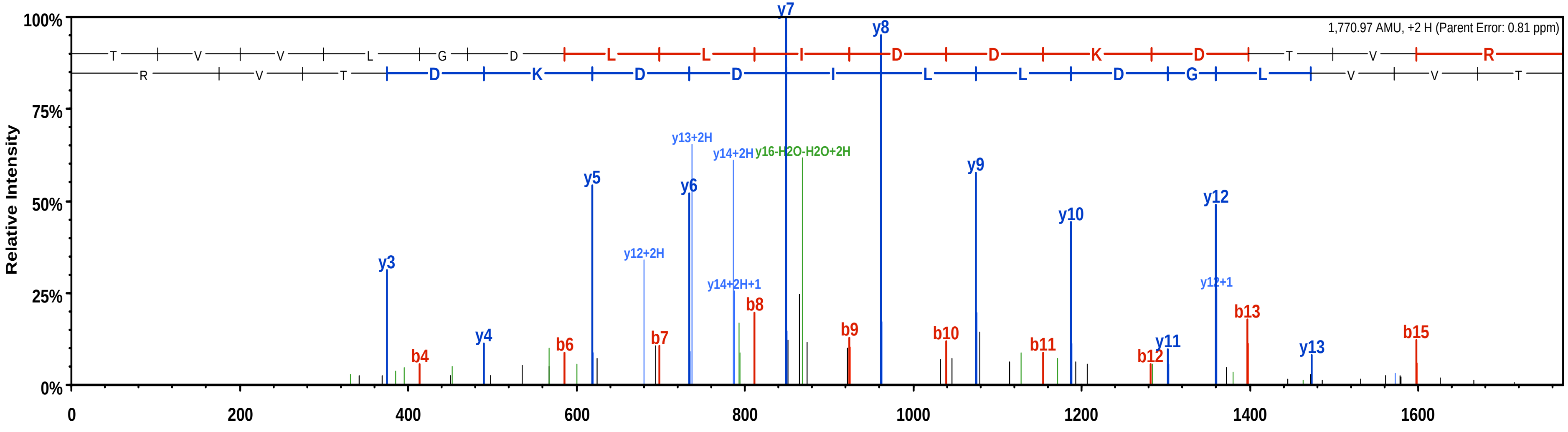


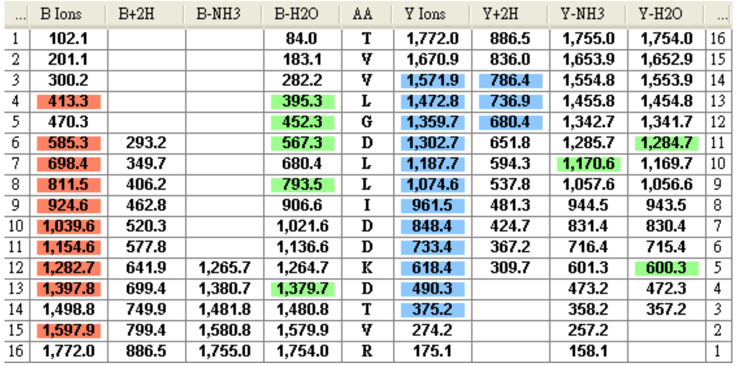


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	164.1				Y	2,005.0	1,003.0	1,988.0	1,987.0	17
2	277.2				L	1,842.0	921.5	1,825.0	1,824.0	16
3	376.2				V	1,728.9	865.0	1,711.9	1,710.9	15
4	505.3			487.3	E	1,629.8	815.4	1,612.8	1,611.8	14
5	604.3			586.3	V	1,500.8	750.9	1,483.8	1,482.8	13
6	733.4	367.2		715.4	E	1,401.7	701.4	1,384.7	1,383.7	12
7	862.4	431.7		844.4	E	1,272.7	636.8	1,255.7	1,254.7	11
8	975.5	488.3		957.5	L	1,143.6	572.3	1,126.6	1,125.6	10
9	1,046.5	523.8		1,028.5	A	1,030.6	515.8	1,013.5	1,012.5	9
10	1,175.6	588.3		1,157.6	E	959.5	480.3	942.5	941.5	8
11	1,304.6	652.8		1,286.6	E	830.5	415.7	813.4	812.5	7
12	1,403.7	702.4		1,385.7	V	701.4	351.2	684.4	683.4	6
13	1,516.8	758.9		1,498.8	L	602.4	301.7	585.3	584.4	5
14	1,587.8	794.4		1,569.8	A	489.3	245.1	472.3	471.3	4
15	1,702.8	851.9		1,684.8	D	418.2	209.6	401.2	400.2	3
16	1,830.9	916.0	1,813.9	1,812.9	K	303.2	152.1	286.2		2
17	2,005.0	1,003.0	1,988.0	1,987.0	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-12	sp|Q8TCD5|NT5C_HUMAN	TVVLGDLLIDDKDTVR	95.01	Unmodified	Light	2	886.49364

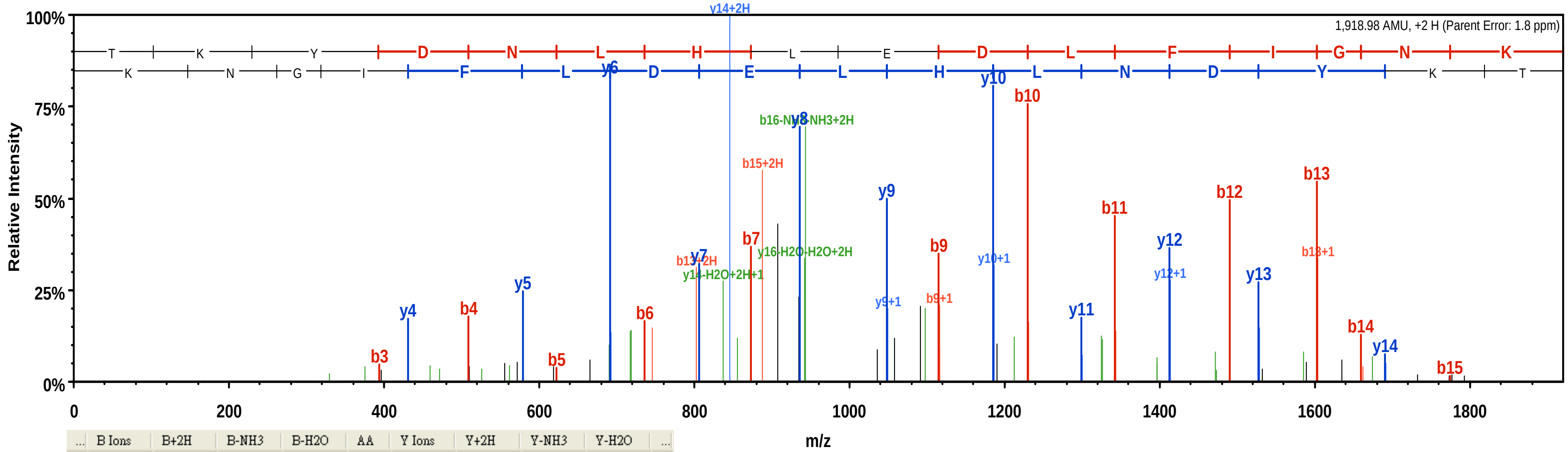


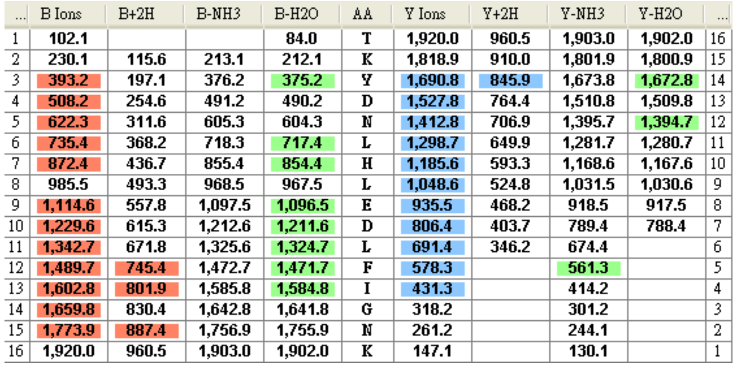


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	102.1			84.0	T	1,772.0	886.5	1,755.0	1,754.0	16
2	201.1			183.1	V	1,670.9	836.0	1,653.9	1,652.9	15
3	300.2			282.2	V	1,571.9	786.4	1,554.8	1,553.9	14
4	413.3			395.3	L	1,472.8	736.9	1,455.8	1,454.8	13
5	470.3			452.3	G	1,359.7	680.4	1,342.7	1,341.7	12
6	585.3	293.2		567.3	D	1,302.7	651.8	1,285.7	1,284.7	11
7	698.4	349.7		680.4	L	1,187.7	594.3	1,170.6	1,169.7	10
8	811.5	406.2		793.5	L	1,074.6	537.8	1,057.6	1,056.6	9
9	924.6	462.8		906.6	I	961.5	481.3	944.5	943.5	8
10	1,039.6	520.3		1,021.6	D	848.4	424.7	831.4	830.4	7
11	1,154.6	577.8		1,136.6	D	733.4	367.2	716.4	715.4	6
12	1,282.7	641.9	1,265.7	1,264.7	K	618.4	309.7	601.3	600.3	5
13	1,397.8	699.4	1,380.7	1,379.7	D	490.3		473.2	472.3	4
14	1,498.8	749.9	1,481.8	1,480.8	T	375.2		358.2	357.2	3
15	1,597.9	799.4	1,580.8	1,579.9	V	274.2		257.2		2
16	1,772.0	886.5	1,755.0	1,754.0	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-13	sp|Q9Y5B8|NDK7_HUMAN	TKYDNLHLEDLFIGNK	94.65	Unmodified	Light	2	960.49672

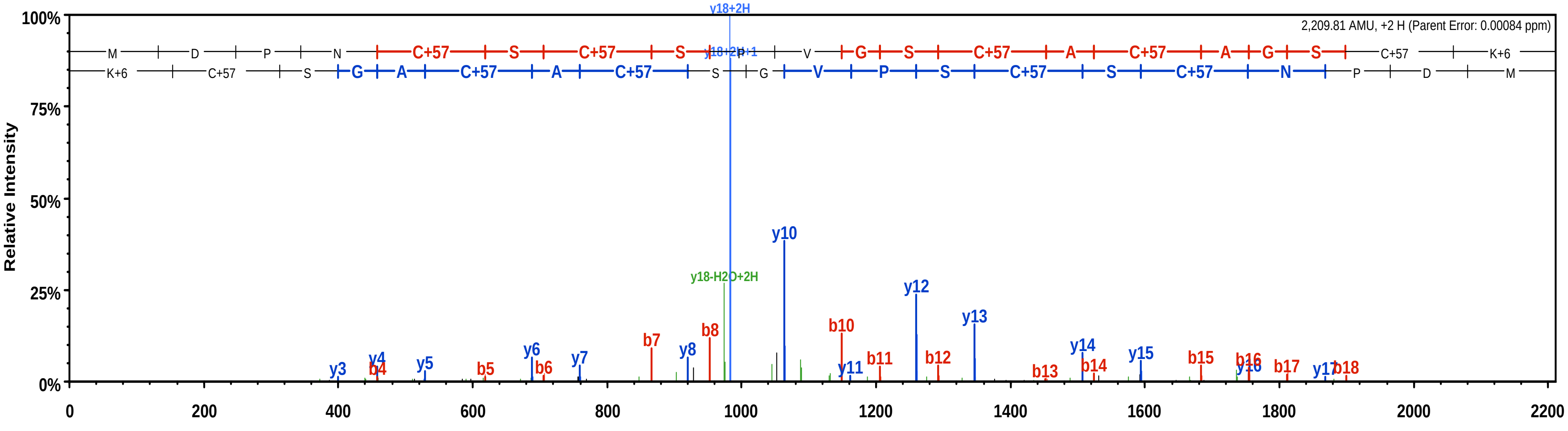


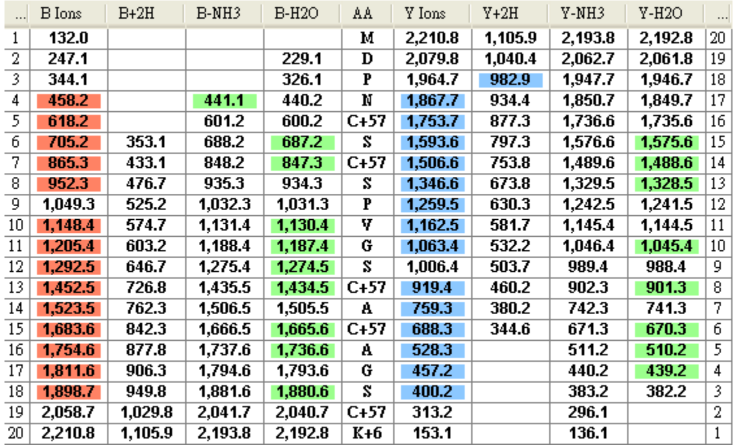


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	102.1			84.0	T	1,920.0	960.5	1,903.0	1,902.0	16
2	230.1	115.6	213.1	212.1	K	1,818.9	910.0	1,801.9	1,800.9	15
3	393.2	197.1	376.2	375.2	Y	1,690.8	845.9	1,673.8	1,672.8	14
4	508.2	254.6	491.2	490.2	D	1,527.8	764.4	1,510.8	1,509.8	13
5	622.3	311.6	605.3	604.3	N	1,412.8	706.9	1,395.7	1,394.7	12
6	735.4	368.2	718.3	717.4	L	1,298.7	649.9	1,281.7	1,280.7	11
7	872.4	436.7	855.4	854.4	H	1,185.6	593.3	1,168.6	1,167.6	10
8	985.5	493.3	968.5	967.5	L	1,048.6	524.8	1,031.5	1,030.6	9
9	1,114.6	557.8	1,097.5	1,096.5	E	935.5	468.2	918.5	917.5	8
10	1,229.6	615.3	1,212.6	1,211.6	D	806.4	403.7	789.4	788.4	7
11	1,342.7	671.8	1,325.6	1,324.7	L	691.4	346.2	674.4		6
12	1,489.7	745.4	1,472.7	1,471.7	F	578.3		561.3		5
13	1,602.8	801.9	1,585.8	1,584.8	I	431.3		414.2		4
14	1,659.8	830.4	1,642.8	1,641.8	G	318.2		301.2		3
15	1,773.9	887.4	1,756.9	1,755.9	N	261.2		244.1		2
16	1,920.0	960.5	1,903.0	1,902.0	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-14	sp|P80297|MT1X_HUMAN	MDPNCSCSPVGSCACAGSCK	94.53	Unmodified	Heavy	2	1102.9014

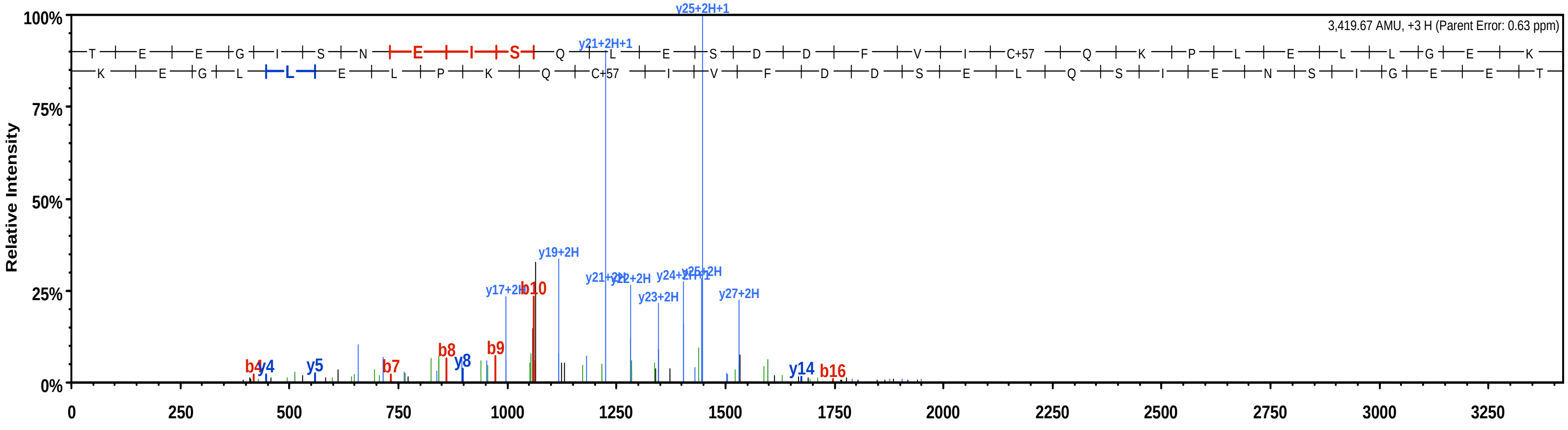


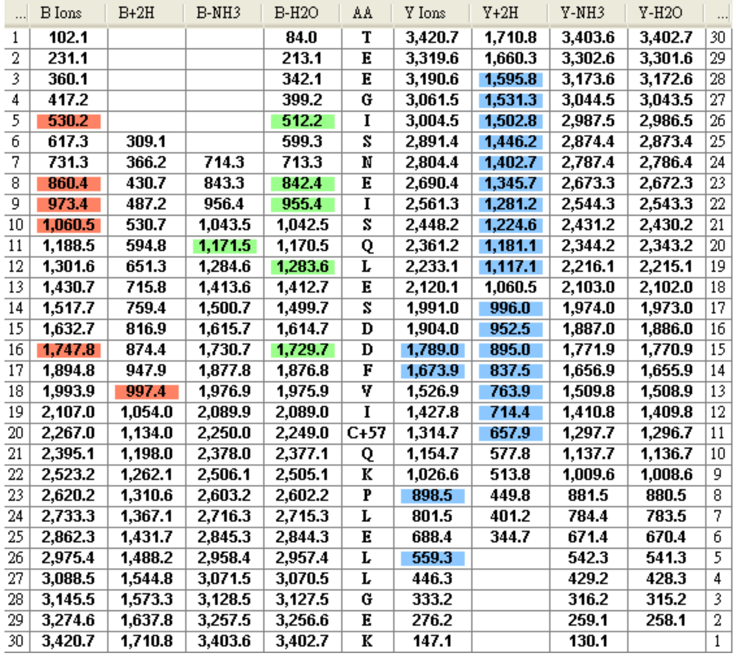


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	132.0				M	2,210.8	1,105.9	2,193.8	2,192.8	20
2	247.1			229.1	D	2,079.8	1,040.4	2,062.7	2,061.8	19
3	344.1			326.1	P	1,964.7	982.9	1,947.7	1,946.7	18
4	458.2		441.1	440.2	N	1,867.7	934.4	1,850.7	1,849.7	17
5	618.2		601.2	600.2	C+57	1,753.7	877.3	1,736.6	1,735.6	16
6	705.2	353.1	688.2	687.2	S	1,593.6	797.3	1,576.6	1,575.6	15
7	865.3	433.1	848.2	847.3	C+57	1,506.6	753.8	1,489.6	1,488.6	14
8	952.3	476.7	935.3	934.3	S	1,346.6	673.8	1,329.5	1,328.5	13
9	1,049.3	525.2	1,032.3	1,031.3	P	1,259.5	630.3	1,242.5	1,241.5	12
10	1,148.4	574.7	1,131.4	1,130.4	V	1,162.5	581.7	1,145.4	1,144.5	11
11	1,205.4	603.2	1,188.4	1,187.4	G	1,063.4	532.2	1,046.4	1,045.4	10
12	1,292.5	646.7	1,275.4	1,274.5	S	1,006.4	503.7	989.4	988.4	9
13	1,452.5	726.8	1,435.5	1,434.5	C+57	919.4	460.2	902.3	901.3	8
14	1,523.5	762.3	1,506.5	1,505.5	A	759.3	380.2	742.3	741.3	7
15	1,683.6	842.3	1,666.5	1,665.6	C+57	688.3	344.6	671.3	670.3	6
16	1,754.6	877.8	1,737.6	1,736.6	A	528.3		511.2	510.2	5
17	1,811.6	906.3	1,794.6	1,793.6	G	457.2		440.2	439.2	4
18	1,898.7	949.8	1,881.6	1,880.6	S	400.2		383.2	382.2	3
19	2,058.7	1,029.8	2,041.7	2,040.7	C+57	313.2		296.1		2
20	2,210.8	1,105.9	2,193.8	2,192.8	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-15	sp|Q969F9|HPS3_HUMAN	TEEGISNEISQLESDDFVICQKPLELLGEK	94.26	Unmodified	Light	3	1140.8957

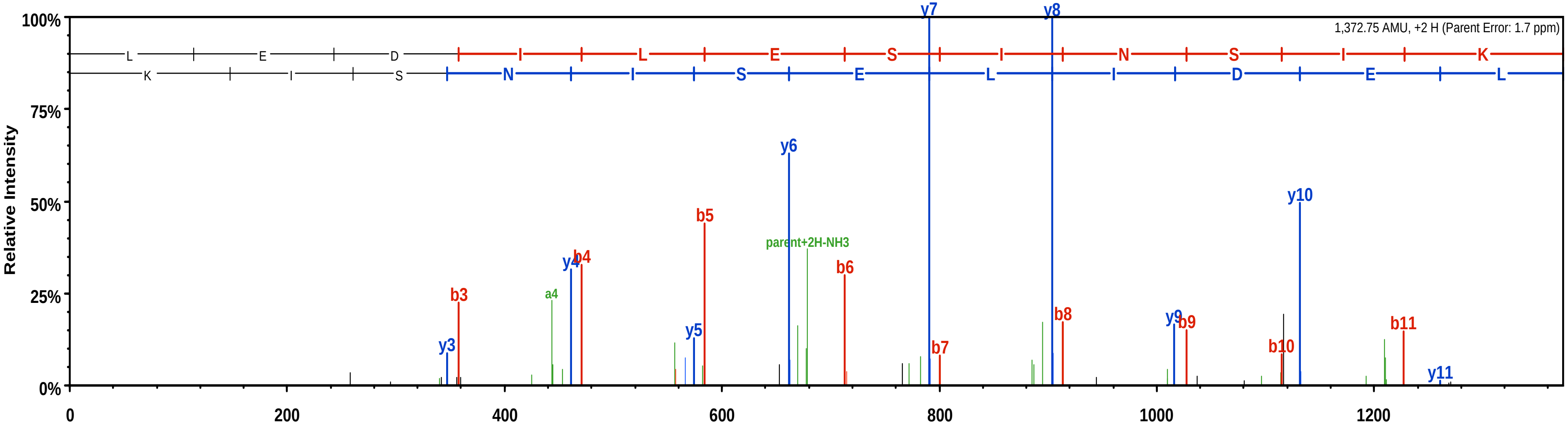


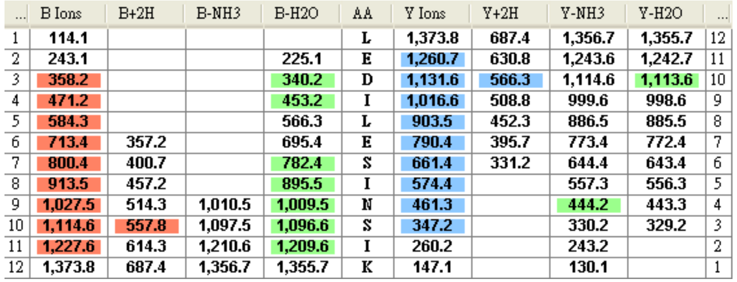


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	102.1			84.0	T	3,420.7	1,710.8	3,403.6	3,402.7	30
2	231.1			213.1	E	3,319.6	1,660.3	3,302.6	3,301.6	29
3	360.1			342.1	E	3,190.6	1,595.8	3,173.6	3,172.6	28
4	417.2			399.2	G	3,061.5	1,531.3	3,044.5	3,043.5	27
5	530.2			512.2	I	3,004.5	1,502.8	2,987.5	2,986.5	26
6	617.3	309.1		599.3	S	2,891.4	1,446.2	2,874.4	2,873.4	25
7	731.3	366.2	714.3	713.3	N	2,804.4	1,402.7	2,787.4	2,786.4	24
8	860.4	430.7	843.3	842.4	E	2,690.4	1,345.7	2,673.3	2,672.3	23
9	973.4	487.2	956.4	955.4	I	2,561.3	1,281.2	2,544.3	2,543.3	22
10	1,060.5	530.7	1,043.5	1,042.5	S	2,448.2	1,224.6	2,431.2	2,430.2	21
11	1,188.5	594.8	1,171.5	1,170.5	Q	2,361.2	1,181.1	2,344.2	2,343.2	20
12	1,301.6	651.3	1,284.6	1,283.6	L	2,233.1	1,117.1	2,216.1	2,215.1	19
13	1,430.7	715.8	1,413.6	1,412.7	E	2,120.1	1,060.5	2,103.0	2,102.0	18
14	1,517.7	759.4	1,500.7	1,499.7	S	1,991.0	996.0	1,974.0	1,973.0	17
15	1,632.7	816.9	1,615.7	1,614.7	D	1,904.0	952.5	1,887.0	1,886.0	16
16	1,747.8	874.4	1,730.7	1,729.7	D	1,789.0	895.0	1,771.9	1,770.9	15
17	1,894.8	947.9	1,877.8	1,876.8	F	1,673.9	837.5	1,656.9	1,655.9	14
18	1,993.9	997.4	1,976.9	1,975.9	V	1,526.9	763.9	1,509.8	1,508.9	13
19	2,107.0	1,054.0	2,089.9	2,089.0	I	1,427.8	714.4	1,410.8	1,409.8	12
20	2,267.0	1,134.0	2,250.0	2,249.0	C+57	1,314.7	657.9	1,297.7	1,296.7	11
21	2,395.1	1,198.0	2,378.0	2,377.1	Q	1,154.7	577.8	1,137.7	1,136.7	10
22	2,523.2	1,262.1	2,506.1	2,505.1	K	1,026.6	513.8	1,009.6	1,008.6	9
23	2,620.2	1,310.6	2,603.2	2,602.2	P	898.5	449.8	881.5	880.5	8
24	2,733.3	1,367.1	2,716.3	2,715.3	L	801.5	401.2	784.4	783.5	7
25	2,862.3	1,431.7	2,845.3	2,844.3	E	688.4	344.7	671.4	670.4	6
26	2,975.4	1,488.2	2,958.4	2,957.4	L	559.3		542.3	541.3	5
27	3,088.5	1,544.8	3,071.5	3,070.5	L	446.3		429.2	428.3	4
28	3,145.5	1,573.3	3,128.5	3,127.5	G	333.2		316.2	315.2	3
29	3,274.6	1,637.8	3,257.5	3,256.6	E	276.2		259.1	258.1	2
30	3,420.7	1,710.8	3,403.6	3,402.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-16	sp|Q9Y3A6|TMED5_HUMAN	LEDILESINSIK	94.24	Unmodified	Light	2	687.37976

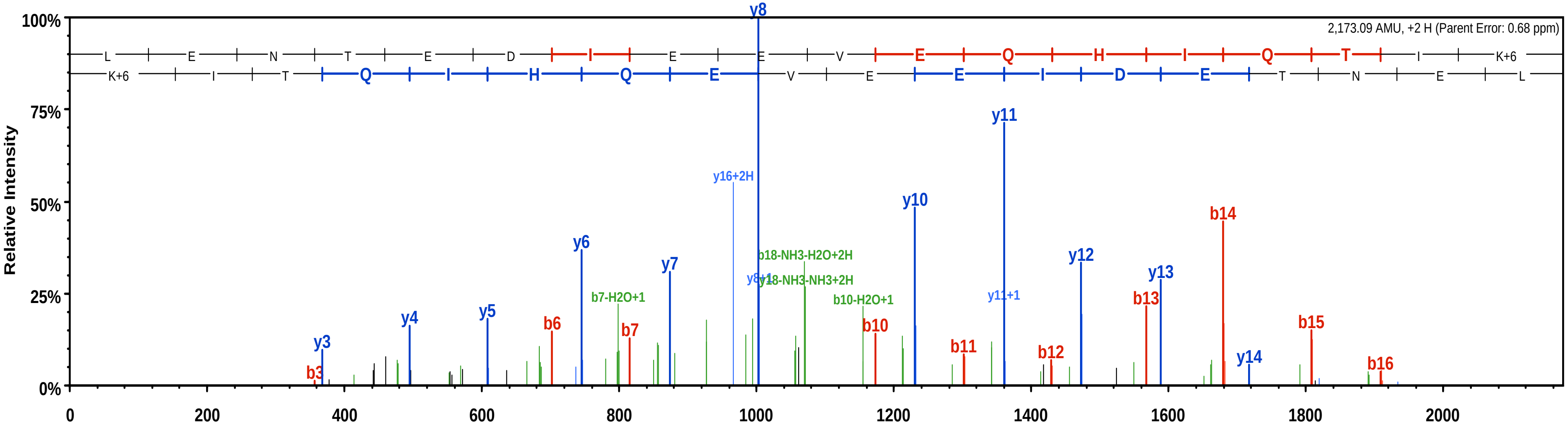


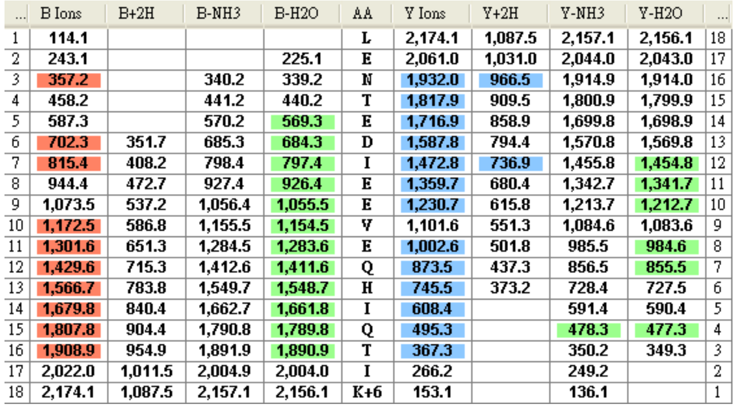


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	1,373.8	687.4	1,356.7	1,355.7	12
2	243.1			225.1	E	1,260.7	630.8	1,243.6	1,242.7	11
3	358.2			340.2	D	1,131.6	566.3	1,114.6	1,113.6	10
4	471.2			453.2	I	1,016.6	508.8	999.6	998.6	9
5	584.3			566.3	L	903.5	452.3	886.5	885.5	8
6	713.4	357.2		695.4	E	790.4	395.7	773.4	772.4	7
7	800.4	400.7		782.4	S	661.4	331.2	644.4	643.4	6
8	913.5	457.2		895.5	I	574.4		557.3	556.3	5
9	1,027.5	514.3	1,010.5	1,009.5	N	461.3		444.2	443.3	4
10	1,114.6	557.8	1,097.5	1,096.6	S	347.2		330.2	329.2	3
11	1,227.6	614.3	1,210.6	1,209.6	I	260.2		243.2		2
12	1,373.8	687.4	1,356.7	1,355.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-17	sp|Q9NUN5|LMBD1_HUMAN	LENTEDIEEVEQHIQTIK	93.9	Unmodified	Heavy	2	1084.5395

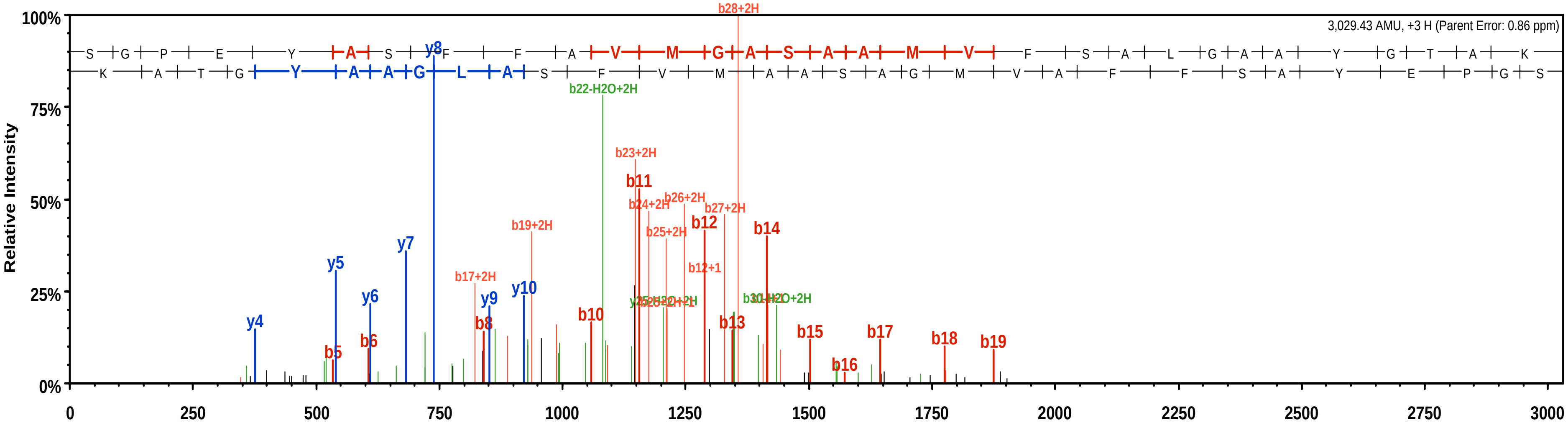


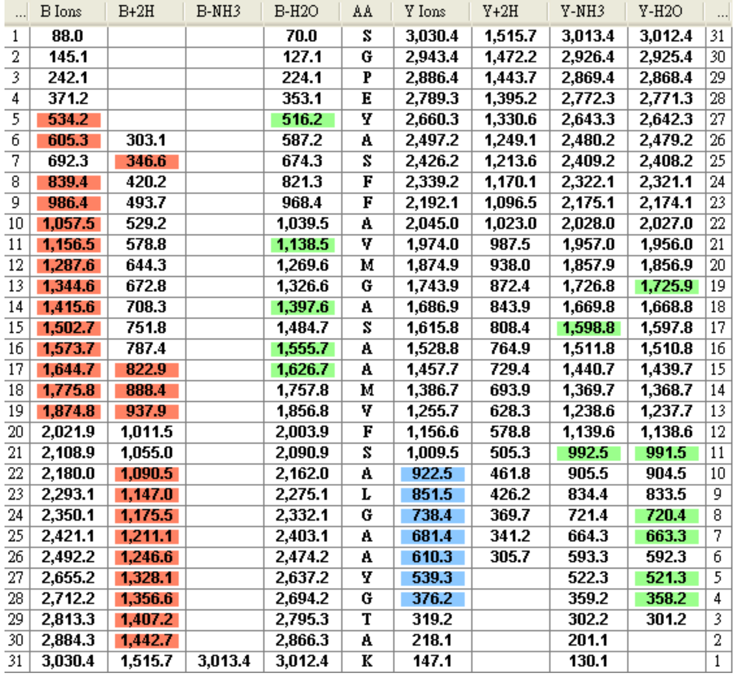


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	2,174.1	1,087.5	2,157.1	2,156.1	18
2	243.1			225.1	E	2,061.0	1,031.0	2,044.0	2,043.0	17
3	357.2		340.2	339.2	N	1,932.0	966.5	1,914.9	1,914.0	16
4	458.2		441.2	440.2	T	1,817.9	909.5	1,800.9	1,799.9	15
5	587.3		570.2	569.3	E	1,716.9	858.9	1,699.8	1,698.9	14
6	702.3	351.7	685.3	684.3	D	1,587.8	794.4	1,570.8	1,569.8	13
7	815.4	408.2	798.4	797.4	I	1,472.8	736.9	1,455.8	1,454.8	12
8	944.4	472.7	927.4	926.4	E	1,359.7	680.4	1,342.7	1,341.7	11
9	1,073.5	537.2	1,056.4	1,055.5	E	1,230.7	615.8	1,213.7	1,212.7	10
10	1,172.5	586.8	1,155.5	1,154.5	V	1,101.6	551.3	1,084.6	1,083.6	9
11	1,301.6	651.3	1,284.5	1,283.6	E	1,002.6	501.8	985.5	984.6	8
12	1,429.6	715.3	1,412.6	1,411.6	Q	873.5	437.3	856.5	855.5	7
13	1,566.7	783.8	1,549.7	1,548.7	H	745.5	373.2	728.4	727.5	6
14	1,679.8	840.4	1,662.7	1,661.8	I	608.4		591.4	590.4	5
15	1,807.8	904.4	1,790.8	1,789.8	Q	495.3		478.3	477.3	4
16	1,908.9	954.9	1,891.9	1,890.9	T	367.3		350.2	349.3	3
17	2,022.0	1,011.5	2,004.9	2,004.0	I	266.2		249.2		2
18	2,174.1	1,087.5	2,157.1	2,156.1	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-18	splP27449lVATL_HUMAN	SGPEYASFFAVMGASAAMVFSALGAAYGTAK	93.89	Unmodified	Light	3	1010.8174

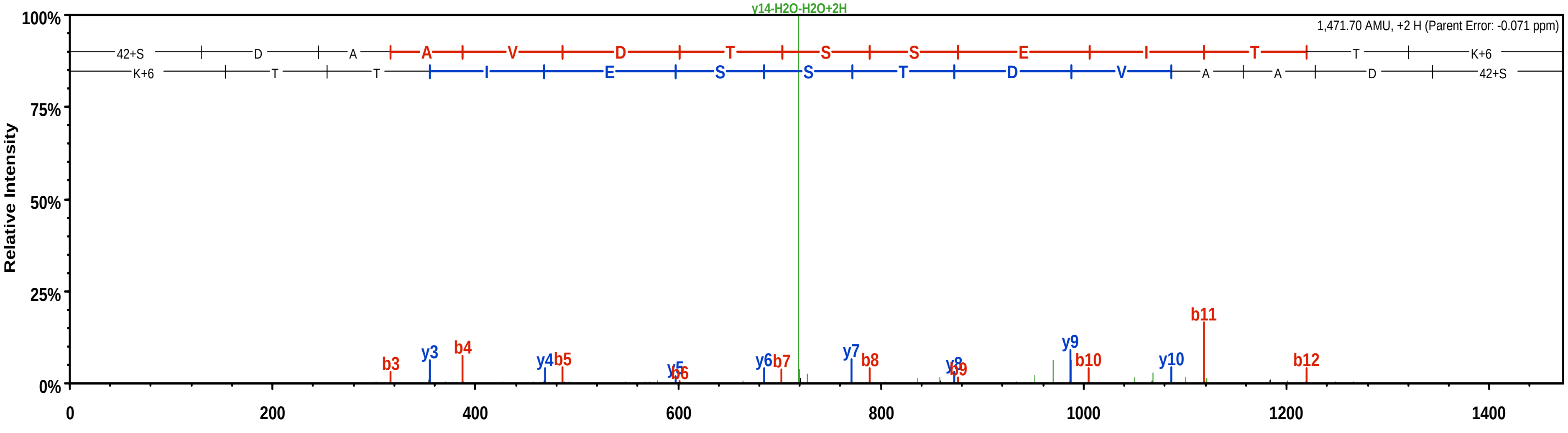


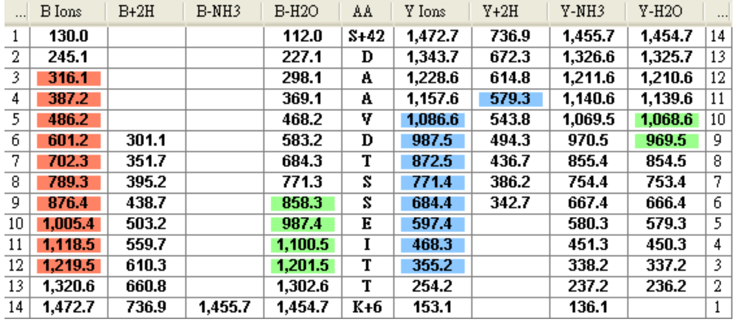


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	3,030.4	1,515.7	3,013.4	3,012.4	31
2	145.1			127.1	G	2,943.4	1,472.2	2,926.4	2,925.4	30
3	242.1			224.1	P	2,886.4	1,443.7	2,869.4	2,868.4	29
4	371.2			353.1	E	2,789.3	1,395.2	2,772.3	2,771.3	28
5	534.2			516.2	Y	2,660.3	1,330.6	2,643.3	2,642.3	27
6	605.3	303.1		587.2	A	2,497.2	1,249.1	2,480.2	2,479.2	26
7	692.3	346.6		674.3	S	2,426.2	1,213.6	2,409.2	2,408.2	25
8	839.4	420.2		821.3	F	2,339.2	1,170.1	2,322.1	2,321.1	24
9	986.4	493.7		968.4	F	2,192.1	1,096.5	2,175.1	2,174.1	23
10	1,057.5	529.2		1,039.5	A	2,045.0	1,023.0	2,028.0	2,027.0	22
11	1,156.5	578.8		1,138.5	V	1,974.0	987.5	1,957.0	1,956.0	21
12	1,287.6	644.3		1,269.6	M	1,874.9	938.0	1,857.9	1,856.9	20
13	1,344.6	672.8		1,326.6	G	1,743.9	872.4	1,726.8	1,725.9	19
14	1,415.6	708.3		1,397.6	A	1,686.9	843.9	1,669.8	1,668.8	18
15	1,502.7	751.8		1,484.7	S	1,615.8	808.4	1,598.8	1,597.8	17
16	1,573.7	787.4		1,555.7	A	1,528.8	764.9	1,511.8	1,510.8	16
17	1,644.7	822.9		1,626.7	A	1,457.7	729.4	1,440.7	1,439.7	15
18	1,775.8	888.4		1,757.8	M	1,386.7	693.9	1,369.7	1,368.7	14
19	1,874.8	937.9		1,856.8	V	1,255.7	628.3	1,238.6	1,237.7	13
20	2,021.9	1,011.5		2,003.9	F	1,156.6	578.8	1,139.6	1,138.6	12
21	2,108.9	1,055.0		2,090.9	S	1,009.5	505.3	992.5	991.5	11
22	2,180.0	1,090.5		2,162.0	A	922.5	461.8	905.5	904.5	10
23	2,293.1	1,147.0		2,275.1	L	851.5	426.2	834.4	833.5	9
24	2,350.1	1,175.5		2,332.1	G	738.4	369.7	721.4	720.4	8
25	2,421.1	1,211.1		2,403.1	A	681.4	341.2	664.3	663.3	7
26	2,492.2	1,246.6		2,474.2	A	610.3	305.7	593.3	592.3	6
27	2,655.2	1,328.1		2,637.2	Y	539.3		522.3	521.3	5
28	2,712.2	1,356.6		2,694.2	G	376.2		359.2	358.2	4
29	2,813.3	1,407.2		2,795.3	T	319.2		302.2	301.2	3
30	2,884.3	1,442.7		2,866.3	A	218.1		201.1		2
31	3,030.4	1,515.7	3,013.4	3,012.4	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-19	sp|P06454|PTMA_HUMAN	SDAAVDTSSEITTK	93.65	Acetyl (Protein N-term)	Heavy	2	733.84648

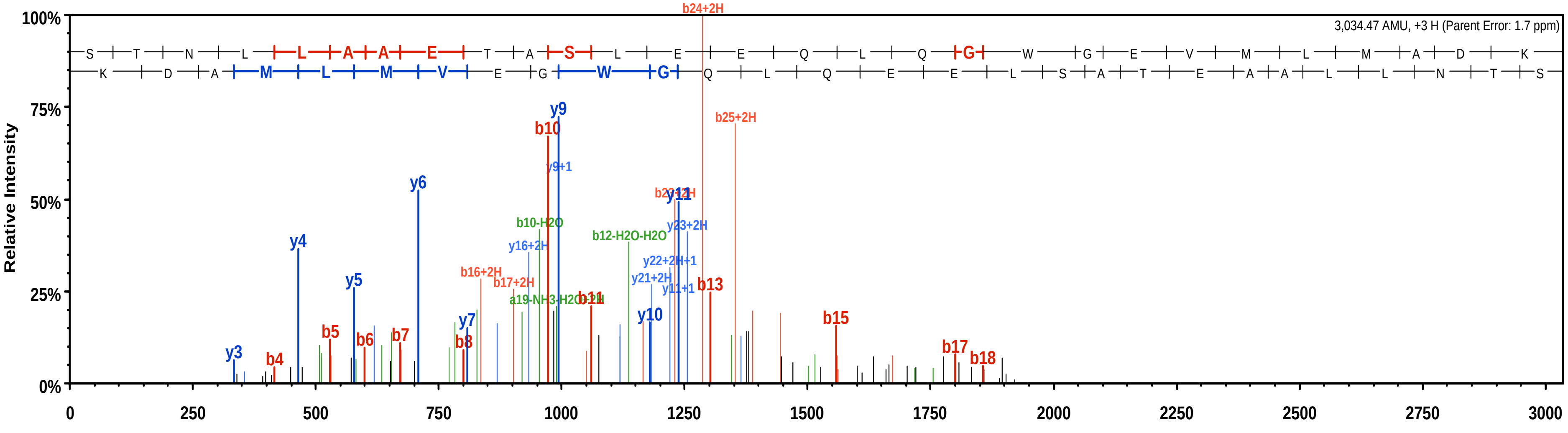


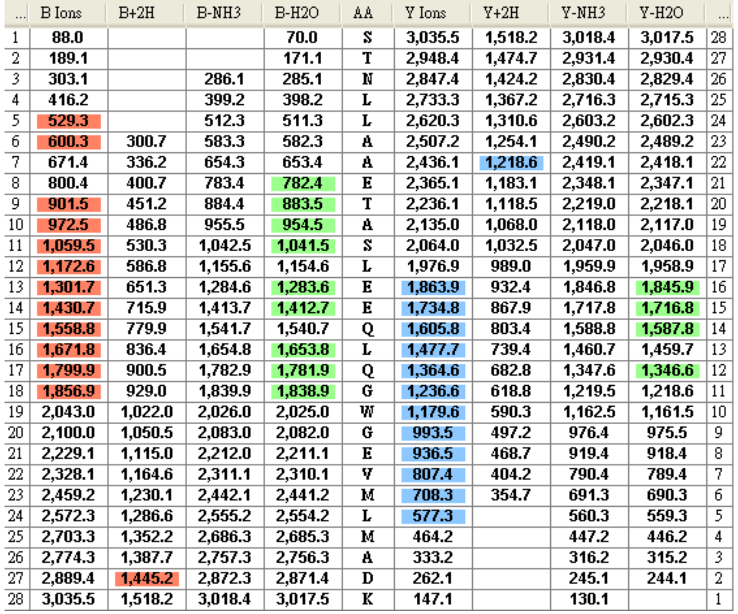


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	S+42	1,472.7	736.9	1,455.7	1,454.7	14
2	245.1			227.1	D	1,343.7	672.3	1,326.6	1,325.7	13
3	316.1			298.1	A	1,228.6	614.8	1,211.6	1,210.6	12
4	387.2			369.1	A	1,157.6	579.3	1,140.6	1,139.6	11
5	486.2			468.2	V	1,086.6	543.8	1,069.5	1,068.6	10
6	601.2	301.1		583.2	D	987.5	494.3	970.5	969.5	9
7	702.3	351.7		684.3	T	872.5	436.7	855.4	854.5	8
8	789.3	395.2		771.3	S	771.4	386.2	754.4	753.4	7
9	876.4	438.7		858.3	S	684.4	342.7	667.4	666.4	6
10	1,005.4	503.2		987.4	E	597.4		580.3	579.3	5
11	1,118.5	559.7		1,100.5	I	468.3		451.3	450.3	4
12	1,219.5	610.3		1,201.5	T	355.2		338.2	337.2	3
13	1,320.6	660.8		1,302.6	T	254.2		237.2	236.2	2
14	1,472.7	736.9	1,455.7	1,454.7	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-20	sp|Q15041|AR6P1_HUMAN	STNLLAAETASLEEQLQGWGEVMLMADK	92.22	Unmodified	Light	2	1518.2386

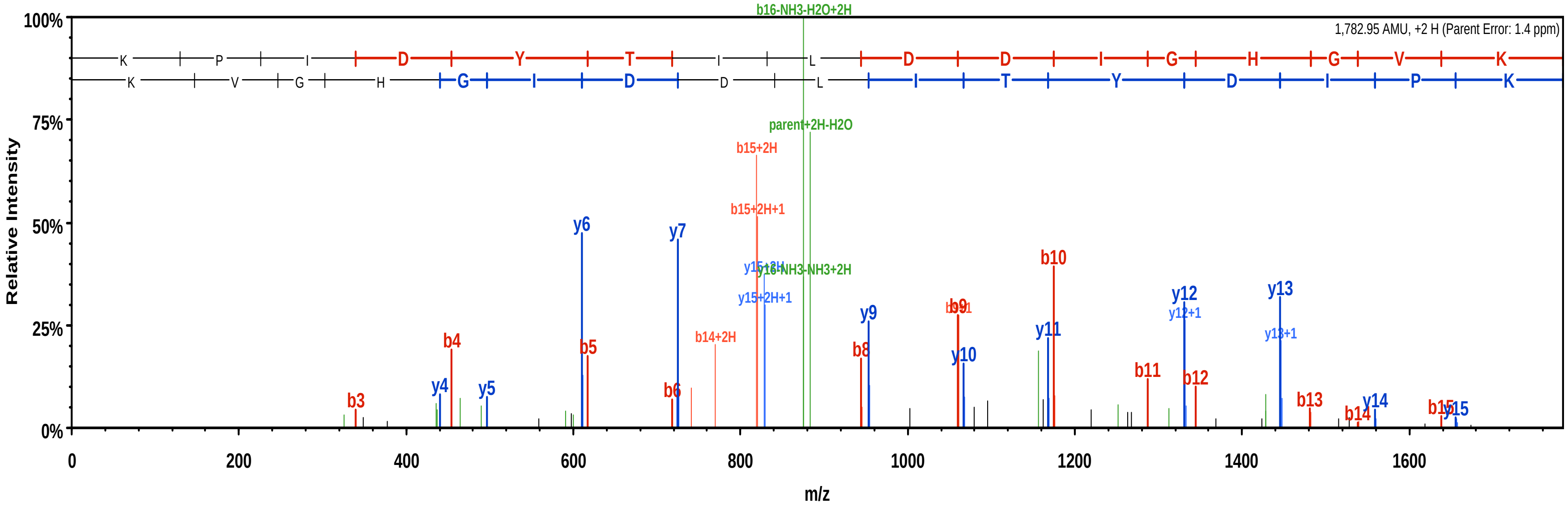


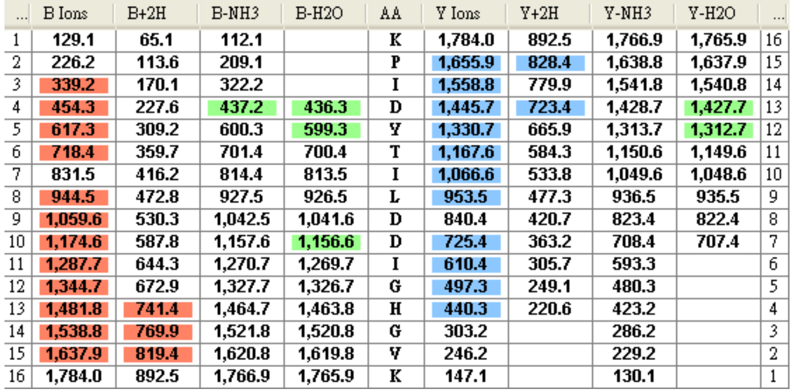


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	3,035.5	1,518.2	3,018.4	3,017.5	28
2	189.1			171.1	T	2,948.4	1,474.7	2,931.4	2,930.4	27
3	303.1		286.1	285.1	N	2,847.4	1,424.2	2,830.4	2,829.4	26
4	416.2		399.2	398.2	L	2,733.3	1,367.2	2,716.3	2,715.3	25
5	529.3		512.3	511.3	L	2,620.3	1,310.6	2,603.2	2,602.3	24
6	600.3	300.7	583.3	582.3	A	2,507.2	1,254.1	2,490.2	2,489.2	23
7	671.4	336.2	654.3	653.4	A	2,436.1	1,218.6	2,419.1	2,418.1	22
8	800.4	400.7	783.4	782.4	E	2,365.1	1,183.1	2,348.1	2,347.1	21
9	901.5	451.2	884.4	883.5	T	2,236.1	1,118.5	2,219.0	2,218.1	20
10	972.5	486.8	955.5	954.5	A	2,135.0	1,068.0	2,118.0	2,117.0	19
11	1,059.5	530.3	1,042.5	1,041.5	S	2,064.0	1,032.5	2,047.0	2,046.0	18
12	1,172.6	586.8	1,155.6	1,154.6	L	1,976.9	989.0	1,959.9	1,958.9	17
13	1,301.7	651.3	1,284.6	1,283.6	E	1,863.9	932.4	1,846.8	1,845.9	16
14	1,430.7	715.9	1,413.7	1,412.7	E	1,734.8	867.9	1,717.8	1,716.8	15
15	1,558.8	779.9	1,541.7	1,540.7	Q	1,605.8	803.4	1,588.8	1,587.8	14
16	1,671.8	836.4	1,654.8	1,653.8	L	1,477.7	739.4	1,460.7	1,459.7	13
17	1,799.9	900.5	1,782.9	1,781.9	Q	1,364.6	682.8	1,347.6	1,346.6	12
18	1,856.9	929.0	1,839.9	1,838.9	G	1,236.6	618.8	1,219.5	1,218.6	11
19	2,043.0	1,022.0	2,026.0	2,025.0	W	1,179.6	590.3	1,162.5	1,161.5	10
20	2,100.0	1,050.5	2,083.0	2,082.0	G	993.5	497.2	976.4	975.5	9
21	2,229.1	1,115.0	2,212.0	2,211.1	E	936.5	468.7	919.4	918.4	8
22	2,328.1	1,164.6	2,311.1	2,310.1	V	807.4	404.2	790.4	789.4	7
23	2,459.2	1,230.1	2,442.1	2,441.2	M	708.3	354.7	691.3	690.3	6
24	2,572.3	1,286.6	2,555.2	2,554.2	L	577.3		560.3	559.3	5
25	2,703.3	1,352.2	2,686.3	2,685.3	M	464.2		447.2	446.2	4
26	2,774.3	1,387.7	2,757.3	2,756.3	A	333.2		316.2	315.2	3
27	2,889.4	1,445.2	2,872.3	2,871.4	D	262.1		245.1	244.1	2
28	3,035.5	1,518.2	3,018.4	3,017.5	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-25	sp|Q9NYB9|ABI2_HUMAN	KPIDYTILDDIGHGVK	92.22	Unmodified	Light	2	892.48308

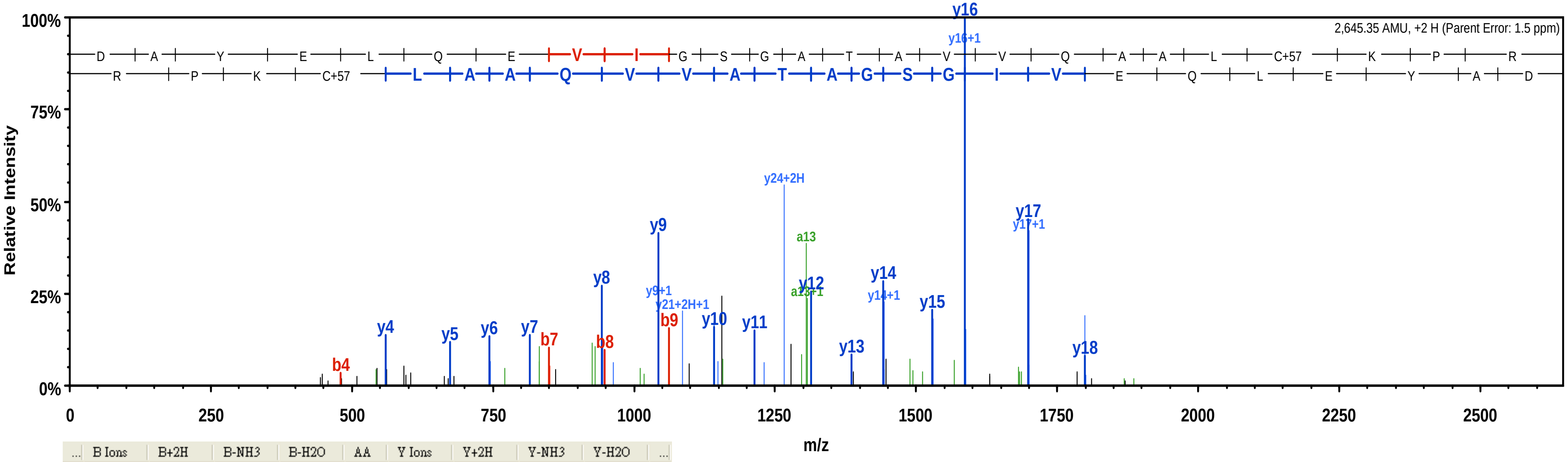


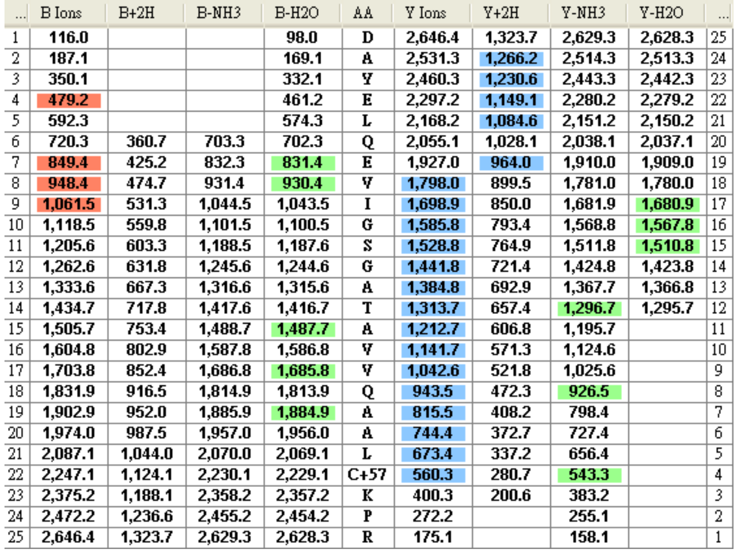


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	129.1	65.1	112.1		K	1,784.0	892.5	1,766.9	1,765.9	16
2	226.2	113.6	209.1		P	1,655.9	828.4	1,638.8	1,637.9	15
3	339.2	170.1	322.2		I	1,558.8	779.9	1,541.8	1,540.8	14
4	454.3	227.6	437.2	436.3	D	1,445.7	723.4	1,428.7	1,427.7	13
5	617.3	309.2	600.3	599.3	Y	1,330.7	665.9	1,313.7	1,312.7	12
6	718.4	359.7	701.4	700.4	T	1,167.6	584.3	1,150.6	1,149.6	11
7	831.5	416.2	814.4	813.5	I	1,066.6	533.8	1,049.6	1,048.6	10
8	944.5	472.8	927.5	926.5	L	953.5	477.3	936.5	935.5	9
9	1,059.6	530.3	1,042.5	1,041.6	D	840.4	420.7	823.4	822.4	8
10	1,174.6	587.8	1,157.6	1,156.6	D	725.4	363.2	708.4	707.4	7
11	1,287.7	644.3	1,270.7	1,269.7	I	610.4	305.7	593.3		6
12	1,344.7	672.9	1,327.7	1,326.7	G	497.3	249.1	480.3		5
13	1,481.8	741.4	1,464.7	1,463.8	H	440.3	220.6	423.2		4
14	1,538.8	769.9	1,521.8	1,520.8	G	303.2		286.2		3
15	1,637.9	819.4	1,620.8	1,619.8	V	246.2		229.2		2
16	1,784.0	892.5	1,766.9	1,765.9	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-21	splQ9UEW8lSTK39_HUMAN	DAYELQEVIGSGATAVVQAALCKPR	91.87	Unmodified	Light	2	1323.6814

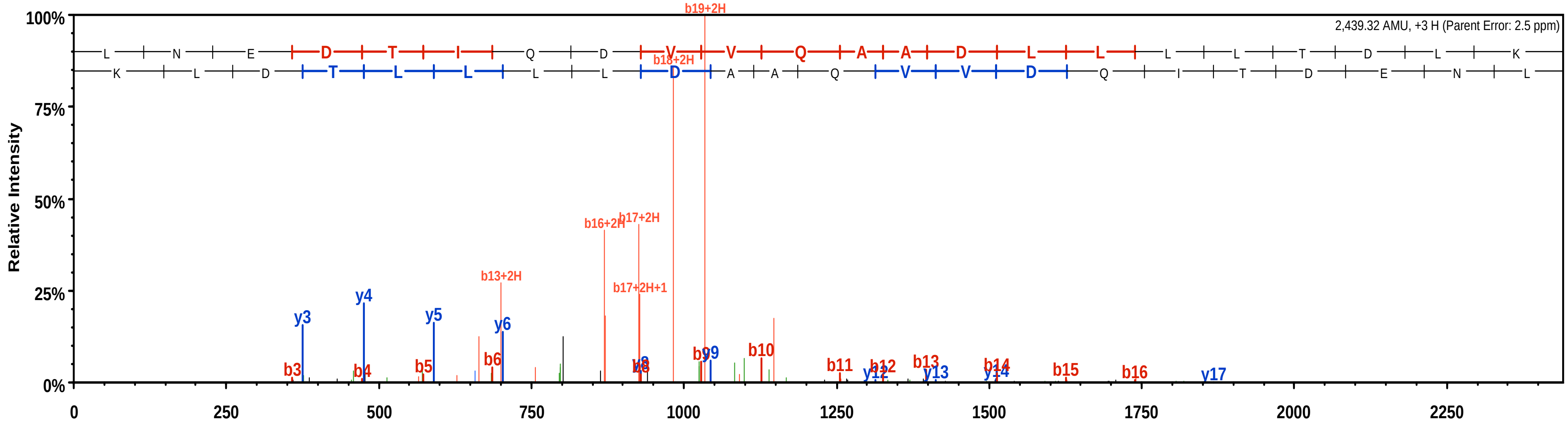


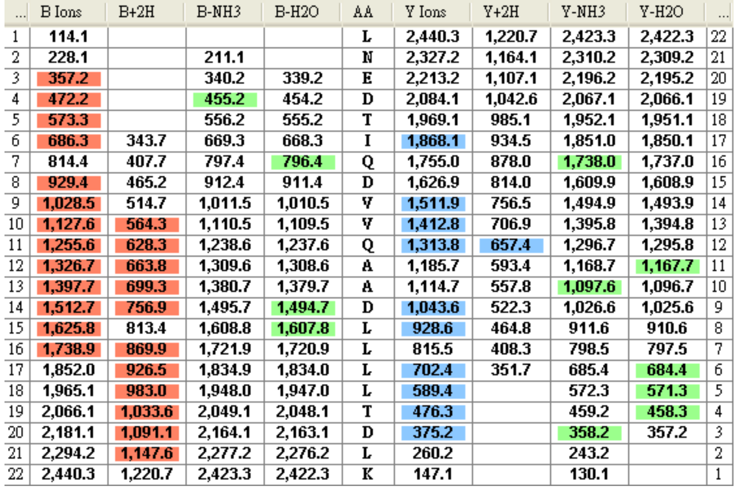


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	2,646.4	1,323.7	2,629.3	2,628.3	25
2	187.1			169.1	A	2,531.3	1,266.2	2,514.3	2,513.3	24
3	350.1			332.1	Y	2,460.3	1,230.6	2,443.3	2,442.3	23
4	479.2			461.2	E	2,297.2	1,149.1	2,280.2	2,279.2	22
5	592.3			574.3	L	2,168.2	1,084.6	2,151.2	2,150.2	21
6	720.3	360.7	703.3	702.3	Q	2,055.1	1,028.1	2,038.1	2,037.1	20
7	849.4	425.2	832.3	831.4	E	1,927.0	964.0	1,910.0	1,909.0	19
8	948.4	474.7	931.4	930.4	V	1,798.0	899.5	1,781.0	1,780.0	18
9	1,061.5	531.3	1,044.5	1,043.5	I	1,698.9	850.0	1,681.9	1,680.9	17
10	1,118.5	559.8	1,101.5	1,100.5	G	1,585.8	793.4	1,568.8	1,567.8	16
11	1,205.6	603.3	1,188.5	1,187.6	S	1,528.8	764.9	1,511.8	1,510.8	15
12	1,262.6	631.8	1,245.6	1,244.6	G	1,441.8	721.4	1,424.8	1,423.8	14
13	1,333.6	667.3	1,316.6	1,315.6	A	1,384.8	692.9	1,367.7	1,366.8	13
14	1,434.7	717.8	1,417.6	1,416.7	T	1,313.7	657.4	1,296.7	1,295.7	12
15	1,505.7	753.4	1,488.7	1,487.7	A	1,212.7	606.8	1,195.7		11
16	1,604.8	802.9	1,587.8	1,586.8	V	1,141.7	571.3	1,124.6		10
17	1,703.8	852.4	1,686.8	1,685.8	V	1,042.6	521.8	1,025.6		9
18	1,831.9	916.5	1,814.9	1,813.9	Q	943.5	472.3	926.5		8
19	1,902.9	952.0	1,885.9	1,884.9	A	815.5	408.2	798.4		7
20	1,974.0	987.5	1,957.0	1,956.0	A	744.4	372.7	727.4		6
21	2,087.1	1,044.0	2,070.0	2,069.1	L	673.4	337.2	656.4		5
22	2,247.1	1,124.1	2,230.1	2,229.1	C+57	560.3	280.7	543.3		4
23	2,375.2	1,188.1	2,358.2	2,357.2	K	400.3	200.6	383.2		3
24	2,472.2	1,236.6	2,455.2	2,454.2	P	272.2		255.1		2
25	2,646.4	1,323.7	2,629.3	2,628.3	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-22	sp|Q9H2C0|GAN_HUMAN	LNEDTIQDVVQAADLLLLTDLK	91.34	Unmodified	Light	3	814.11089

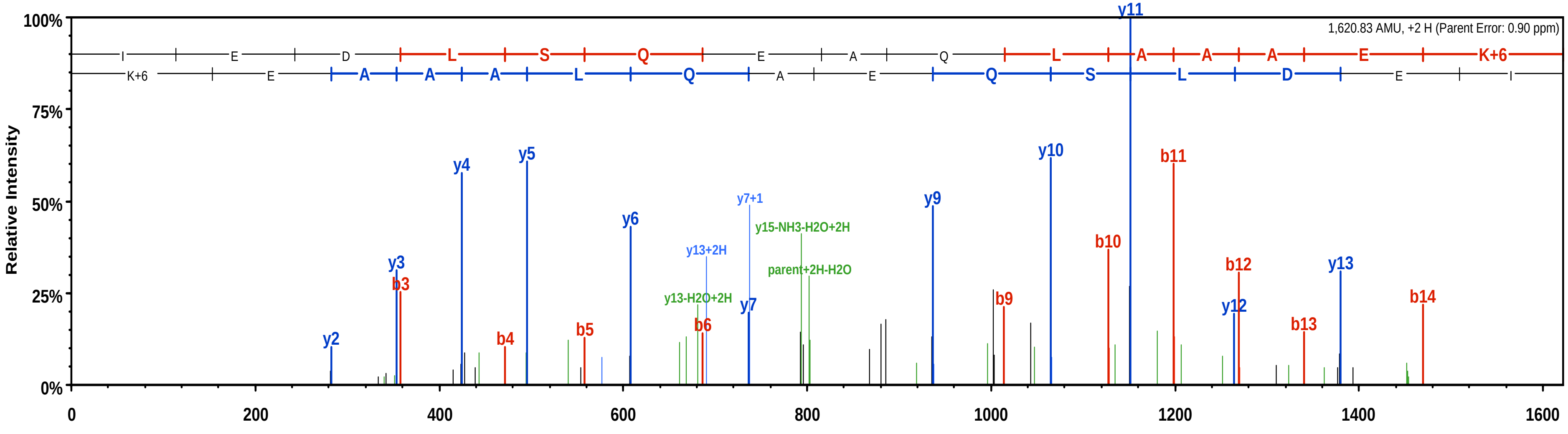


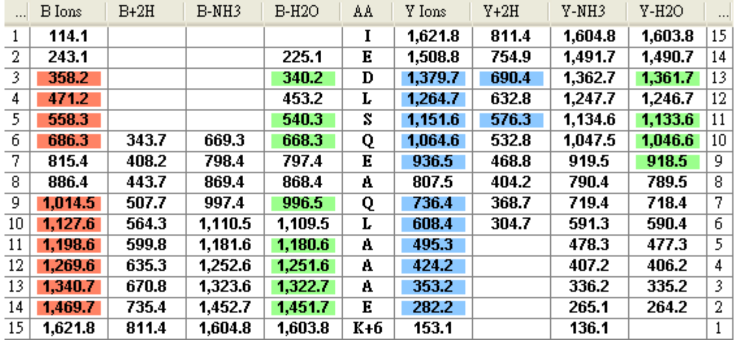


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	2,440.3	1,220.7	2,423.3	2,422.3	22
2	228.1		211.1		N	2,327.2	1,164.1	2,310.2	2,309.2	21
3	357.2		340.2	339.2	E	2,213.2	1,107.1	2,196.2	2,195.2	20
4	472.2		455.2	454.2	D	2,084.1	1,042.6	2,067.1	2,066.1	19
5	573.3		556.2	555.2	T	1,969.1	985.1	1,952.1	1,951.1	18
6	686.3	343.7	669.3	668.3	I	1,868.1	934.5	1,851.0	1,850.1	17
7	814.4	407.7	797.4	796.4	Q	1,755.0	878.0	1,738.0	1,737.0	16
8	929.4	465.2	912.4	911.4	D	1,626.9	814.0	1,609.9	1,608.9	15
9	1,028.5	514.7	1,011.5	1,010.5	V	1,511.9	756.5	1,494.9	1,493.9	14
10	1,127.6	564.3	1,110.5	1,109.5	V	1,412.8	706.9	1,395.8	1,394.8	13
11	1,255.6	628.3	1,238.6	1,237.6	Q	1,313.8	657.4	1,296.7	1,295.8	12
12	1,326.7	663.8	1,309.6	1,308.6	A	1,185.7	593.4	1,168.7	1,167.7	11
13	1,397.7	699.3	1,380.7	1,379.7	A	1,114.7	557.8	1,097.6	1,096.7	10
14	1,512.7	756.9	1,495.7	1,494.7	D	1,043.6	522.3	1,026.6	1,025.6	9
15	1,625.8	813.4	1,608.8	1,607.8	L	928.6	464.8	911.6	910.6	8
16	1,738.9	869.9	1,721.9	1,720.9	L	815.5	408.3	798.5	797.5	7
17	1,852.0	926.5	1,834.9	1,834.0	L	702.4	351.7	685.4	684.4	6
18	1,965.1	983.0	1,948.0	1,947.0	L	589.4		572.3	571.3	5
19	2,066.1	1,033.6	2,049.1	2,048.1	T	476.3		459.2	458.3	4
20	2,181.1	1,091.1	2,164.1	2,163.1	D	375.2		358.2	357.2	3
21	2,294.2	1,147.6	2,277.2	2,276.2	L	260.2		243.2		2
22	2,440.3	1,220.7	2,423.3	2,422.3	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-23	sp|Q9BZK3|NACP1_HUMAN	IEDLSQEAQLAAAEK	91.02	Unmodified	Heavy	2	808.41232

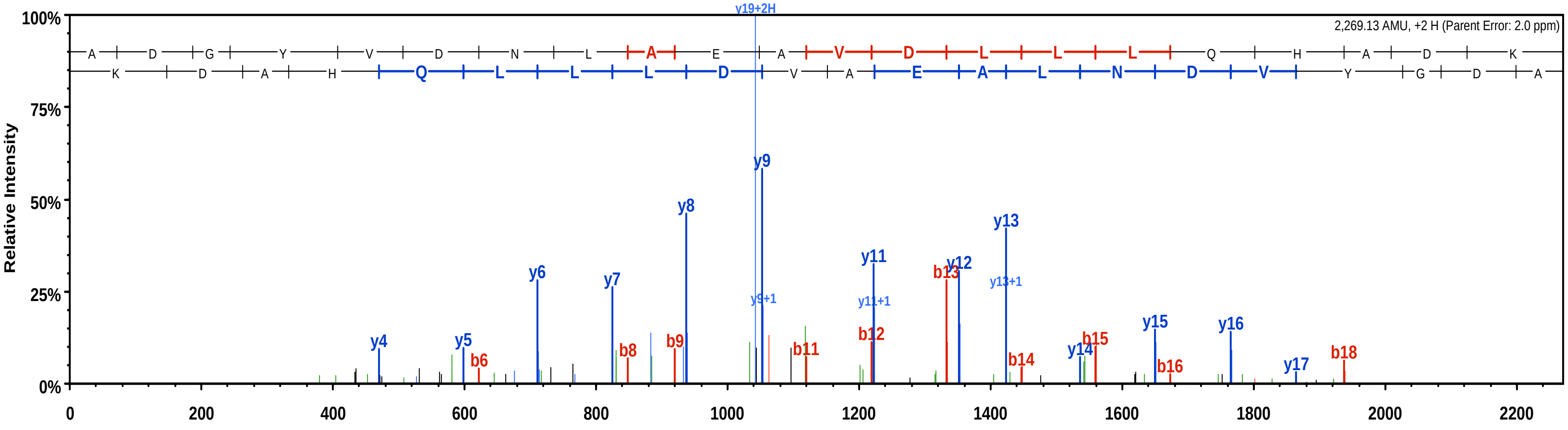


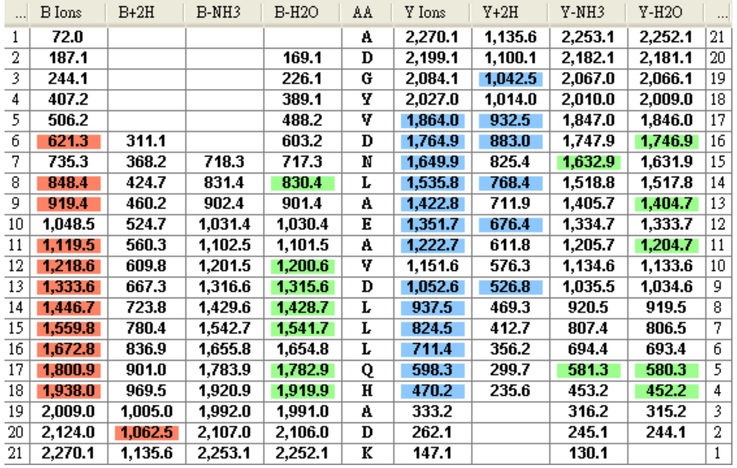


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	1,621.8	811.4	1,604.8	1,603.8	15
2	243.1			225.1	E	1,508.8	754.9	1,491.7	1,490.7	14
3	358.2			340.2	D	1,379.7	690.4	1,362.7	1,361.7	13
4	471.2			453.2	L	1,264.7	632.8	1,247.7	1,246.7	12
5	558.3			540.3	S	1,151.6	576.3	1,134.6	1,133.6	11
6	686.3	343.7	669.3	668.3	Q	1,064.6	532.8	1,047.5	1,046.6	10
7	815.4	408.2	798.4	797.4	E	936.5	468.8	919.5	918.5	9
8	886.4	443.7	869.4	868.4	A	807.5	404.2	790.4	789.5	8
9	1,014.5	507.7	997.4	996.5	Q	736.4	368.7	719.4	718.4	7
10	1,127.6	564.3	1,110.5	1,109.5	L	608.4	304.7	591.3	590.4	6
11	1,198.6	599.8	1,181.6	1,180.6	A	495.3		478.3	477.3	5
12	1,269.6	635.3	1,252.6	1,251.6	A	424.2		407.2	406.2	4
13	1,340.7	670.8	1,323.6	1,322.7	A	353.2		336.2	335.2	3
14	1,469.7	735.4	1,452.7	1,451.7	E	282.2		265.1	264.2	2
15	1,621.8	811.4	1,604.8	1,603.8	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-24	splQ9H008lLHPP_HUMAN	ADGYVDNLAEAVDLLLQHADK	90.14	Unmodified	Light	2	1135.5686

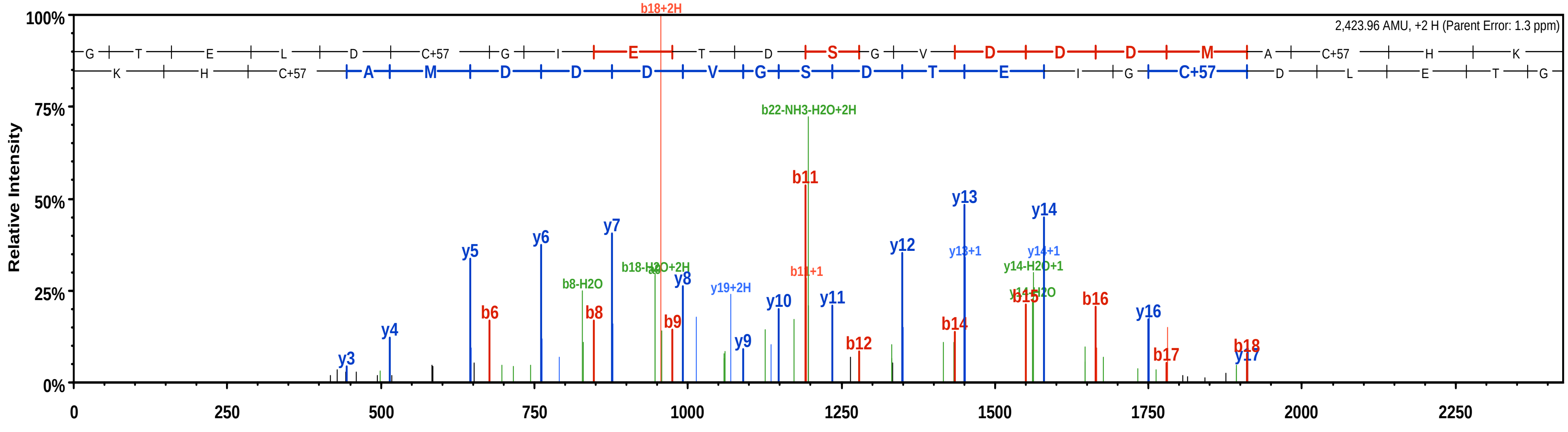


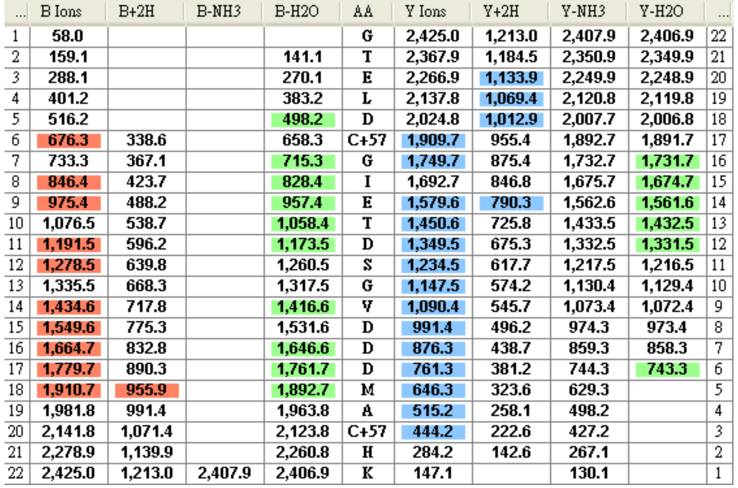


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	2,270.1	1,135.6	2,253.1	2,252.1	21
2	187.1			169.1	D	2,199.1	1,100.1	2,182.1	2,181.1	20
3	244.1			226.1	G	2,084.1	1,042.5	2,067.0	2,066.1	19
4	407.2			389.1	Y	2,027.0	1,014.0	2,010.0	2,009.0	18
5	506.2			488.2	V	1,864.0	932.5	1,847.0	1,846.0	17
6	621.3	311.1		603.2	D	1,764.9	883.0	1,747.9	1,746.9	16
7	735.3	368.2	718.3	717.3	N	1,649.9	825.4	1,632.9	1,631.9	15
8	848.4	424.7	831.4	830.4	L	1,535.8	768.4	1,518.8	1,517.8	14
9	919.4	460.2	902.4	901.4	A	1,422.8	711.9	1,405.7	1,404.7	13
10	1,048.5	524.7	1,031.4	1,030.4	E	1,351.7	676.4	1,334.7	1,333.7	12
11	1,119.5	560.3	1,102.5	1,101.5	A	1,222.7	611.8	1,205.7	1,204.7	11
12	1,218.6	609.8	1,201.5	1,200.6	V	1,151.6	576.3	1,134.6	1,133.6	10
13	1,333.6	667.3	1,316.6	1,315.6	D	1,052.6	526.8	1,035.5	1,034.6	9
14	1,446.7	723.8	1,429.6	1,428.7	L	937.5	469.3	920.5	919.5	8
15	1,559.8	780.4	1,542.7	1,541.7	L	824.5	412.7	807.4	806.5	7
16	1,672.8	836.9	1,655.8	1,654.8	L	711.4	356.2	694.4	693.4	6
17	1,800.9	901.0	1,783.9	1,782.9	Q	598.3	299.7	581.3	580.3	5
18	1,938.0	969.5	1,920.9	1,919.9	H	470.2	235.6	453.2	452.2	4
19	2,009.0	1,005.0	1,992.0	1,991.0	A	333.2		316.2	315.2	3
20	2,124.0	1,062.5	2,107.0	2,106.0	D	262.1		245.1	244.1	2
21	2,270.1	1,135.6	2,253.1	2,252.1	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-25	sp|P42574|CASP3_HUMAN	GTELDCGIETDSGVDDDMACHK	89.27	Unmodified	Light	2	1212.983

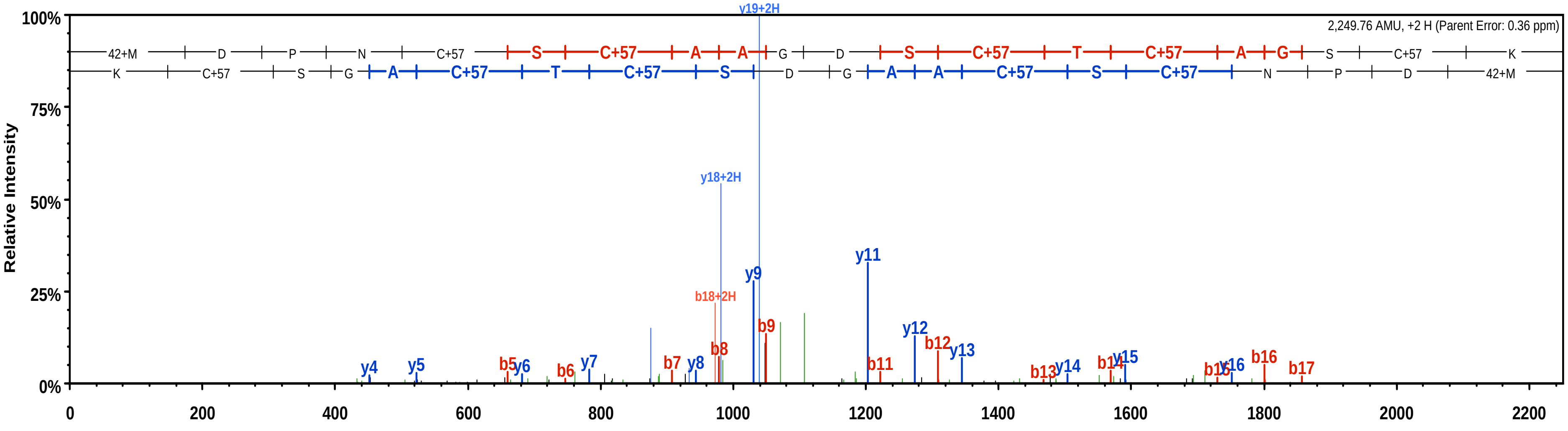


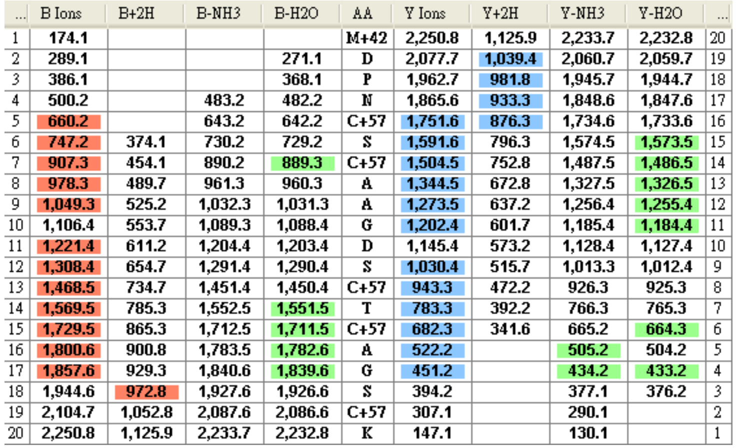


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	2,425.0	1,213.0	2,407.9	2,406.9	22
2	159.1			141.1	T	2,367.9	1,184.5	2,350.9	2,349.9	21
3	288.1			270.1	E	2,266.9	1,133.9	2,249.9	2,248.9	20
4	401.2			383.2	L	2,137.8	1,069.4	2,120.8	2,119.8	19
5	516.2			498.2	D	2,024.8	1,012.9	2,007.7	2,006.8	18
6	676.3	338.6		658.3	C+57	1,909.7	955.4	1,892.7	1,891.7	17
7	733.3	367.1		715.3	G	1,749.7	875.4	1,732.7	1,731.7	16
8	846.4	423.7		828.4	I	1,692.7	846.8	1,675.7	1,674.7	15
9	975.4	488.2		957.4	E	1,579.6	790.3	1,562.6	1,561.6	14
10	1,076.5	538.7		1,058.4	T	1,450.6	725.8	1,433.5	1,432.5	13
11	1,191.5	596.2		1,173.5	D	1,349.5	675.3	1,332.5	1,331.5	12
12	1,278.5	639.8		1,260.5	S	1,234.5	617.7	1,217.5	1,216.5	11
13	1,335.5	668.3		1,317.5	G	1,147.5	574.2	1,130.4	1,129.4	10
14	1,434.6	717.8		1,416.6	V	1,090.4	545.7	1,073.4	1,072.4	9
15	1,549.6	775.3		1,531.6	D	991.4	496.2	974.3	973.4	8
16	1,664.7	832.8		1,646.6	D	876.3	438.7	859.3	858.3	7
17	1,779.7	890.3		1,761.7	D	761.3	381.2	744.3	743.3	6
18	1,910.7	955.9		1,892.7	M	646.3	323.6	629.3		5
19	1,981.8	991.4		1,963.8	A	515.2	258.1	498.2		4
20	2,141.8	1,071.4		2,123.8	C+57	444.2	222.6	427.2		3
21	2,278.9	1,139.9		2,260.8	H	284.2	142.6	267.1		2
22	2,425.0	1,213.0	2,407.9	2,406.9	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-26	splP02795lMT2_HUMAN	MDPNCSCAAGDSCTCAGSCK	89.1	Acetyl (Protein N-term)	Light	2	1125.886

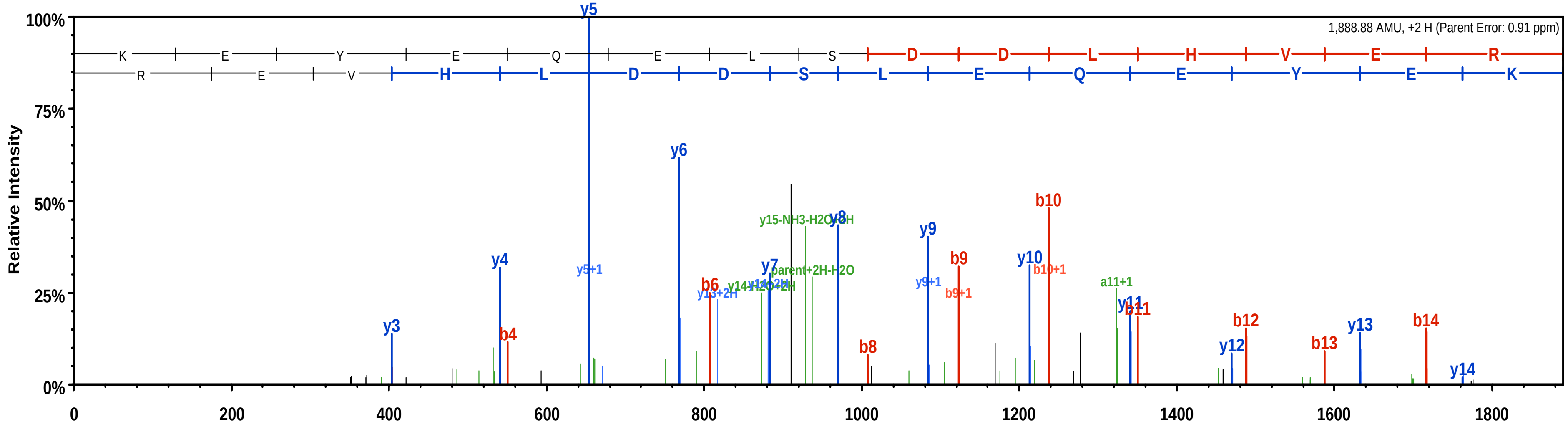


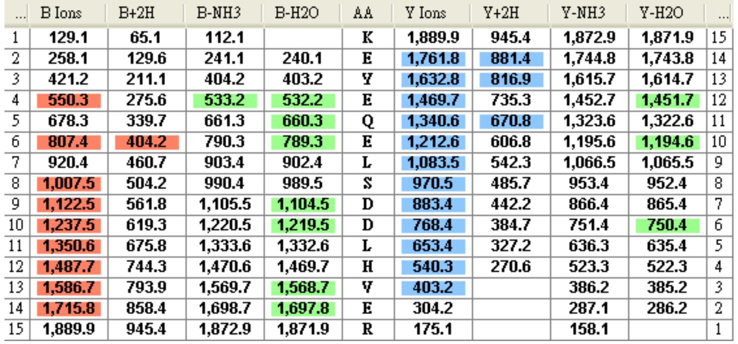


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	174.1				M+42	2,250.8	1,125.9	2,233.7	2,232.8	20
2	289.1			271.1	D	2,077.7	1,039.4	2,060.7	2,059.7	19
3	386.1			368.1	P	1,962.7	981.8	1,945.7	1,944.7	18
4	500.2		483.2	482.2	N	1,865.6	933.3	1,848.6	1,847.6	17
5	660.2		643.2	642.2	C+57	1,751.6	876.3	1,734.6	1,733.6	16
6	747.2	374.1	730.2	729.2	S	1,591.6	796.3	1,574.5	1,573.5	15
7	907.3	454.1	890.2	889.3	C+57	1,504.5	752.8	1,487.5	1,486.5	14
8	978.3	489.7	961.3	960.3	A	1,344.5	672.8	1,327.5	1,326.5	13
9	1,049.3	525.2	1,032.3	1,031.3	A	1,273.5	637.2	1,256.4	1,255.4	12
10	1,106.4	553.7	1,089.3	1,088.4	G	1,202.4	601.7	1,185.4	1,184.4	11
11	1,221.4	611.2	1,204.4	1,203.4	D	1,145.4	573.2	1,128.4	1,127.4	10
12	1,308.4	654.7	1,291.4	1,290.4	S	1,030.4	515.7	1,013.3	1,012.4	9
13	1,468.5	734.7	1,451.4	1,450.4	C+57	943.3	472.2	926.3	925.3	8
14	1,569.5	785.3	1,552.5	1,551.5	T	783.3	392.2	766.3	765.3	7
15	1,729.5	865.3	1,712.5	1,711.5	C+57	682.3	341.6	665.2	664.3	6
16	1,800.6	900.8	1,783.5	1,782.6	A	522.2		505.2	504.2	5
17	1,857.6	929.3	1,840.6	1,839.6	G	451.2		434.2	433.2	4
18	1,944.6	972.8	1,927.6	1,926.6	S	394.2		377.1	376.2	3
19	2,104.7	1,052.8	2,087.6	2,086.6	C+57	307.1		290.1		2
20	2,250.8	1,125.9	2,233.7	2,232.8	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-27	sp|Q7Z7F7|RM55_HUMAN	KEYEQELSDDLHVER	86.16	Unmodified	Light	2	945.44742

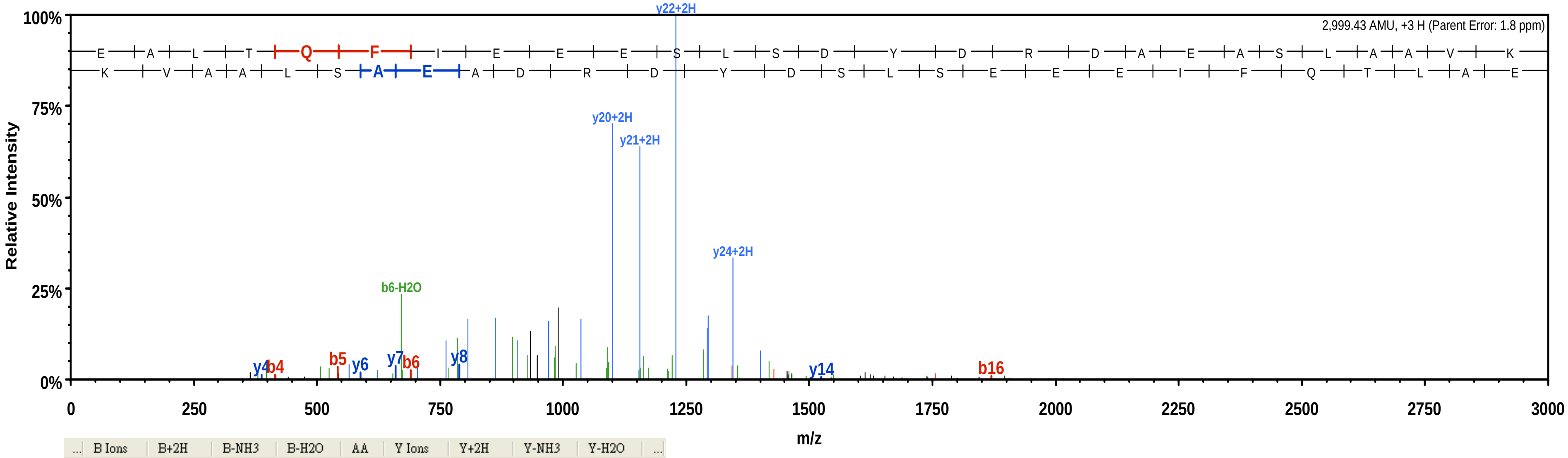


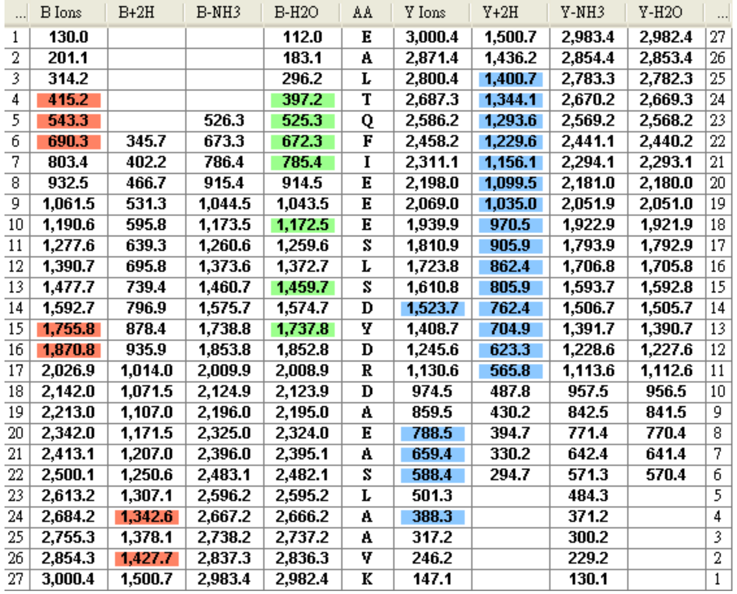


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	129.1	65.1	112.1		K	1,889.9	945.4	1,872.9	1,871.9	15
2	258.1	129.6	241.1	240.1	E	1,761.8	881.4	1,744.8	1,743.8	14
3	421.2	211.1	404.2	403.2	Y	1,632.8	816.9	1,615.7	1,614.7	13
4	550.3	275.6	533.2	532.2	E	1,469.7	735.3	1,452.7	1,451.7	12
5	678.3	339.7	661.3	660.3	Q	1,340.6	670.8	1,323.6	1,322.6	11
6	807.4	404.2	790.3	789.3	E	1,212.6	606.8	1,195.6	1,194.6	10
7	920.4	460.7	903.4	902.4	L	1,083.5	542.3	1,066.5	1,065.5	9
8	1,007.5	504.2	990.4	989.5	S	970.5	485.7	953.4	952.4	8
9	1,122.5	561.8	1,105.5	1,104.5	D	883.4	442.2	866.4	865.4	7
10	1,237.5	619.3	1,220.5	1,219.5	D	768.4	384.7	751.4	750.4	6
11	1,350.6	675.8	1,333.6	1,332.6	L	653.4	327.2	636.3	635.4	5
12	1,487.7	744.3	1,470.6	1,469.7	H	540.3	270.6	523.3	522.3	4
13	1,586.7	793.9	1,569.7	1,568.7	V	403.2		386.2	385.2	3
14	1,715.8	858.4	1,698.7	1,697.8	E	304.2		287.1	286.2	2
15	1,889.9	945.4	1,872.9	1,871.9	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-28	sp|Q9NQ89|CL004_HUMAN	EALTQFIEEESLSDYDRDAEASLAAVK	85.83	Unmodified	Light	3	1000.8155

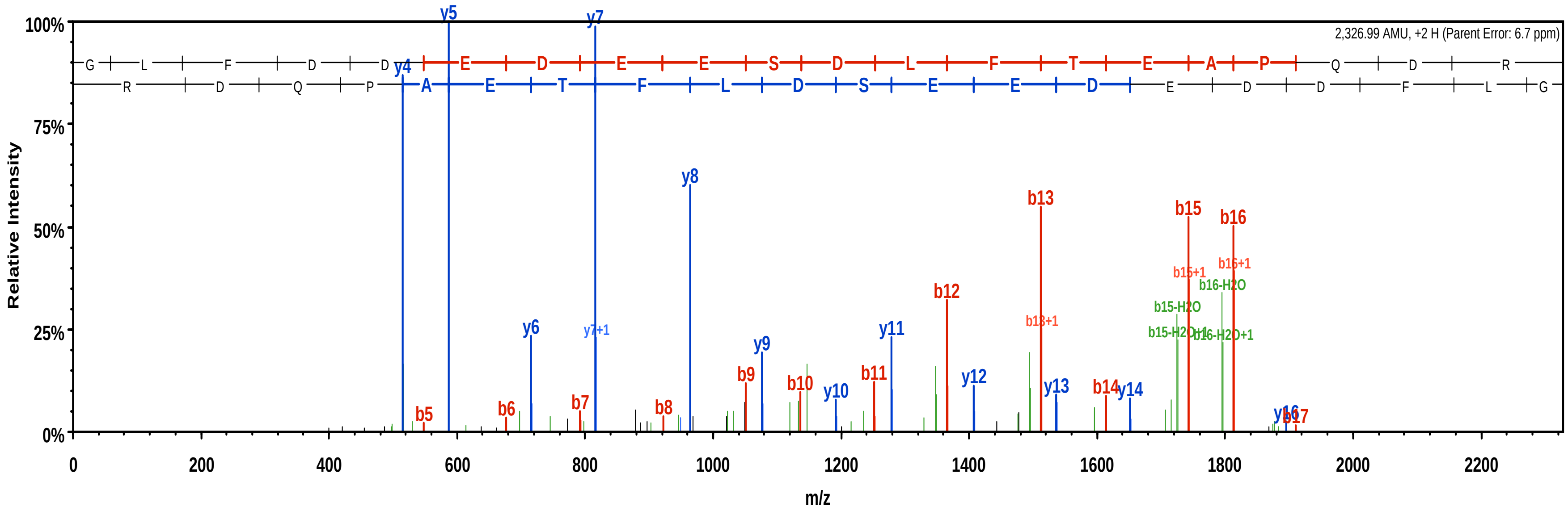


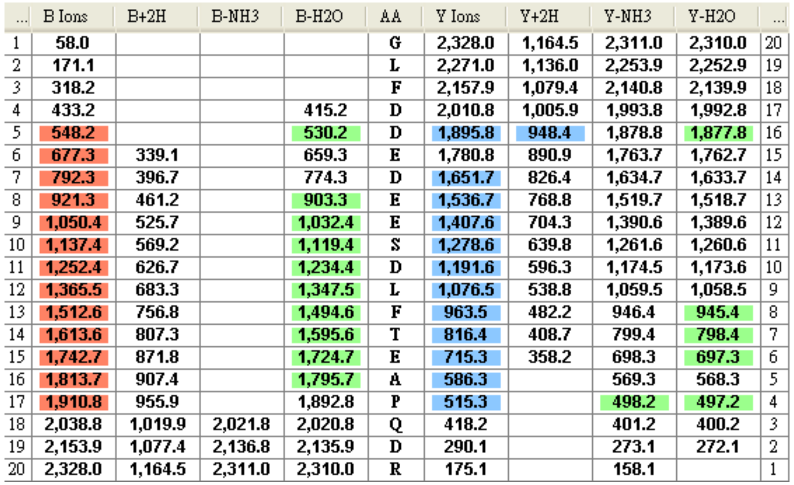


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	3,000.4	1,500.7	2,983.4	2,982.4	27
2	201.1			183.1	A	2,871.4	1,436.2	2,854.4	2,853.4	26
3	314.2			296.2	L	2,800.4	1,400.7	2,783.3	2,782.3	25
4	415.2			397.2	T	2,687.3	1,344.1	2,670.2	2,669.3	24
5	543.3		526.3	525.3	Q	2,586.2	1,293.6	2,569.2	2,568.2	23
6	690.3	345.7	673.3	672.3	F	2,458.2	1,229.6	2,441.1	2,440.2	22
7	803.4	402.2	786.4	785.4	I	2,311.1	1,156.1	2,294.1	2,293.1	21
8	932.5	466.7	915.4	914.5	E	2,198.0	1,099.5	2,181.0	2,180.0	20
9	1,061.5	531.3	1,044.5	1,043.5	E	2,069.0	1,035.0	2,051.9	2,051.0	19
10	1,190.6	595.8	1,173.5	1,172.5	E	1,939.9	970.5	1,922.9	1,921.9	18
11	1,277.6	639.3	1,260.6	1,259.6	S	1,810.9	905.9	1,793.9	1,792.9	17
12	1,390.7	695.8	1,373.6	1,372.7	L	1,723.8	862.4	1,706.8	1,705.8	16
13	1,477.7	739.4	1,460.7	1,459.7	S	1,610.8	805.9	1,593.7	1,592.8	15
14	1,592.7	796.9	1,575.7	1,574.7	D	1,523.7	762.4	1,506.7	1,505.7	14
15	1,755.8	878.4	1,738.8	1,737.8	Y	1,408.7	704.9	1,391.7	1,390.7	13
16	1,870.8	935.9	1,853.8	1,852.8	D	1,245.6	623.3	1,228.6	1,227.6	12
17	2,026.9	1,014.0	2,009.9	2,008.9	R	1,130.6	565.8	1,113.6	1,112.6	11
18	2,142.0	1,071.5	2,124.9	2,123.9	D	974.5	487.8	957.5	956.5	10
19	2,213.0	1,107.0	2,196.0	2,195.0	A	859.5	430.2	842.5	841.5	9
20	2,342.0	1,171.5	2,325.0	2,324.0	E	788.5	394.7	771.4	770.4	8
21	2,413.1	1,207.0	2,396.0	2,395.1	A	659.4	330.2	642.4	641.4	7
22	2,500.1	1,250.6	2,483.1	2,482.1	S	588.4	294.7	571.3	570.4	6
23	2,613.2	1,307.1	2,596.2	2,595.2	L	501.3		484.3		5
24	2,684.2	1,342.6	2,667.2	2,666.2	A	388.3		371.2		4
25	2,755.3	1,378.1	2,738.2	2,737.2	A	317.2		300.2		3
26	2,854.3	1,427.7	2,837.3	2,836.3	V	246.2		229.2		2
27	3,000.4	1,500.7	2,983.4	2,982.4	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-34	sp|Q641Q2|FA21A_HUMAN	GLFDDEDEESDLFTEAPQDR	85.38	Unmodified		2	1164.4929

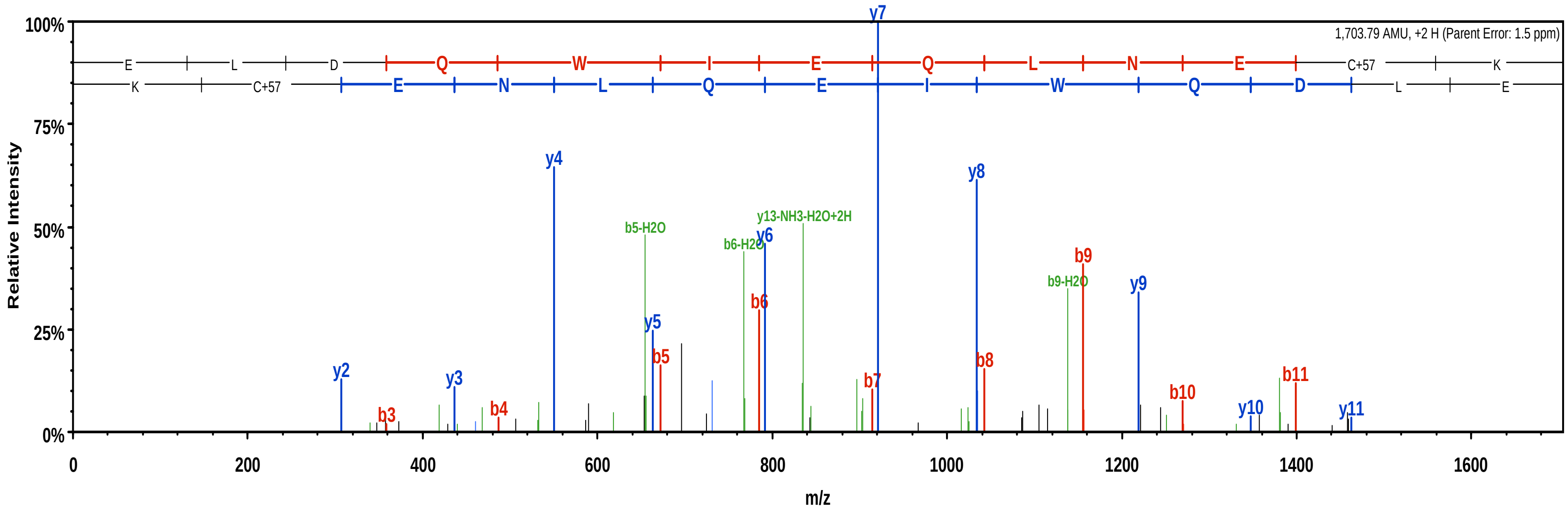


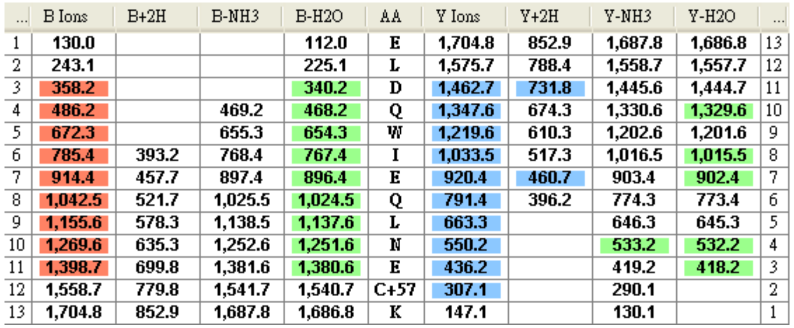


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	2,328.0	1,164.5	2,311.0	2,310.0	20
2	171.1				L	2,271.0	1,136.0	2,253.9	2,252.9	19
3	318.2				F	2,157.9	1,079.4	2,140.8	2,139.9	18
4	433.2			415.2	D	2,010.8	1,005.9	1,993.8	1,992.8	17
5	548.2			530.2	D	1,895.8	948.4	1,878.8	1,877.8	16
6	677.3	339.1		659.3	E	1,780.8	890.9	1,763.7	1,762.7	15
7	792.3	396.7		774.3	D	1,651.7	826.4	1,634.7	1,633.7	14
8	921.3	461.2		903.3	E	1,536.7	768.8	1,519.7	1,518.7	13
9	1,050.4	525.7		1,032.4	E	1,407.6	704.3	1,390.6	1,389.6	12
10	1,137.4	569.2		1,119.4	S	1,278.6	639.8	1,261.6	1,260.6	11
11	1,252.4	626.7		1,234.4	D	1,191.6	596.3	1,174.5	1,173.6	10
12	1,365.5	683.3		1,347.5	L	1,076.5	538.8	1,059.5	1,058.5	9
13	1,512.6	756.8		1,494.6	F	963.5	482.2	946.4	945.4	8
14	1,613.6	807.3		1,595.6	T	816.4	408.7	799.4	798.4	7
15	1,742.7	871.8		1,724.7	E	715.3	358.2	698.3	697.3	6
16	1,813.7	907.4		1,795.7	A	586.3		569.3	568.3	5
17	1,910.8	955.9		1,892.8	P	515.3		498.2	497.2	4
18	2,038.8	1,019.9	2,021.8	2,020.8	Q	418.2		401.2	400.2	3
19	2,153.9	1,077.4	2,136.8	2,135.9	D	290.1		273.1	272.1	2
20	2,328.0	1,164.5	2,311.0	2,310.0	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-35	sp|P67775|PP2AA_HUMAN	ELDQWIEQLNECK	85.22	Unmodified	Light	2	852.89852

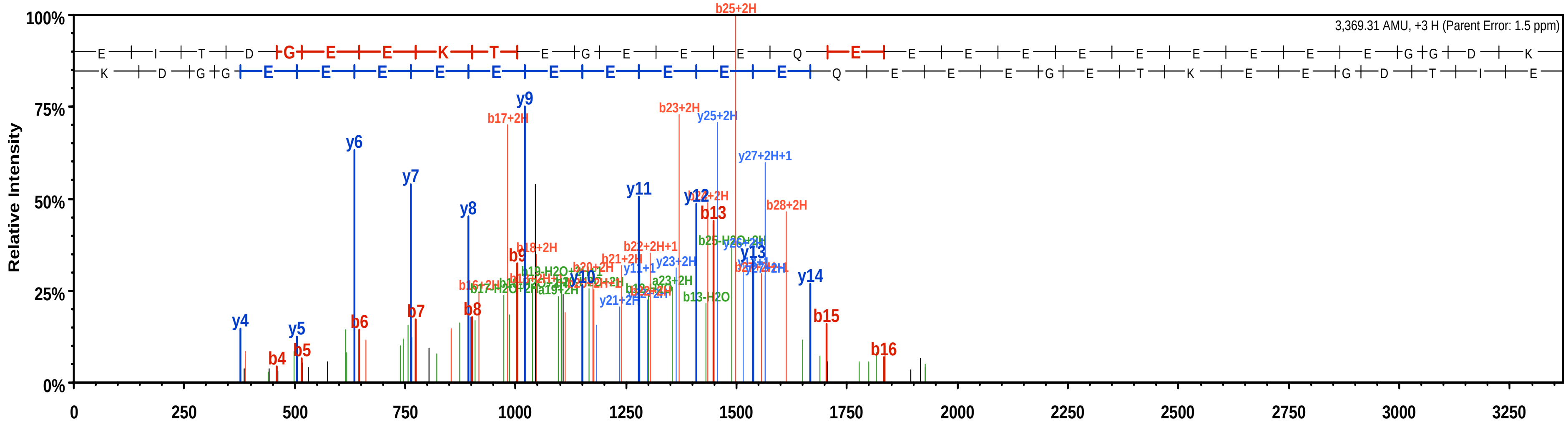


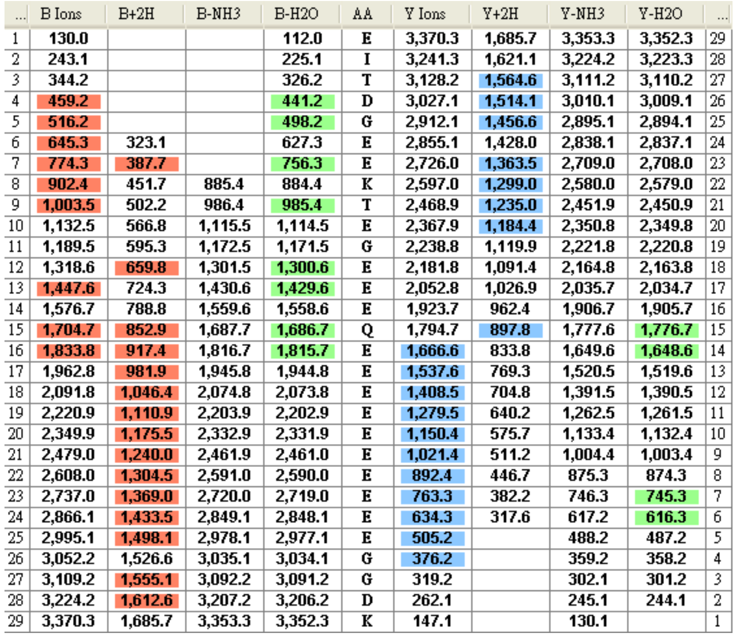


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	1,704.8	852.9	1,687.8	1,686.8	13
2	243.1			225.1	L	1,575.7	788.4	1,558.7	1,557.7	12
3	358.2			340.2	D	1,462.7	731.8	1,445.6	1,444.7	11
4	486.2		469.2	468.2	Q	1,347.6	674.3	1,330.6	1,329.6	10
5	672.3		655.3	654.3	W	1,219.6	610.3	1,202.6	1,201.6	9
6	785.4	393.2	768.4	767.4	I	1,033.5	517.3	1,016.5	1,015.5	8
7	914.4	457.7	897.4	896.4	E	920.4	460.7	903.4	902.4	7
8	1,042.5	521.7	1,025.5	1,024.5	Q	791.4	396.2	774.3	773.4	6
9	1,155.6	578.3	1,138.5	1,137.6	L	663.3		646.3	645.3	5
10	1,269.6	635.3	1,252.6	1,251.6	N	550.2		533.2	532.2	4
11	1,398.7	699.8	1,381.6	1,380.6	E	436.2		419.2	418.2	3
12	1,558.7	779.8	1,541.7	1,540.7	C+57	307.1		290.1		2
13	1,704.8	852.9	1,687.8	1,686.8	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-29	sp|Q8N129|CNPY4_HUMAN	EITDGEEKTEGEEEQEEEEEEEEEEGGDK	84.72	Unmodified	Light	3	1124.108

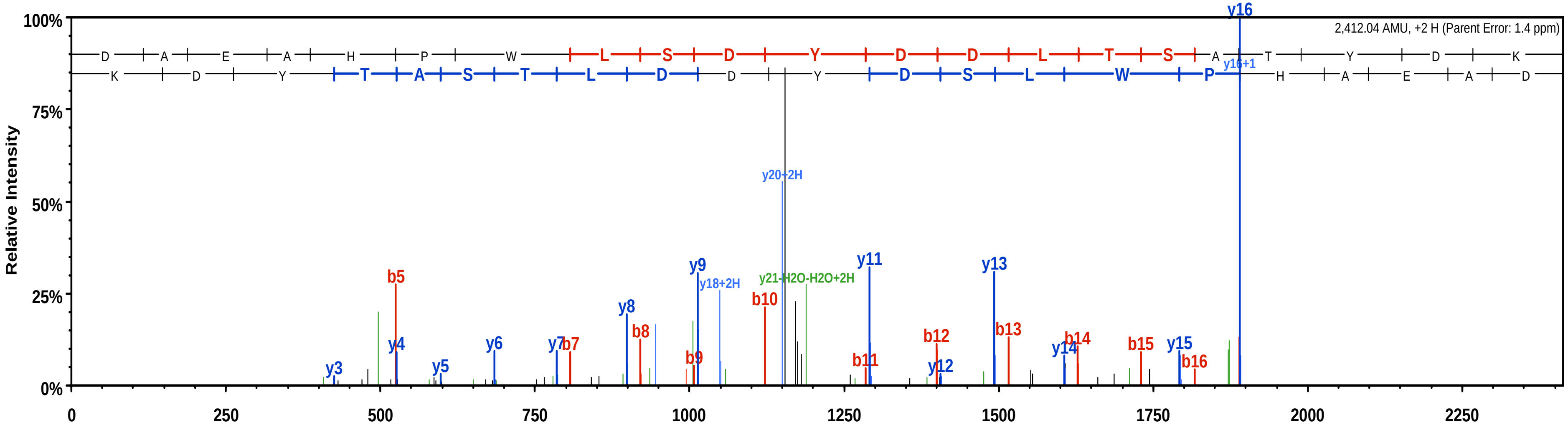


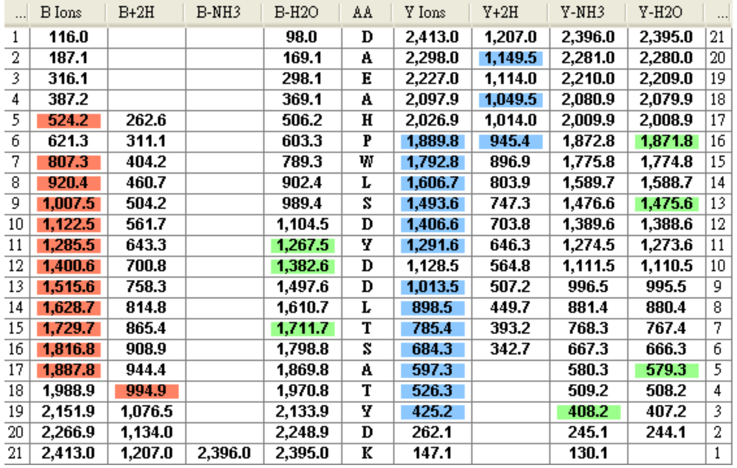


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	3,370.3	1,685.7	3,353.3	3,352.3	29
2	243.1			225.1	I	3,241.3	1,621.1	3,224.2	3,223.3	28
3	344.2			326.2	T	3,128.2	1,564.6	3,111.2	3,110.2	27
4	459.2			441.2	D	3,027.1	1,514.1	3,010.1	3,009.1	26
5	516.2			498.2	G	2,912.1	1,456.6	2,895.1	2,894.1	25
6	645.3	323.1		627.3	E	2,855.1	1,428.0	2,838.1	2,837.1	24
7	774.3	387.7		756.3	E	2,726.0	1,363.5	2,709.0	2,708.0	23
8	902.4	451.7	885.4	884.4	K	2,597.0	1,299.0	2,580.0	2,579.0	22
9	1,003.5	502.2	986.4	985.4	T	2,468.9	1,235.0	2,451.9	2,450.9	21
10	1,132.5	566.8	1,115.5	1,114.5	E	2,367.9	1,184.4	2,350.8	2,349.8	20
11	1,189.5	595.3	1,172.5	1,171.5	G	2,238.8	1,119.9	2,221.8	2,220.8	19
12	1,318.6	659.8	1,301.5	1,300.6	E	2,181.8	1,091.4	2,164.8	2,163.8	18
13	1,447.6	724.3	1,430.6	1,429.6	E	2,052.8	1,026.9	2,035.7	2,034.7	17
14	1,576.7	788.8	1,559.6	1,558.6	E	1,923.7	962.4	1,906.7	1,905.7	16
15	1,704.7	852.9	1,687.7	1,686.7	Q	1,794.7	897.8	1,777.6	1,776.7	15
16	1,833.8	917.4	1,816.7	1,815.7	E	1,666.6	833.8	1,649.6	1,648.6	14
17	1,962.8	981.9	1,945.8	1,944.8	E	1,537.6	769.3	1,520.5	1,519.6	13
18	2,091.8	1,046.4	2,074.8	2,073.8	E	1,408.5	704.8	1,391.5	1,390.5	12
19	2,220.9	1,110.9	2,203.9	2,202.9	E	1,279.5	640.2	1,262.5	1,261.5	11
20	2,349.9	1,175.5	2,332.9	2,331.9	E	1,150.4	575.7	1,133.4	1,132.4	10
21	2,479.0	1,240.0	2,461.9	2,461.0	E	1,021.4	511.2	1,004.4	1,003.4	9
22	2,608.0	1,304.5	2,591.0	2,590.0	E	892.4	446.7	875.3	874.3	8
23	2,737.0	1,369.0	2,720.0	2,719.0	E	763.3	382.2	746.3	745.3	7
24	2,866.1	1,433.5	2,849.1	2,848.1	E	634.3	317.6	617.2	616.3	6
25	2,995.1	1,498.1	2,978.1	2,977.1	E	505.2		488.2	487.2	5
26	3,052.2	1,526.6	3,035.1	3,034.1	G	376.2		359.2	358.2	4
27	3,109.2	1,555.1	3,092.2	3,091.2	G	319.2		302.1	301.2	3
28	3,224.2	1,612.6	3,207.2	3,206.2	D	262.1		245.1	244.1	2
29	3,370.3	1,685.7	3,353.3	3,352.3	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-30	sp|P50542|PEX5_HUMAN	DAEAHPWLSDYDDLTSATYDK	84.51	Unmodified	Light	2	1207.027

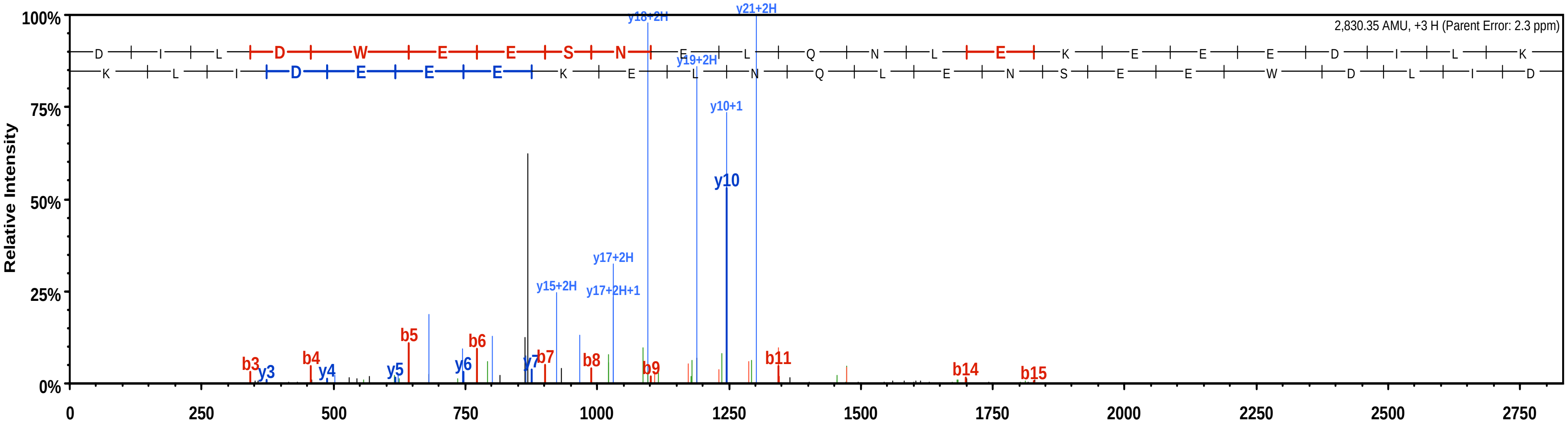




...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	2,413.0	1,207.0	2,396.0	2,395.0	21
2	187.1			169.1	A	2,298.0	1,149.5	2,281.0	2,280.0	20
3	316.1			298.1	E	2,227.0	1,114.0	2,210.0	2,209.0	19
4	387.2			369.1	A	2,097.9	1,049.5	2,080.9	2,079.9	18
5	524.2	262.6		506.2	H	2,026.9	1,014.0	2,009.9	2,008.9	17
6	621.3	311.1		603.3	P	1,889.8	945.4	1,872.8	1,871.8	16
7	807.3	404.2		789.3	W	1,792.8	896.9	1,775.8	1,774.8	15
8	920.4	460.7		902.4	L	1,606.7	803.9	1,589.7	1,588.7	14
9	1,007.5	504.2		989.4	S	1,493.6	747.3	1,476.6	1,475.6	13
10	1,122.5	561.7		1,104.5	D	1,406.6	703.8	1,389.6	1,388.6	12
11	1,285.5	643.3		1,267.5	Y	1,291.6	646.3	1,274.5	1,273.6	11
12	1,400.6	700.8		1,382.6	D	1,128.5	564.8	1,111.5	1,110.5	10
13	1,515.6	758.3		1,497.6	D	1,013.5	507.2	996.5	995.5	9
14	1,628.7	814.8		1,610.7	L	898.5	449.7	881.4	880.4	8
15	1,729.7	865.4		1,711.7	T	785.4	393.2	768.3	767.4	7
16	1,816.8	908.9		1,798.8	S	684.3	342.7	667.3	666.3	6
17	1,887.8	944.4		1,869.8	A	597.3		580.3	579.3	5
18	1,988.9	994.9		1,970.8	T	526.3		509.2	508.2	4
19	2,151.9	1,076.5		2,133.9	Y	425.2		408.2	407.2	3
20	2,266.9	1,134.0		2,248.9	D	262.1		245.1	244.1	2
21	2,413.0	1,207.0	2,396.0	2,395.0	K	147.1		130.1		1

Whole proteome

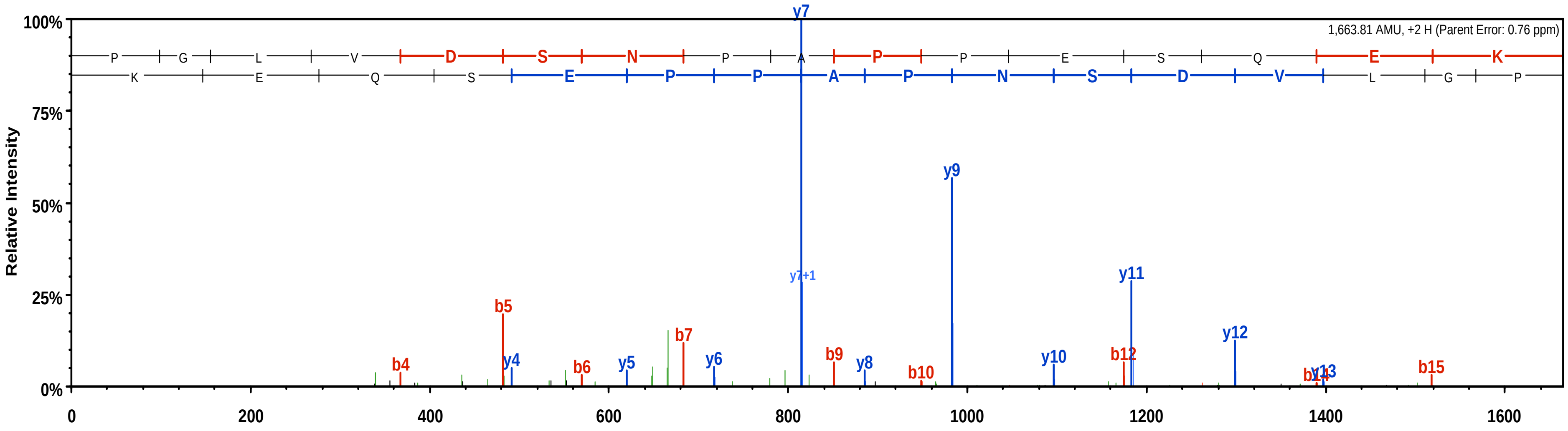
Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-31	sp|Q9C035|TRIM5_HUMAN	DILDWEESNELQNLEKEEEDILK	84.15	Unmodified	Light	3	944.45382

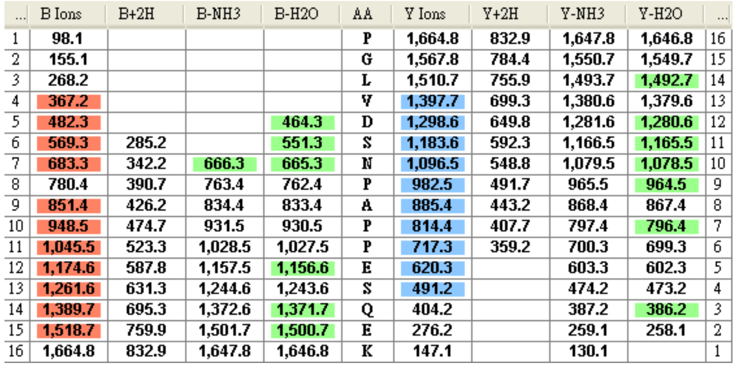


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	2,831.3	1,416.2	2,814.3	2,813.3	23
2	229.1			211.1	I	2,716.3	1,358.7	2,699.3	2,698.3	22
3	342.2			324.2	L	2,603.2	1,302.1	2,586.2	2,585.2	21
4	457.2			439.2	D	2,490.2	1,245.6	2,473.1	2,472.1	20
5	643.3			625.3	W	2,375.1	1,188.1	2,358.1	2,357.1	19
6	772.4	386.7		754.3	E	2,189.0	1,095.0	2,172.0	2,171.0	18
7	901.4	451.2		883.4	E	2,060.0	1,030.5	2,043.0	2,042.0	17
8	988.4	494.7		970.4	S	1,931.0	966.0	1,913.9	1,912.9	16
9	1,102.5	551.7	1,085.4	1,084.5	N	1,843.9	922.5	1,826.9	1,825.9	15
10	1,231.5	616.3	1,214.5	1,213.5	E	1,729.9	865.4	1,712.9	1,711.9	14
11	1,344.6	672.8	1,327.6	1,326.6	L	1,600.8	800.9	1,583.8	1,582.8	13
12	1,472.7	736.8	1,455.6	1,454.6	Q	1,487.8	744.4	1,470.7	1,469.7	12
13	1,586.7	793.9	1,569.7	1,568.7	N	1,359.7	680.4	1,342.7	1,341.7	11
14	1,699.8	850.4	1,682.8	1,681.8	L	1,245.7	623.3	1,228.6	1,227.6	10
15	1,828.8	914.9	1,811.8	1,810.8	E	1,132.6	566.8	1,115.5	1,114.6	9
16	1,956.9	979.0	1,939.9	1,938.9	K	1,003.5	502.3	986.5	985.5	8
17	2,086.0	1,043.5	2,068.9	2,068.0	E	875.4	438.2	858.4	857.4	7
18	2,215.0	1,108.0	2,198.0	2,197.0	E	746.4	373.7	729.4	728.4	6
19	2,344.0	1,172.5	2,327.0	2,326.0	E	617.4		600.3	599.3	5
20	2,459.1	1,230.0	2,442.0	2,441.1	D	488.3		471.3	470.3	4
21	2,572.2	1,286.6	2,555.1	2,554.1	I	373.3		356.3		3
22	2,685.2	1,343.1	2,668.2	2,667.2	L	260.2		243.2		2
23	2,831.3	1,416.2	2,814.3	2,813.3	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-32	sp|Q14061|COX17_HUMAN	PGLVDSNPAPPESQEK	83.93	Unmodified	Light	2	832.90994

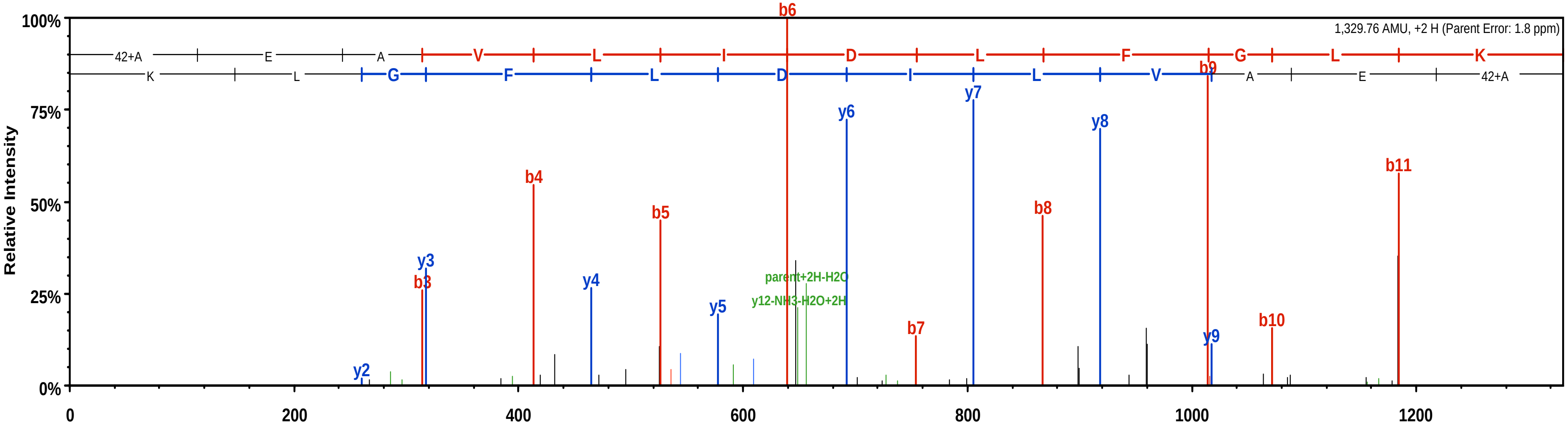




...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	98.1				P	1,664.8	832.9	1,647.8	1,646.8	16
2	155.1				G	1,567.8	784.4	1,550.7	1,549.7	15
3	268.2				L	1,510.7	755.9	1,493.7	1,492.7	14
4	367.2				V	1,397.7	699.3	1,380.6	1,379.6	13
5	482.3			464.3	D	1,298.6	649.8	1,281.6	1,280.6	12
6	569.3	285.2		551.3	S	1,183.6	592.3	1,166.5	1,165.5	11
7	683.3	342.2	666.3	665.3	N	1,096.5	548.8	1,079.5	1,078.5	10
8	780.4	390.7	763.4	762.4	P	982.5	491.7	965.5	964.5	9
9	851.4	426.2	834.4	833.4	A	885.4	443.2	868.4	867.4	8
10	948.5	474.7	931.5	930.5	P	814.4	407.7	797.4	796.4	7
11	1,045.5	523.3	1,028.5	1,027.5	P	717.3	359.2	700.3	699.3	6
12	1,174.6	587.8	1,157.5	1,156.6	E	620.3		603.3	602.3	5
13	1,261.6	631.3	1,244.6	1,243.6	S	491.2		474.2	473.2	4
14	1,389.7	695.3	1,372.6	1,371.7	Q	404.2		387.2	386.2	3
15	1,518.7	759.9	1,501.7	1,500.7	E	276.2		259.1	258.1	2
16	1,664.8	832.9	1,647.8	1,646.8	K	147.1		130.1		1

Whole proteome

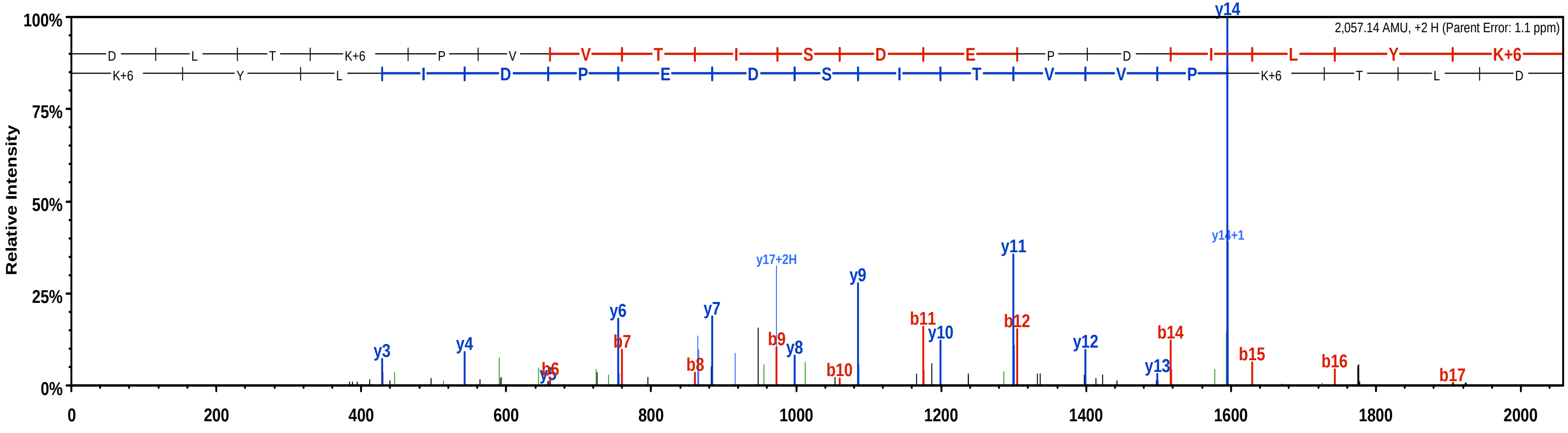
Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-33	sp|Q8IV20|CM031_HUMAN	AEAVLIDLFGLK	82.22	Acetyl (Protein N-term)	Light	2	665.88448

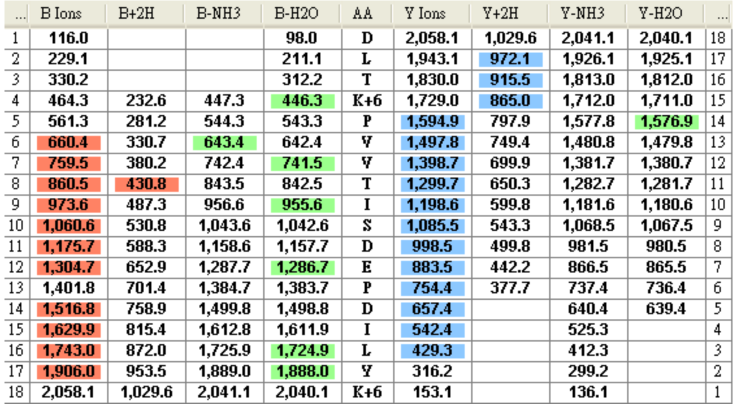


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	1,330.8	665.9	1,313.7	1,312.8	12
2	243.1			225.1	E	1,217.7	609.4	1,200.7	1,199.7	11
3	314.1			296.1	A	1,088.7	544.8	1,071.6	1,070.7	10
4	413.2			395.2	V	1,017.6	509.3	1,000.6	999.6	9
5	526.3			508.3	L	918.6	459.8	901.5	900.6	8
6	639.4	320.2		621.4	I	805.5	403.2	788.5	787.5	7
7	754.4	377.7		736.4	D	692.4	346.7	675.4	674.4	6
8	867.5	434.2		849.5	L	577.4		560.3		5
9	1,014.6	507.8		996.5	F	464.3		447.3		4
10	1,071.6	536.3		1,053.6	G	317.2		300.2		3
11	1,184.7	592.8		1,166.6	L	260.2		243.2		2
12	1,330.8	665.9	1,313.7	1,312.8	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-34	sp|P82664|RT10_HUMAN	DLTKPVVTISDEPDILYK	81.44	Unmodified	Heavy	2	1023.5539

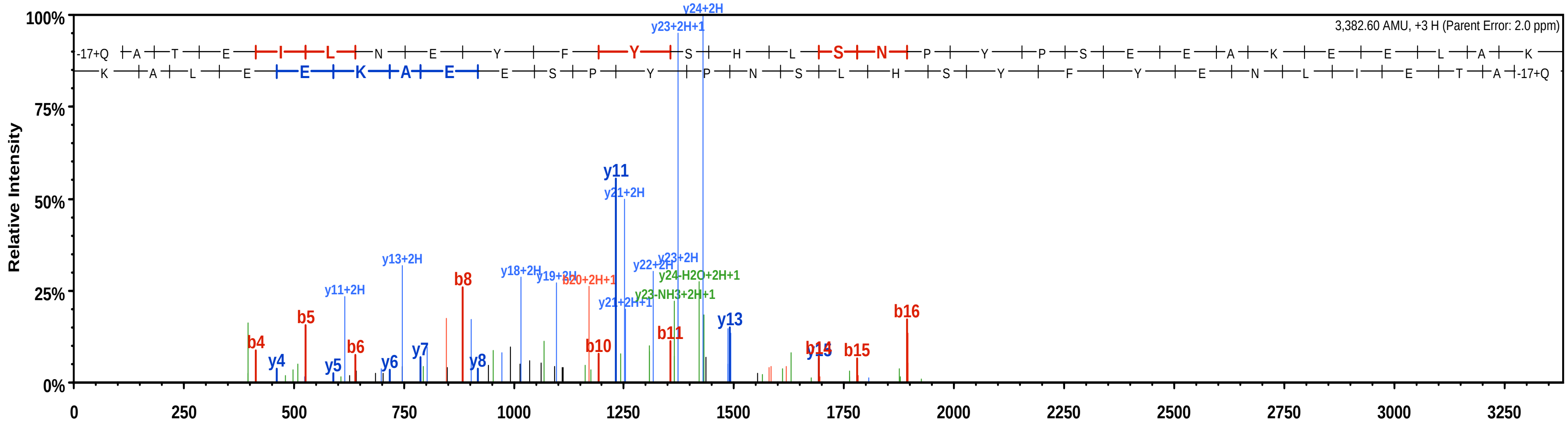


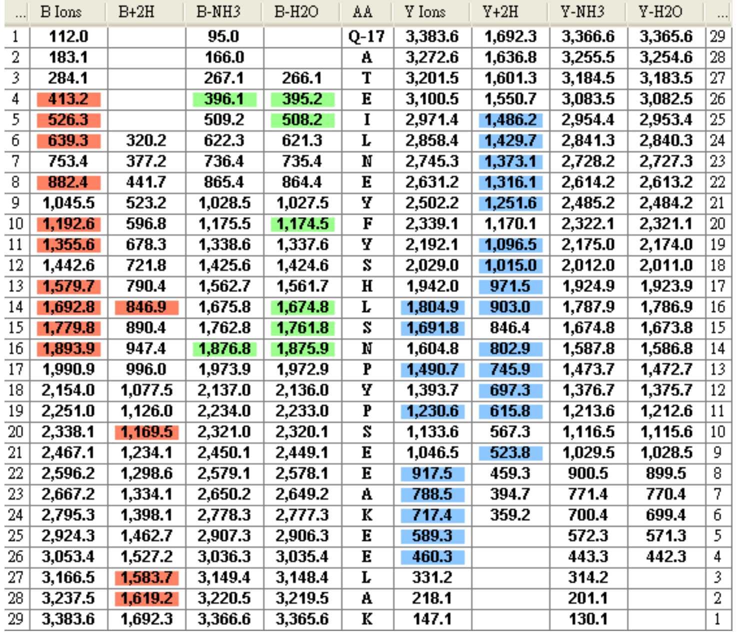


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	2,058.1	1,029.6	2,041.1	2,040.1	18
2	229.1			211.1	L	1,943.1	972.1	1,926.1	1,925.1	17
3	330.2			312.2	T	1,830.0	915.5	1,813.0	1,812.0	16
4	464.3	232.6	447.3	446.3	K+6	1,729.0	865.0	1,712.0	1,711.0	15
5	561.3	281.2	544.3	543.3	P	1,594.9	797.9	1,577.8	1,576.9	14
6	660.4	330.7	643.4	642.4	V	1,497.8	749.4	1,480.8	1,479.8	13
7	759.5	380.2	742.4	741.5	V	1,398.7	699.9	1,381.7	1,380.7	12
8	860.5	430.8	843.5	842.5	T	1,299.7	650.3	1,282.7	1,281.7	11
9	973.6	487.3	956.6	955.6	I	1,198.6	599.8	1,181.6	1,180.6	10
10	1,060.6	530.8	1,043.6	1,042.6	S	1,085.5	543.3	1,068.5	1,067.5	9
11	1,175.7	588.3	1,158.6	1,157.7	D	998.5	499.8	981.5	980.5	8
12	1,304.7	652.9	1,287.7	1,286.7	E	883.5	442.2	866.5	865.5	7
13	1,401.8	701.4	1,384.7	1,383.7	P	754.4	377.7	737.4	736.4	6
14	1,516.8	758.9	1,499.8	1,498.8	D	657.4		640.4	639.4	5
15	1,629.9	815.4	1,612.8	1,611.9	I	542.4		525.3		4
16	1,743.0	872.0	1,725.9	1,724.9	L	429.3		412.3		3
17	1,906.0	953.5	1,889.0	1,888.0	Y	316.2		299.2		2
18	2,058.1	1,029.6	2,041.1	2,040.1	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-35	sp|P40426|PBX3_HUMAN	QATEILNEYFYSHLSNPYPSEEAKEELAK	80.37	Gln->pyro-Glu (N-term Q)	Light	3	1128.5367

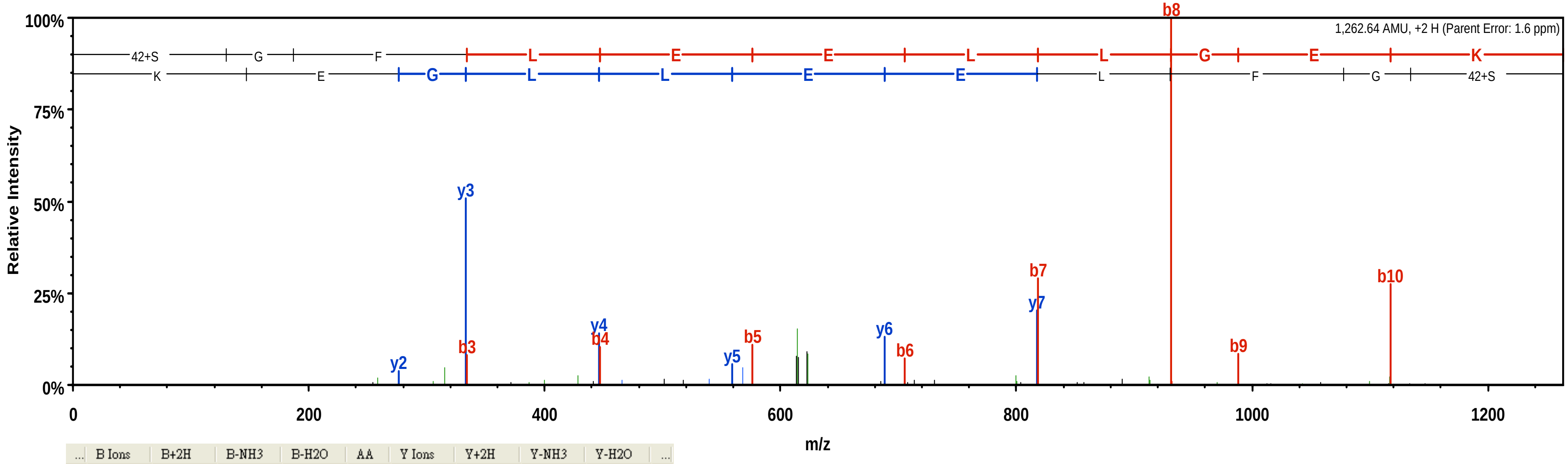


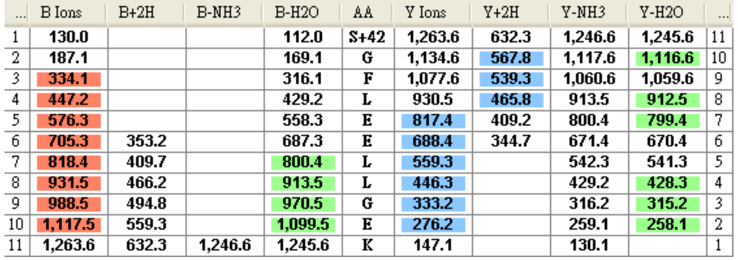


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	3,383.6	1,692.3	3,366.6	3,365.6	29
2	183.1		166.0		A	3,272.6	1,636.8	3,255.5	3,254.6	28
3	284.1		267.1	266.1	T	3,201.5	1,601.3	3,184.5	3,183.5	27
4	413.2		396.1	395.2	E	3,100.5	1,550.7	3,083.5	3,082.5	26
5	526.3		509.2	508.2	I	2,971.4	1,486.2	2,954.4	2,953.4	25
6	639.3	320.2	622.3	621.3	L	2,858.4	1,429.7	2,841.3	2,840.3	24
7	753.4	377.2	736.4	735.4	N	2,745.3	1,373.1	2,728.2	2,727.3	23
8	882.4	441.7	865.4	864.4	E	2,631.2	1,316.1	2,614.2	2,613.2	22
9	1,045.5	523.2	1,028.5	1,027.5	Y	2,502.2	1,251.6	2,485.2	2,484.2	21
10	1,192.6	596.8	1,175.5	1,174.5	F	2,339.1	1,170.1	2,322.1	2,321.1	20
11	1,355.6	678.3	1,338.6	1,337.6	Y	2,192.1	1,096.5	2,175.0	2,174.0	19
12	1,442.6	721.8	1,425.6	1,424.6	S	2,029.0	1,015.0	2,012.0	2,011.0	18
13	1,579.7	790.4	1,562.7	1,561.7	H	1,942.0	971.5	1,924.9	1,923.9	17
14	1,692.8	846.9	1,675.8	1,674.8	L	1,804.9	903.0	1,787.9	1,786.9	16
15	1,779.8	890.4	1,762.8	1,761.8	S	1,691.8	846.4	1,674.8	1,673.8	15
16	1,893.9	947.4	1,876.8	1,875.9	N	1,604.8	802.9	1,587.8	1,586.8	14
17	1,990.9	996.0	1,973.9	1,972.9	P	1,490.7	745.9	1,473.7	1,472.7	13
18	2,154.0	1,077.5	2,137.0	2,136.0	Y	1,393.7	697.3	1,376.7	1,375.7	12
19	2,251.0	1,126.0	2,234.0	2,233.0	P	1,230.6	615.8	1,213.6	1,212.6	11
20	2,338.1	1,169.5	2,321.0	2,320.1	S	1,133.6	567.3	1,116.5	1,115.6	10
21	2,467.1	1,234.1	2,450.1	2,449.1	E	1,046.5	523.8	1,029.5	1,028.5	9
22	2,596.2	1,298.6	2,579.1	2,578.1	E	917.5	459.3	900.5	899.5	8
23	2,667.2	1,334.1	2,650.2	2,649.2	A	788.5	394.7	771.4	770.4	7
24	2,795.3	1,398.1	2,778.3	2,777.3	K	717.4	359.2	700.4	699.4	6
25	2,924.3	1,462.7	2,907.3	2,906.3	E	589.3		572.3	571.3	5
26	3,053.4	1,527.2	3,036.3	3,035.4	E	460.3		443.3	442.3	4
27	3,166.5	1,583.7	3,149.4	3,148.4	L	331.2		314.2		3
28	3,237.5	1,619.2	3,220.5	3,219.5	A	218.1		201.1		2
29	3,383.6	1,692.3	3,366.6	3,365.6	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-36	sp|Q6DKJ4|NXN_HUMAN	SGFLEELLGEK	79.49	Acetyl (Protein N-term)	Light	2	632.32699

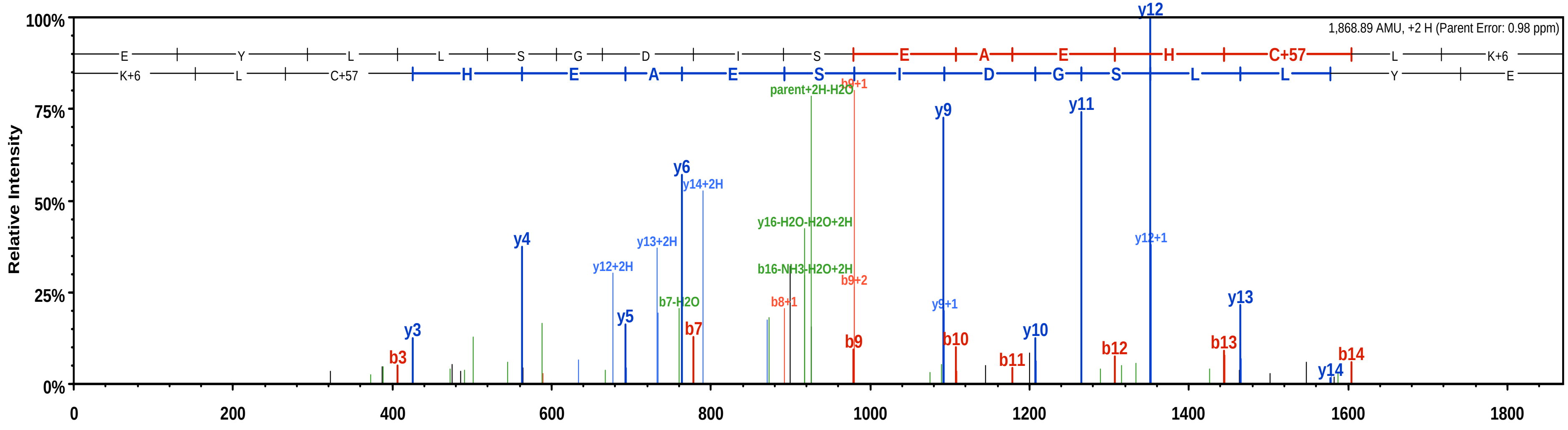


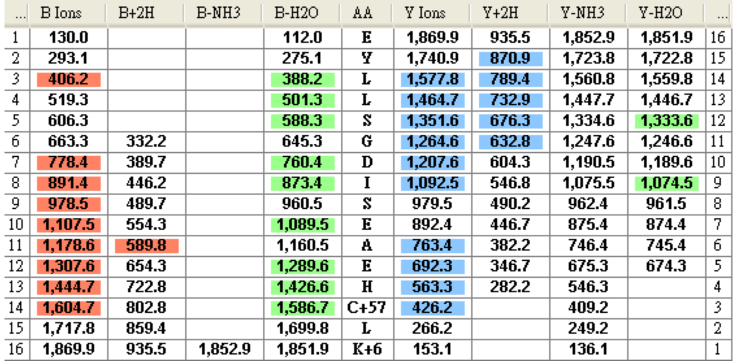


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	S+42	1,263.6	632.3	1,246.6	1,245.6	11
2	187.1			169.1	G	1,134.6	567.8	1,117.6	1,116.6	10
3	334.1			316.1	F	1,077.6	539.3	1,060.6	1,059.6	9
4	447.2			429.2	L	930.5	465.8	913.5	912.5	8
5	576.3			558.3	E	817.4	409.2	800.4	799.4	7
6	705.3	353.2		687.3	E	688.4	344.7	671.4	670.4	6
7	818.4	409.7		800.4	L	559.3		542.3	541.3	5
8	931.5	466.2		913.5	L	446.3		429.2	428.3	4
9	988.5	494.8		970.5	G	333.2		316.2	315.2	3
10	1,117.5	559.3		1,099.5	E	276.2		259.1	258.1	2
11	1,263.6	632.3	1,246.6	1,245.6	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-44	sp|Q53EL6|PDCD4_HUMAN	EYLLSGDISEAEHCLK	79.31	Unmodified	Heavy	2	932.44329

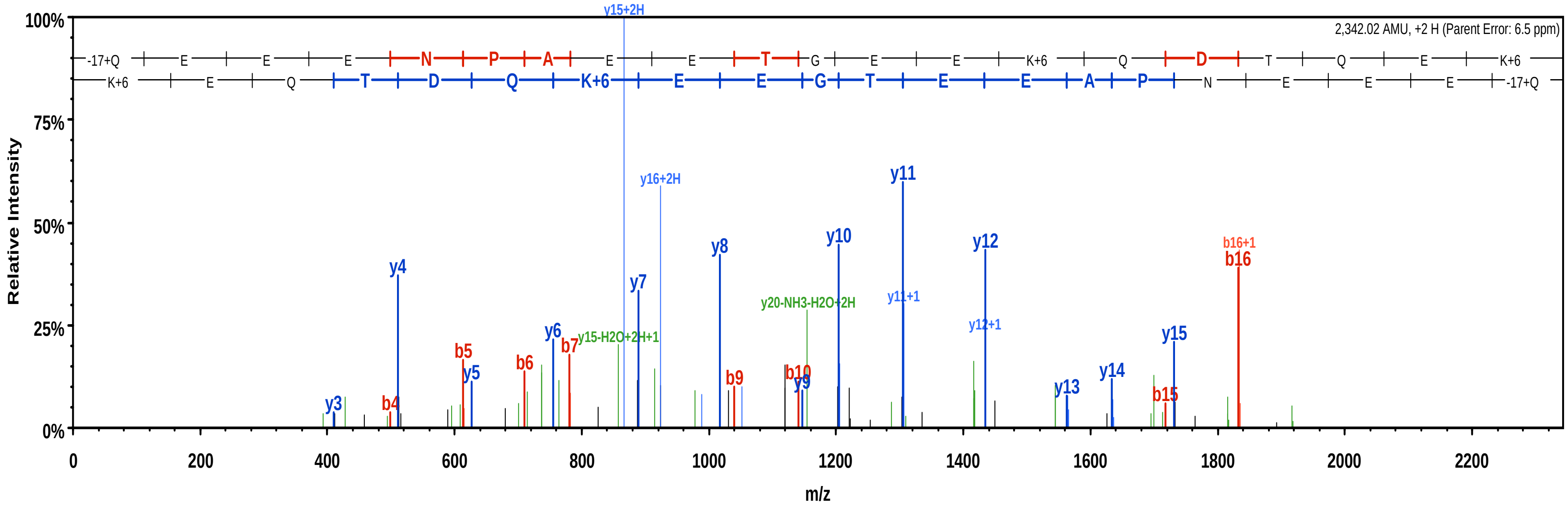


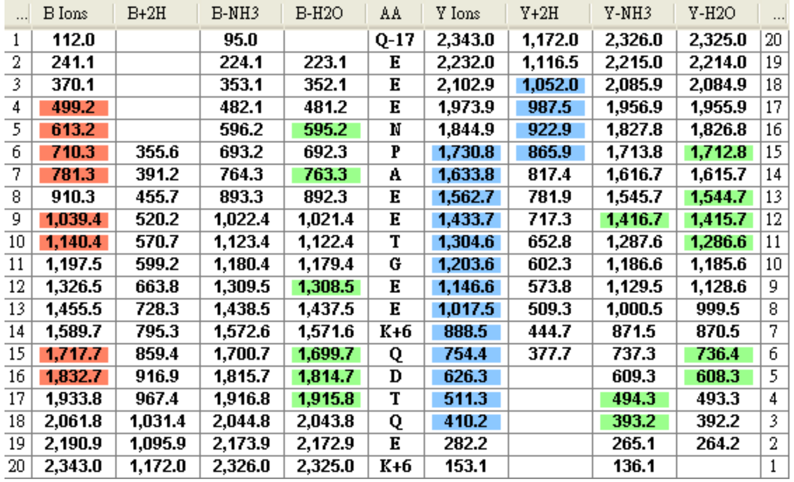


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	1,869.9	935.5	1,852.9	1,851.9	16
2	293.1			275.1	Y	1,740.9	870.9	1,723.8	1,722.8	15
3	406.2			388.2	L	1,577.8	789.4	1,560.8	1,559.8	14
4	519.3			501.3	L	1,464.7	732.9	1,447.7	1,446.7	13
5	606.3			588.3	S	1,351.6	676.3	1,334.6	1,333.6	12
6	663.3	332.2		645.3	G	1,264.6	632.8	1,247.6	1,246.6	11
7	778.4	389.7		760.4	D	1,207.6	604.3	1,190.5	1,189.6	10
8	891.4	446.2		873.4	I	1,092.5	546.8	1,075.5	1,074.5	9
9	978.5	489.7		960.5	S	979.5	490.2	962.4	961.5	8
10	1,107.5	554.3		1,089.5	E	892.4	446.7	875.4	874.4	7
11	1,178.6	589.8		1,160.5	A	763.4	382.2	746.4	745.4	6
12	1,307.6	654.3		1,289.6	E	692.3	346.7	675.3	674.3	5
13	1,444.7	722.8		1,426.6	H	563.3	282.2	546.3		4
14	1,604.7	802.8		1,586.7	C+57	426.2		409.2		3
15	1,717.8	859.4		1,699.8	L	266.2		249.2		2
16	1,869.9	935.5	1,852.9	1,851.9	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-45	sp|O43768|ENSA_HUMAN	QEEENPAEETGEEKQDTQEK	79.2	Gln->pyro-Glu (N-term Q)	Heavy	2	1165.9908

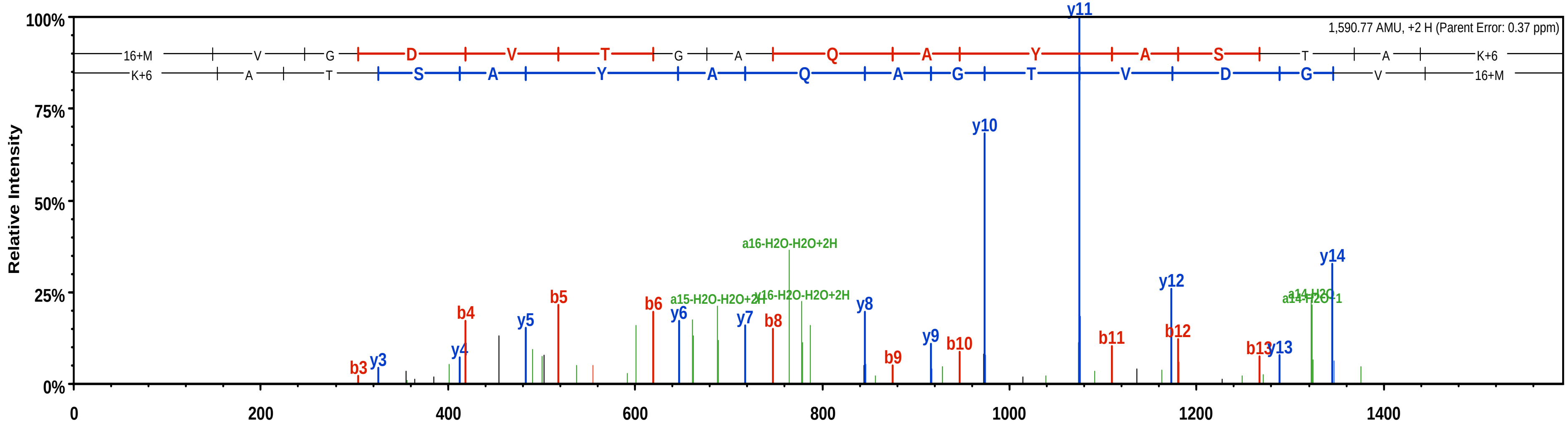


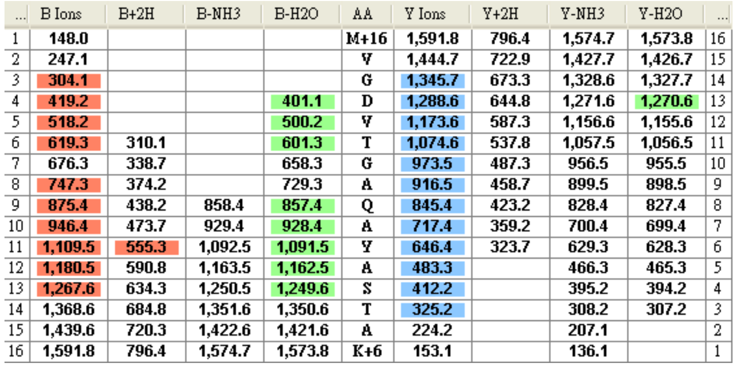


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	2,343.0	1,172.0	2,326.0	2,325.0	20
2	241.1		224.1	223.1	E	2,232.0	1,116.5	2,215.0	2,214.0	19
3	370.1		353.1	352.1	E	2,102.9	1,052.0	2,085.9	2,084.9	18
4	499.2		482.1	481.2	E	1,973.9	987.5	1,956.9	1,955.9	17
5	613.2		596.2	595.2	N	1,844.9	922.9	1,827.8	1,826.8	16
6	710.3	355.6	693.2	692.3	P	1,730.8	865.9	1,713.8	1,712.8	15
7	781.3	391.2	764.3	763.3	A	1,633.8	817.4	1,616.7	1,615.7	14
8	910.3	455.7	893.3	892.3	E	1,562.7	781.9	1,545.7	1,544.7	13
9	1,039.4	520.2	1,022.4	1,021.4	E	1,433.7	717.3	1,416.7	1,415.7	12
10	1,140.4	570.7	1,123.4	1,122.4	T	1,304.6	652.8	1,287.6	1,286.6	11
11	1,197.5	599.2	1,180.4	1,179.4	G	1,203.6	602.3	1,186.6	1,185.6	10
12	1,326.5	663.8	1,309.5	1,308.5	E	1,146.6	573.8	1,129.5	1,128.6	9
13	1,455.5	728.3	1,438.5	1,437.5	E	1,017.5	509.3	1,000.5	999.5	8
14	1,589.7	795.3	1,572.6	1,571.6	K+6	888.5	444.7	871.5	870.5	7
15	1,717.7	859.4	1,700.7	1,699.7	Q	754.4	377.7	737.3	736.4	6
16	1,832.7	916.9	1,815.7	1,814.7	D	626.3		609.3	608.3	5
17	1,933.8	967.4	1,916.8	1,915.8	T	511.3		494.3	493.3	4
18	2,061.8	1,031.4	2,044.8	2,043.8	Q	410.2		393.2	392.2	3
19	2,190.9	1,095.9	2,173.9	2,172.9	E	282.2		265.1	264.2	2
20	2,343.0	1,172.0	2,326.0	2,325.0	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-46	sp|Q01628|IFM3_HUMAN	MVGDVTGAQAYASTAK	78.22	Oxidation (M)	Heavy	2	793.37996

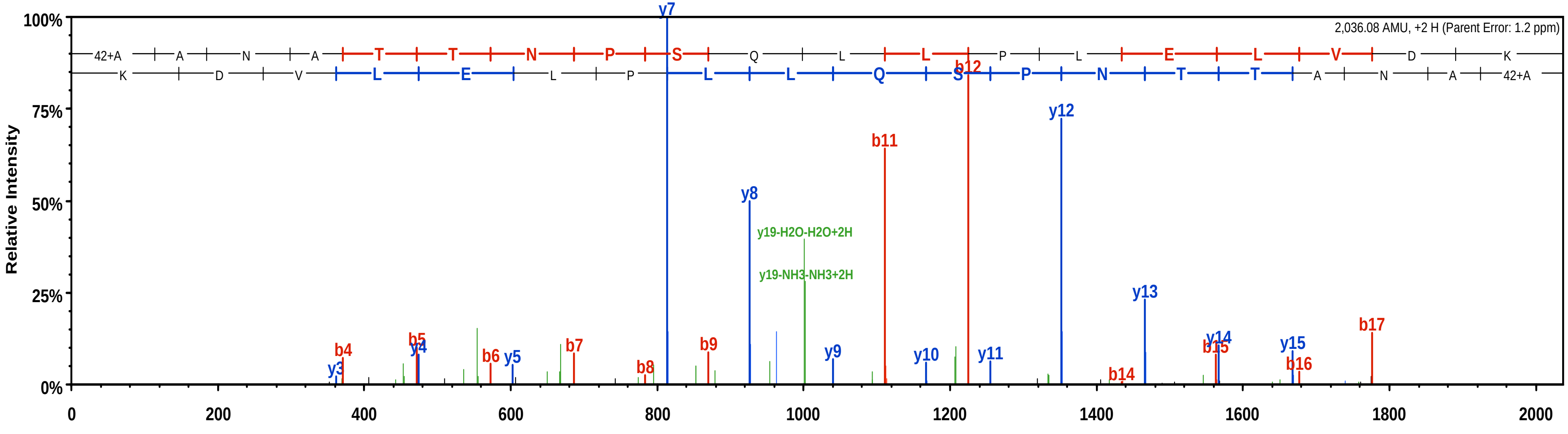


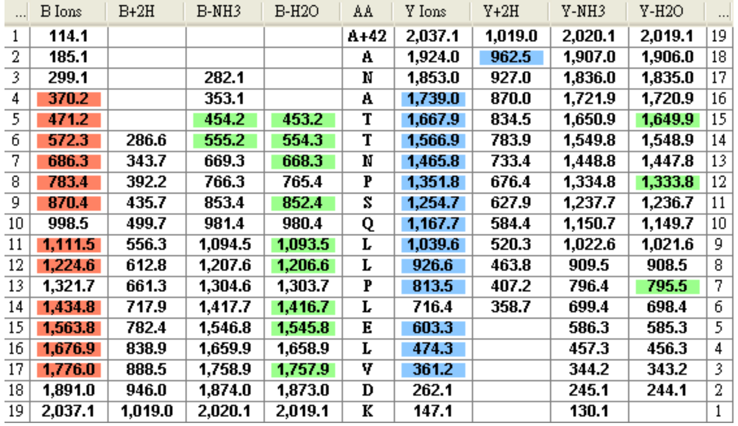


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.0				M+16	1,591.8	796.4	1,574.7	1,573.8	16
2	247.1				V	1,444.7	722.9	1,427.7	1,426.7	15
3	304.1				G	1,345.7	673.3	1,328.6	1,327.7	14
4	419.2			401.1	D	1,288.6	644.8	1,271.6	1,270.6	13
5	518.2			500.2	V	1,173.6	587.3	1,156.6	1,155.6	12
6	619.3	310.1		601.3	T	1,074.6	537.8	1,057.5	1,056.5	11
7	676.3	338.7		658.3	G	973.5	487.3	956.5	955.5	10
8	747.3	374.2		729.3	A	916.5	458.7	899.5	898.5	9
9	875.4	438.2	858.4	857.4	Q	845.4	423.2	828.4	827.4	8
10	946.4	473.7	929.4	928.4	A	717.4	359.2	700.4	699.4	7
11	1,109.5	555.3	1,092.5	1,091.5	Y	646.4	323.7	629.3	628.3	6
12	1,180.5	590.8	1,163.5	1,162.5	A	483.3		466.3	465.3	5
13	1,267.6	634.3	1,250.5	1,249.6	S	412.2		395.2	394.2	4
14	1,368.6	684.8	1,351.6	1,350.6	T	325.2		308.2	307.2	3
15	1,439.6	720.3	1,422.6	1,421.6	A	224.2		207.1		2
16	1,591.8	796.4	1,574.7	1,573.8	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-47	sp|Q9Y4Y9|LSM5_HUMAN	AANATTNPSQLLPLELVDK	77.77	Acetyl (Protein N-term)	Light	2	1019.0468

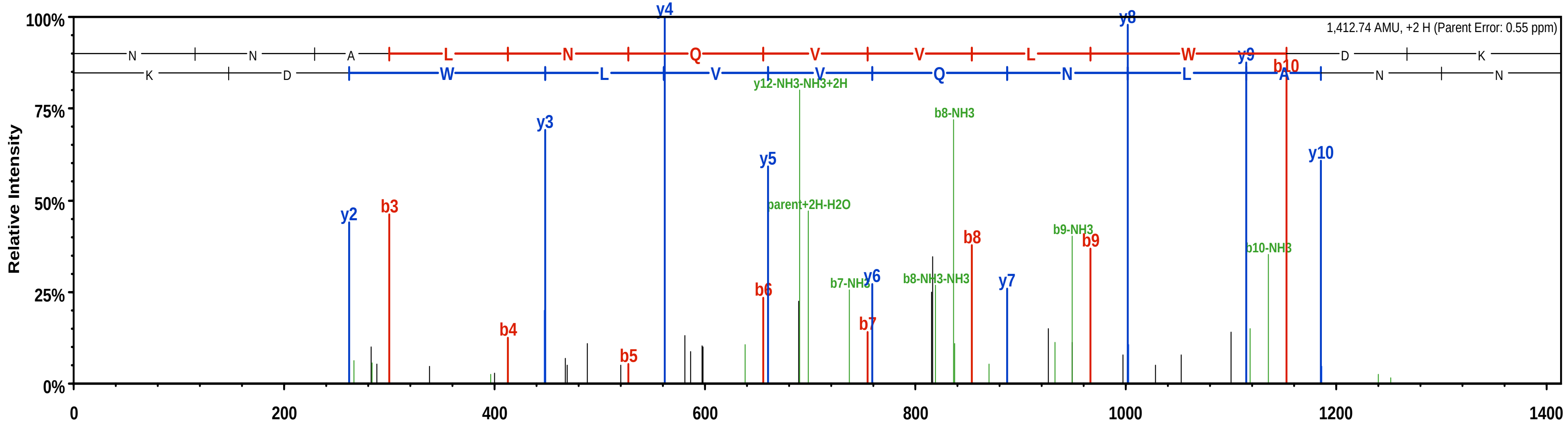


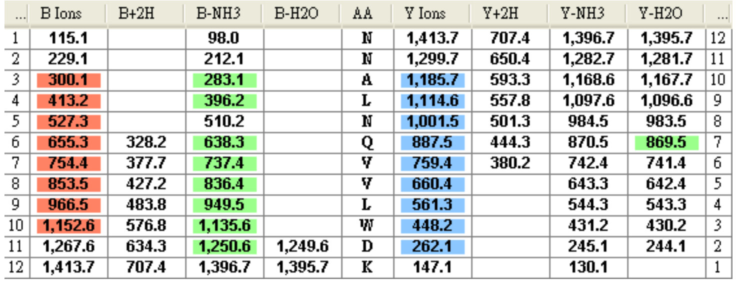


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	2,037.1	1,019.0	2,020.1	2,019.1	19
2	185.1				A	1,924.0	962.5	1,907.0	1,906.0	18
3	299.1		282.1		N	1,853.0	927.0	1,836.0	1,835.0	17
4	370.2		353.1		A	1,739.0	870.0	1,721.9	1,720.9	16
5	471.2		454.2	453.2	T	1,667.9	834.5	1,650.9	1,649.9	15
6	572.3	286.6	555.2	554.3	T	1,566.9	783.9	1,549.8	1,548.9	14
7	686.3	343.7	669.3	668.3	N	1,465.8	733.4	1,448.8	1,447.8	13
8	783.4	392.2	766.3	765.4	P	1,351.8	676.4	1,334.8	1,333.8	12
9	870.4	435.7	853.4	852.4	S	1,254.7	627.9	1,237.7	1,236.7	11
10	998.5	499.7	981.4	980.4	Q	1,167.7	584.4	1,150.7	1,149.7	10
11	1,111.5	556.3	1,094.5	1,093.5	L	1,039.6	520.3	1,022.6	1,021.6	9
12	1,224.6	612.8	1,207.6	1,206.6	L	926.6	463.8	909.5	908.5	8
13	1,321.7	661.3	1,304.6	1,303.7	P	813.5	407.2	796.4	795.5	7
14	1,434.8	717.9	1,417.7	1,416.7	L	716.4	358.7	699.4	698.4	6
15	1,563.8	782.4	1,546.8	1,545.8	E	603.3		586.3	585.3	5
16	1,676.9	838.9	1,659.9	1,658.9	L	474.3		457.3	456.3	4
17	1,776.0	888.5	1,758.9	1,757.9	V	361.2		344.2	343.2	3
18	1,891.0	946.0	1,874.0	1,873.0	D	262.1		245.1	244.1	2
19	2,037.1	1,019.0	2,020.1	2,019.1	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-48	sp|P61009|SPCS3_HUMAN	NNALNQVVLWDK	77.11	Unmodified	Light	2	707.37788

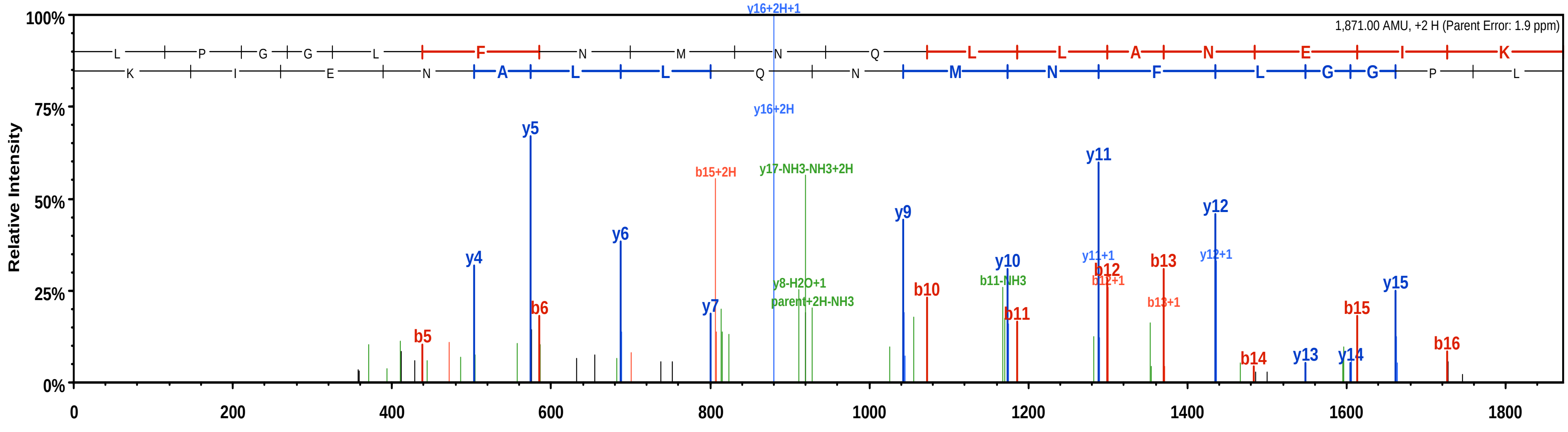


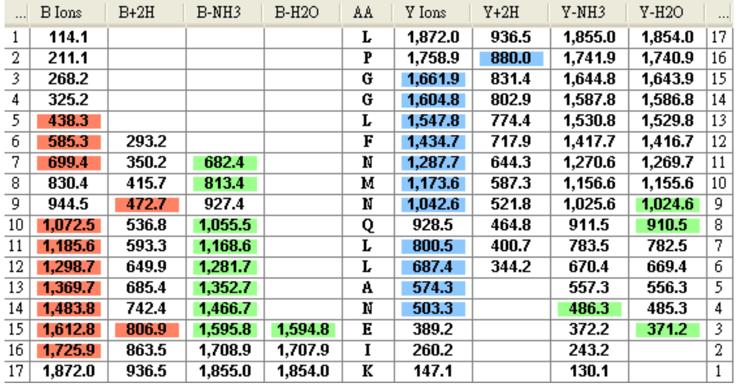


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	115.1		98.0		N	1,413.7	707.4	1,396.7	1,395.7	12
2	229.1		212.1		N	1,299.7	650.4	1,282.7	1,281.7	11
3	300.1		283.1		A	1,185.7	593.3	1,168.6	1,167.7	10
4	413.2		396.2		L	1,114.6	557.8	1,097.6	1,096.6	9
5	527.3		510.2		N	1,001.5	501.3	984.5	983.5	8
6	655.3	328.2	638.3		Q	887.5	444.3	870.5	869.5	7
7	754.4	377.7	737.4		V	759.4	380.2	742.4	741.4	6
8	853.5	427.2	836.4		V	660.4		643.3	642.4	5
9	966.5	483.8	949.5		L	561.3		544.3	543.3	4
10	1,152.6	576.8	1,135.6		W	448.2		431.2	430.2	3
11	1,267.6	634.3	1,250.6	1,249.6	D	262.1		245.1	244.1	2
12	1,413.7	707.4	1,396.7	1,395.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-49	sp|Q9ULI2|RIMKB_HUMAN	LPGGLFNMNQLLANEIK	74.86	Unmodified	Light	2	936.50603

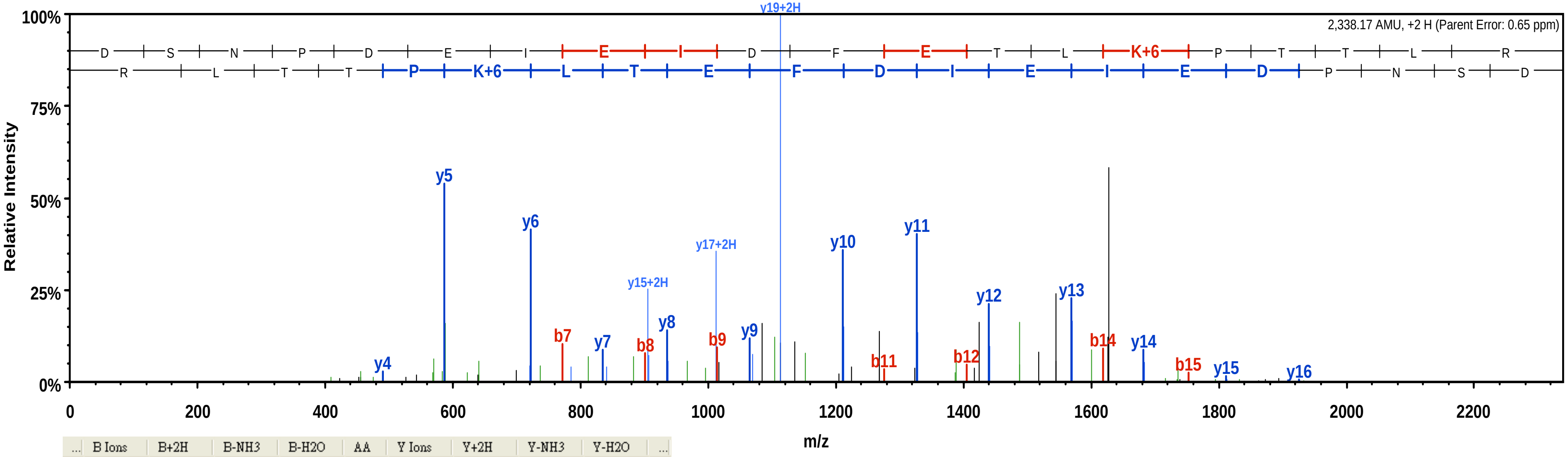


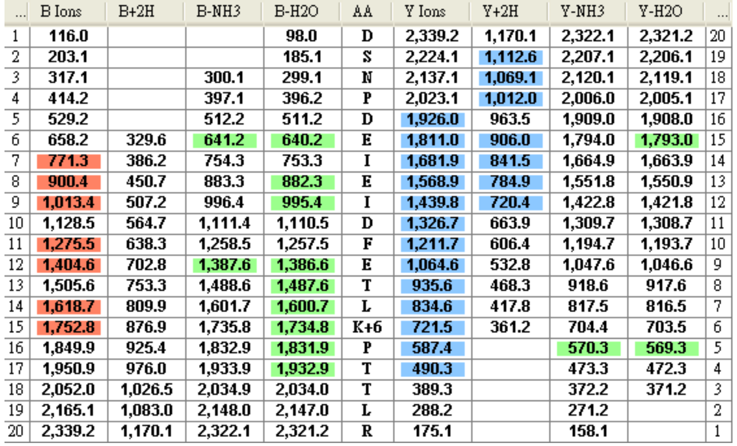


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	1,872.0	936.5	1,855.0	1,854.0	17
2	211.1				P	1,758.9	880.0	1,741.9	1,740.9	16
3	268.2				G	1,661.9	831.4	1,644.8	1,643.9	15
4	325.2				G	1,604.8	802.9	1,587.8	1,586.8	14
5	438.3				L	1,547.8	774.4	1,530.8	1,529.8	13
6	585.3	293.2			F	1,434.7	717.9	1,417.7	1,416.7	12
7	699.4	350.2	682.4		N	1,287.7	644.3	1,270.6	1,269.7	11
8	830.4	415.7	813.4		M	1,173.6	587.3	1,156.6	1,155.6	10
9	944.5	472.7	927.4		N	1,042.6	521.8	1,025.6	1,024.6	9
10	1,072.5	536.8	1,055.5		Q	928.5	464.8	911.5	910.5	8
11	1,185.6	593.3	1,168.6		L	800.5	400.7	783.5	782.5	7
12	1,298.7	649.9	1,281.7		L	687.4	344.2	670.4	669.4	6
13	1,369.7	685.4	1,352.7		A	574.3		557.3	556.3	5
14	1,483.8	742.4	1,466.7		N	503.3		486.3	485.3	4
15	1,612.8	806.9	1,595.8	1,594.8	E	389.2		372.2	371.2	3
16	1,725.9	863.5	1,708.9	1,707.9	I	260.2		243.2		2
17	1,872.0	936.5	1,855.0	1,854.0	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-50	sp|Q15059|BRD3_HUMAN	DSNPDEIEIDFETLKPTTLR	74.58	Unmodified	Heavy	2	1167.079

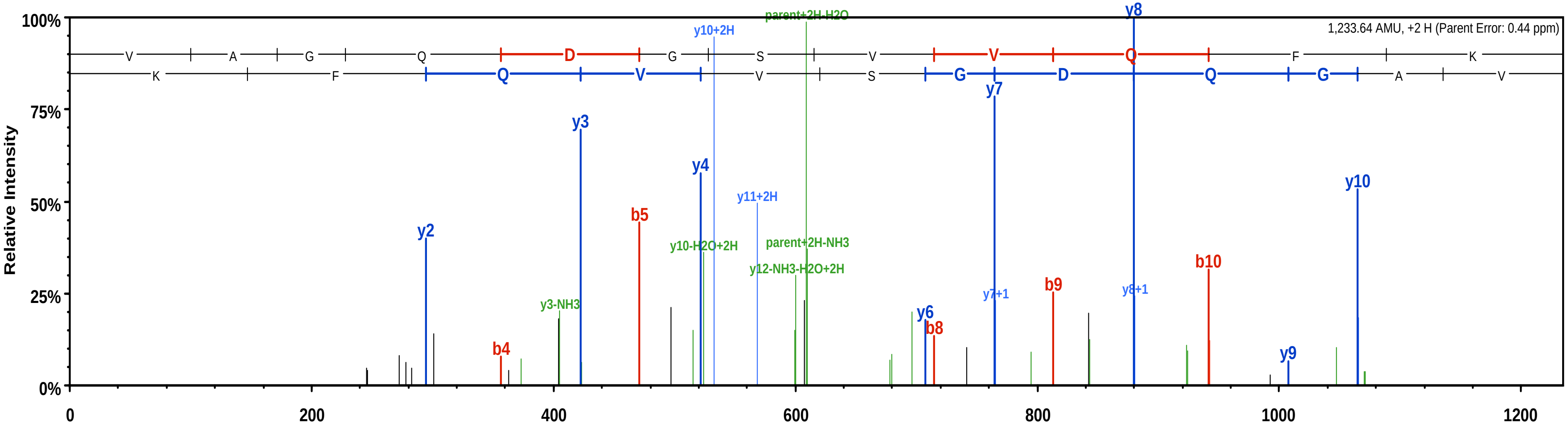


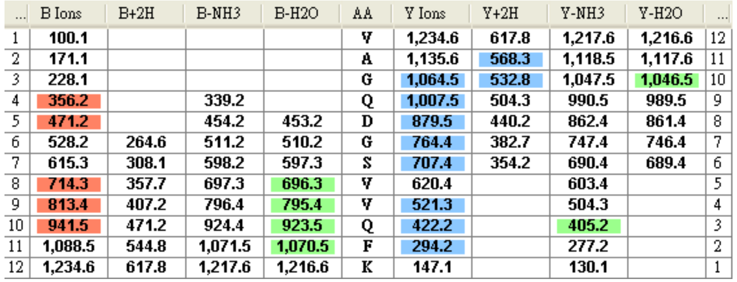


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	2,339.2	1,170.1	2,322.1	2,321.2	20
2	203.1			185.1	S	2,224.1	1,112.6	2,207.1	2,206.1	19
3	317.1		300.1	299.1	N	2,137.1	1,069.1	2,120.1	2,119.1	18
4	414.2		397.1	396.2	P	2,023.1	1,012.0	2,006.0	2,005.1	17
5	529.2		512.2	511.2	D	1,926.0	963.5	1,909.0	1,908.0	16
6	658.2	329.6	641.2	640.2	E	1,811.0	906.0	1,794.0	1,793.0	15
7	771.3	386.2	754.3	753.3	I	1,681.9	841.5	1,664.9	1,663.9	14
8	900.4	450.7	883.3	882.3	E	1,568.9	784.9	1,551.8	1,550.9	13
9	1,013.4	507.2	996.4	995.4	I	1,439.8	720.4	1,422.8	1,421.8	12
10	1,128.5	564.7	1,111.4	1,110.5	D	1,326.7	663.9	1,309.7	1,308.7	11
11	1,275.5	638.3	1,258.5	1,257.5	F	1,211.7	606.4	1,194.7	1,193.7	10
12	1,404.6	702.8	1,387.6	1,386.6	E	1,064.6	532.8	1,047.6	1,046.6	9
13	1,505.6	753.3	1,488.6	1,487.6	T	935.6	468.3	918.6	917.6	8
14	1,618.7	809.9	1,601.7	1,600.7	L	834.6	417.8	817.5	816.5	7
15	1,752.8	876.9	1,735.8	1,734.8	K+6	721.5	361.2	704.4	703.5	6
16	1,849.9	925.4	1,832.9	1,831.9	P	587.4		570.3	569.3	5
17	1,950.9	976.0	1,933.9	1,932.9	T	490.3		473.3	472.3	4
18	2,052.0	1,026.5	2,034.9	2,034.0	T	389.3		372.2	371.2	3
19	2,165.1	1,083.0	2,148.0	2,147.0	L	288.2		271.2		2
20	2,339.2	1,170.1	2,322.1	2,321.2	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-51	sp|P55854|SUMO3_HUMAN	VAGQDGSVVQFK	74.48	Unmodified	Light	2	617.82495

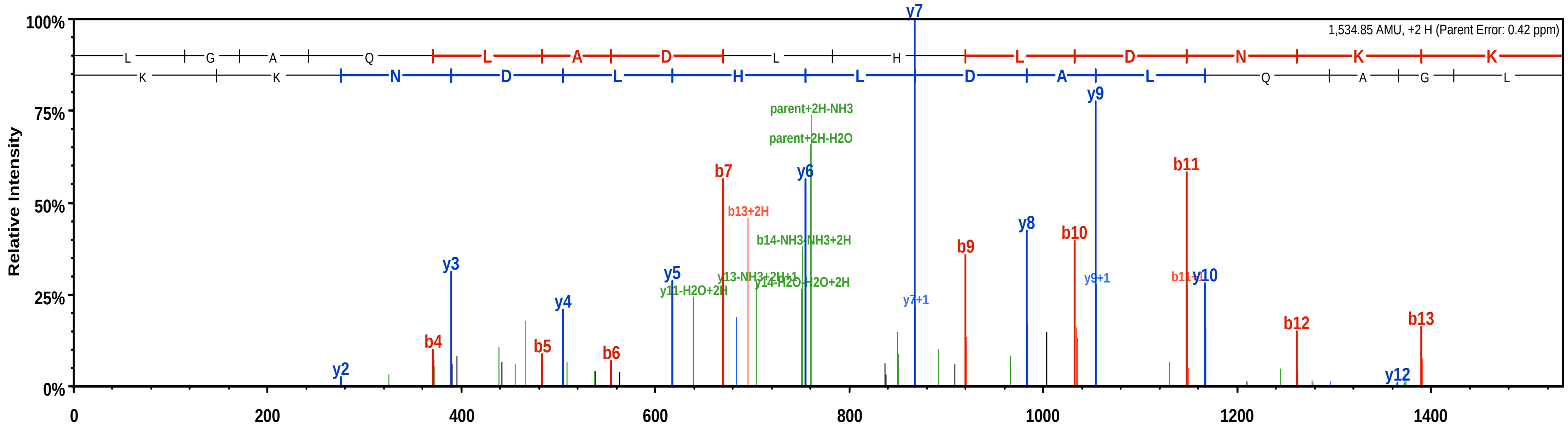


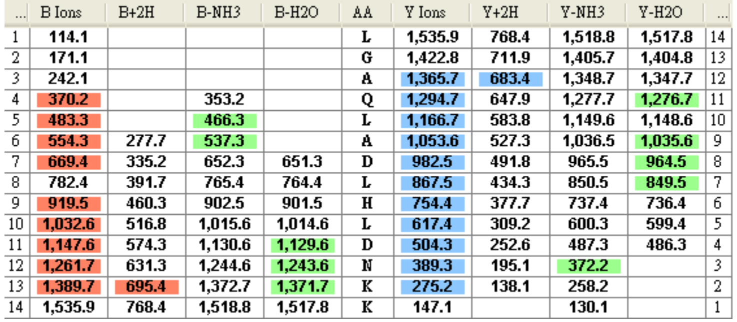


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	1,234.6	617.8	1,217.6	1,216.6	12
2	171.1				A	1,135.6	568.3	1,118.5	1,117.6	11
3	228.1				G	1,064.5	532.8	1,047.5	1,046.5	10
4	356.2		339.2		Q	1,007.5	504.3	990.5	989.5	9
5	471.2		454.2	453.2	D	879.5	440.2	862.4	861.4	8
6	528.2	264.6	511.2	510.2	G	764.4	382.7	747.4	746.4	7
7	615.3	308.1	598.2	597.3	S	707.4	354.2	690.4	689.4	6
8	714.3	357.7	697.3	696.3	V	620.4		603.4		5
9	813.4	407.2	796.4	795.4	V	521.3		504.3		4
10	941.5	471.2	924.4	923.5	Q	422.2		405.2		3
11	1,088.5	544.8	1,071.5	1,070.5	F	294.2		277.2		2
12	1,234.6	617.8	1,217.6	1,216.6	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-52	sp|Q9HA64|KT3K_HUMAN	LGAQLADLHLDNKK	74.23	Unmodified	Light	2	768.43065

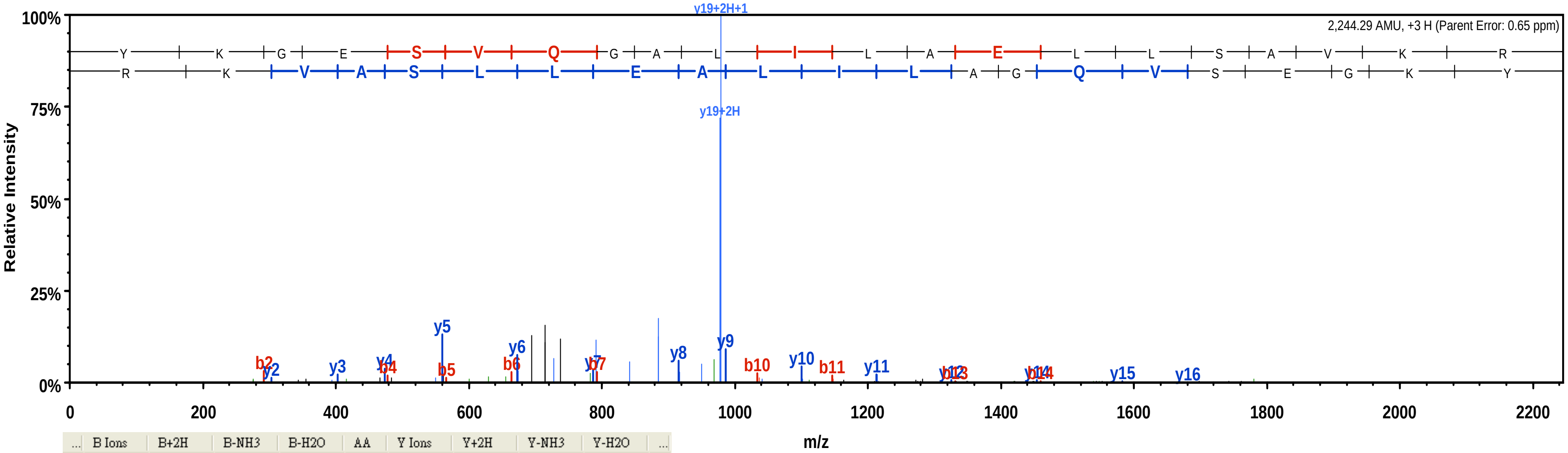


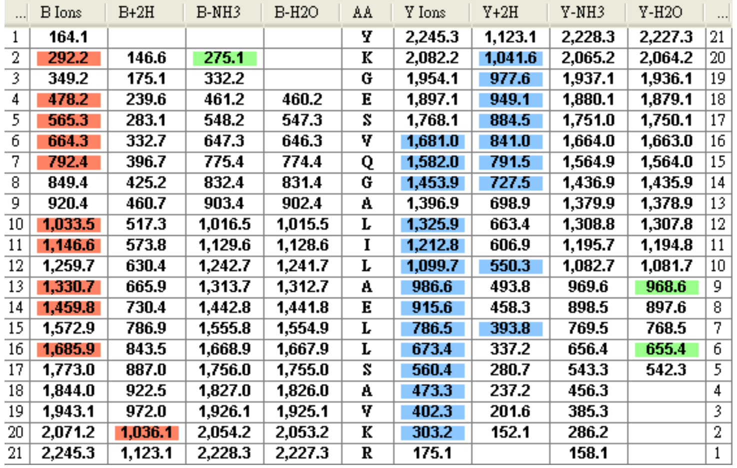


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	1,535.9	768.4	1,518.8	1,517.8	14
2	171.1				G	1,422.8	711.9	1,405.7	1,404.8	13
3	242.1				A	1,365.7	683.4	1,348.7	1,347.7	12
4	370.2		353.2		Q	1,294.7	647.9	1,277.7	1,276.7	11
5	483.3		466.3		L	1,166.7	583.8	1,149.6	1,148.6	10
6	554.3	277.7	537.3		A	1,053.6	527.3	1,036.5	1,035.6	9
7	669.4	335.2	652.3	651.3	D	982.5	491.8	965.5	964.5	8
8	782.4	391.7	765.4	764.4	L	867.5	434.3	850.5	849.5	7
9	919.5	460.3	902.5	901.5	H	754.4	377.7	737.4	736.4	6
10	1,032.6	516.8	1,015.6	1,014.6	L	617.4	309.2	600.3	599.4	5
11	1,147.6	574.3	1,130.6	1,129.6	D	504.3	252.6	487.3	486.3	4
12	1,261.7	631.3	1,244.6	1,243.6	N	389.3	195.1	372.2		3
13	1,389.7	695.4	1,372.7	1,371.7	K	275.2	138.1	258.2		2
14	1,535.9	768.4	1,518.8	1,517.8	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-53	sp|Q8NBN3|TM87A_HUMAN	YKGESVQGALILAELLSAVKR	72.71	Unmodified	Light	3	749.102

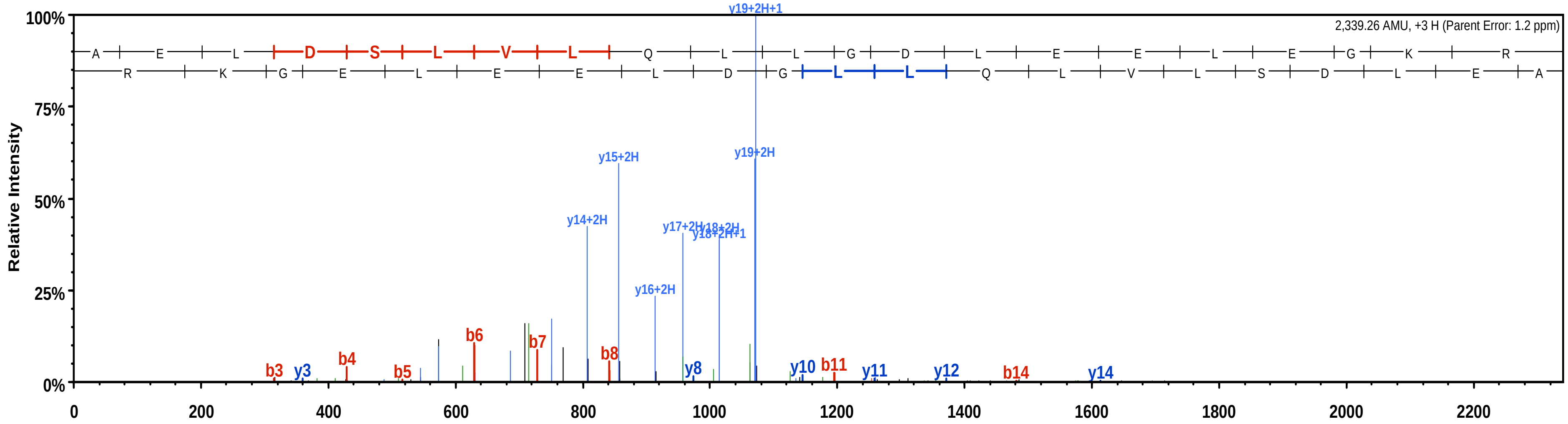


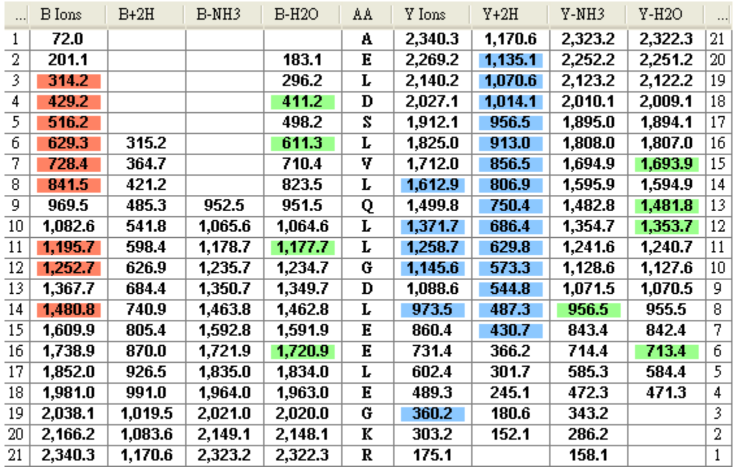


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	164.1				Y	2,245.3	1,123.1	2,228.3	2,227.3	21
2	292.2	146.6	275.1		K	2,082.2	1,041.6	2,065.2	2,064.2	20
3	349.2	175.1	332.2		G	1,954.1	977.6	1,937.1	1,936.1	19
4	478.2	239.6	461.2	460.2	E	1,897.1	949.1	1,880.1	1,879.1	18
5	565.3	283.1	548.2	547.3	S	1,768.1	884.5	1,751.0	1,750.1	17
6	664.3	332.7	647.3	646.3	V	1,681.0	841.0	1,664.0	1,663.0	16
7	792.4	396.7	775.4	774.4	Q	1,582.0	791.5	1,564.9	1,564.0	15
8	849.4	425.2	832.4	831.4	G	1,453.9	727.5	1,436.9	1,435.9	14
9	920.4	460.7	903.4	902.4	A	1,396.9	698.9	1,379.9	1,378.9	13
10	1,033.5	517.3	1,016.5	1,015.5	L	1,325.9	663.4	1,308.8	1,307.8	12
11	1,146.6	573.8	1,129.6	1,128.6	I	1,212.8	606.9	1,195.7	1,194.8	11
12	1,259.7	630.4	1,242.7	1,241.7	L	1,099.7	550.3	1,082.7	1,081.7	10
13	1,330.7	665.9	1,313.7	1,312.7	A	986.6	493.8	969.6	968.6	9
14	1,459.8	730.4	1,442.8	1,441.8	E	915.6	458.3	898.5	897.6	8
15	1,572.9	786.9	1,555.8	1,554.9	L	786.5	393.8	769.5	768.5	7
16	1,685.9	843.5	1,668.9	1,667.9	L	673.4	337.2	656.4	655.4	6
17	1,773.0	887.0	1,756.0	1,755.0	S	560.4	280.7	543.3	542.3	5
18	1,844.0	922.5	1,827.0	1,826.0	A	473.3	237.2	456.3		4
19	1,943.1	972.0	1,926.1	1,925.1	V	402.3	201.6	385.3		3
20	2,071.2	1,036.1	2,054.2	2,053.2	K	303.2	152.1	286.2		2
21	2,245.3	1,123.1	2,228.3	2,227.3	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-54	sp|Q96NT0|CC115_HUMAN	AELDSLVLQLLGDLEELEGKR	72.34	Unmodified	Light	3	780.76008

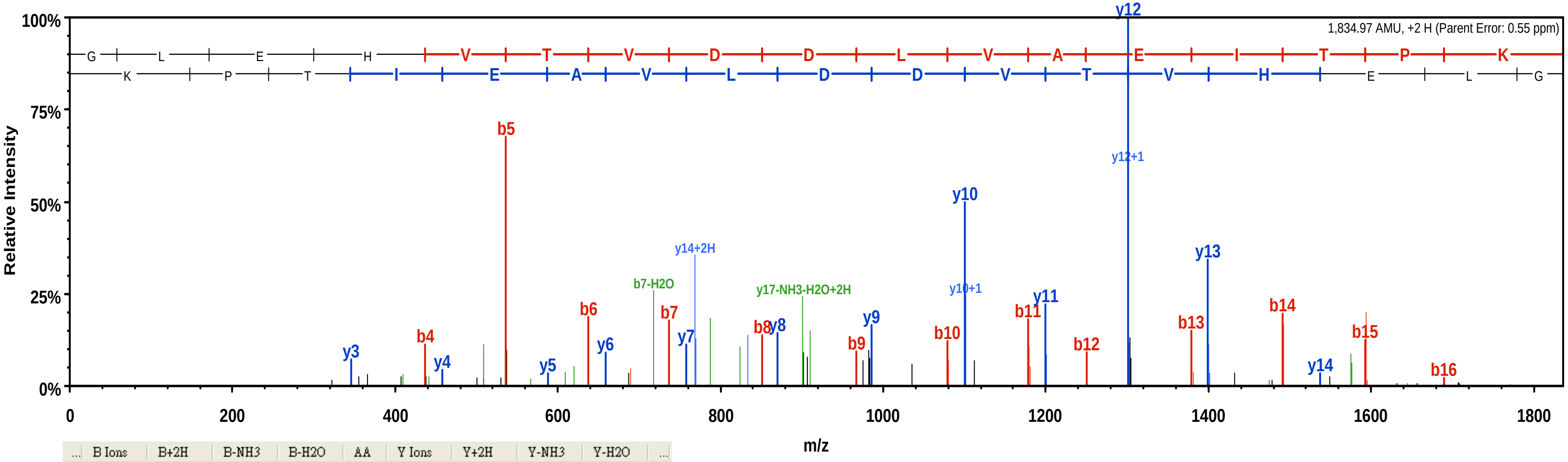


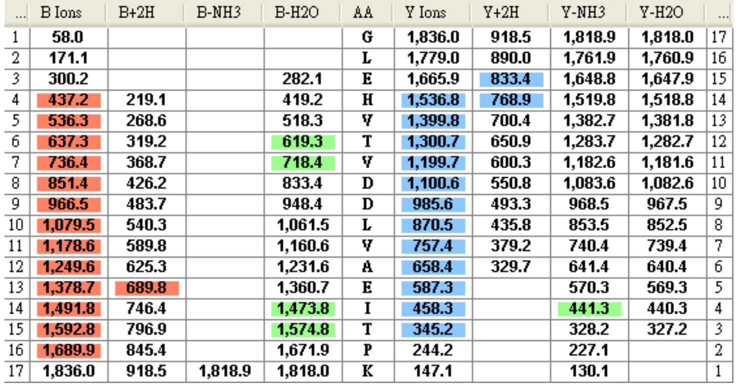


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	2,340.3	1,170.6	2,323.2	2,322.3	21
2	201.1			183.1	E	2,269.2	1,135.1	2,252.2	2,251.2	20
3	314.2			296.2	L	2,140.2	1,070.6	2,123.2	2,122.2	19
4	429.2			411.2	D	2,027.1	1,014.1	2,010.1	2,009.1	18
5	516.2			498.2	S	1,912.1	956.5	1,895.0	1,894.1	17
6	629.3	315.2		611.3	L	1,825.0	913.0	1,808.0	1,807.0	16
7	728.4	364.7		710.4	V	1,712.0	856.5	1,694.9	1,693.9	15
8	841.5	421.2		823.5	L	1,612.9	806.9	1,595.9	1,594.9	14
9	969.5	485.3	952.5	951.5	Q	1,499.8	750.4	1,482.8	1,481.8	13
10	1,082.6	541.8	1,065.6	1,064.6	L	1,371.7	686.4	1,354.7	1,353.7	12
11	1,195.7	598.4	1,178.7	1,177.7	L	1,258.7	629.8	1,241.6	1,240.7	11
12	1,252.7	626.9	1,235.7	1,234.7	G	1,145.6	573.3	1,128.6	1,127.6	10
13	1,367.7	684.4	1,350.7	1,349.7	D	1,088.6	544.8	1,071.5	1,070.5	9
14	1,480.8	740.9	1,463.8	1,462.8	L	973.5	487.3	956.5	955.5	8
15	1,609.9	805.4	1,592.8	1,591.9	E	860.4	430.7	843.4	842.4	7
16	1,738.9	870.0	1,721.9	1,720.9	E	731.4	366.2	714.4	713.4	6
17	1,852.0	926.5	1,835.0	1,834.0	L	602.4	301.7	585.3	584.4	5
18	1,981.0	991.0	1,964.0	1,963.0	E	489.3	245.1	472.3	471.3	4
19	2,038.1	1,019.5	2,021.0	2,020.0	G	360.2	180.6	343.2		3
20	2,166.2	1,083.6	2,149.1	2,148.1	K	303.2	152.1	286.2		2
21	2,340.3	1,170.6	2,323.2	2,322.3	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-55	sp|Q9NPA8|ENY2_HUMAN	GLEHVTVDDLVAEITPK	71.92	Unmodified	Light	2	918.4911

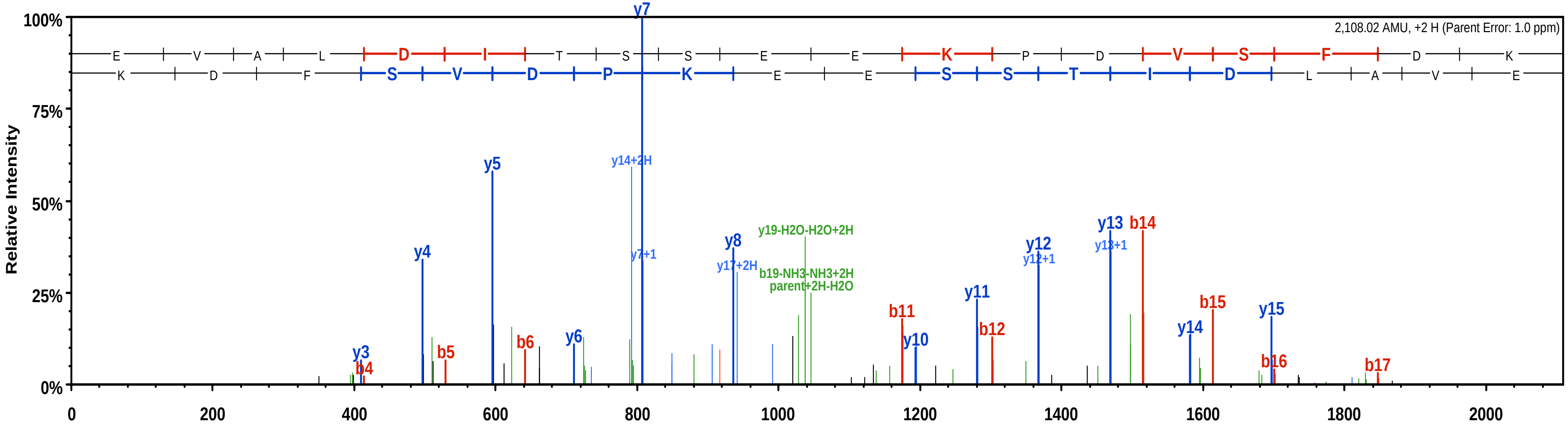


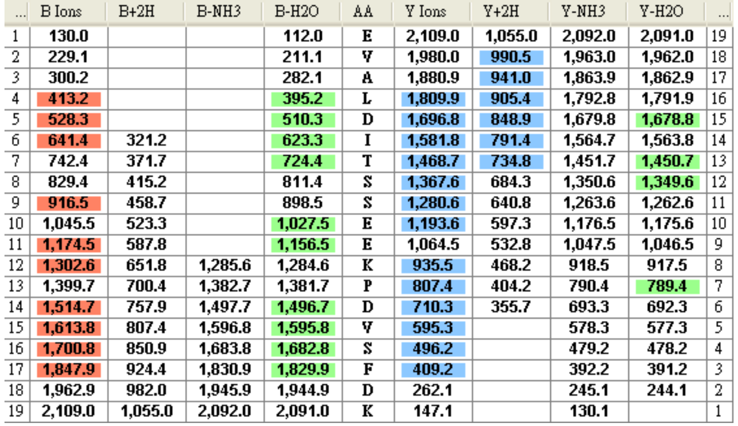


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	1,836.0	918.5	1,818.9	1,818.0	17
2	171.1				L	1,779.0	890.0	1,761.9	1,760.9	16
3	300.2			282.1	E	1,665.9	833.4	1,648.8	1,647.9	15
4	437.2	219.1		419.2	H	1,536.8	768.9	1,519.8	1,518.8	14
5	536.3	268.6		518.3	V	1,399.8	700.4	1,382.7	1,381.8	13
6	637.3	319.2		619.3	T	1,300.7	650.9	1,283.7	1,282.7	12
7	736.4	368.7		718.4	V	1,199.7	600.3	1,182.6	1,181.6	11
8	851.4	426.2		833.4	D	1,100.6	550.8	1,083.6	1,082.6	10
9	966.5	483.7		948.4	D	985.6	493.3	968.5	967.5	9
10	1,079.5	540.3		1,061.5	L	870.5	435.8	853.5	852.5	8
11	1,178.6	589.8		1,160.6	V	757.4	379.2	740.4	739.4	7
12	1,249.6	625.3		1,231.6	A	658.4	329.7	641.4	640.4	6
13	1,378.7	689.8		1,360.7	E	587.3		570.3	569.3	5
14	1,491.8	746.4		1,473.8	I	458.3		441.3	440.3	4
15	1,592.8	796.9		1,574.8	T	345.2		328.2	327.2	3
16	1,689.9	845.4		1,671.9	P	244.2		227.1		2
17	1,836.0	918.5	1,818.9	1,818.0	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-26	sp|Q9Y375|CIA30_HUMAN	EVALDITSSEEKPDVSFDK	71.92	Unmodified	Light	2	1055.0153

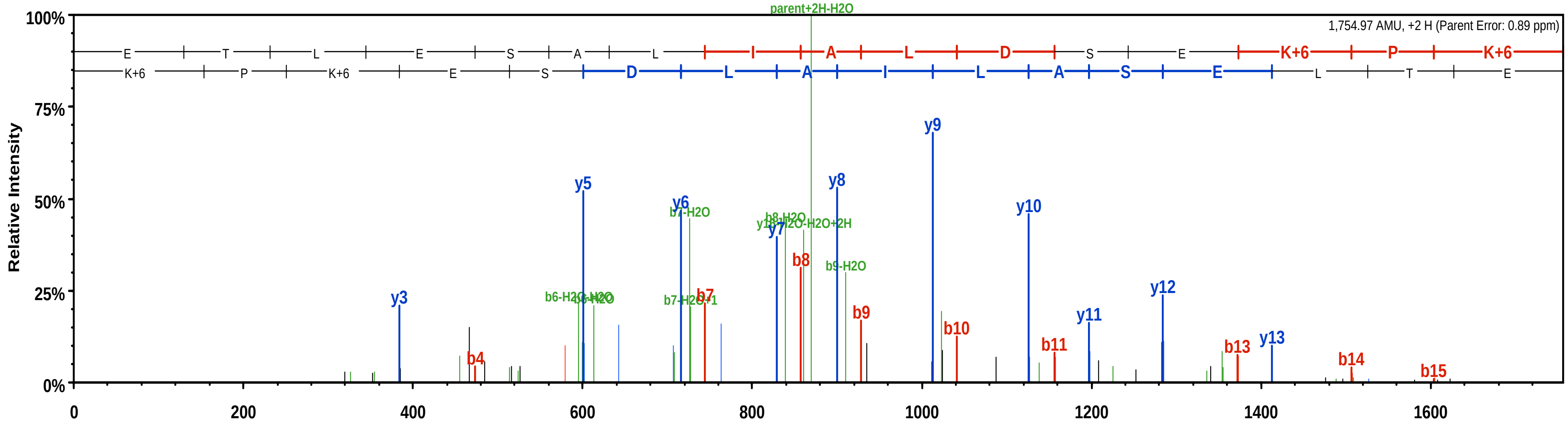


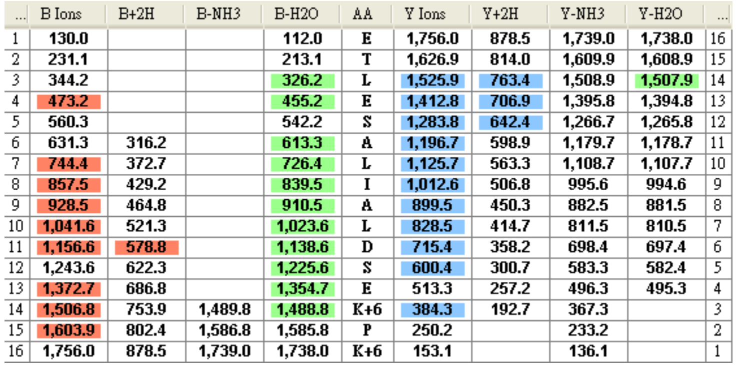


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	2,109.0	1,055.0	2,092.0	2,091.0	19
2	229.1			211.1	V	1,980.0	990.5	1,963.0	1,962.0	18
3	300.2			282.1	A	1,880.9	941.0	1,863.9	1,862.9	17
4	413.2			395.2	L	1,809.9	905.4	1,792.8	1,791.9	16
5	528.3			510.3	D	1,696.8	848.9	1,679.8	1,678.8	15
6	641.4	321.2		623.3	I	1,581.8	791.4	1,564.7	1,563.8	14
7	742.4	371.7		724.4	T	1,468.7	734.8	1,451.7	1,450.7	13
8	829.4	415.2		811.4	S	1,367.6	684.3	1,350.6	1,349.6	12
9	916.5	458.7		898.5	S	1,280.6	640.8	1,263.6	1,262.6	11
10	1,045.5	523.3		1,027.5	E	1,193.6	597.3	1,176.5	1,175.6	10
11	1,174.5	587.8		1,156.5	E	1,064.5	532.8	1,047.5	1,046.5	9
12	1,302.6	651.8	1,285.6	1,284.6	K	935.5	468.2	918.5	917.5	8
13	1,399.7	700.4	1,382.7	1,381.7	P	807.4	404.2	790.4	789.4	7
14	1,514.7	757.9	1,497.7	1,496.7	D	710.3	355.7	693.3	692.3	6
15	1,613.8	807.4	1,596.8	1,595.8	V	595.3		578.3	577.3	5
16	1,700.8	850.9	1,683.8	1,682.8	S	496.2		479.2	478.2	4
17	1,847.9	924.4	1,830.9	1,829.9	F	409.2		392.2	391.2	3
18	1,962.9	982.0	1,945.9	1,944.9	D	262.1		245.1	244.1	2
19	2,109.0	1,055.0	2,092.0	2,091.0	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-57	sp|Q9H9B1|EHMT1_HUMAN	ETLESALIALDSEKPK	71.6	Unmodified	Heavy	2	872.47237

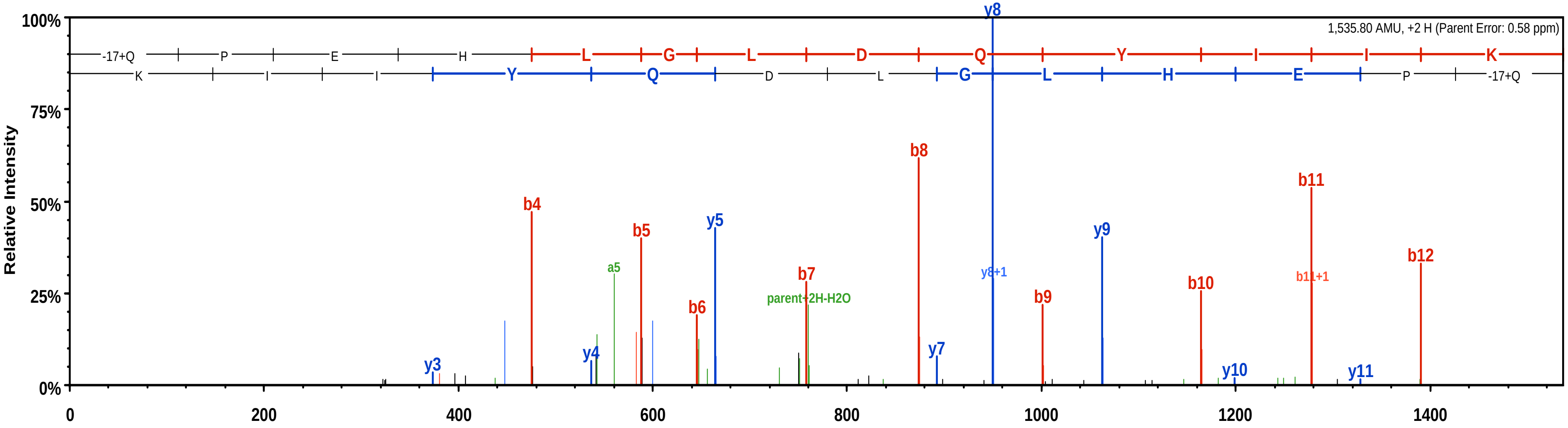


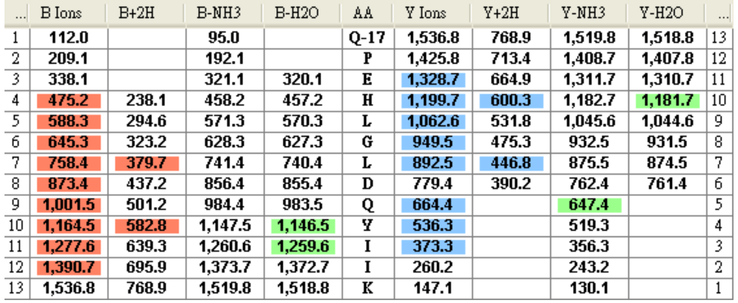


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	1,756.0	878.5	1,739.0	1,738.0	16
2	231.1			213.1	T	1,626.9	814.0	1,609.9	1,608.9	15
3	344.2			326.2	L	1,525.9	763.4	1,508.9	1,507.9	14
4	473.2			455.2	E	1,412.8	706.9	1,395.8	1,394.8	13
5	560.3			542.2	S	1,283.8	642.4	1,266.7	1,265.8	12
6	631.3	316.2		613.3	A	1,196.7	598.9	1,179.7	1,178.7	11
7	744.4	372.7		726.4	L	1,125.7	563.3	1,108.7	1,107.7	10
8	857.5	429.2		839.5	I	1,012.6	506.8	995.6	994.6	9
9	928.5	464.8		910.5	A	899.5	450.3	882.5	881.5	8
10	1,041.6	521.3		1,023.6	L	828.5	414.7	811.5	810.5	7
11	1,156.6	578.8		1,138.6	D	715.4	358.2	698.4	697.4	6
12	1,243.6	622.3		1,225.6	S	600.4	300.7	583.3	582.4	5
13	1,372.7	686.8		1,354.7	E	513.3	257.2	496.3	495.3	4
14	1,506.8	753.9	1,489.8	1,488.8	K+6	384.3	192.7	367.3		3
15	1,603.9	802.4	1,586.8	1,585.8	P	250.2		233.2		2
16	1,756.0	878.5	1,739.0	1,738.0	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-58	sp|Q9BPX6|CBAA1_HUMAN	QPEHLGLDQYIIK	71.04	Gln->pyro-Glu (N-term Q)	Light	2	768.90647

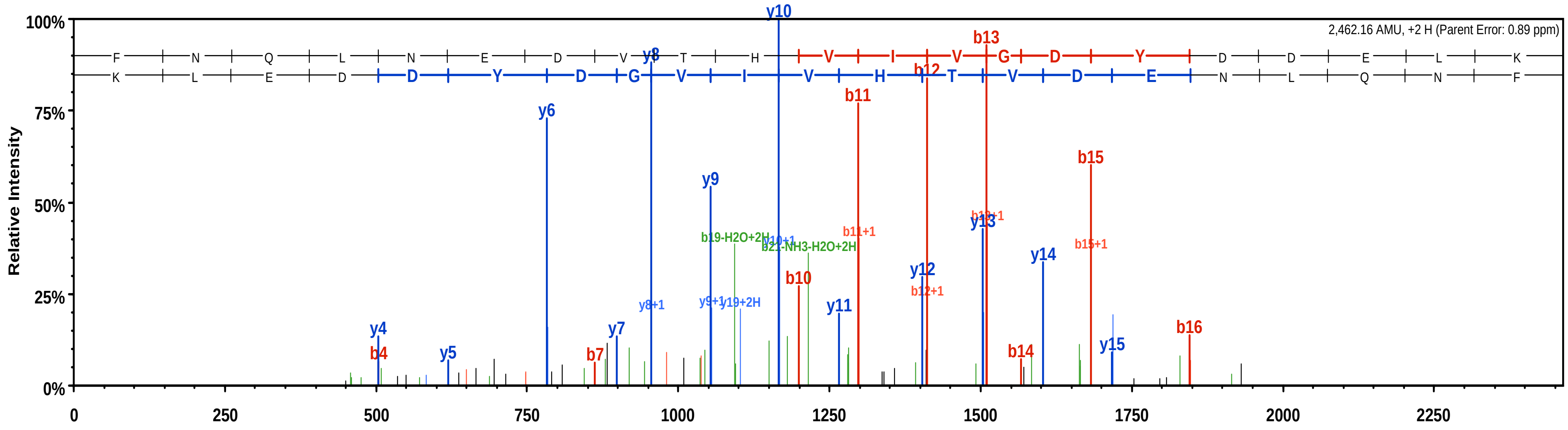


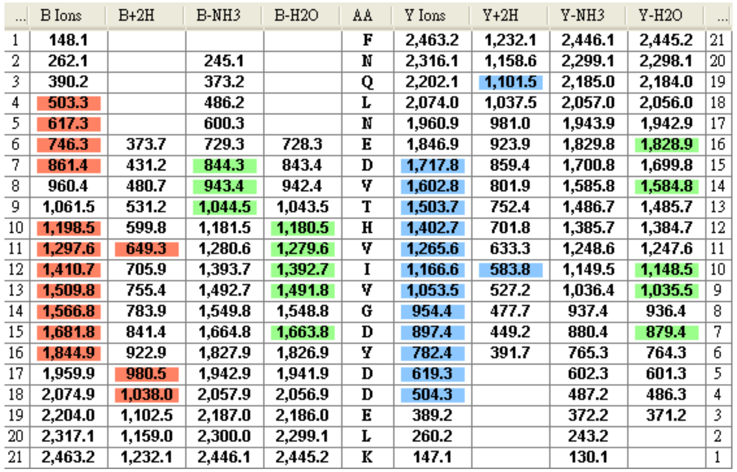


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	1,536.8	768.9	1,519.8	1,518.8	13
2	209.1		192.1		P	1,425.8	713.4	1,408.7	1,407.8	12
3	338.1		321.1	320.1	E	1,328.7	664.9	1,311.7	1,310.7	11
4	475.2	238.1	458.2	457.2	H	1,199.7	600.3	1,182.7	1,181.7	10
5	588.3	294.6	571.3	570.3	L	1,062.6	531.8	1,045.6	1,044.6	9
6	645.3	323.2	628.3	627.3	G	949.5	475.3	932.5	931.5	8
7	758.4	379.7	741.4	740.4	L	892.5	446.8	875.5	874.5	7
8	873.4	437.2	856.4	855.4	D	779.4	390.2	762.4	761.4	6
9	1,001.5	501.2	984.4	983.5	Q	664.4		647.4		5
10	1,164.5	582.8	1,147.5	1,146.5	Y	536.3		519.3		4
11	1,277.6	639.3	1,260.6	1,259.6	I	373.3		356.3		3
12	1,390.7	695.9	1,373.7	1,372.7	I	260.2		243.2		2
13	1,536.8	768.9	1,519.8	1,518.8	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-59	sp|Q92547|TOPB1_HUMAN	FNQLNEDVTHVIVGDYDDELK	69.78	Unmodified	Light	2	1232.0874

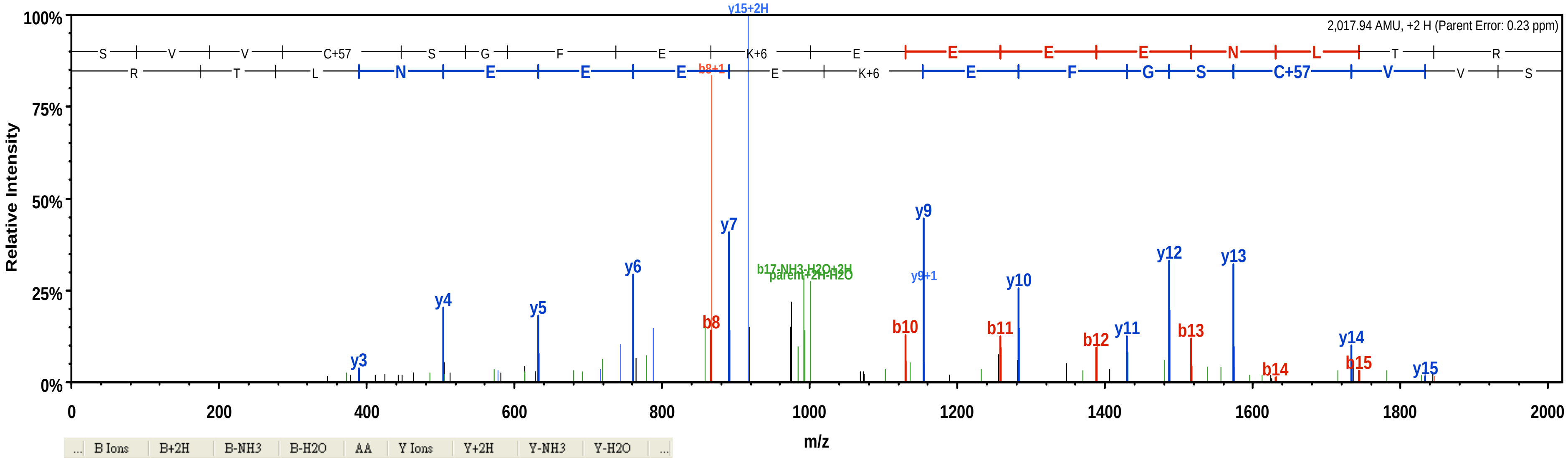


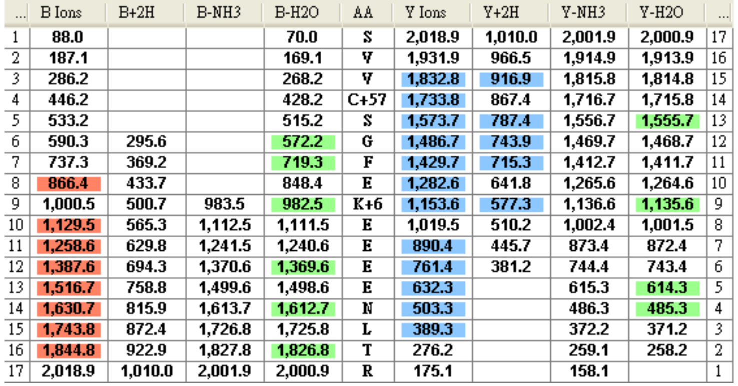


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.1				F	2,463.2	1,232.1	2,446.1	2,445.2	21
2	262.1		245.1		N	2,316.1	1,158.6	2,299.1	2,298.1	20
3	390.2		373.2		Q	2,202.1	1,101.5	2,185.0	2,184.0	19
4	503.3		486.2		L	2,074.0	1,037.5	2,057.0	2,056.0	18
5	617.3		600.3		N	1,960.9	981.0	1,943.9	1,942.9	17
6	746.3	373.7	729.3	728.3	E	1,846.9	923.9	1,829.8	1,828.9	16
7	861.4	431.2	844.3	843.4	D	1,717.8	859.4	1,700.8	1,699.8	15
8	960.4	480.7	943.4	942.4	V	1,602.8	801.9	1,585.8	1,584.8	14
9	1,061.5	531.2	1,044.5	1,043.5	T	1,503.7	752.4	1,486.7	1,485.7	13
10	1,198.5	599.8	1,181.5	1,180.5	H	1,402.7	701.8	1,385.7	1,384.7	12
11	1,297.6	649.3	1,280.6	1,279.6	V	1,265.6	633.3	1,248.6	1,247.6	11
12	1,410.7	705.9	1,393.7	1,392.7	I	1,166.6	583.8	1,149.5	1,148.5	10
13	1,509.8	755.4	1,492.7	1,491.8	V	1,053.5	527.2	1,036.4	1,035.5	9
14	1,566.8	783.9	1,549.8	1,548.8	G	954.4	477.7	937.4	936.4	8
15	1,681.8	841.4	1,664.8	1,663.8	D	897.4	449.2	880.4	879.4	7
16	1,844.9	922.9	1,827.9	1,826.9	Y	782.4	391.7	765.3	764.3	6
17	1,959.9	980.5	1,942.9	1,941.9	D	619.3		602.3	601.3	5
18	2,074.9	1,038.0	2,057.9	2,056.9	D	504.3		487.2	486.3	4
19	2,204.0	1,102.5	2,187.0	2,186.0	E	389.2		372.2	371.2	3
20	2,317.1	1,159.0	2,300.0	2,299.1	L	260.2		243.2		2
21	2,463.2	1,232.1	2,446.1	2,445.2	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-60	sp|P56277|MTCPA_HUMAN	SVVCSGFEKEEEENLTR	69.48	Unmodified	Heavy	2	1006.9651

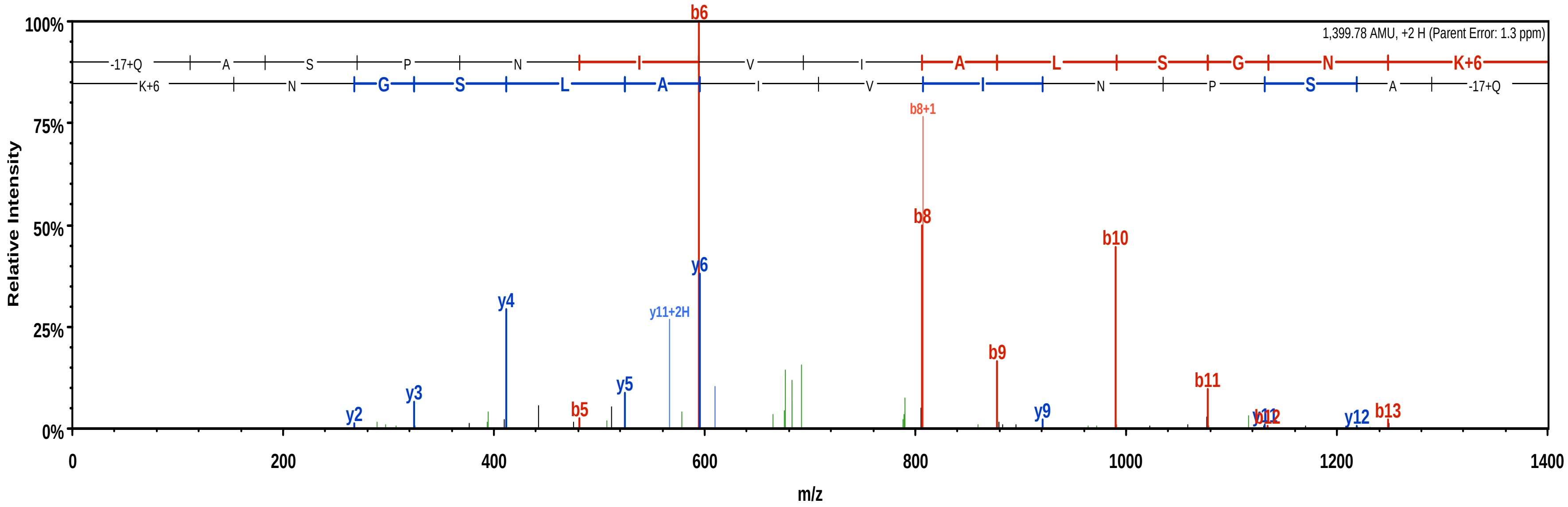


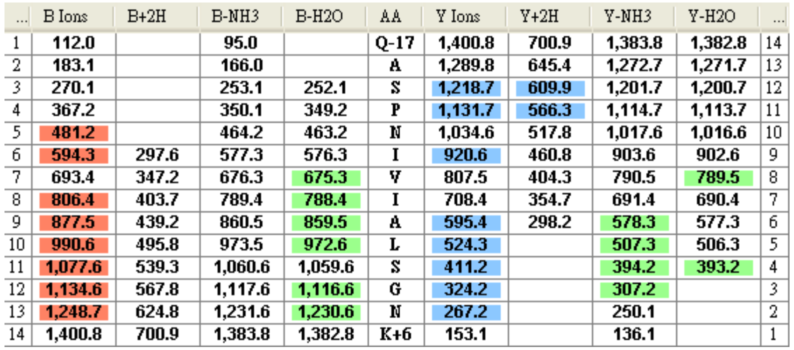


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	2,018.9	1,010.0	2,001.9	2,000.9	17
2	187.1			169.1	V	1,931.9	966.5	1,914.9	1,913.9	16
3	286.2			268.2	V	1,832.8	916.9	1,815.8	1,814.8	15
4	446.2			428.2	C+57	1,733.8	867.4	1,716.7	1,715.8	14
5	533.2			515.2	S	1,573.7	787.4	1,556.7	1,555.7	13
6	590.3	295.6		572.2	G	1,486.7	743.9	1,469.7	1,468.7	12
7	737.3	369.2		719.3	F	1,429.7	715.3	1,412.7	1,411.7	11
8	866.4	433.7		848.4	E	1,282.6	641.8	1,265.6	1,264.6	10
9	1,000.5	500.7	983.5	982.5	K+6	1,153.6	577.3	1,136.6	1,135.6	9
10	1,129.5	565.3	1,112.5	1,111.5	E	1,019.5	510.2	1,002.4	1,001.5	8
11	1,258.6	629.8	1,241.5	1,240.6	E	890.4	445.7	873.4	872.4	7
12	1,387.6	694.3	1,370.6	1,369.6	E	761.4	381.2	744.4	743.4	6
13	1,516.7	758.8	1,499.6	1,498.6	E	632.3		615.3	614.3	5
14	1,630.7	815.9	1,613.7	1,612.7	N	503.3		486.3	485.3	4
15	1,743.8	872.4	1,726.8	1,725.8	L	389.3		372.2	371.2	3
16	1,844.8	922.9	1,827.8	1,826.8	T	276.2		259.1	258.2	2
17	2,018.9	1,010.0	2,001.9	2,000.9	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-61	sp|P20339|RAB5A_HUMAN	QASPNIVIALSGNK	69.14	Gln->pyro-Glu (N-term Q)	Heavy	2	697.88554

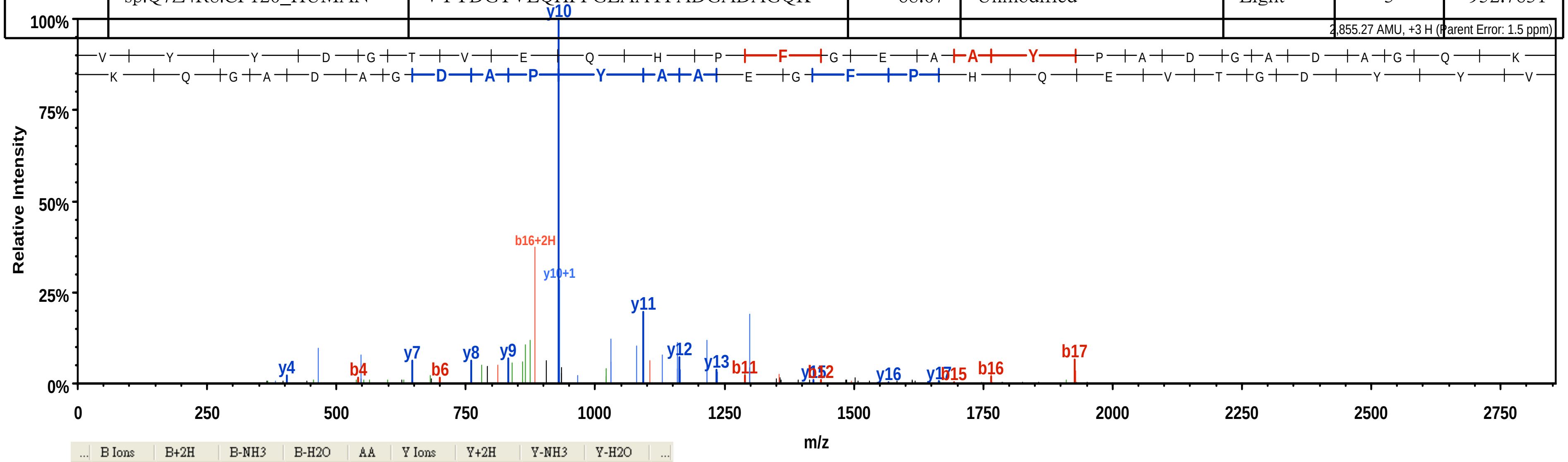


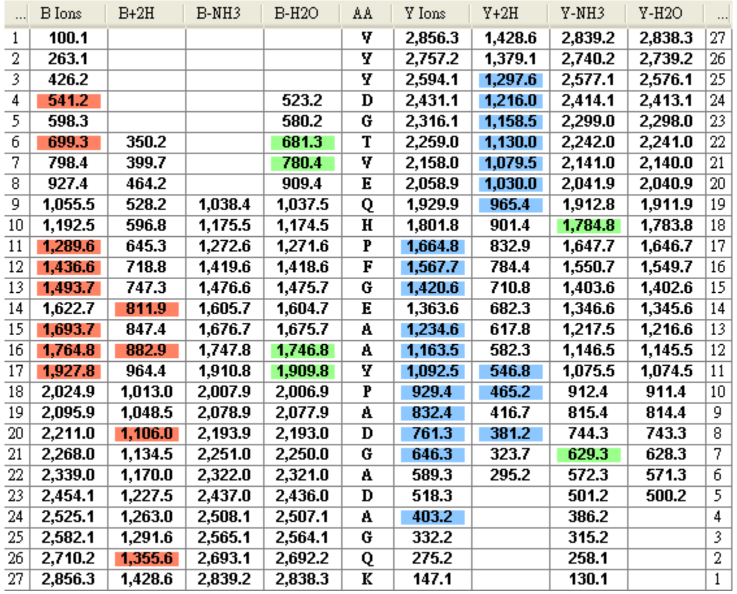


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	1,400.8	700.9	1,383.8	1,382.8	14
2	183.1		166.0		A	1,289.8	645.4	1,272.7	1,271.7	13
3	270.1		253.1	252.1	S	1,218.7	609.9	1,201.7	1,200.7	12
4	367.2		350.1	349.2	P	1,131.7	566.3	1,114.7	1,113.7	11
5	481.2		464.2	463.2	N	1,034.6	517.8	1,017.6	1,016.6	10
6	594.3	297.6	577.3	576.3	I	920.6	460.8	903.6	902.6	9
7	693.4	347.2	676.3	675.3	V	807.5	404.3	790.5	789.5	8
8	806.4	403.7	789.4	788.4	I	708.4	354.7	691.4	690.4	7
9	877.5	439.2	860.5	859.5	A	595.4	298.2	578.3	577.3	6
10	990.6	495.8	973.5	972.6	L	524.3		507.3	506.3	5
11	1,077.6	539.3	1,060.6	1,059.6	S	411.2		394.2	393.2	4
12	1,134.6	567.8	1,117.6	1,116.6	G	324.2		307.2		3
13	1,248.7	624.8	1,231.6	1,230.6	N	267.2		250.1		2
14	1,400.8	700.9	1,383.8	1,382.8	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-62	splQ7Z4R8lCF120_HUMAN	VYYDGTVEQHPFGEAAYPADGADAGQK	68.07	Unmodified	Light	3	952.7631

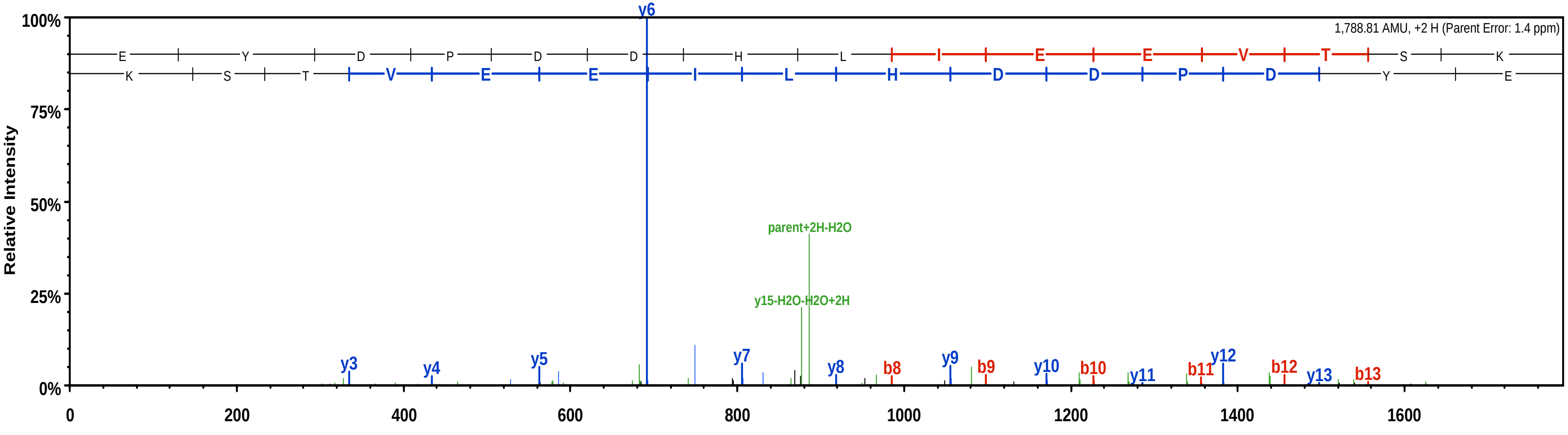


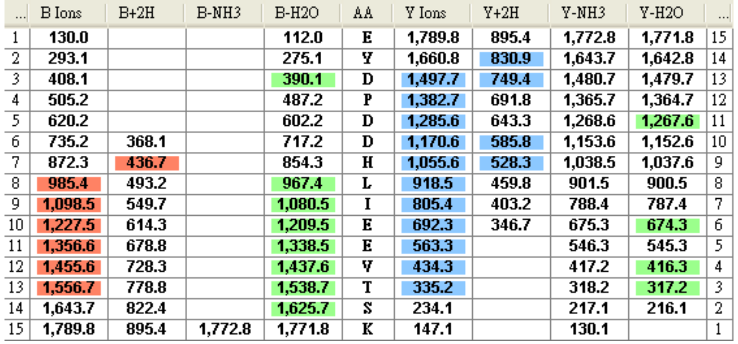


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	2,856.3	1,428.6	2,839.2	2,838.3	27
2	263.1				Y	2,757.2	1,379.1	2,740.2	2,739.2	26
3	426.2				Y	2,594.1	1,297.6	2,577.1	2,576.1	25
4	541.2			523.2	D	2,431.1	1,216.0	2,414.1	2,413.1	24
5	598.3			580.2	G	2,316.1	1,158.5	2,299.0	2,298.0	23
6	699.3	350.2		681.3	T	2,259.0	1,130.0	2,242.0	2,241.0	22
7	798.4	399.7		780.4	V	2,158.0	1,079.5	2,141.0	2,140.0	21
8	927.4	464.2		909.4	E	2,058.9	1,030.0	2,041.9	2,040.9	20
9	1,055.5	528.2	1,038.4	1,037.5	Q	1,929.9	965.4	1,912.8	1,911.9	19
10	1,192.5	596.8	1,175.5	1,174.5	H	1,801.8	901.4	1,784.8	1,783.8	18
11	1,289.6	645.3	1,272.6	1,271.6	P	1,664.8	832.9	1,647.7	1,646.7	17
12	1,436.6	718.8	1,419.6	1,418.6	F	1,567.7	784.4	1,550.7	1,549.7	16
13	1,493.7	747.3	1,476.6	1,475.7	G	1,420.6	710.8	1,403.6	1,402.6	15
14	1,622.7	811.9	1,605.7	1,604.7	E	1,363.6	682.3	1,346.6	1,345.6	14
15	1,693.7	847.4	1,676.7	1,675.7	A	1,234.6	617.8	1,217.5	1,216.6	13
16	1,764.8	882.9	1,747.8	1,746.8	A	1,163.5	582.3	1,146.5	1,145.5	12
17	1,927.8	964.4	1,910.8	1,909.8	Y	1,092.5	546.8	1,075.5	1,074.5	11
18	2,024.9	1,013.0	2,007.9	2,006.9	P	929.4	465.2	912.4	911.4	10
19	2,095.9	1,048.5	2,078.9	2,077.9	A	832.4	416.7	815.4	814.4	9
20	2,211.0	1,106.0	2,193.9	2,193.0	D	761.3	381.2	744.3	743.3	8
21	2,268.0	1,134.5	2,251.0	2,250.0	G	646.3	323.7	629.3	628.3	7
22	2,339.0	1,170.0	2,322.0	2,321.0	A	589.3	295.2	572.3	571.3	6
23	2,454.1	1,227.5	2,437.0	2,436.0	D	518.3		501.2	500.2	5
24	2,525.1	1,263.0	2,508.1	2,507.1	A	403.2		386.2		4
25	2,582.1	1,291.6	2,565.1	2,564.1	G	332.2		315.2		3
26	2,710.2	1,355.6	2,693.1	2,692.2	Q	275.2		258.1		2
27	2,856.3	1,428.6	2,839.2	2,838.3	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-63	sp|Q9NV66|TYW1_HUMAN	EYDPDDHLIEEVTSK	67.72	Unmodified	Light	2	895.40997

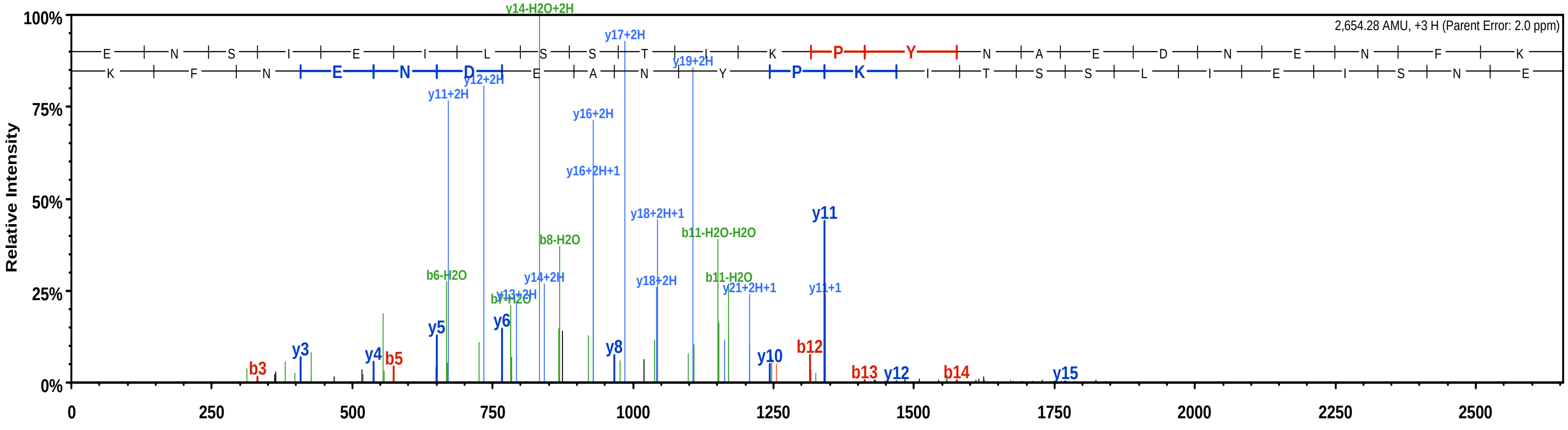


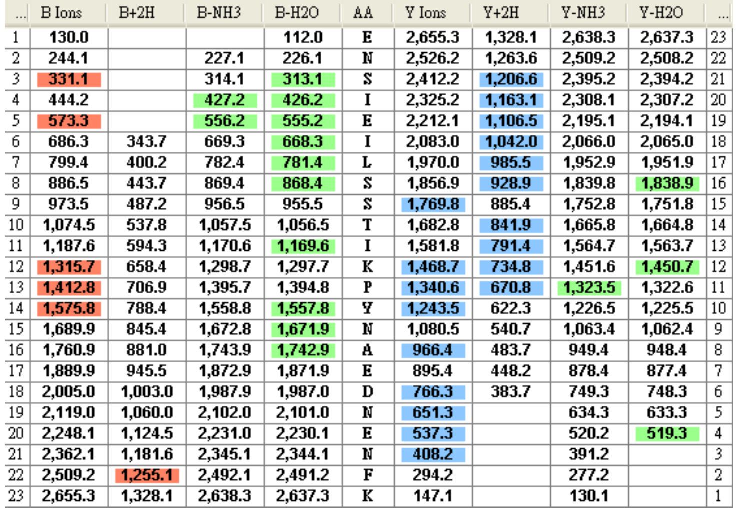


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	1,789.8	895.4	1,772.8	1,771.8	15
2	293.1			275.1	Y	1,660.8	830.9	1,643.7	1,642.8	14
3	408.1			390.1	D	1,497.7	749.4	1,480.7	1,479.7	13
4	505.2			487.2	P	1,382.7	691.8	1,365.7	1,364.7	12
5	620.2			602.2	D	1,285.6	643.3	1,268.6	1,267.6	11
6	735.2	368.1		717.2	D	1,170.6	585.8	1,153.6	1,152.6	10
7	872.3	436.7		854.3	H	1,055.6	528.3	1,038.5	1,037.6	9
8	985.4	493.2		967.4	L	918.5	459.8	901.5	900.5	8
9	1,098.5	549.7		1,080.5	I	805.4	403.2	788.4	787.4	7
10	1,227.5	614.3		1,209.5	E	692.3	346.7	675.3	674.3	6
11	1,356.6	678.8		1,338.5	E	563.3		546.3	545.3	5
12	1,455.6	728.3		1,437.6	V	434.3		417.2	416.3	4
13	1,556.7	778.8		1,538.7	T	335.2		318.2	317.2	3
14	1,643.7	822.4		1,625.7	S	234.1		217.1	216.1	2
15	1,789.8	895.4	1,772.8	1,771.8	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-64	sp|Q9NWV4|CA123_HUMAN	ENSIEILSSTIKPYNAEDNENFK	66.21	Unmodified	Light	3	885.76433

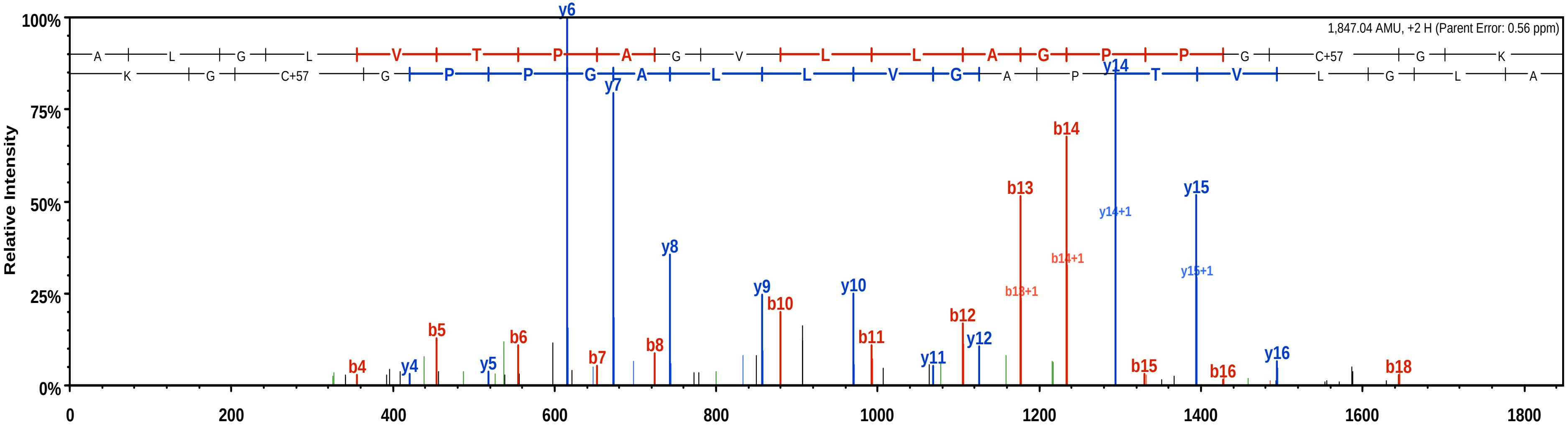


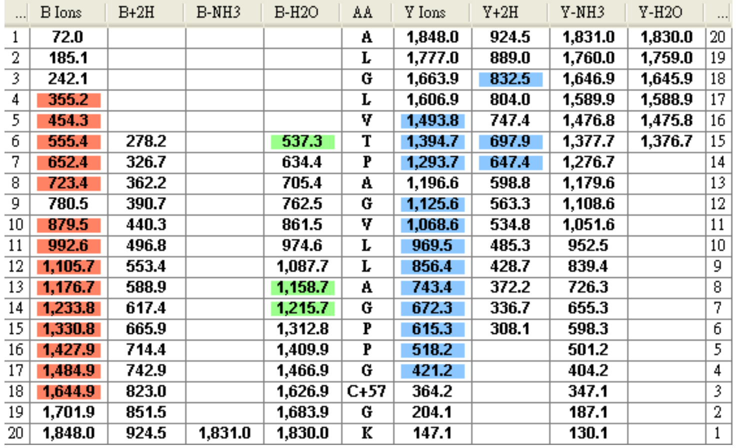


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	2,655.3	1,328.1	2,638.3	2,637.3	23
2	244.1		227.1	226.1	N	2,526.2	1,263.6	2,509.2	2,508.2	22
3	331.1		314.1	313.1	S	2,412.2	1,206.6	2,395.2	2,394.2	21
4	444.2		427.2	426.2	I	2,325.2	1,163.1	2,308.1	2,307.2	20
5	573.3		556.2	555.2	E	2,212.1	1,106.5	2,195.1	2,194.1	19
6	686.3	343.7	669.3	668.3	I	2,083.0	1,042.0	2,066.0	2,065.0	18
7	799.4	400.2	782.4	781.4	L	1,970.0	985.5	1,952.9	1,951.9	17
8	886.5	443.7	869.4	868.4	S	1,856.9	928.9	1,839.8	1,838.9	16
9	973.5	487.2	956.5	955.5	S	1,769.8	885.4	1,752.8	1,751.8	15
10	1,074.5	537.8	1,057.5	1,056.5	T	1,682.8	841.9	1,665.8	1,664.8	14
11	1,187.6	594.3	1,170.6	1,169.6	I	1,581.8	791.4	1,564.7	1,563.7	13
12	1,315.7	658.4	1,298.7	1,297.7	K	1,468.7	734.8	1,451.6	1,450.7	12
13	1,412.8	706.9	1,395.7	1,394.8	P	1,340.6	670.8	1,323.5	1,322.6	11
14	1,575.8	788.4	1,558.8	1,557.8	Y	1,243.5	622.3	1,226.5	1,225.5	10
15	1,689.9	845.4	1,672.8	1,671.9	N	1,080.5	540.7	1,063.4	1,062.4	9
16	1,760.9	881.0	1,743.9	1,742.9	A	966.4	483.7	949.4	948.4	8
17	1,889.9	945.5	1,872.9	1,871.9	E	895.4	448.2	878.4	877.4	7
18	2,005.0	1,003.0	1,987.9	1,987.0	D	766.3	383.7	749.3	748.3	6
19	2,119.0	1,060.0	2,102.0	2,101.0	N	651.3		634.3	633.3	5
20	2,248.1	1,124.5	2,231.0	2,230.1	E	537.3		520.2	519.3	4
21	2,362.1	1,181.6	2,345.1	2,344.1	N	408.2		391.2		3
22	2,509.2	1,255.1	2,492.1	2,491.2	F	294.2		277.2		2
23	2,655.3	1,328.1	2,638.3	2,637.3	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-65	sp|O15381|NVL_HUMAN	ALGLVTPAGVLLAGPPGCGK	65.54	Unmodified	Light	2	924.52422

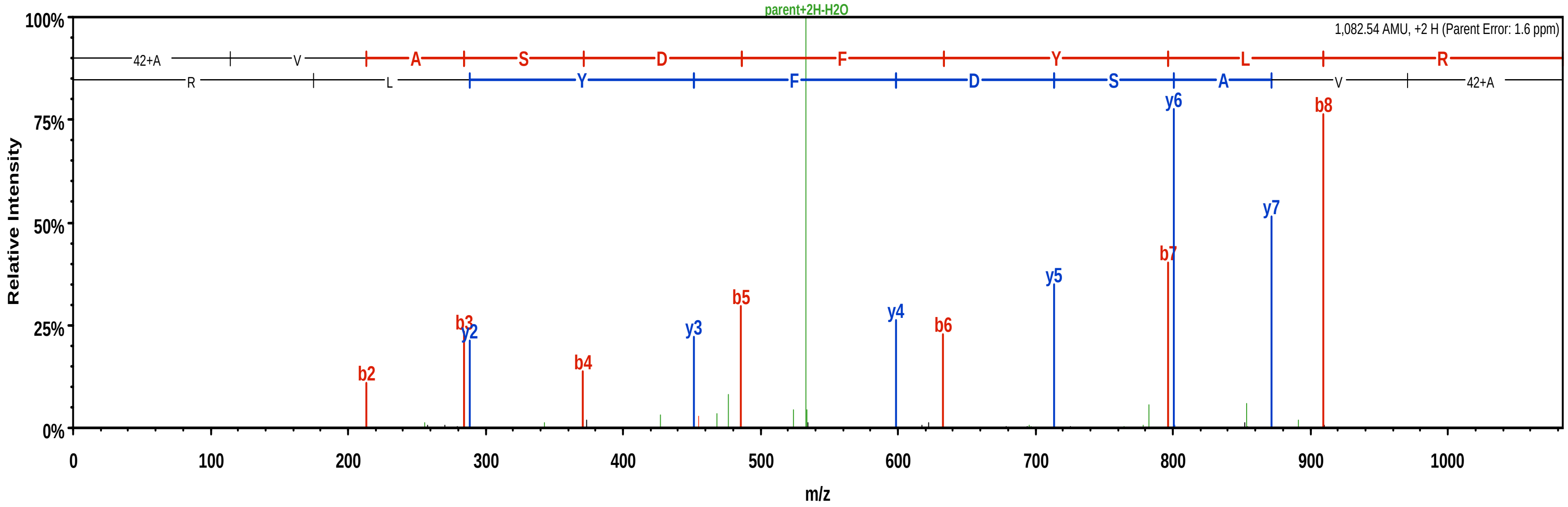


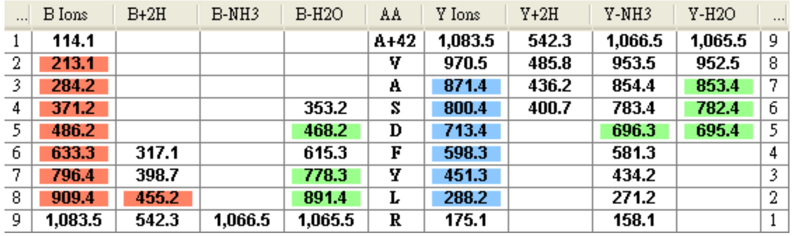


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	1,848.0	924.5	1,831.0	1,830.0	20
2	185.1				L	1,777.0	889.0	1,760.0	1,759.0	19
3	242.1				G	1,663.9	832.5	1,646.9	1,645.9	18
4	355.2				L	1,606.9	804.0	1,589.9	1,588.9	17
5	454.3				V	1,493.8	747.4	1,476.8	1,475.8	16
6	555.4	278.2		537.3	T	1,394.7	697.9	1,377.7	1,376.7	15
7	652.4	326.7		634.4	P	1,293.7	647.4	1,276.7		14
8	723.4	362.2		705.4	A	1,196.6	598.8	1,179.6		13
9	780.5	390.7		762.5	G	1,125.6	563.3	1,108.6		12
10	879.5	440.3		861.5	V	1,068.6	534.8	1,051.6		11
11	992.6	496.8		974.6	L	969.5	485.3	952.5		10
12	1,105.7	553.4		1,087.7	L	856.4	428.7	839.4		9
13	1,176.7	588.9		1,158.7	A	743.4	372.2	726.3		8
14	1,233.8	617.4		1,215.7	G	672.3	336.7	655.3		7
15	1,330.8	665.9		1,312.8	P	615.3	308.1	598.3		6
16	1,427.9	714.4		1,409.9	P	518.2		501.2		5
17	1,484.9	742.9		1,466.9	G	421.2		404.2		4
18	1,644.9	823.0		1,626.9	C+57	364.2		347.1		3
19	1,701.9	851.5		1,683.9	G	204.1		187.1		2
20	1,848.0	924.5	1,831.0	1,830.0	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-66	sp|Q96A72|MGN2_HUMAN	AVASDFYLR	65	Acetyl (Protein N-term)		2	542.27711

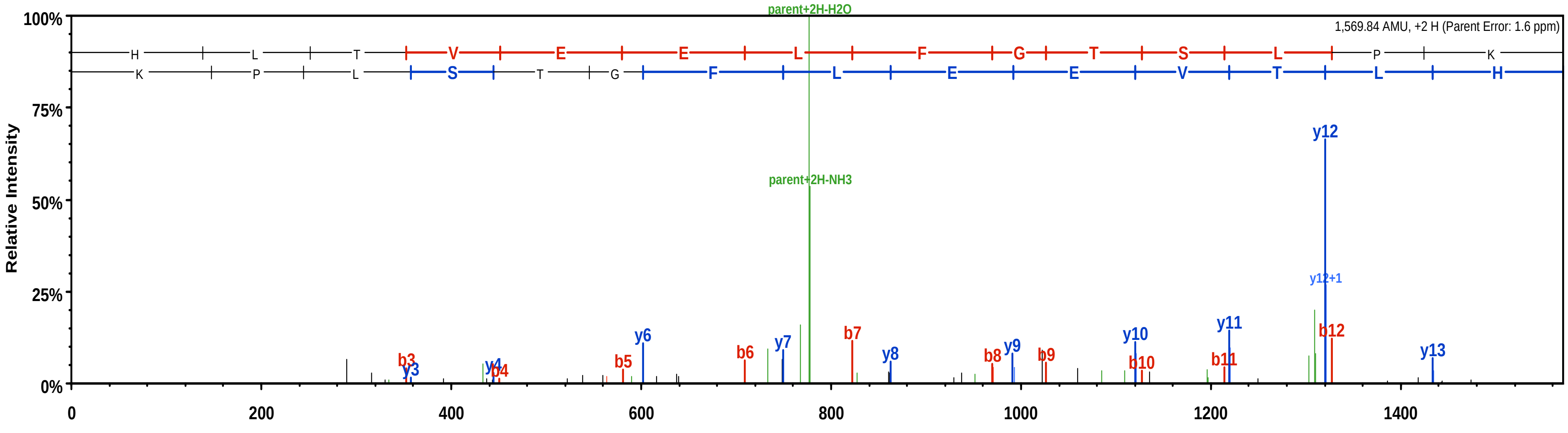


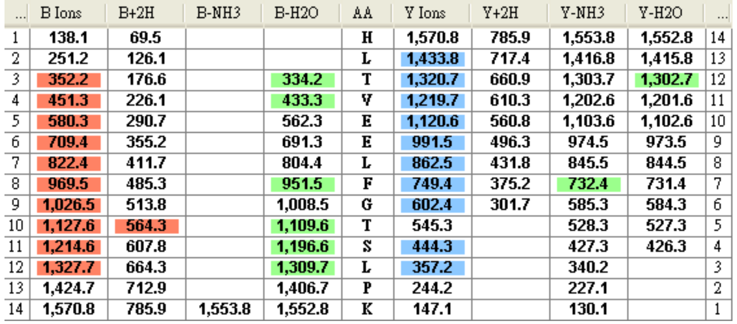


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	1,083.5	542.3	1,066.5	1,065.5	9
2	213.1				V	970.5	485.8	953.5	952.5	8
3	284.2				A	871.4	436.2	854.4	853.4	7
4	371.2			353.2	S	800.4	400.7	783.4	782.4	6
5	486.2			468.2	D	713.4		696.3	695.4	5
6	633.3	317.1		615.3	F	598.3		581.3		4
7	796.4	398.7		778.3	Y	451.3		434.2		3
8	909.4	455.2		891.4	L	288.2		271.2		2
9	1,083.5	542.3	1,066.5	1,065.5	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-67	sp|Q9NPI6|DCP1A_HUMAN	HLTVEELFGTSLPK	63.36	Unmodified	Light	2	785.92741

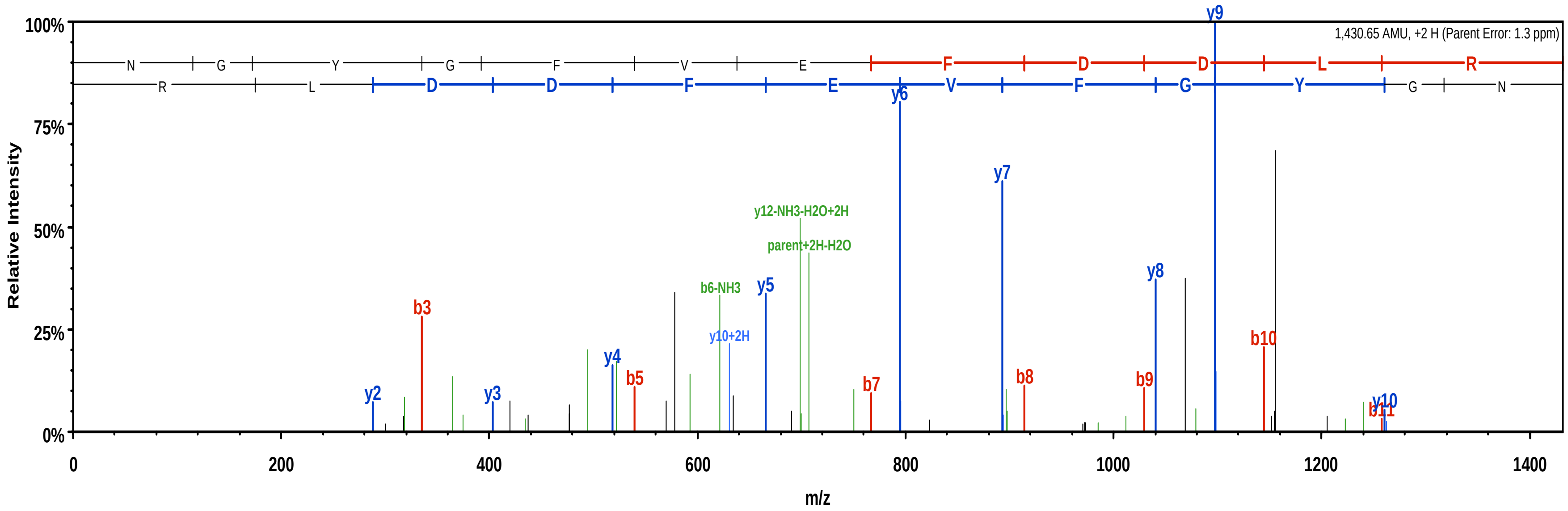


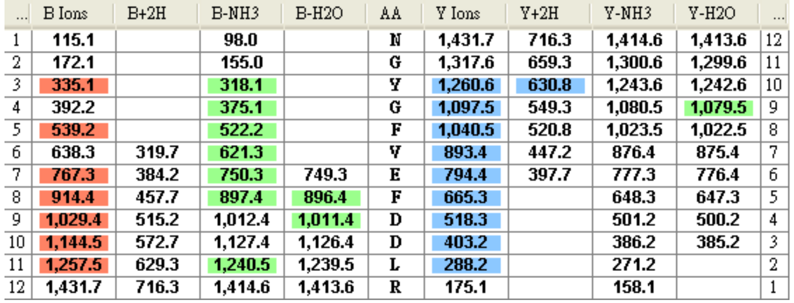


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	138.1	69.5			H	1,570.8	785.9	1,553.8	1,552.8	14
2	251.2	126.1			L	1,433.8	717.4	1,416.8	1,415.8	13
3	352.2	176.6		334.2	T	1,320.7	660.9	1,303.7	1,302.7	12
4	451.3	226.1		433.3	V	1,219.7	610.3	1,202.6	1,201.6	11
5	580.3	290.7		562.3	E	1,120.6	560.8	1,103.6	1,102.6	10
6	709.4	355.2		691.3	E	991.5	496.3	974.5	973.5	9
7	822.4	411.7		804.4	L	862.5	431.8	845.5	844.5	8
8	969.5	485.3		951.5	F	749.4	375.2	732.4	731.4	7
9	1,026.5	513.8		1,008.5	G	602.4	301.7	585.3	584.3	6
10	1,127.6	564.3		1,109.6	T	545.3		528.3	527.3	5
11	1,214.6	607.8		1,196.6	S	444.3		427.3	426.3	4
12	1,327.7	664.3		1,309.7	L	357.2		340.2		3
13	1,424.7	712.9		1,406.7	P	244.2		227.1		2
14	1,570.8	785.9	1,553.8	1,552.8	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-68	sp|Q08170|SFRS4_HUMAN	NGYGFVEFDDLR	62.78	Unmodified		2	716.3306

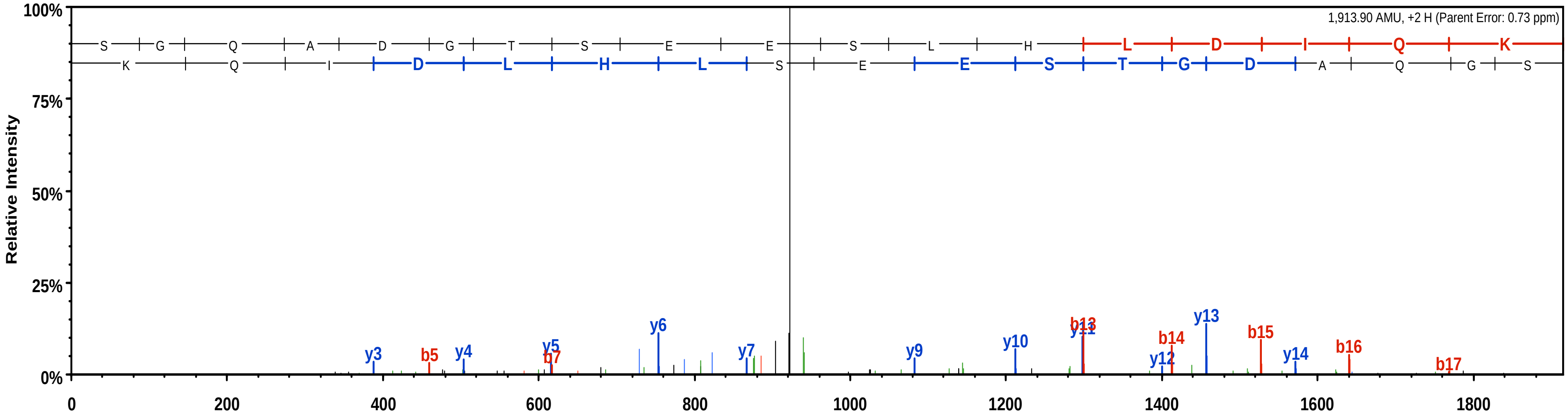


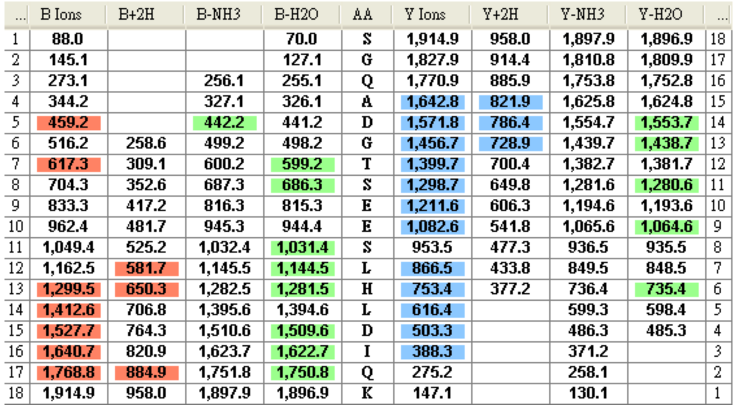


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	115.1		98.0		N	1,431.7	716.3	1,414.6	1,413.6	12
2	172.1		155.0		G	1,317.6	659.3	1,300.6	1,299.6	11
3	335.1		318.1		Y	1,260.6	630.8	1,243.6	1,242.6	10
4	392.2		375.1		G	1,097.5	549.3	1,080.5	1,079.5	9
5	539.2		522.2		F	1,040.5	520.8	1,023.5	1,022.5	8
6	638.3	319.7	621.3		V	893.4	447.2	876.4	875.4	7
7	767.3	384.2	750.3	749.3	E	794.4	397.7	777.3	776.4	6
8	914.4	457.7	897.4	896.4	F	665.3		648.3	647.3	5
9	1,029.4	515.2	1,012.4	1,011.4	D	518.3		501.2	500.2	4
10	1,144.5	572.7	1,127.4	1,126.4	D	403.2		386.2	385.2	3
11	1,257.5	629.3	1,240.5	1,239.5	L	288.2		271.2		2
12	1,431.7	716.3	1,414.6	1,413.6	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-69	sp|Q1ZZU3|CI119_HUMAN	SGQADGTSEESLHLDIQK	61.22	Unmodified	Light	2	957.95561

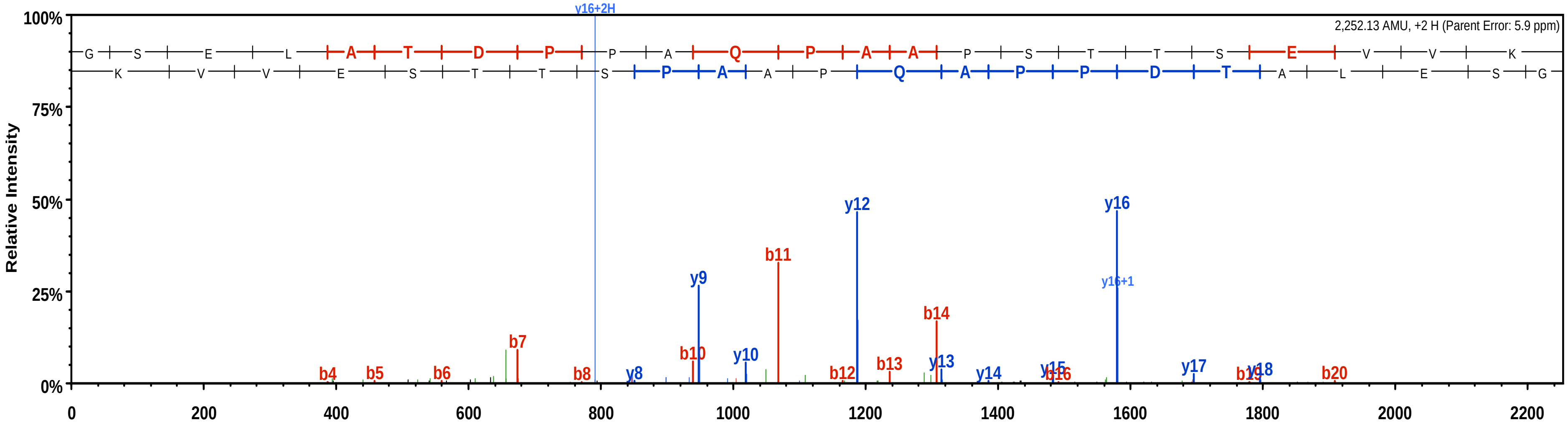


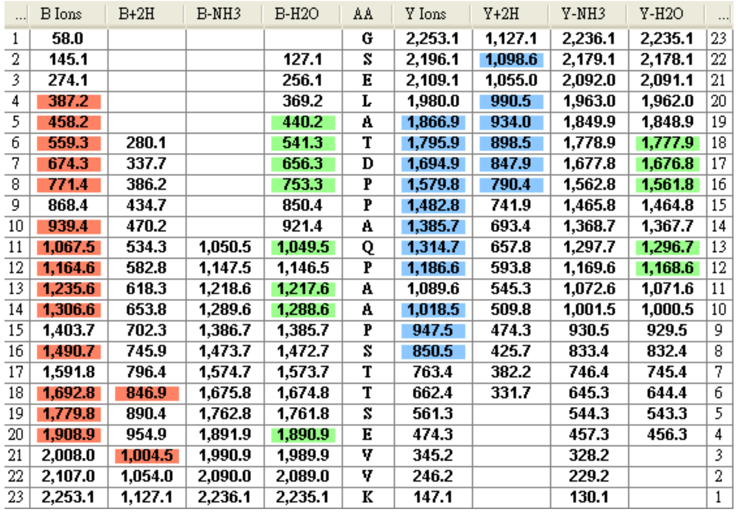


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	1,914.9	958.0	1,897.9	1,896.9	18
2	145.1			127.1	G	1,827.9	914.4	1,810.8	1,809.9	17
3	273.1		256.1	255.1	Q	1,770.9	885.9	1,753.8	1,752.8	16
4	344.2		327.1	326.1	A	1,642.8	821.9	1,625.8	1,624.8	15
5	459.2		442.2	441.2	D	1,571.8	786.4	1,554.7	1,553.7	14
6	516.2	258.6	499.2	498.2	G	1,456.7	728.9	1,439.7	1,438.7	13
7	617.3	309.1	600.2	599.2	T	1,399.7	700.4	1,382.7	1,381.7	12
8	704.3	352.6	687.3	686.3	S	1,298.7	649.8	1,281.6	1,280.6	11
9	833.3	417.2	816.3	815.3	E	1,211.6	606.3	1,194.6	1,193.6	10
10	962.4	481.7	945.3	944.4	E	1,082.6	541.8	1,065.6	1,064.6	9
11	1,049.4	525.2	1,032.4	1,031.4	S	953.5	477.3	936.5	935.5	8
12	1,162.5	581.7	1,145.5	1,144.5	L	866.5	433.8	849.5	848.5	7
13	1,299.5	650.3	1,282.5	1,281.5	H	753.4	377.2	736.4	735.4	6
14	1,412.6	706.8	1,395.6	1,394.6	L	616.4		599.3	598.4	5
15	1,527.7	764.3	1,510.6	1,509.6	D	503.3		486.3	485.3	4
16	1,640.7	820.9	1,623.7	1,622.7	I	388.3		371.2		3
17	1,768.8	884.9	1,751.8	1,750.8	Q	275.2		258.1		2
18	1,914.9	958.0	1,897.9	1,896.9	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-70	sp|O00562|PITM1_HUMAN	GSELATDPPAQPAAPSTTSEVVK	61.15	Unmodified	Light	2	1127.0659

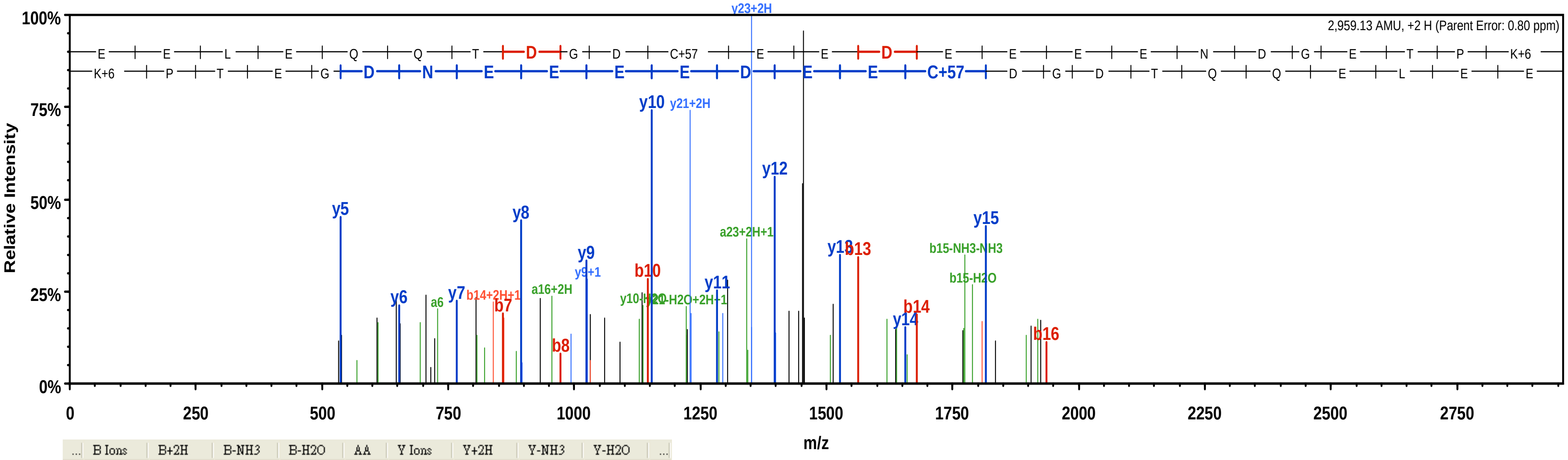


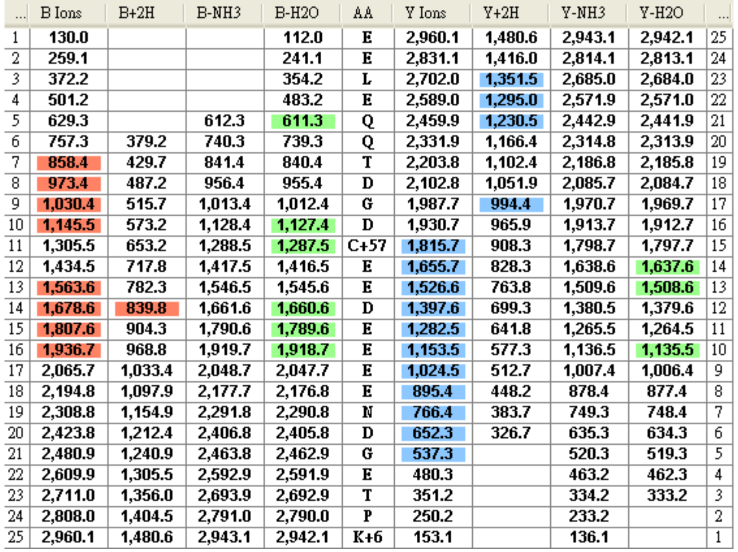


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	2,253.1	1,127.1	2,236.1	2,235.1	23
2	145.1			127.1	S	2,196.1	1,098.6	2,179.1	2,178.1	22
3	274.1			256.1	E	2,109.1	1,055.0	2,092.0	2,091.1	21
4	387.2			369.2	L	1,980.0	990.5	1,963.0	1,962.0	20
5	458.2			440.2	A	1,866.9	934.0	1,849.9	1,848.9	19
6	559.3	280.1		541.3	T	1,795.9	898.5	1,778.9	1,777.9	18
7	674.3	337.7		656.3	D	1,694.9	847.9	1,677.8	1,676.8	17
8	771.4	386.2		753.3	P	1,579.8	790.4	1,562.8	1,561.8	16
9	868.4	434.7		850.4	P	1,482.8	741.9	1,465.8	1,464.8	15
10	939.4	470.2		921.4	A	1,385.7	693.4	1,368.7	1,367.7	14
11	1,067.5	534.3	1,050.5	1,049.5	Q	1,314.7	657.8	1,297.7	1,296.7	13
12	1,164.6	582.8	1,147.5	1,146.5	P	1,186.6	593.8	1,169.6	1,168.6	12
13	1,235.6	618.3	1,218.6	1,217.6	A	1,089.6	545.3	1,072.6	1,071.6	11
14	1,306.6	653.8	1,289.6	1,288.6	A	1,018.5	509.8	1,001.5	1,000.5	10
15	1,403.7	702.3	1,386.7	1,385.7	P	947.5	474.3	930.5	929.5	9
16	1,490.7	745.9	1,473.7	1,472.7	S	850.5	425.7	833.4	832.4	8
17	1,591.8	796.4	1,574.7	1,573.7	T	763.4	382.2	746.4	745.4	7
18	1,692.8	846.9	1,675.8	1,674.8	T	662.4	331.7	645.3	644.4	6
19	1,779.8	890.4	1,762.8	1,761.8	S	561.3		544.3	543.3	5
20	1,908.9	954.9	1,891.9	1,890.9	E	474.3		457.3	456.3	4
21	2,008.0	1,004.5	1,990.9	1,989.9	V	345.2		328.2		3
22	2,107.0	1,054.0	2,090.0	2,089.0	V	246.2		229.2		2
23	2,253.1	1,127.1	2,236.1	2,235.1	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-71	sp|Q99442|SEC62_HUMAN	EELEQQTDGDCEEDEEEENDGETPK	61.13	Unmodified	Heavy	2	1477.5598

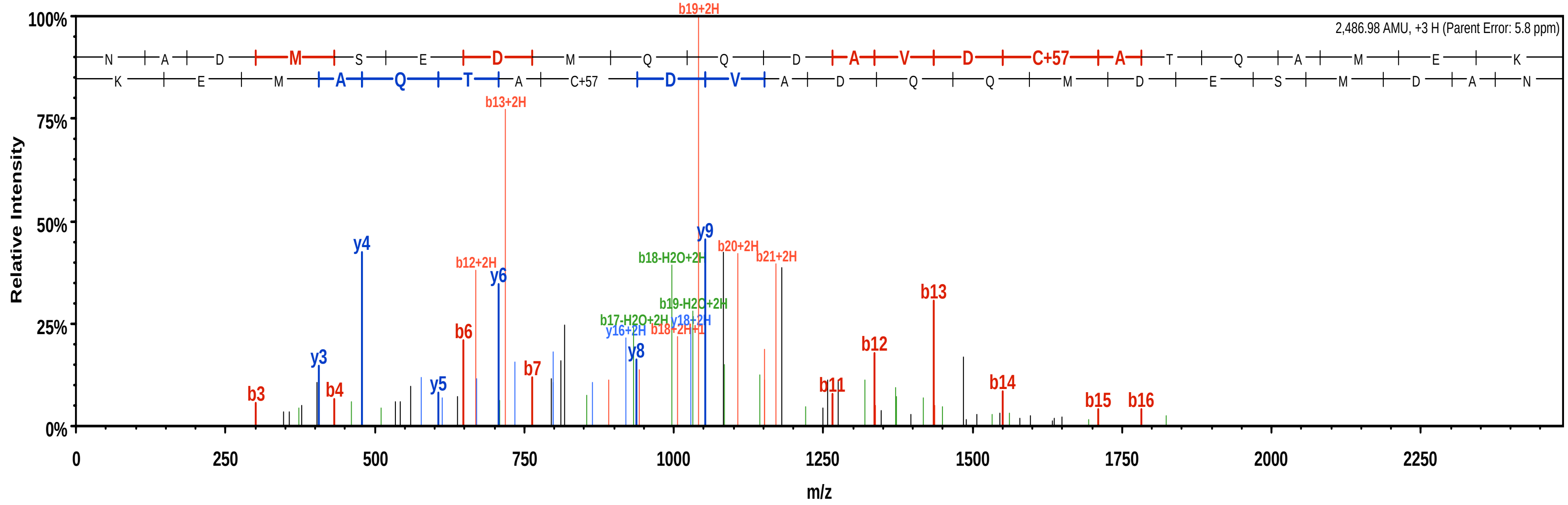


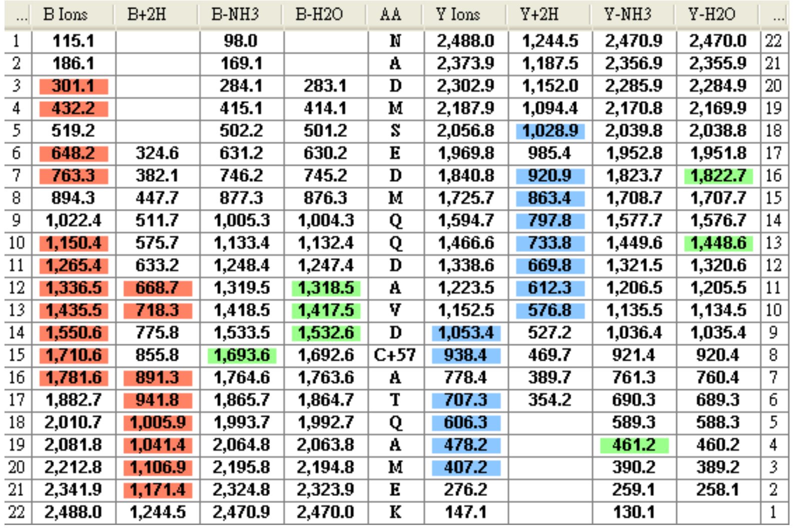


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	2,960.1	1,480.6	2,943.1	2,942.1	25
2	259.1			241.1	E	2,831.1	1,416.0	2,814.1	2,813.1	24
3	372.2			354.2	L	2,702.0	1,351.5	2,685.0	2,684.0	23
4	501.2			483.2	E	2,589.0	1,295.0	2,571.9	2,571.0	22
5	629.3		612.3	611.3	Q	2,459.9	1,230.5	2,442.9	2,441.9	21
6	757.3	379.2	740.3	739.3	Q	2,331.9	1,166.4	2,314.8	2,313.9	20
7	858.4	429.7	841.4	840.4	T	2,203.8	1,102.4	2,186.8	2,185.8	19
8	973.4	487.2	956.4	955.4	D	2,102.8	1,051.9	2,085.7	2,084.7	18
9	1,030.4	515.7	1,013.4	1,012.4	G	1,987.7	994.4	1,970.7	1,969.7	17
10	1,145.5	573.2	1,128.4	1,127.4	D	1,930.7	965.9	1,913.7	1,912.7	16
11	1,305.5	653.2	1,288.5	1,287.5	C+57	1,815.7	908.3	1,798.7	1,797.7	15
12	1,434.5	717.8	1,417.5	1,416.5	E	1,655.7	828.3	1,638.6	1,637.6	14
13	1,563.6	782.3	1,546.5	1,545.6	E	1,526.6	763.8	1,509.6	1,508.6	13
14	1,678.6	839.8	1,661.6	1,660.6	D	1,397.6	699.3	1,380.5	1,379.6	12
15	1,807.6	904.3	1,790.6	1,789.6	E	1,282.5	641.8	1,265.5	1,264.5	11
16	1,936.7	968.8	1,919.7	1,918.7	E	1,153.5	577.3	1,136.5	1,135.5	10
17	2,065.7	1,033.4	2,048.7	2,047.7	E	1,024.5	512.7	1,007.4	1,006.4	9
18	2,194.8	1,097.9	2,177.7	2,176.8	E	895.4	448.2	878.4	877.4	8
19	2,308.8	1,154.9	2,291.8	2,290.8	N	766.4	383.7	749.3	748.4	7
20	2,423.8	1,212.4	2,406.8	2,405.8	D	652.3	326.7	635.3	634.3	6
21	2,480.9	1,240.9	2,463.8	2,462.9	G	537.3		520.3	519.3	5
22	2,609.9	1,305.5	2,592.9	2,591.9	E	480.3		463.2	462.3	4
23	2,711.0	1,356.0	2,693.9	2,692.9	T	351.2		334.2	333.2	3
24	2,808.0	1,404.5	2,791.0	2,790.0	P	250.2		233.2		2
25	2,960.1	1,480.6	2,943.1	2,942.1	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-72	sp|Q96FJ2|DYL2_HUMAN	NADMSEDMQQDAVDCATQAMEK	61.11	Unmodified	Light	3	829.99588

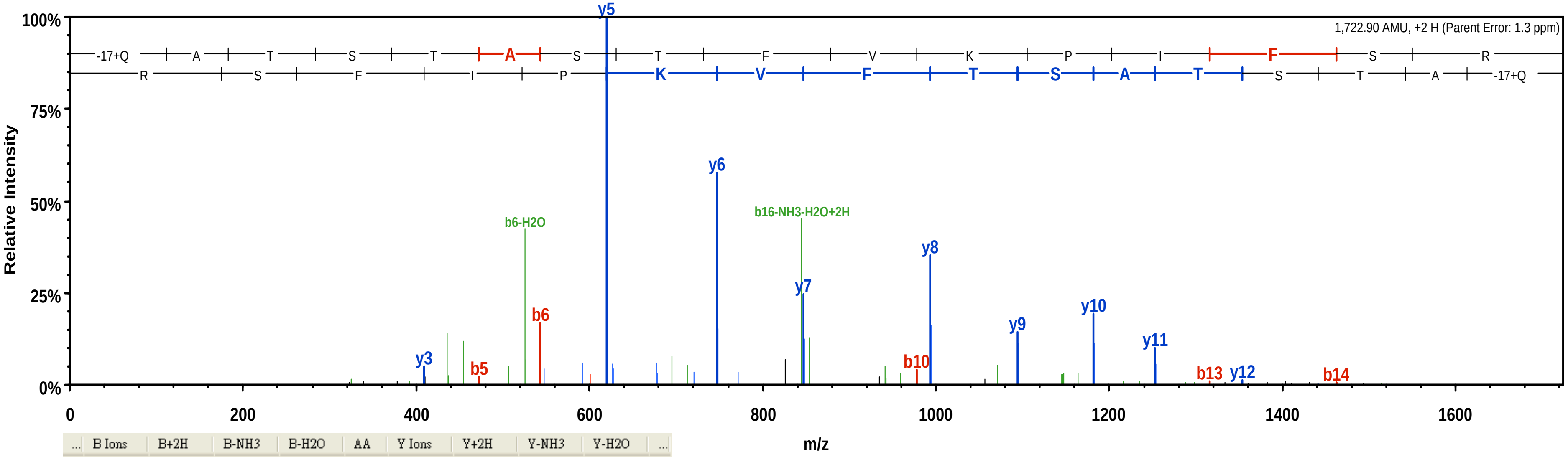


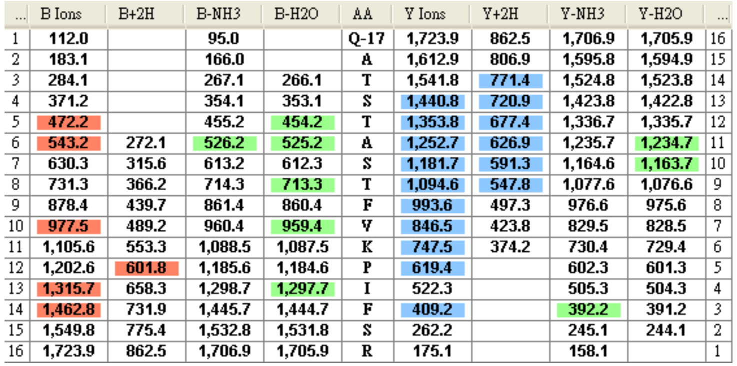


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	115.1		98.0		N	2,488.0	1,244.5	2,470.9	2,470.0	22
2	186.1		169.1		A	2,373.9	1,187.5	2,356.9	2,355.9	21
3	301.1		284.1	283.1	D	2,302.9	1,152.0	2,285.9	2,284.9	20
4	432.2		415.1	414.1	M	2,187.9	1,094.4	2,170.8	2,169.9	19
5	519.2		502.2	501.2	S	2,056.8	1,028.9	2,039.8	2,038.8	18
6	648.2	324.6	631.2	630.2	E	1,969.8	985.4	1,952.8	1,951.8	17
7	763.3	382.1	746.2	745.2	D	1,840.8	920.9	1,823.7	1,822.7	16
8	894.3	447.7	877.3	876.3	M	1,725.7	863.4	1,708.7	1,707.7	15
9	1,022.4	511.7	1,005.3	1,004.3	Q	1,594.7	797.8	1,577.7	1,576.7	14
10	1,150.4	575.7	1,133.4	1,132.4	Q	1,466.6	733.8	1,449.6	1,448.6	13
11	1,265.4	633.2	1,248.4	1,247.4	D	1,338.6	669.8	1,321.5	1,320.6	12
12	1,336.5	668.7	1,319.5	1,318.5	A	1,223.5	612.3	1,206.5	1,205.5	11
13	1,435.5	718.3	1,418.5	1,417.5	V	1,152.5	576.8	1,135.5	1,134.5	10
14	1,550.6	775.8	1,533.5	1,532.6	D	1,053.4	527.2	1,036.4	1,035.4	9
15	1,710.6	855.8	1,693.6	1,692.6	C+57	938.4	469.7	921.4	920.4	8
16	1,781.6	891.3	1,764.6	1,763.6	A	778.4	389.7	761.3	760.4	7
17	1,882.7	941.8	1,865.7	1,864.7	T	707.3	354.2	690.3	689.3	6
18	2,010.7	1,005.9	1,993.7	1,992.7	Q	606.3		589.3	588.3	5
19	2,081.8	1,041.4	2,064.8	2,063.8	A	478.2		461.2	460.2	4
20	2,212.8	1,106.9	2,195.8	2,194.8	M	407.2		390.2	389.2	3
21	2,341.9	1,171.4	2,324.8	2,323.9	E	276.2		259.1	258.1	2
22	2,488.0	1,244.5	2,470.9	2,470.0	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-73	sp|P56556|NDUA6_HUMAN	QATSTASTFVKPIFSR	60.94	Gln->pyro-Glu (N-term Q)	Heavy	2	862.45432

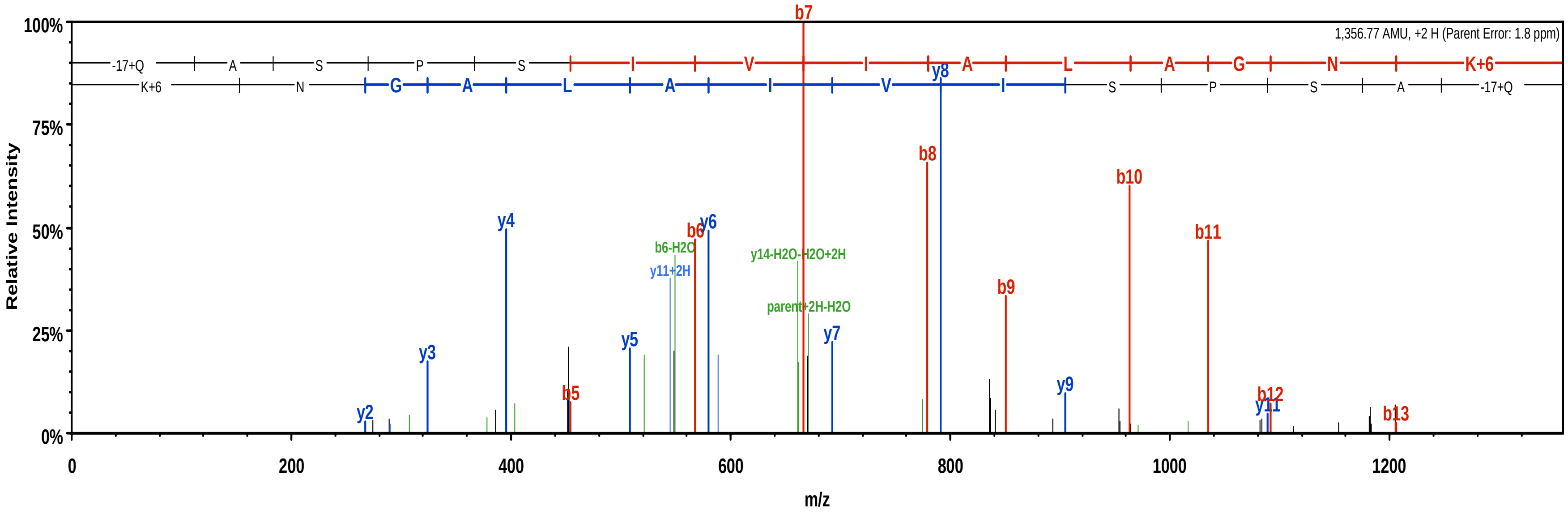


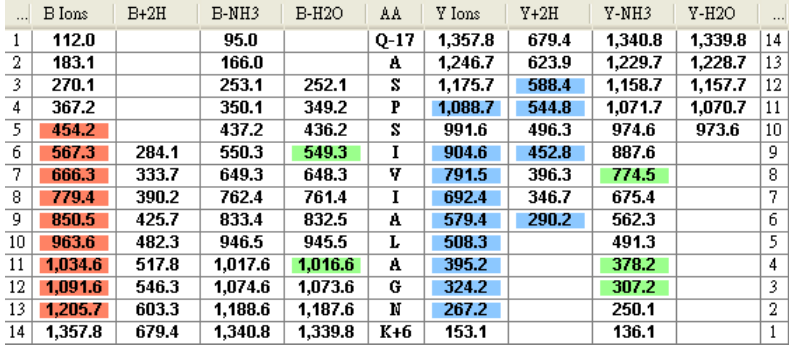


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	1,723.9	862.5	1,706.9	1,705.9	16
2	183.1		166.0		A	1,612.9	806.9	1,595.8	1,594.9	15
3	284.1		267.1	266.1	T	1,541.8	771.4	1,524.8	1,523.8	14
4	371.2		354.1	353.1	S	1,440.8	720.9	1,423.8	1,422.8	13
5	472.2		455.2	454.2	T	1,353.8	677.4	1,336.7	1,335.7	12
6	543.2	272.1	526.2	525.2	A	1,252.7	626.9	1,235.7	1,234.7	11
7	630.3	315.6	613.2	612.3	S	1,181.7	591.3	1,164.6	1,163.7	10
8	731.3	366.2	714.3	713.3	T	1,094.6	547.8	1,077.6	1,076.6	9
9	878.4	439.7	861.4	860.4	F	993.6	497.3	976.6	975.6	8
10	977.5	489.2	960.4	959.4	V	846.5	423.8	829.5	828.5	7
11	1,105.6	553.3	1,088.5	1,087.5	K	747.5	374.2	730.4	729.4	6
12	1,202.6	601.8	1,185.6	1,184.6	P	619.4		602.3	601.3	5
13	1,315.7	658.3	1,298.7	1,297.7	I	522.3		505.3	504.3	4
14	1,462.8	731.9	1,445.7	1,444.7	F	409.2		392.2	391.2	3
15	1,549.8	775.4	1,532.8	1,531.8	S	262.2		245.1	244.1	2
16	1,723.9	862.5	1,706.9	1,705.9	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-74	sp|P61020|RAB5B_HUMAN	QASPSIVIALAGNK	59.34	Gln->pyro-Glu (N-term Q)	Heavy	2	676.38263

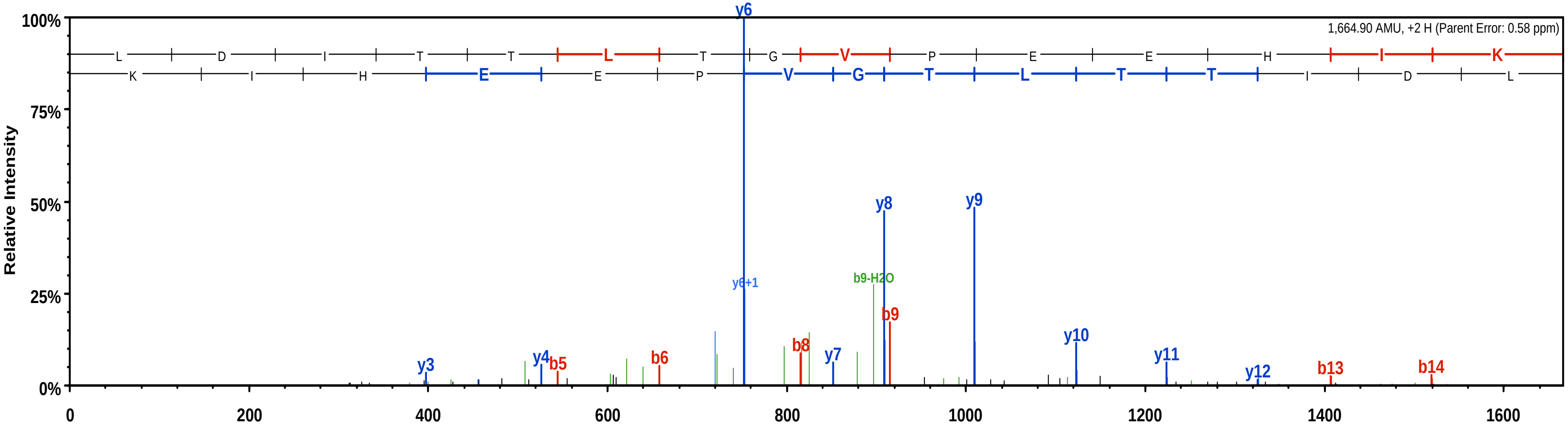


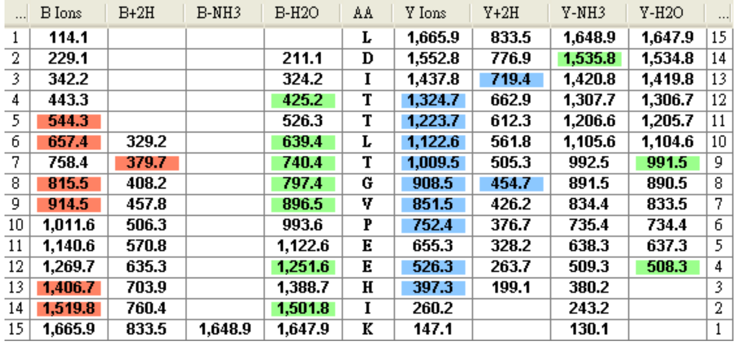


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	1,357.8	679.4	1,340.8	1,339.8	14
2	183.1		166.0		A	1,246.7	623.9	1,229.7	1,228.7	13
3	270.1		253.1	252.1	S	1,175.7	588.4	1,158.7	1,157.7	12
4	367.2		350.1	349.2	P	1,088.7	544.8	1,071.7	1,070.7	11
5	454.2		437.2	436.2	S	991.6	496.3	974.6	973.6	10
6	567.3	284.1	550.3	549.3	I	904.6	452.8	887.6		9
7	666.3	333.7	649.3	648.3	V	791.5	396.3	774.5		8
8	779.4	390.2	762.4	761.4	I	692.4	346.7	675.4		7
9	850.5	425.7	833.4	832.5	A	579.4	290.2	562.3		6
10	963.6	482.3	946.5	945.5	L	508.3		491.3		5
11	1,034.6	517.8	1,017.6	1,016.6	A	395.2		378.2		4
12	1,091.6	546.3	1,074.6	1,073.6	G	324.2		307.2		3
13	1,205.7	603.3	1,188.6	1,187.6	N	267.2		250.1		2
14	1,357.8	679.4	1,340.8	1,339.8	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-75	sp|O43181|NDUS4_HUMAN	LDITTLTGVPEEHIK	59.17	Unmodified	Light	2	833.45653

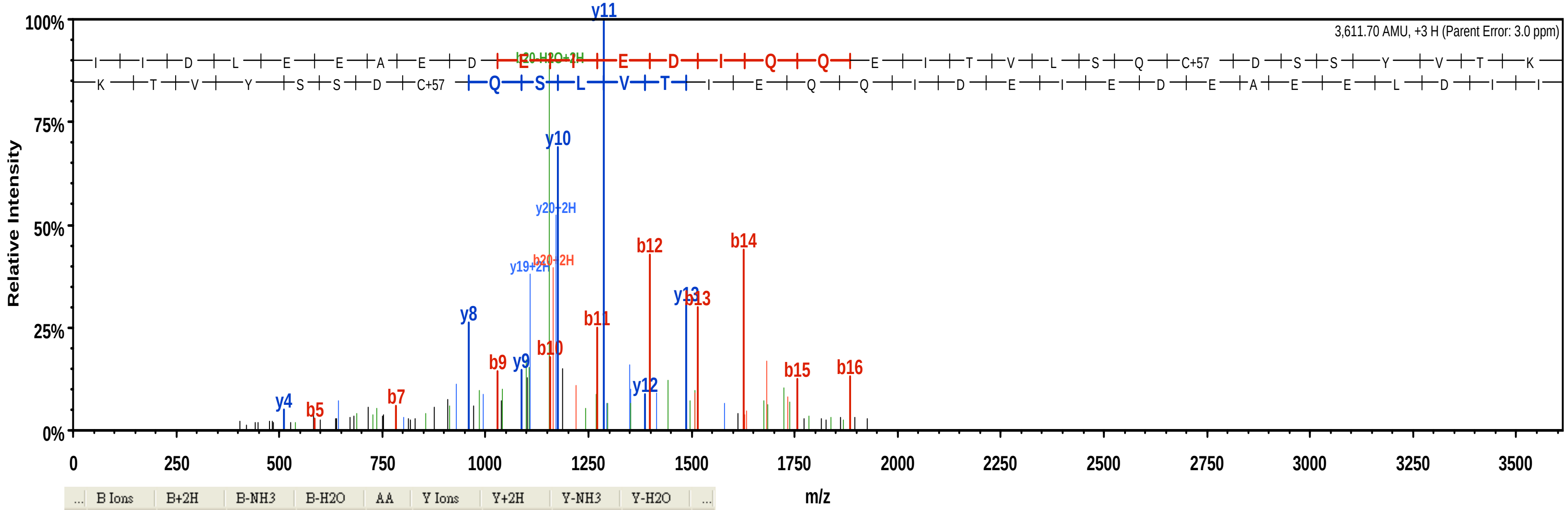


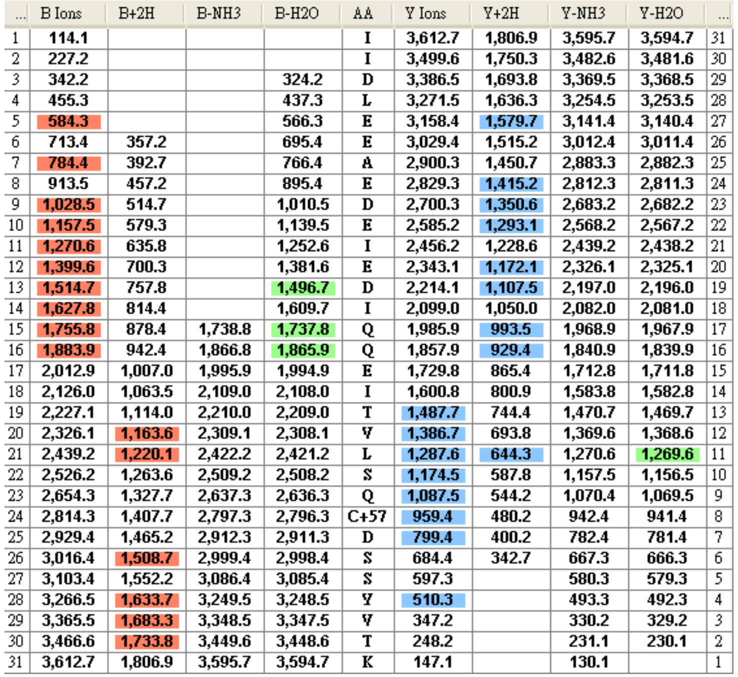


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	1,665.9	833.5	1,648.9	1,647.9	15
2	229.1			211.1	D	1,552.8	776.9	1,535.8	1,534.8	14
3	342.2			324.2	I	1,437.8	719.4	1,420.8	1,419.8	13
4	443.3			425.2	T	1,324.7	662.9	1,307.7	1,306.7	12
5	544.3			526.3	T	1,223.7	612.3	1,206.6	1,205.7	11
6	657.4	329.2		639.4	L	1,122.6	561.8	1,105.6	1,104.6	10
7	758.4	379.7		740.4	T	1,009.5	505.3	992.5	991.5	9
8	815.5	408.2		797.4	G	908.5	454.7	891.5	890.5	8
9	914.5	457.8		896.5	V	851.5	426.2	834.4	833.5	7
10	1,011.6	506.3		993.6	P	752.4	376.7	735.4	734.4	6
11	1,140.6	570.8		1,122.6	E	655.3	328.2	638.3	637.3	5
12	1,269.7	635.3		1,251.6	E	526.3	263.7	509.3	508.3	4
13	1,406.7	703.9		1,388.7	H	397.3	199.1	380.2		3
14	1,519.8	760.4		1,501.8	I	260.2		243.2		2
15	1,665.9	833.5	1,648.9	1,647.9	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-76	sp|Q9P289|MST4_HUMAN	IIDLEEAEDEIEDIQQEITVLSQCDSSYVTK	59.17	Unmodified	Light	3	1204.9047

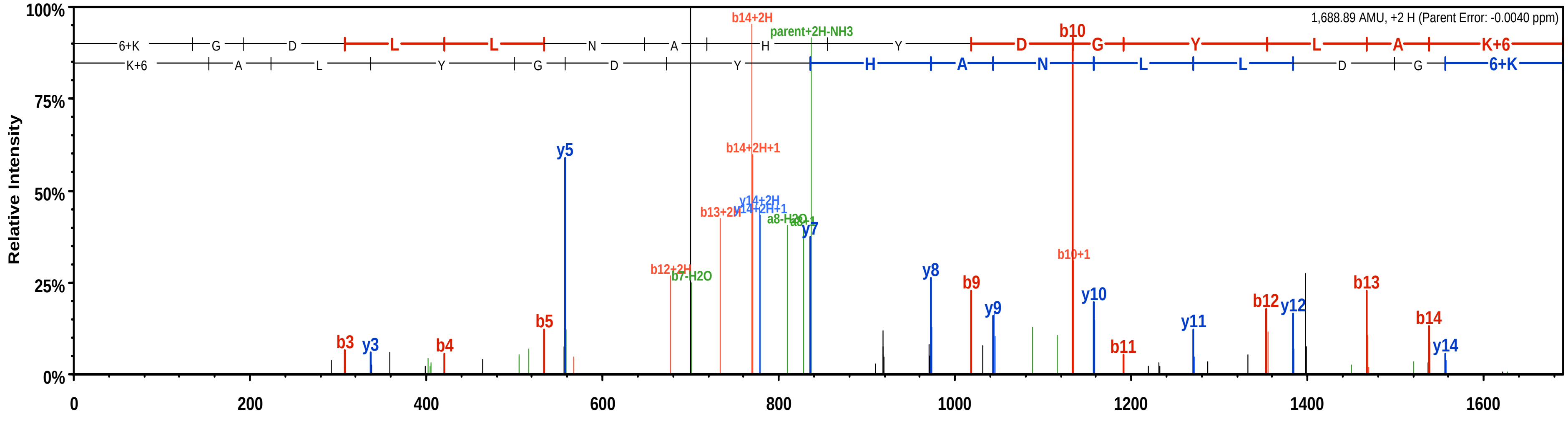


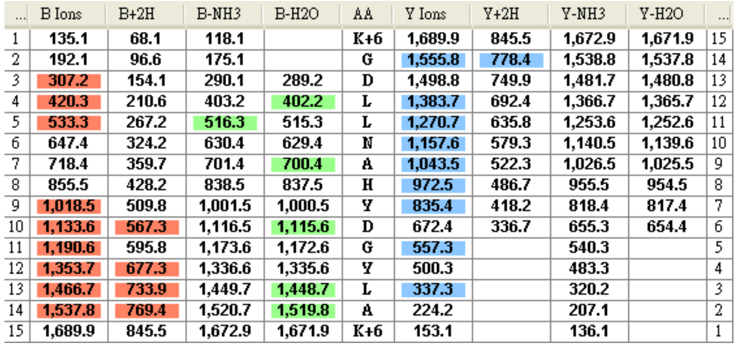


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	3,612.7	1,806.9	3,595.7	3,594.7	31
2	227.2				I	3,499.6	1,750.3	3,482.6	3,481.6	30
3	342.2			324.2	D	3,386.5	1,693.8	3,369.5	3,368.5	29
4	455.3			437.3	L	3,271.5	1,636.3	3,254.5	3,253.5	28
5	584.3			566.3	E	3,158.4	1,579.7	3,141.4	3,140.4	27
6	713.4	357.2		695.4	E	3,029.4	1,515.2	3,012.4	3,011.4	26
7	784.4	392.7		766.4	A	2,900.3	1,450.7	2,883.3	2,882.3	25
8	913.5	457.2		895.4	E	2,829.3	1,415.2	2,812.3	2,811.3	24
9	1,028.5	514.7		1,010.5	D	2,700.3	1,350.6	2,683.2	2,682.2	23
10	1,157.5	579.3		1,139.5	E	2,585.2	1,293.1	2,568.2	2,567.2	22
11	1,270.6	635.8		1,252.6	I	2,456.2	1,228.6	2,439.2	2,438.2	21
12	1,399.6	700.3		1,381.6	E	2,343.1	1,172.1	2,326.1	2,325.1	20
13	1,514.7	757.8		1,496.7	D	2,214.1	1,107.5	2,197.0	2,196.0	19
14	1,627.8	814.4		1,609.7	I	2,099.0	1,050.0	2,082.0	2,081.0	18
15	1,755.8	878.4	1,738.8	1,737.8	Q	1,985.9	993.5	1,968.9	1,967.9	17
16	1,883.9	942.4	1,866.8	1,865.9	Q	1,857.9	929.4	1,840.9	1,839.9	16
17	2,012.9	1,007.0	1,995.9	1,994.9	E	1,729.8	865.4	1,712.8	1,711.8	15
18	2,126.0	1,063.5	2,109.0	2,108.0	I	1,600.8	800.9	1,583.8	1,582.8	14
19	2,227.1	1,114.0	2,210.0	2,209.0	T	1,487.7	744.4	1,470.7	1,469.7	13
20	2,326.1	1,163.6	2,309.1	2,308.1	V	1,386.7	693.8	1,369.6	1,368.6	12
21	2,439.2	1,220.1	2,422.2	2,421.2	L	1,287.6	644.3	1,270.6	1,269.6	11
22	2,526.2	1,263.6	2,509.2	2,508.2	S	1,174.5	587.8	1,157.5	1,156.5	10
23	2,654.3	1,327.7	2,637.3	2,636.3	Q	1,087.5	544.2	1,070.4	1,069.5	9
24	2,814.3	1,407.7	2,797.3	2,796.3	C+57	959.4	480.2	942.4	941.4	8
25	2,929.4	1,465.2	2,912.3	2,911.3	D	799.4	400.2	782.4	781.4	7
26	3,016.4	1,508.7	2,999.4	2,998.4	S	684.4	342.7	667.3	666.3	6
27	3,103.4	1,552.2	3,086.4	3,085.4	S	597.3		580.3	579.3	5
28	3,266.5	1,633.7	3,249.5	3,248.5	Y	510.3		493.3	492.3	4
29	3,365.5	1,683.3	3,348.5	3,347.5	V	347.2		330.2	329.2	3
30	3,466.6	1,733.8	3,449.6	3,448.6	T	248.2		231.1	230.1	2
31	3,612.7	1,806.9	3,595.7	3,594.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-77	sp|Q9Y680|FKBP7_HUMAN	KGDLLNAHYDGYLAK	58.69	Unmodified	Heavy	2	839.43339

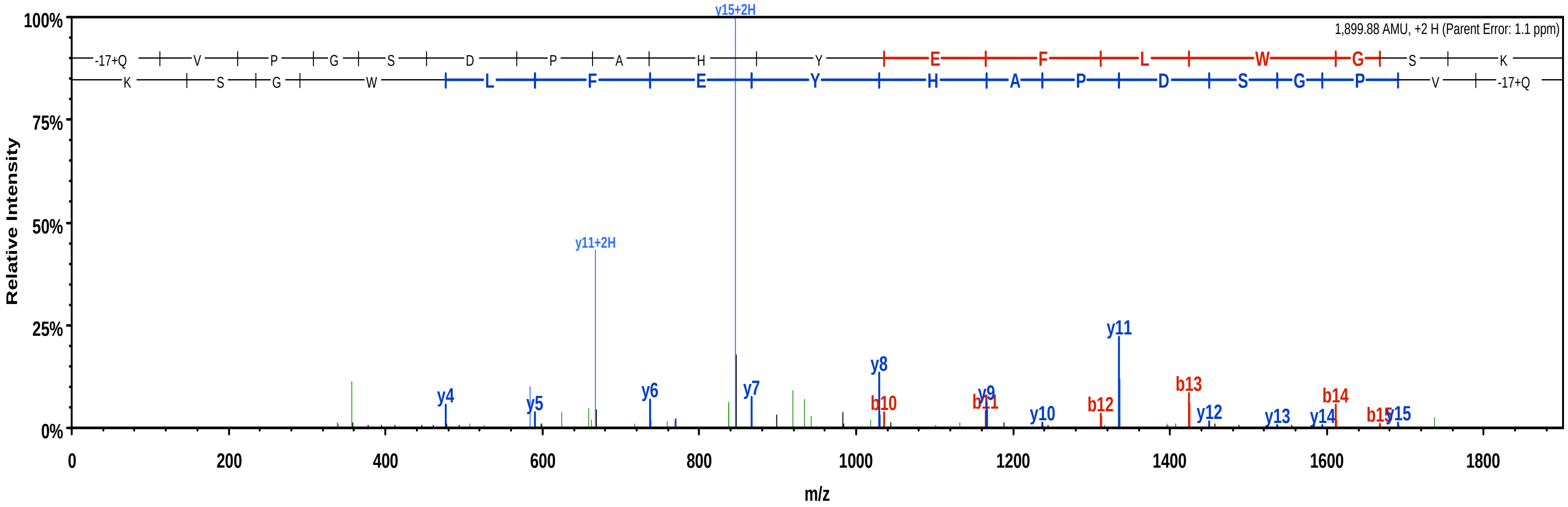


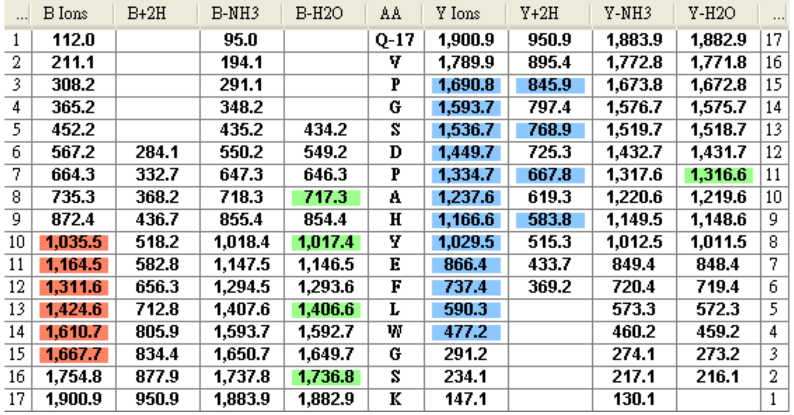


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	135.1	68.1	118.1		K+6	1,689.9	845.5	1,672.9	1,671.9	15
2	192.1	96.6	175.1		G	1,555.8	778.4	1,538.8	1,537.8	14
3	307.2	154.1	290.1	289.2	D	1,498.8	749.9	1,481.7	1,480.8	13
4	420.3	210.6	403.2	402.2	L	1,383.7	692.4	1,366.7	1,365.7	12
5	533.3	267.2	516.3	515.3	L	1,270.7	635.8	1,253.6	1,252.6	11
6	647.4	324.2	630.4	629.4	N	1,157.6	579.3	1,140.5	1,139.6	10
7	718.4	359.7	701.4	700.4	A	1,043.5	522.3	1,026.5	1,025.5	9
8	855.5	428.2	838.5	837.5	H	972.5	486.7	955.5	954.5	8
9	1,018.5	509.8	1,001.5	1,000.5	Y	835.4	418.2	818.4	817.4	7
10	1,133.6	567.3	1,116.5	1,115.6	D	672.4	336.7	655.3	654.4	6
11	1,190.6	595.8	1,173.6	1,172.6	G	557.3		540.3		5
12	1,353.7	677.3	1,336.6	1,335.6	Y	500.3		483.3		4
13	1,466.7	733.9	1,449.7	1,448.7	L	337.3		320.2		3
14	1,537.8	769.4	1,520.7	1,519.8	A	224.2		207.1		2
15	1,689.9	845.5	1,672.9	1,671.9	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-78	splP43362lMAGA9_HUMAN	QVPGSDPAHYEFLWGSK	58.24	Gln->pyro-Glu (N-term Q)	Light	2	950.94686

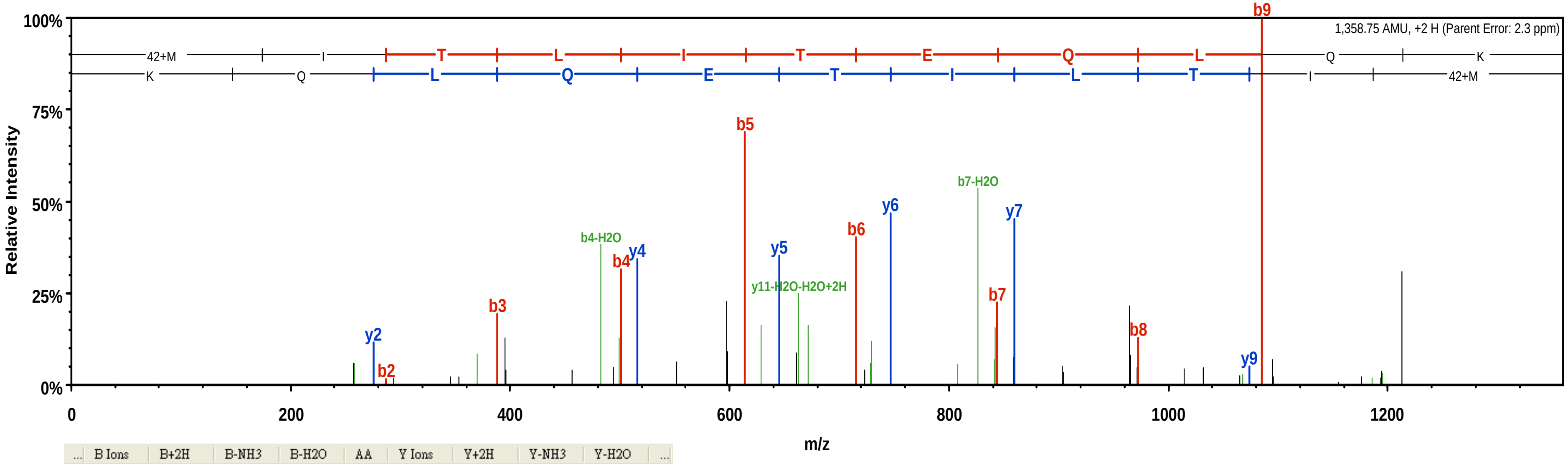


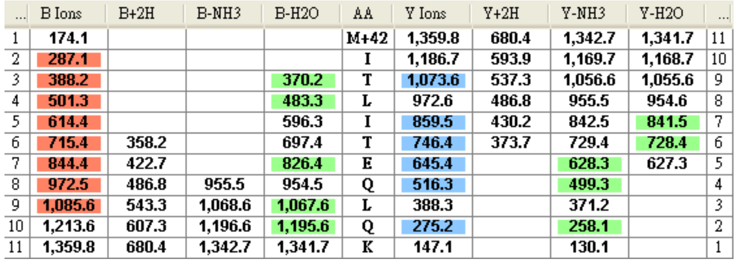


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	1,900.9	950.9	1,883.9	1,882.9	17
2	211.1		194.1		V	1,789.9	895.4	1,772.8	1,771.8	16
3	308.2		291.1		P	1,690.8	845.9	1,673.8	1,672.8	15
4	365.2		348.2		G	1,593.7	797.4	1,576.7	1,575.7	14
5	452.2		435.2	434.2	S	1,536.7	768.9	1,519.7	1,518.7	13
6	567.2	284.1	550.2	549.2	D	1,449.7	725.3	1,432.7	1,431.7	12
7	664.3	332.7	647.3	646.3	P	1,334.7	667.8	1,317.6	1,316.6	11
8	735.3	368.2	718.3	717.3	A	1,237.6	619.3	1,220.6	1,219.6	10
9	872.4	436.7	855.4	854.4	H	1,166.6	583.8	1,149.5	1,148.6	9
10	1,035.5	518.2	1,018.4	1,017.4	Y	1,029.5	515.3	1,012.5	1,011.5	8
11	1,164.5	582.8	1,147.5	1,146.5	E	866.4	433.7	849.4	848.4	7
12	1,311.6	656.3	1,294.5	1,293.6	F	737.4	369.2	720.4	719.4	6
13	1,424.6	712.8	1,407.6	1,406.6	L	590.3		573.3	572.3	5
14	1,610.7	805.9	1,593.7	1,592.7	W	477.2		460.2	459.2	4
15	1,667.7	834.4	1,650.7	1,649.7	G	291.2		274.1	273.2	3
16	1,754.8	877.9	1,737.8	1,736.8	S	234.1		217.1	216.1	2
17	1,900.9	950.9	1,883.9	1,882.9	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-79	sp|Q9NYF3|FA53C_HUMAN	MITLITEQLQK	58.11	Acetyl (Protein N-term)	Light	2	680.38125

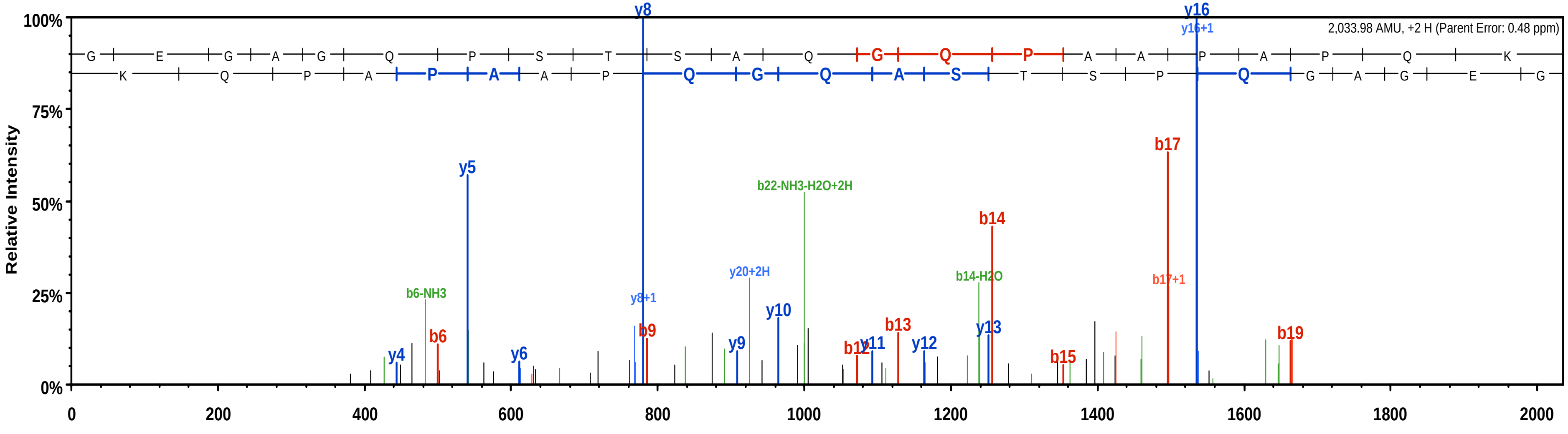


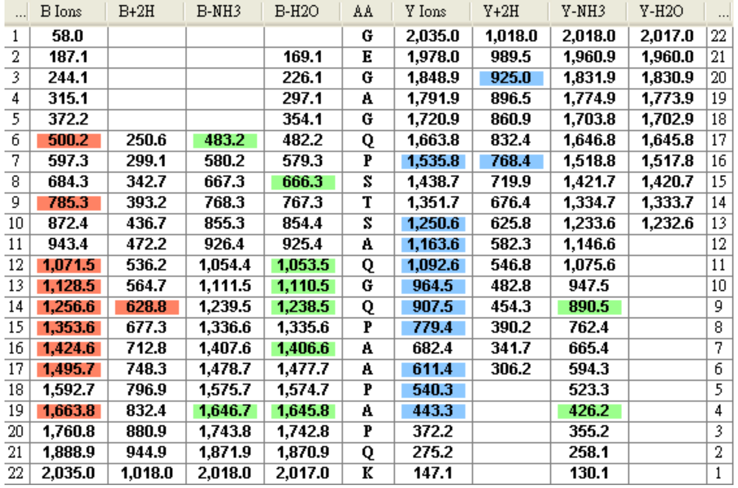


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	174.1				M+42	1,359.8	680.4	1,342.7	1,341.7	11
2	287.1				I	1,186.7	593.9	1,169.7	1,168.7	10
3	388.2			370.2	T	1,073.6	537.3	1,056.6	1,055.6	9
4	501.3			483.3	L	972.6	486.8	955.5	954.6	8
5	614.4			596.3	I	859.5	430.2	842.5	841.5	7
6	715.4	358.2		697.4	T	746.4	373.7	729.4	728.4	6
7	844.4	422.7		826.4	E	645.4		628.3	627.3	5
8	972.5	486.8	955.5	954.5	Q	516.3		499.3		4
9	1,085.6	543.3	1,068.6	1,067.6	L	388.3		371.2		3
10	1,213.6	607.3	1,196.6	1,195.6	Q	275.2		258.1		2
11	1,359.8	680.4	1,342.7	1,341.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-80	sp|P52926|HMGA2_HUMAN	GEGAGQPSTSAQGQPAAPAPQK	57.88	Unmodified	Light	2	1017.9956

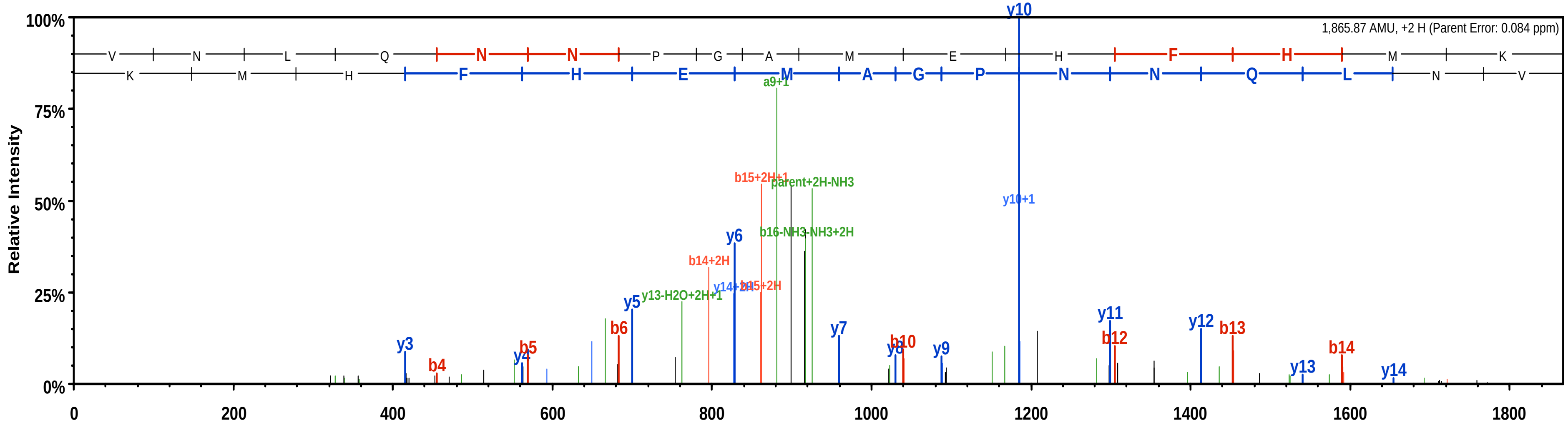


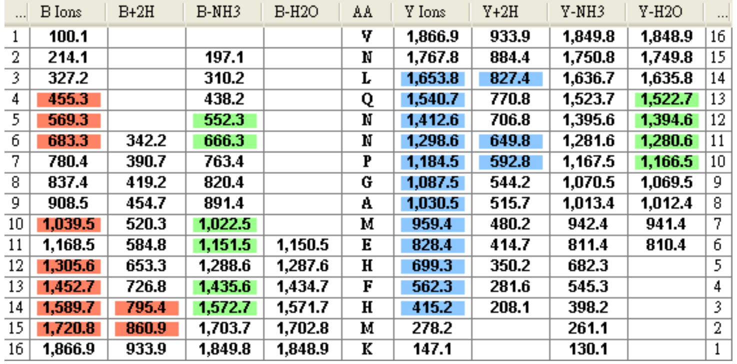


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	2,035.0	1,018.0	2,018.0	2,017.0	22
2	187.1			169.1	E	1,978.0	989.5	1,960.9	1,960.0	21
3	244.1			226.1	G	1,848.9	925.0	1,831.9	1,830.9	20
4	315.1			297.1	A	1,791.9	896.5	1,774.9	1,773.9	19
5	372.2			354.1	G	1,720.9	860.9	1,703.8	1,702.9	18
6	500.2	250.6	483.2	482.2	Q	1,663.8	832.4	1,646.8	1,645.8	17
7	597.3	299.1	580.2	579.3	P	1,535.8	768.4	1,518.8	1,517.8	16
8	684.3	342.7	667.3	666.3	S	1,438.7	719.9	1,421.7	1,420.7	15
9	785.3	393.2	768.3	767.3	T	1,351.7	676.4	1,334.7	1,333.7	14
10	872.4	436.7	855.3	854.4	S	1,250.6	625.8	1,233.6	1,232.6	13
11	943.4	472.2	926.4	925.4	A	1,163.6	582.3	1,146.6		12
12	1,071.5	536.2	1,054.4	1,053.5	Q	1,092.6	546.8	1,075.6		11
13	1,128.5	564.7	1,111.5	1,110.5	G	964.5	482.8	947.5		10
14	1,256.6	628.8	1,239.5	1,238.5	Q	907.5	454.3	890.5		9
15	1,353.6	677.3	1,336.6	1,335.6	P	779.4	390.2	762.4		8
16	1,424.6	712.8	1,407.6	1,406.6	A	682.4	341.7	665.4		7
17	1,495.7	748.3	1,478.7	1,477.7	A	611.4	306.2	594.3		6
18	1,592.7	796.9	1,575.7	1,574.7	P	540.3		523.3		5
19	1,663.8	832.4	1,646.7	1,645.8	A	443.3		426.2		4
20	1,760.8	880.9	1,743.8	1,742.8	P	372.2		355.2		3
21	1,888.9	944.9	1,871.9	1,870.9	Q	275.2		258.1		2
22	2,035.0	1,018.0	2,018.0	2,017.0	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-81	splP51572lBAP31_HUMAN	VNLQNNPGAMEHFHMK	56.37	Unmodified	Light	2	933.94053

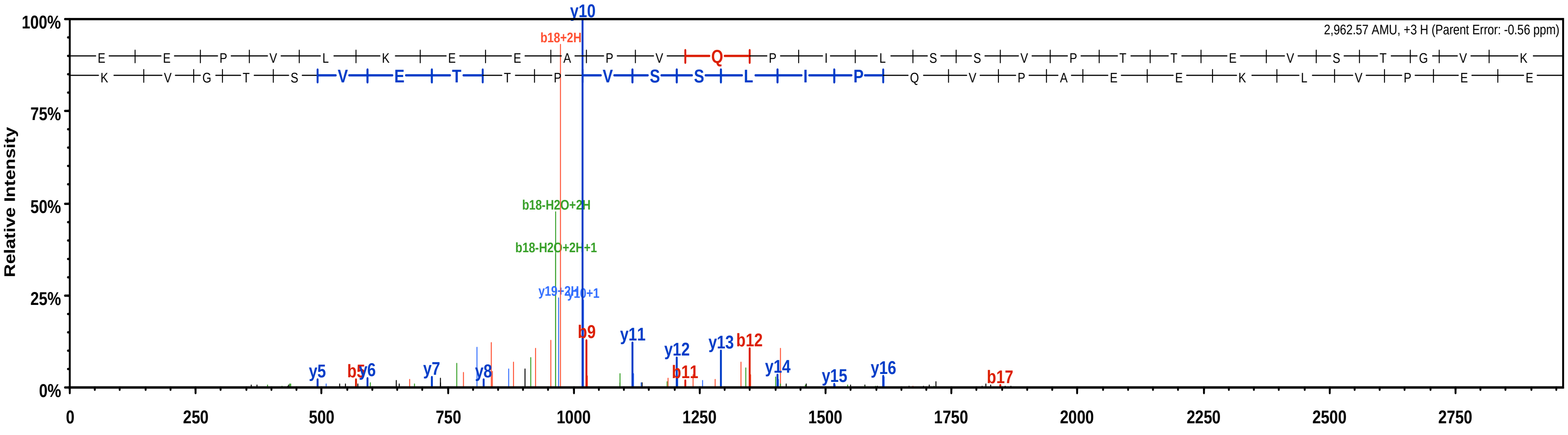


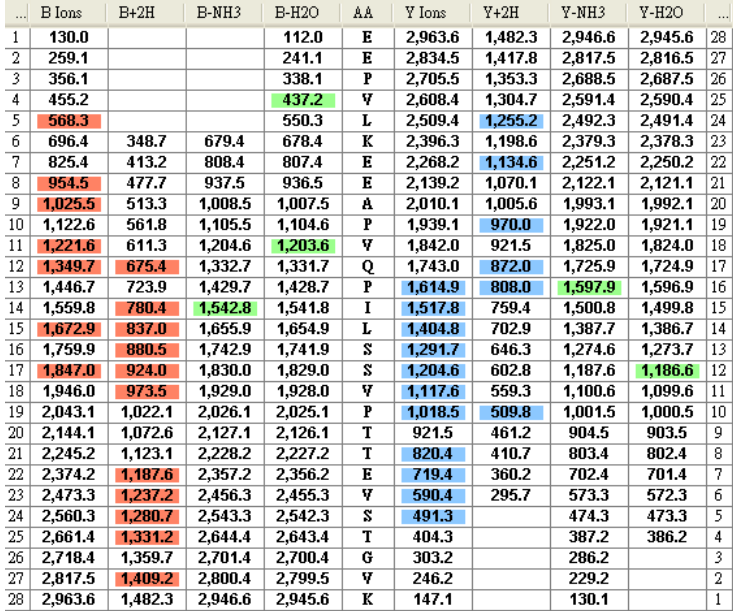


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	1,866.9	933.9	1,849.8	1,848.9	16
2	214.1		197.1		N	1,767.8	884.4	1,750.8	1,749.8	15
3	327.2		310.2		L	1,653.8	827.4	1,636.7	1,635.8	14
4	455.3		438.2		Q	1,540.7	770.8	1,523.7	1,522.7	13
5	569.3		552.3		N	1,412.6	706.8	1,395.6	1,394.6	12
6	683.3	342.2	666.3		N	1,298.6	649.8	1,281.6	1,280.6	11
7	780.4	390.7	763.4		P	1,184.5	592.8	1,167.5	1,166.5	10
8	837.4	419.2	820.4		G	1,087.5	544.2	1,070.5	1,069.5	9
9	908.5	454.7	891.4		A	1,030.5	515.7	1,013.4	1,012.4	8
10	1,039.5	520.3	1,022.5		M	959.4	480.2	942.4	941.4	7
11	1,168.5	584.8	1,151.5	1,150.5	E	828.4	414.7	811.4	810.4	6
12	1,305.6	653.3	1,288.6	1,287.6	H	699.3	350.2	682.3		5
13	1,452.7	726.8	1,435.6	1,434.7	F	562.3	281.6	545.3		4
14	1,589.7	795.4	1,572.7	1,571.7	H	415.2	208.1	398.2		3
15	1,720.8	860.9	1,703.7	1,702.8	M	278.2		261.1		2
16	1,866.9	933.9	1,849.8	1,848.9	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-82	splQ9BZ95lNSD3_HUMAN	EEPVLKEEAPVQPILSSVPTTEVSTGVK	55.94	Unmodified	Light	3	988.53229

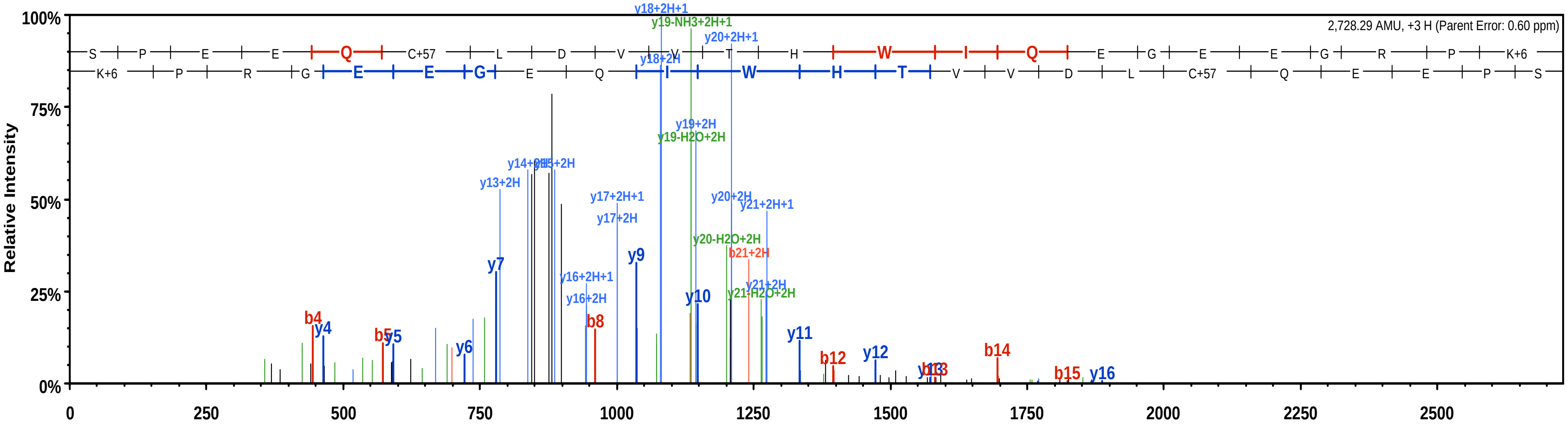


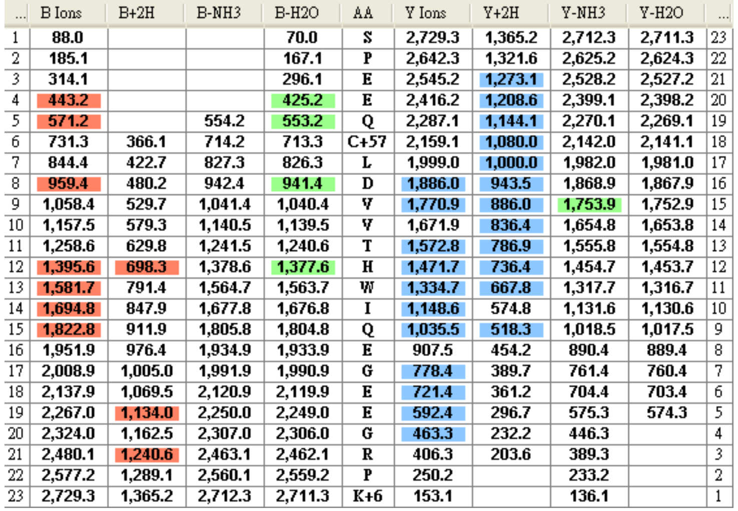


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	2,963.6	1,482.3	2,946.6	2,945.6	28
2	259.1			241.1	E	2,834.5	1,417.8	2,817.5	2,816.5	27
3	356.1			338.1	P	2,705.5	1,353.3	2,688.5	2,687.5	26
4	455.2			437.2	V	2,608.4	1,304.7	2,591.4	2,590.4	25
5	568.3			550.3	L	2,509.4	1,255.2	2,492.3	2,491.4	24
6	696.4	348.7	679.4	678.4	K	2,396.3	1,198.6	2,379.3	2,378.3	23
7	825.4	413.2	808.4	807.4	E	2,268.2	1,134.6	2,251.2	2,250.2	22
8	954.5	477.7	937.5	936.5	E	2,139.2	1,070.1	2,122.1	2,121.1	21
9	1,025.5	513.3	1,008.5	1,007.5	A	2,010.1	1,005.6	1,993.1	1,992.1	20
10	1,122.6	561.8	1,105.5	1,104.6	P	1,939.1	970.0	1,922.0	1,921.1	19
11	1,221.6	611.3	1,204.6	1,203.6	V	1,842.0	921.5	1,825.0	1,824.0	18
12	1,349.7	675.4	1,332.7	1,331.7	Q	1,743.0	872.0	1,725.9	1,724.9	17
13	1,446.7	723.9	1,429.7	1,428.7	P	1,614.9	808.0	1,597.9	1,596.9	16
14	1,559.8	780.4	1,542.8	1,541.8	I	1,517.8	759.4	1,500.8	1,499.8	15
15	1,672.9	837.0	1,655.9	1,654.9	L	1,404.8	702.9	1,387.7	1,386.7	14
16	1,759.9	880.5	1,742.9	1,741.9	S	1,291.7	646.3	1,274.6	1,273.7	13
17	1,847.0	924.0	1,830.0	1,829.0	S	1,204.6	602.8	1,187.6	1,186.6	12
18	1,946.0	973.5	1,929.0	1,928.0	V	1,117.6	559.3	1,100.6	1,099.6	11
19	2,043.1	1,022.1	2,026.1	2,025.1	P	1,018.5	509.8	1,001.5	1,000.5	10
20	2,144.1	1,072.6	2,127.1	2,126.1	T	921.5	461.2	904.5	903.5	9
21	2,245.2	1,123.1	2,228.2	2,227.2	T	820.4	410.7	803.4	802.4	8
22	2,374.2	1,187.6	2,357.2	2,356.2	E	719.4	360.2	702.4	701.4	7
23	2,473.3	1,237.2	2,456.3	2,455.3	V	590.4	295.7	573.3	572.3	6
24	2,560.3	1,280.7	2,543.3	2,542.3	S	491.3		474.3	473.3	5
25	2,661.4	1,331.2	2,644.4	2,643.4	T	404.3		387.2	386.2	4
26	2,718.4	1,359.7	2,701.4	2,700.4	G	303.2		286.2		3
27	2,817.5	1,409.2	2,800.4	2,799.5	V	246.2		229.2		2
28	2,963.6	1,482.3	2,946.6	2,945.6	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-83	sp|Q03405|UPAR_HUMAN	SPEEQCLDVVTHWIQEGEEGRPK	54.68	Unmodified	Heavy	3	908.42917

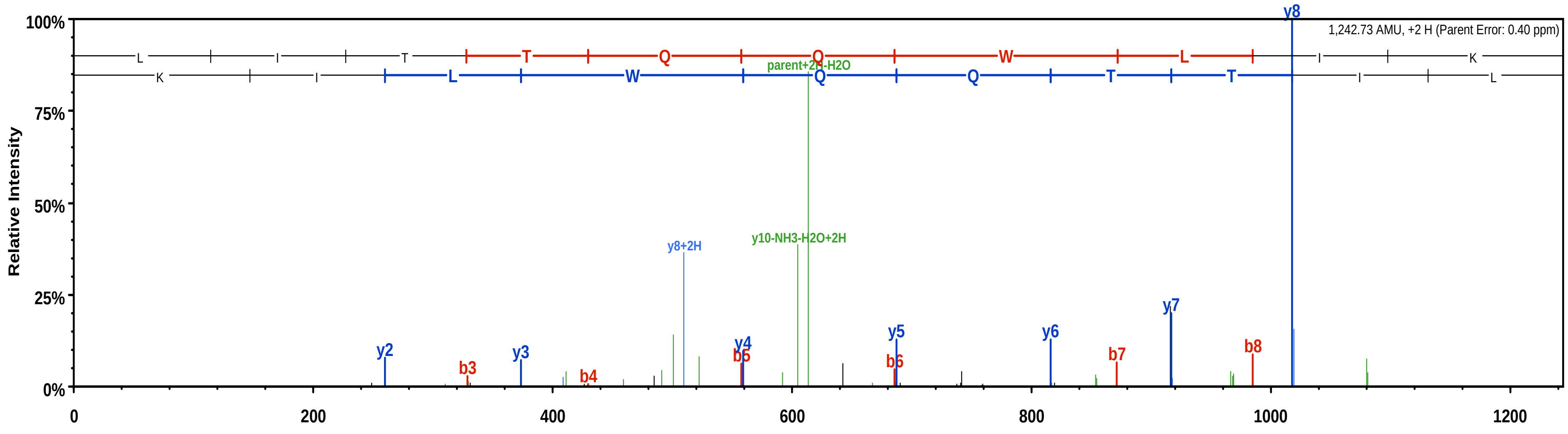


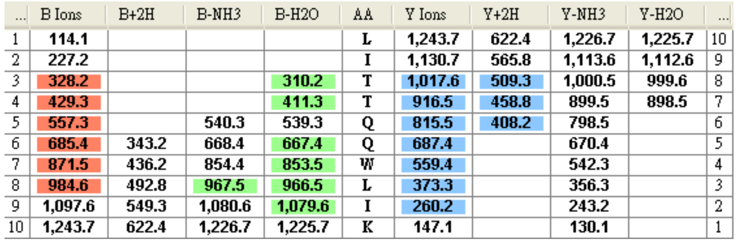


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	2,729.3	1,365.2	2,712.3	2,711.3	23
2	185.1			167.1	P	2,642.3	1,321.6	2,625.2	2,624.3	22
3	314.1			296.1	E	2,545.2	1,273.1	2,528.2	2,527.2	21
4	443.2			425.2	E	2,416.2	1,208.6	2,399.1	2,398.2	20
5	571.2		554.2	553.2	Q	2,287.1	1,144.1	2,270.1	2,269.1	19
6	731.3	366.1	714.2	713.3	C+57	2,159.1	1,080.0	2,142.0	2,141.1	18
7	844.4	422.7	827.3	826.3	L	1,999.0	1,000.0	1,982.0	1,981.0	17
8	959.4	480.2	942.4	941.4	D	1,886.0	943.5	1,868.9	1,867.9	16
9	1,058.4	529.7	1,041.4	1,040.4	V	1,770.9	886.0	1,753.9	1,752.9	15
10	1,157.5	579.3	1,140.5	1,139.5	V	1,671.9	836.4	1,654.8	1,653.8	14
11	1,258.6	629.8	1,241.5	1,240.6	T	1,572.8	786.9	1,555.8	1,554.8	13
12	1,395.6	698.3	1,378.6	1,377.6	H	1,471.7	736.4	1,454.7	1,453.7	12
13	1,581.7	791.4	1,564.7	1,563.7	W	1,334.7	667.8	1,317.7	1,316.7	11
14	1,694.8	847.9	1,677.8	1,676.8	I	1,148.6	574.8	1,131.6	1,130.6	10
15	1,822.8	911.9	1,805.8	1,804.8	Q	1,035.5	518.3	1,018.5	1,017.5	9
16	1,951.9	976.4	1,934.9	1,933.9	E	907.5	454.2	890.4	889.4	8
17	2,008.9	1,005.0	1,991.9	1,990.9	G	778.4	389.7	761.4	760.4	7
18	2,137.9	1,069.5	2,120.9	2,119.9	E	721.4	361.2	704.4	703.4	6
19	2,267.0	1,134.0	2,250.0	2,249.0	E	592.4	296.7	575.3	574.3	5
20	2,324.0	1,162.5	2,307.0	2,306.0	G	463.3	232.2	446.3		4
21	2,480.1	1,240.6	2,463.1	2,462.1	R	406.3	203.6	389.3		3
22	2,577.2	1,289.1	2,560.1	2,559.2	P	250.2		233.2		2
23	2,729.3	1,365.2	2,712.3	2,711.3	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-84	sp|P00846|ATP6_HUMAN	LITTQQWLIK	54.17	Unmodified	Light	2	622.37408

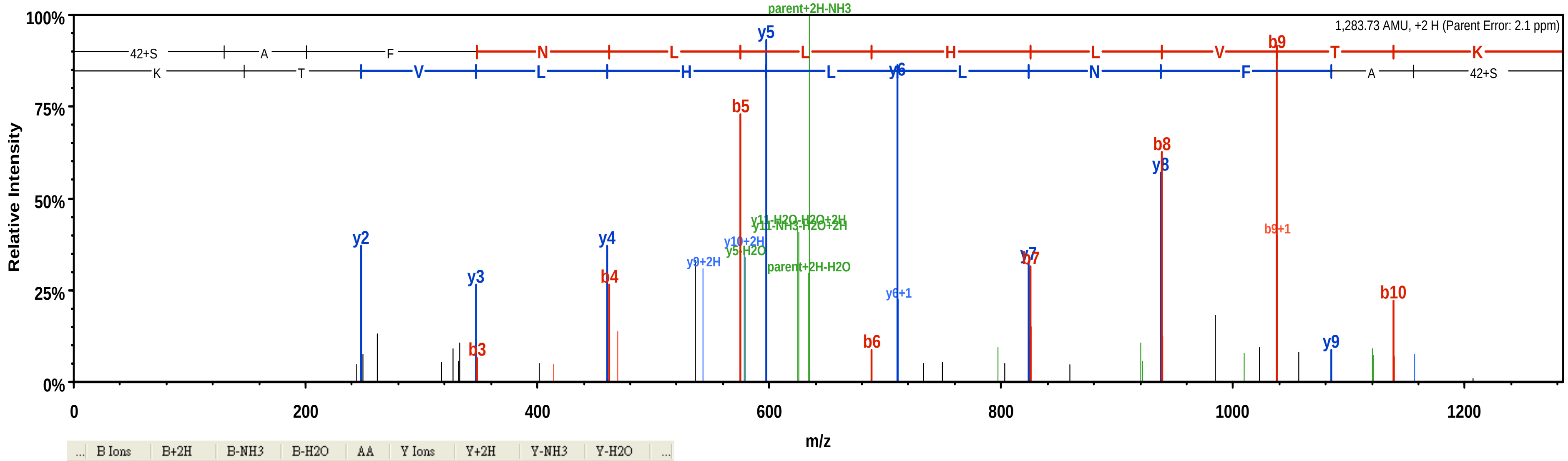


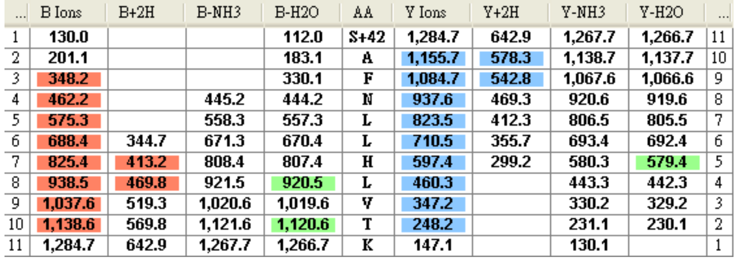


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	1,243.7	622.4	1,226.7	1,225.7	10
2	227.2				I	1,130.7	565.8	1,113.6	1,112.6	9
3	328.2			310.2	T	1,017.6	509.3	1,000.5	999.6	8
4	429.3			411.3	T	916.5	458.8	899.5	898.5	7
5	557.3		540.3	539.3	Q	815.5	408.2	798.5		6
6	685.4	343.2	668.4	667.4	Q	687.4		670.4		5
7	871.5	436.2	854.4	853.5	W	559.4		542.3		4
8	984.6	492.8	967.5	966.5	L	373.3		356.3		3
9	1,097.6	549.3	1,080.6	1,079.6	I	260.2		243.2		2
10	1,243.7	622.4	1,226.7	1,225.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-85	splQ8IXL7lMSRB3_HUMAN	SAFNLLHLVTK	54.16	Acetyl (Protein N-term)	Light	2	642.86916

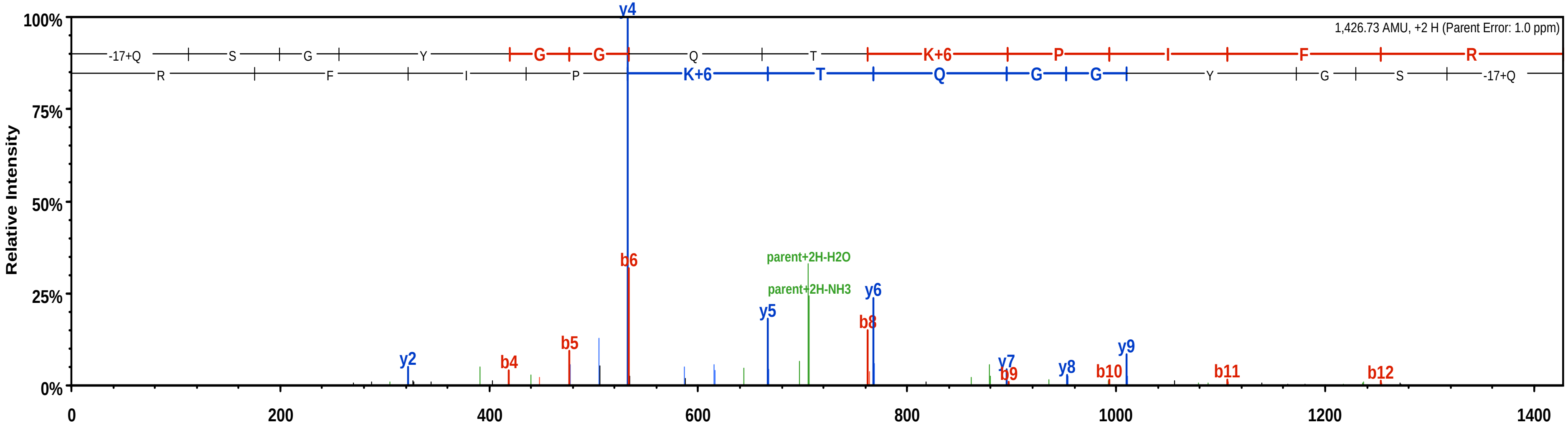


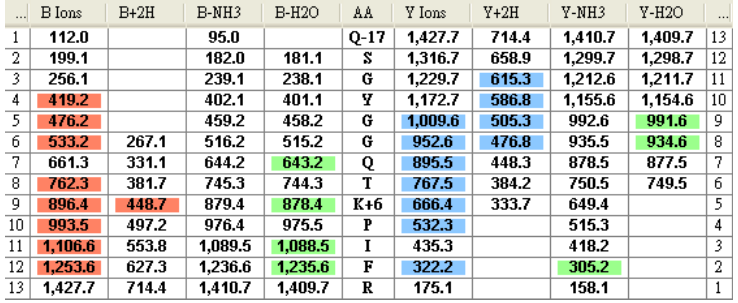


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	S+42	1,284.7	642.9	1,267.7	1,266.7	11
2	201.1			183.1	A	1,155.7	578.3	1,138.7	1,137.7	10
3	348.2			330.1	F	1,084.7	542.8	1,067.6	1,066.6	9
4	462.2		445.2	444.2	N	937.6	469.3	920.6	919.6	8
5	575.3		558.3	557.3	L	823.5	412.3	806.5	805.5	7
6	688.4	344.7	671.3	670.4	L	710.5	355.7	693.4	692.4	6
7	825.4	413.2	808.4	807.4	H	597.4	299.2	580.3	579.4	5
8	938.5	469.8	921.5	920.5	L	460.3		443.3	442.3	4
9	1,037.6	519.3	1,020.6	1,019.6	V	347.2		330.2	329.2	3
10	1,138.6	569.8	1,121.6	1,120.6	T	248.2		231.1	230.1	2
11	1,284.7	642.9	1,267.7	1,266.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-86	sp|P83881|RL36A_HUMAN	QSGYGGQTKPIFR	53.27	Gln->pyro-Glu (N-term Q)	Heavy	2	711.36223

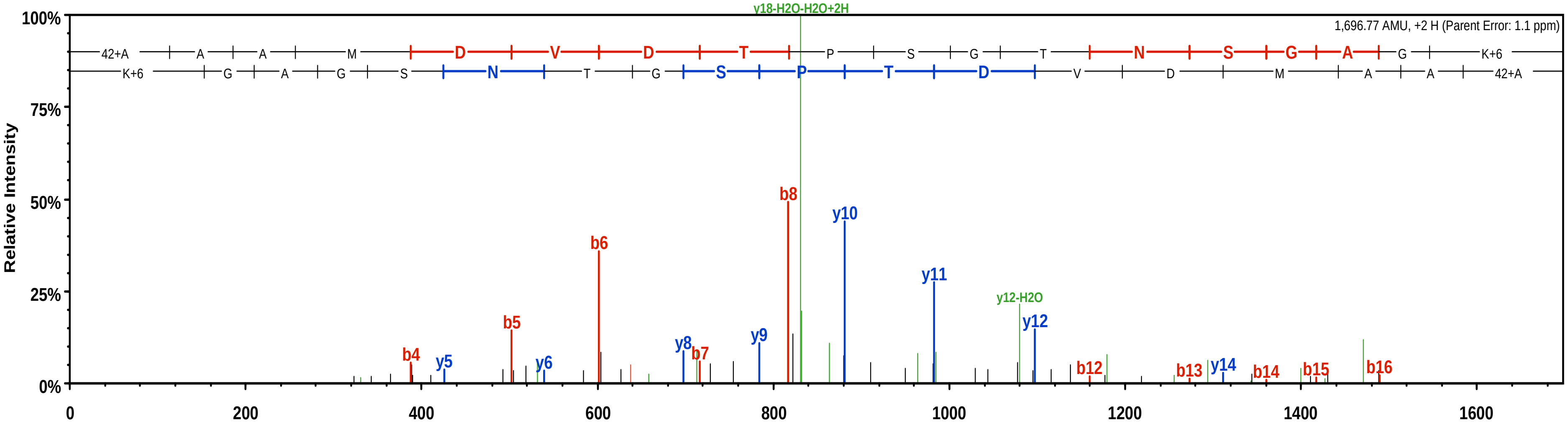


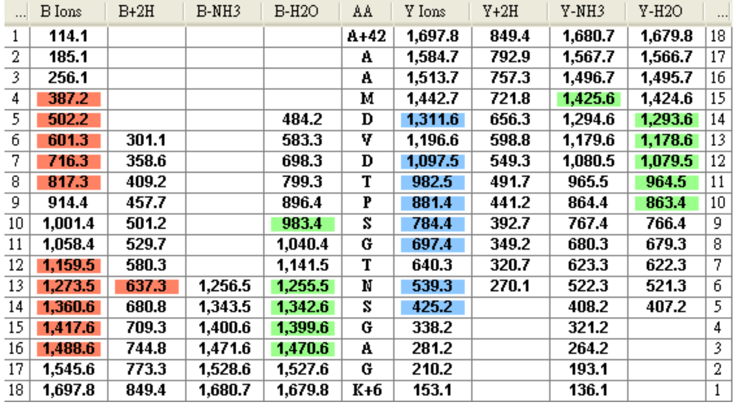


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	1,427.7	714.4	1,410.7	1,409.7	13
2	199.1		182.0	181.1	S	1,316.7	658.9	1,299.7	1,298.7	12
3	256.1		239.1	238.1	G	1,229.7	615.3	1,212.6	1,211.7	11
4	419.2		402.1	401.1	Y	1,172.7	586.8	1,155.6	1,154.6	10
5	476.2		459.2	458.2	G	1,009.6	505.3	992.6	991.6	9
6	533.2	267.1	516.2	515.2	G	952.6	476.8	935.5	934.6	8
7	661.3	331.1	644.2	643.2	Q	895.5	448.3	878.5	877.5	7
8	762.3	381.7	745.3	744.3	T	767.5	384.2	750.5	749.5	6
9	896.4	448.7	879.4	878.4	K+6	666.4	333.7	649.4		5
10	993.5	497.2	976.4	975.5	P	532.3		515.3		4
11	1,106.6	553.8	1,089.5	1,088.5	I	435.3		418.2		3
12	1,253.6	627.3	1,236.6	1,235.6	F	322.2		305.2		2
13	1,427.7	714.4	1,410.7	1,409.7	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-87	sp|P62877|RBX1_HUMAN	AAAMDVDTPSGTNSGAGK	53.25	Acetyl (Protein N-term)	Heavy	2	846.38069

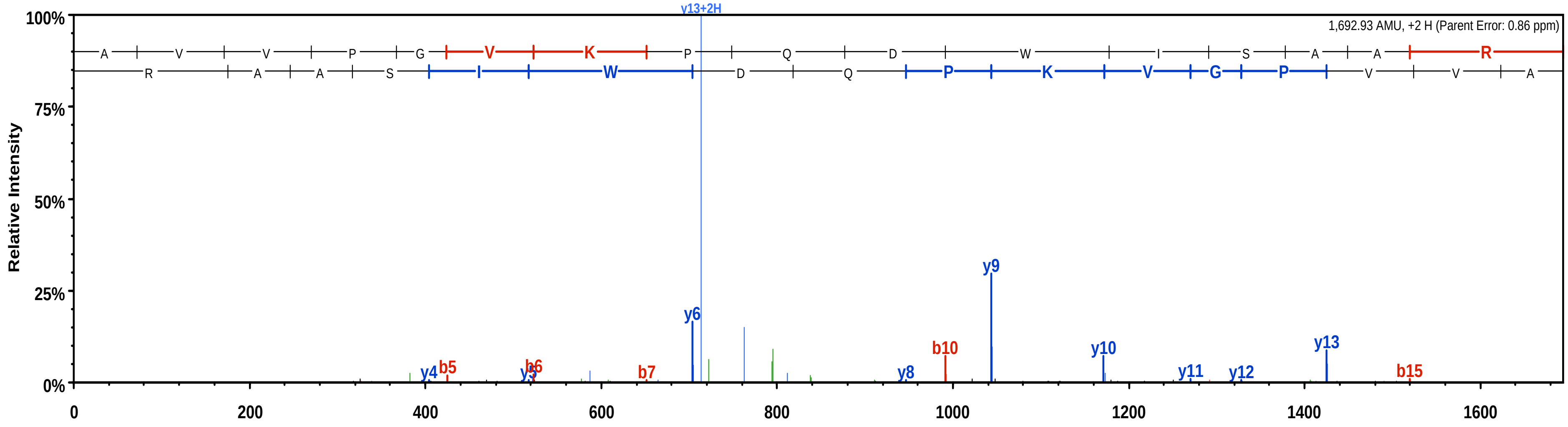


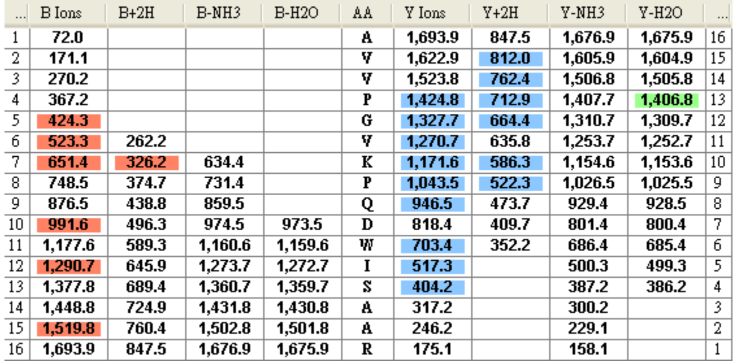


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	1,697.8	849.4	1,680.7	1,679.8	18
2	185.1				A	1,584.7	792.9	1,567.7	1,566.7	17
3	256.1				A	1,513.7	757.3	1,496.7	1,495.7	16
4	387.2				M	1,442.7	721.8	1,425.6	1,424.6	15
5	502.2			484.2	D	1,311.6	656.3	1,294.6	1,293.6	14
6	601.3	301.1		583.3	V	1,196.6	598.8	1,179.6	1,178.6	13
7	716.3	358.6		698.3	D	1,097.5	549.3	1,080.5	1,079.5	12
8	817.3	409.2		799.3	T	982.5	491.7	965.5	964.5	11
9	914.4	457.7		896.4	P	881.4	441.2	864.4	863.4	10
10	1,001.4	501.2		983.4	S	784.4	392.7	767.4	766.4	9
11	1,058.4	529.7		1,040.4	G	697.4	349.2	680.3	679.3	8
12	1,159.5	580.3		1,141.5	T	640.3	320.7	623.3	622.3	7
13	1,273.5	637.3	1,256.5	1,255.5	N	539.3	270.1	522.3	521.3	6
14	1,360.6	680.8	1,343.5	1,342.6	S	425.2		408.2	407.2	5
15	1,417.6	709.3	1,400.6	1,399.6	G	338.2		321.2		4
16	1,488.6	744.8	1,471.6	1,470.6	A	281.2		264.2		3
17	1,545.6	773.3	1,528.6	1,527.6	G	210.2		193.1		2
18	1,697.8	849.4	1,680.7	1,679.8	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-88	sp|Q9NPA0|CO024_HUMAN	AVVPGVKPQDWISAAR	53.11	Unmodified	Light	2	847.47285

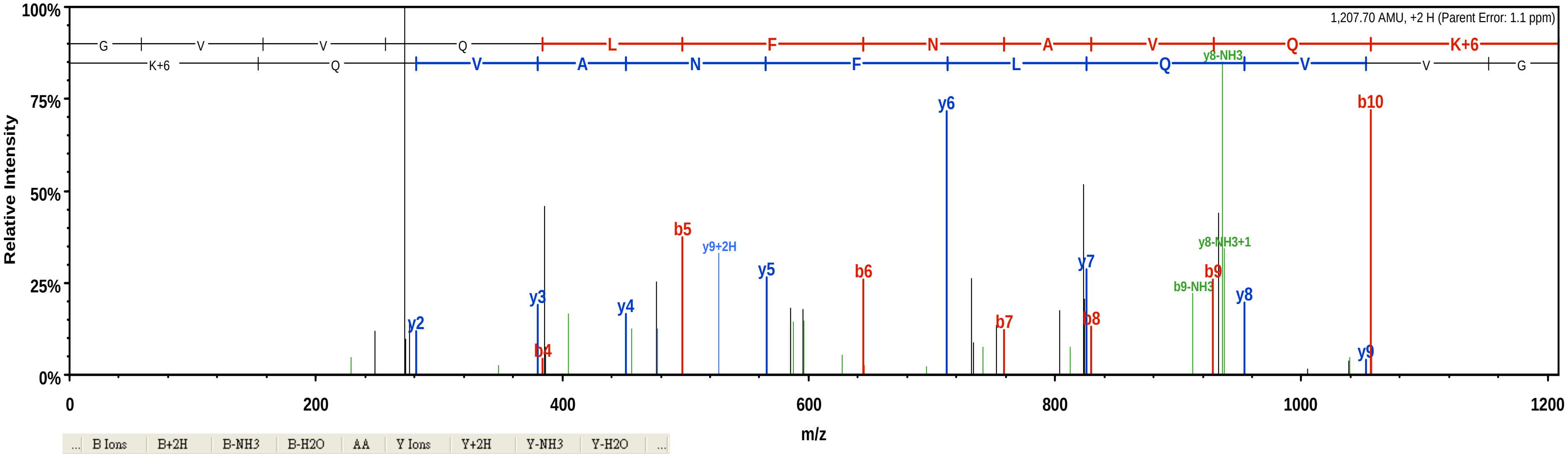


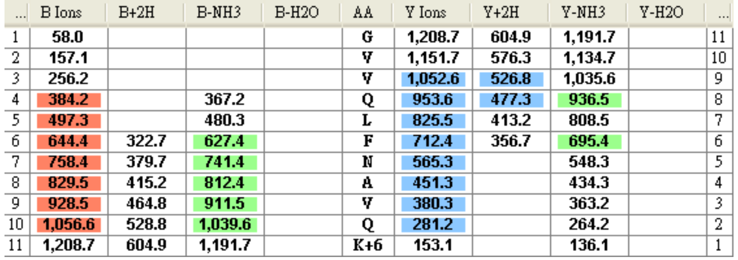


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	1,693.9	847.5	1,676.9	1,675.9	16
2	171.1				V	1,622.9	812.0	1,605.9	1,604.9	15
3	270.2				V	1,523.8	762.4	1,506.8	1,505.8	14
4	367.2				P	1,424.8	712.9	1,407.7	1,406.8	13
5	424.3				G	1,327.7	664.4	1,310.7	1,309.7	12
6	523.3	262.2			V	1,270.7	635.8	1,253.7	1,252.7	11
7	651.4	326.2	634.4		K	1,171.6	586.3	1,154.6	1,153.6	10
8	748.5	374.7	731.4		P	1,043.5	522.3	1,026.5	1,025.5	9
9	876.5	438.8	859.5		Q	946.5	473.7	929.4	928.5	8
10	991.6	496.3	974.5	973.5	D	818.4	409.7	801.4	800.4	7
11	1,177.6	589.3	1,160.6	1,159.6	W	703.4	352.2	686.4	685.4	6
12	1,290.7	645.9	1,273.7	1,272.7	I	517.3		500.3	499.3	5
13	1,377.8	689.4	1,360.7	1,359.7	S	404.2		387.2	386.2	4
14	1,448.8	724.9	1,431.8	1,430.8	A	317.2		300.2		3
15	1,519.8	760.4	1,502.8	1,501.8	A	246.2		229.1		2
16	1,693.9	847.5	1,676.9	1,675.9	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-89	sp|Q9Y3B9|RRP15_HUMAN	GVVQLFNAVQK	51.26	Unmodified	Heavy	2	601.84823

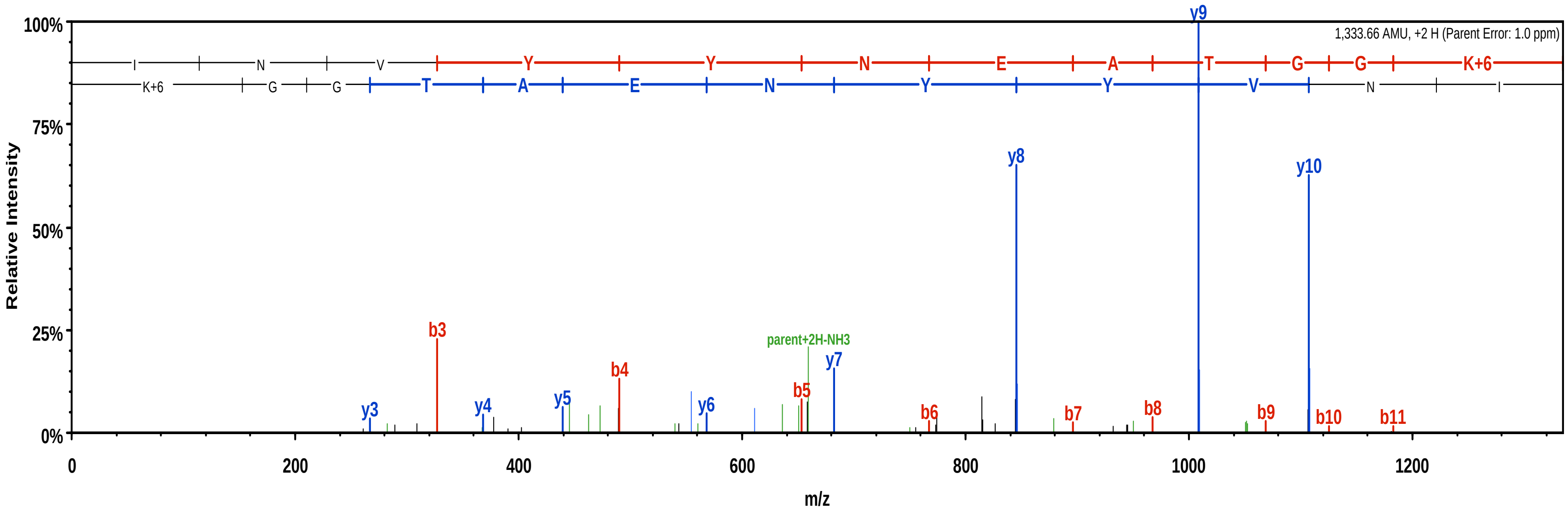


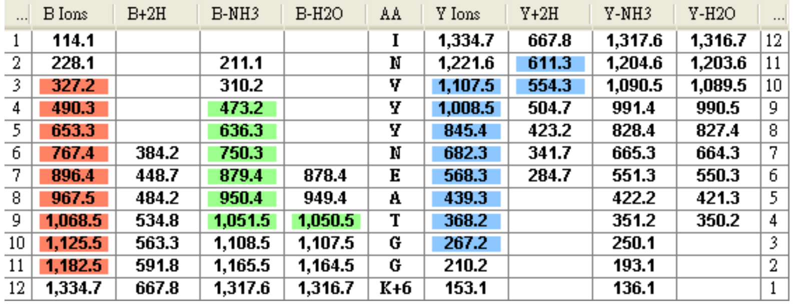


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	1,208.7	604.9	1,191.7		11
2	157.1				V	1,151.7	576.3	1,134.7		10
3	256.2				V	1,052.6	526.8	1,035.6		9
4	384.2		367.2		Q	953.6	477.3	936.5		8
5	497.3		480.3		L	825.5	413.2	808.5		7
6	644.4	322.7	627.4		F	712.4	356.7	695.4		6
7	758.4	379.7	741.4		N	565.3		548.3		5
8	829.5	415.2	812.4		A	451.3		434.3		4
9	928.5	464.8	911.5		V	380.3		363.2		3
10	1,056.6	528.8	1,039.6		Q	281.2		264.2		2
11	1,208.7	604.9	1,191.7		K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-90	sp|P68371|TBB2C_HUMAN	INVYYNEATGGK	51.18	Unmodified	Heavy	2	664.82769

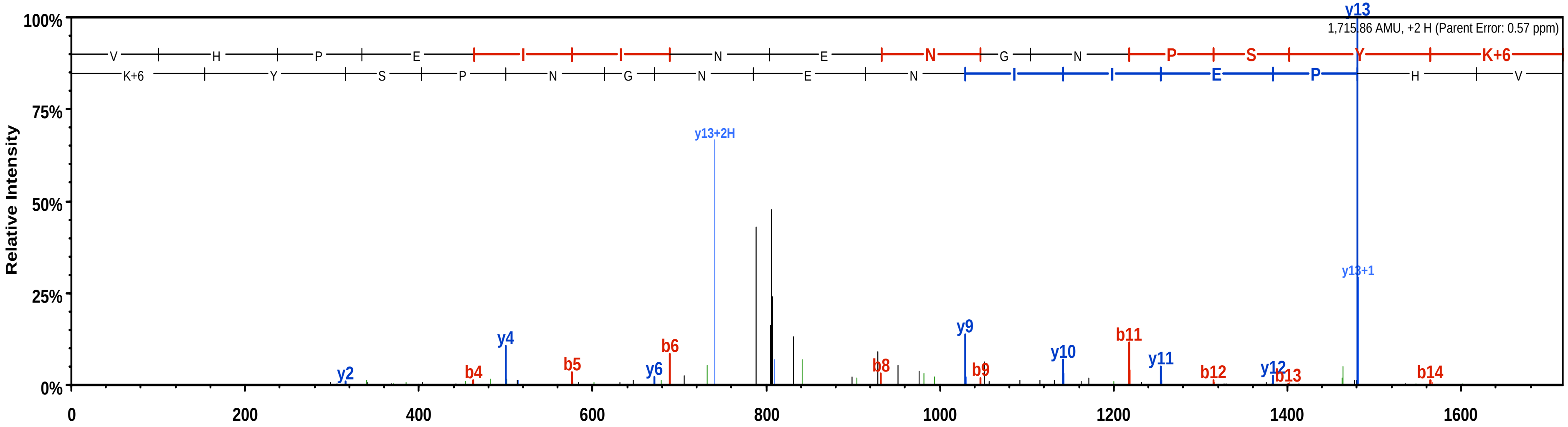


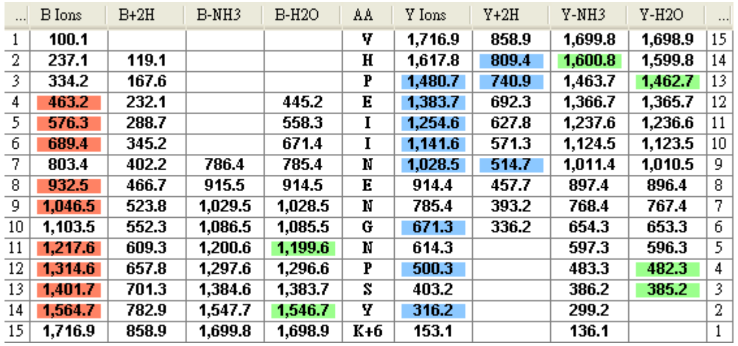


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	1,334.7	667.8	1,317.6	1,316.7	12
2	228.1		211.1		N	1,221.6	611.3	1,204.6	1,203.6	11
3	327.2		310.2		V	1,107.5	554.3	1,090.5	1,089.5	10
4	490.3		473.2		Y	1,008.5	504.7	991.4	990.5	9
5	653.3		636.3		Y	845.4	423.2	828.4	827.4	8
6	767.4	384.2	750.3		N	682.3	341.7	665.3	664.3	7
7	896.4	448.7	879.4	878.4	E	568.3	284.7	551.3	550.3	6
8	967.5	484.2	950.4	949.4	A	439.3		422.2	421.3	5
9	1,068.5	534.8	1,051.5	1,050.5	T	368.2		351.2	350.2	4
10	1,125.5	563.3	1,108.5	1,107.5	G	267.2		250.1		3
11	1,182.5	591.8	1,165.5	1,164.5	G	210.2		193.1		2
12	1,334.7	667.8	1,317.6	1,316.7	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-91	sp|O95881|TXD12_HUMAN	VHPEIINENGNPSYK	50.01	Unmodified	Heavy	2	855.92593

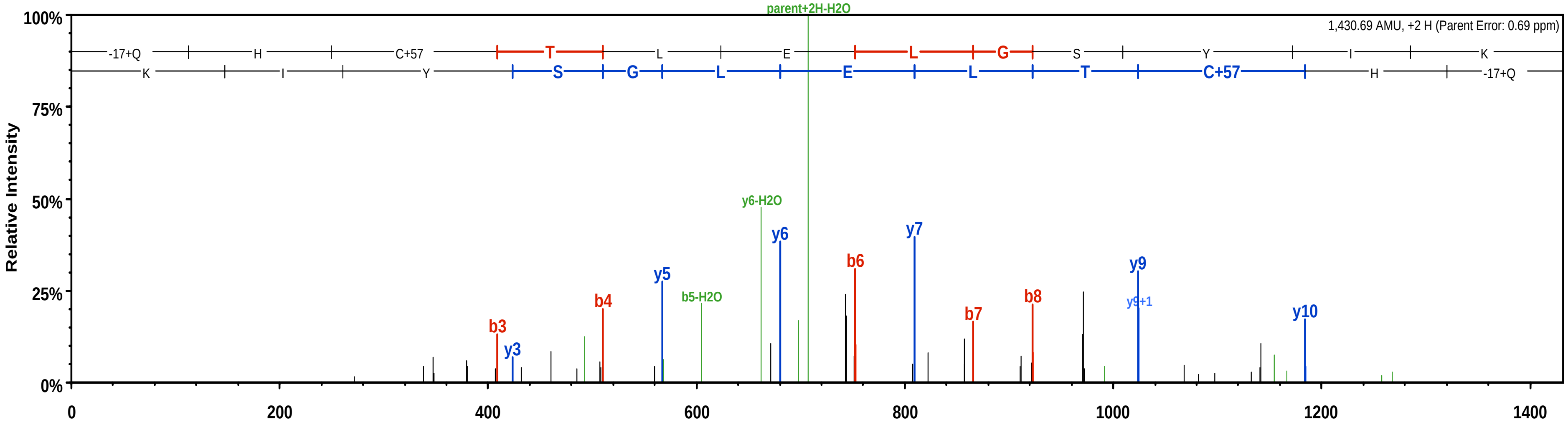


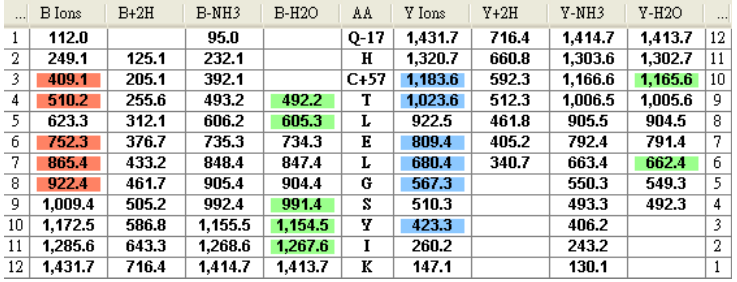


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	1,716.9	858.9	1,699.8	1,698.9	15
2	237.1	119.1			H	1,617.8	809.4	1,600.8	1,599.8	14
3	334.2	167.6			P	1,480.7	740.9	1,463.7	1,462.7	13
4	463.2	232.1		445.2	E	1,383.7	692.3	1,366.7	1,365.7	12
5	576.3	288.7		558.3	I	1,254.6	627.8	1,237.6	1,236.6	11
6	689.4	345.2		671.4	I	1,141.6	571.3	1,124.5	1,123.5	10
7	803.4	402.2	786.4	785.4	N	1,028.5	514.7	1,011.4	1,010.5	9
8	932.5	466.7	915.5	914.5	E	914.4	457.7	897.4	896.4	8
9	1,046.5	523.8	1,029.5	1,028.5	N	785.4	393.2	768.4	767.4	7
10	1,103.5	552.3	1,086.5	1,085.5	G	671.3	336.2	654.3	653.3	6
11	1,217.6	609.3	1,200.6	1,199.6	N	614.3		597.3	596.3	5
12	1,314.6	657.8	1,297.6	1,296.6	P	500.3		483.3	482.3	4
13	1,401.7	701.3	1,384.6	1,383.7	S	403.2		386.2	385.2	3
14	1,564.7	782.9	1,547.7	1,546.7	Y	316.2		299.2		2
15	1,716.9	858.9	1,699.8	1,698.9	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-92	sp|O95476|DULRD_HUMAN	QHCTLELGSYIK	49.94	Gln->pyro-Glu (N-term Q)	Light	2	716.35047

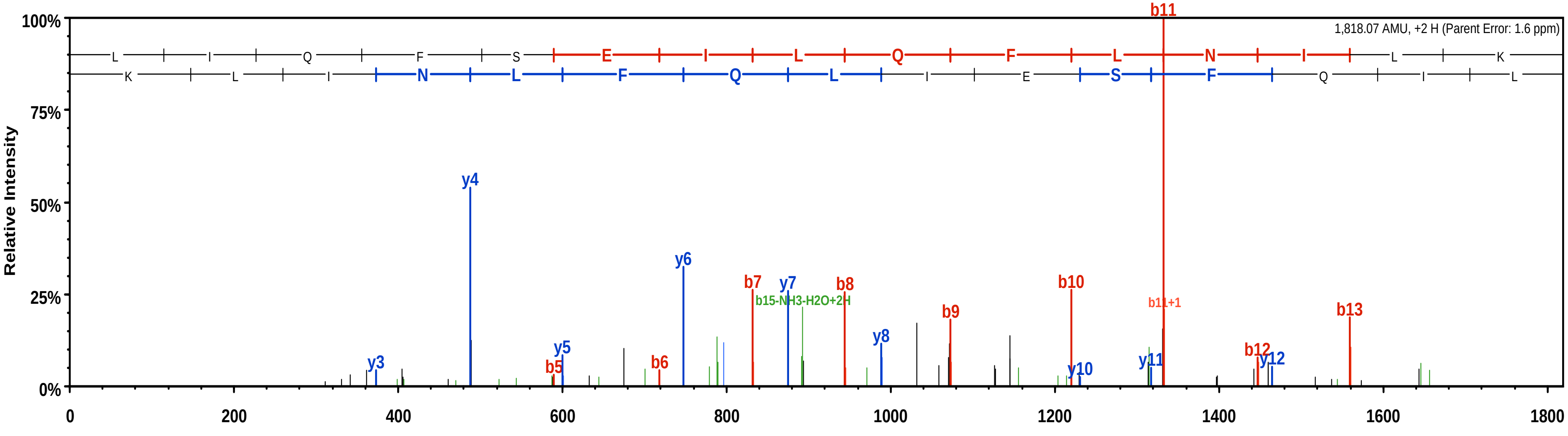


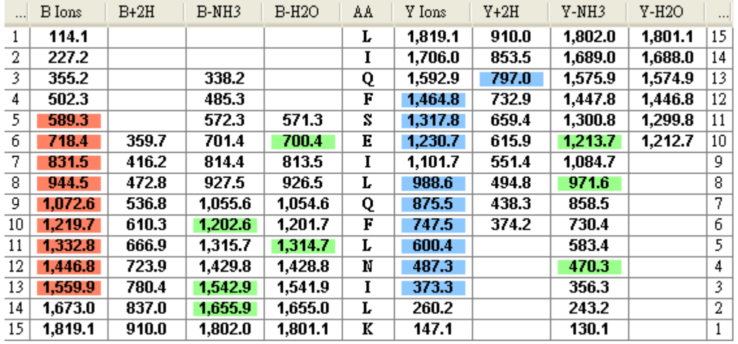


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	1,431.7	716.4	1,414.7	1,413.7	12
2	249.1	125.1	232.1		H	1,320.7	660.8	1,303.6	1,302.7	11
3	409.1	205.1	392.1		C+57	1,183.6	592.3	1,166.6	1,165.6	10
4	510.2	255.6	493.2	492.2	T	1,023.6	512.3	1,006.5	1,005.6	9
5	623.3	312.1	606.2	605.3	L	922.5	461.8	905.5	904.5	8
6	752.3	376.7	735.3	734.3	E	809.4	405.2	792.4	791.4	7
7	865.4	433.2	848.4	847.4	L	680.4	340.7	663.4	662.4	6
8	922.4	461.7	905.4	904.4	G	567.3		550.3	549.3	5
9	1,009.4	505.2	992.4	991.4	S	510.3		493.3	492.3	4
10	1,172.5	586.8	1,155.5	1,154.5	Y	423.3		406.2		3
11	1,285.6	643.3	1,268.6	1,267.6	I	260.2		243.2		2
12	1,431.7	716.4	1,414.7	1,413.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-93	sp|Q12791|KCMA1_HUMAN	LIQFSEILQFLNILK	49.53	Unmodified	Light	2	910.04003

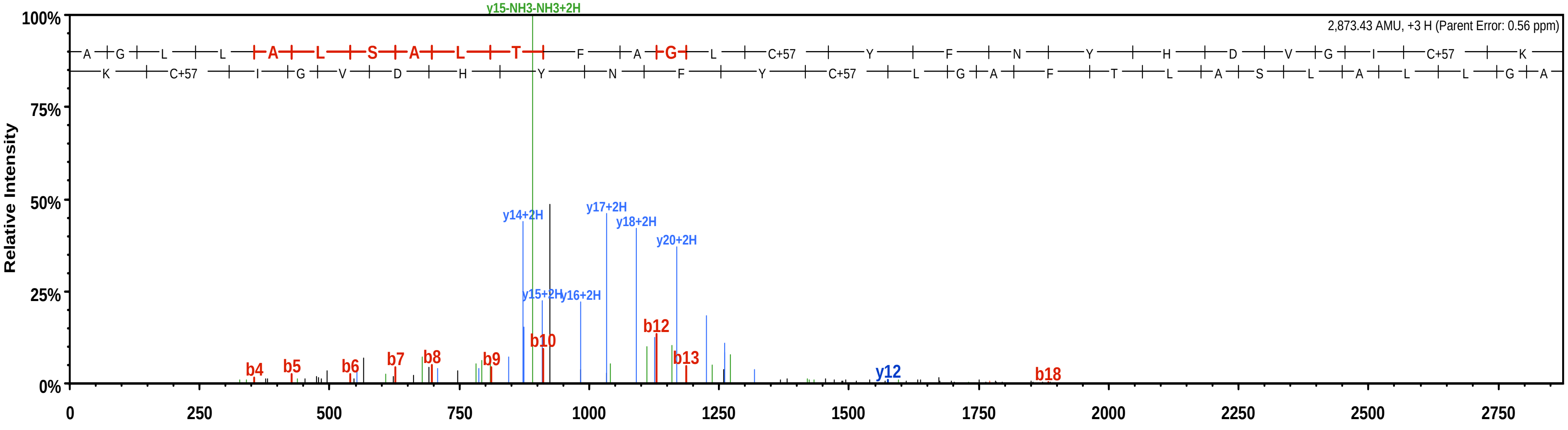


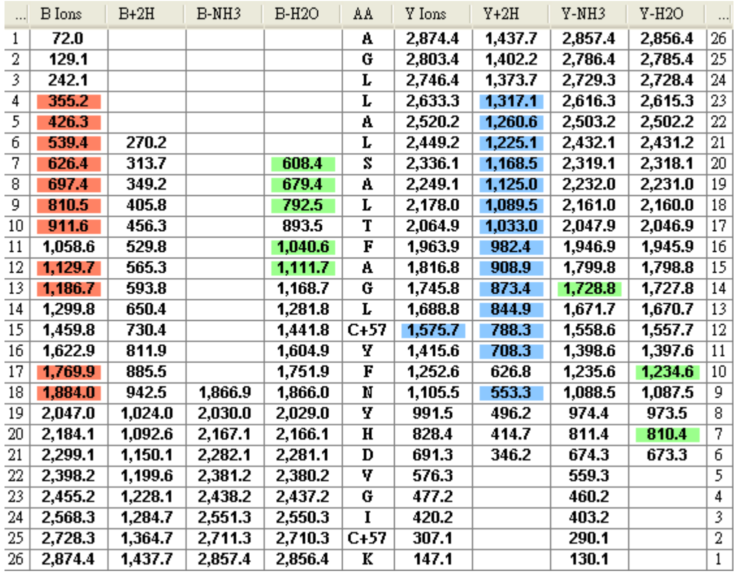


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	1,819.1	910.0	1,802.0	1,801.1	15
2	227.2				I	1,706.0	853.5	1,689.0	1,688.0	14
3	355.2		338.2		Q	1,592.9	797.0	1,575.9	1,574.9	13
4	502.3		485.3		F	1,464.8	732.9	1,447.8	1,446.8	12
5	589.3		572.3	571.3	S	1,317.8	659.4	1,300.8	1,299.8	11
6	718.4	359.7	701.4	700.4	E	1,230.7	615.9	1,213.7	1,212.7	10
7	831.5	416.2	814.4	813.5	I	1,101.7	551.4	1,084.7		9
8	944.5	472.8	927.5	926.5	L	988.6	494.8	971.6		8
9	1,072.6	536.8	1,055.6	1,054.6	Q	875.5	438.3	858.5		7
10	1,219.7	610.3	1,202.6	1,201.7	F	747.5	374.2	730.4		6
11	1,332.8	666.9	1,315.7	1,314.7	L	600.4		583.4		5
12	1,446.8	723.9	1,429.8	1,428.8	N	487.3		470.3		4
13	1,559.9	780.4	1,542.9	1,541.9	I	373.3		356.3		3
14	1,673.0	837.0	1,655.9	1,655.0	L	260.2		243.2		2
15	1,819.1	910.0	1,802.0	1,801.1	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-94	sp|O14521|DHSD_HUMAN	AGLLALSALTFAGLCYFNYHDVGICK	49.45	Unmodified	Light	3	958.81542

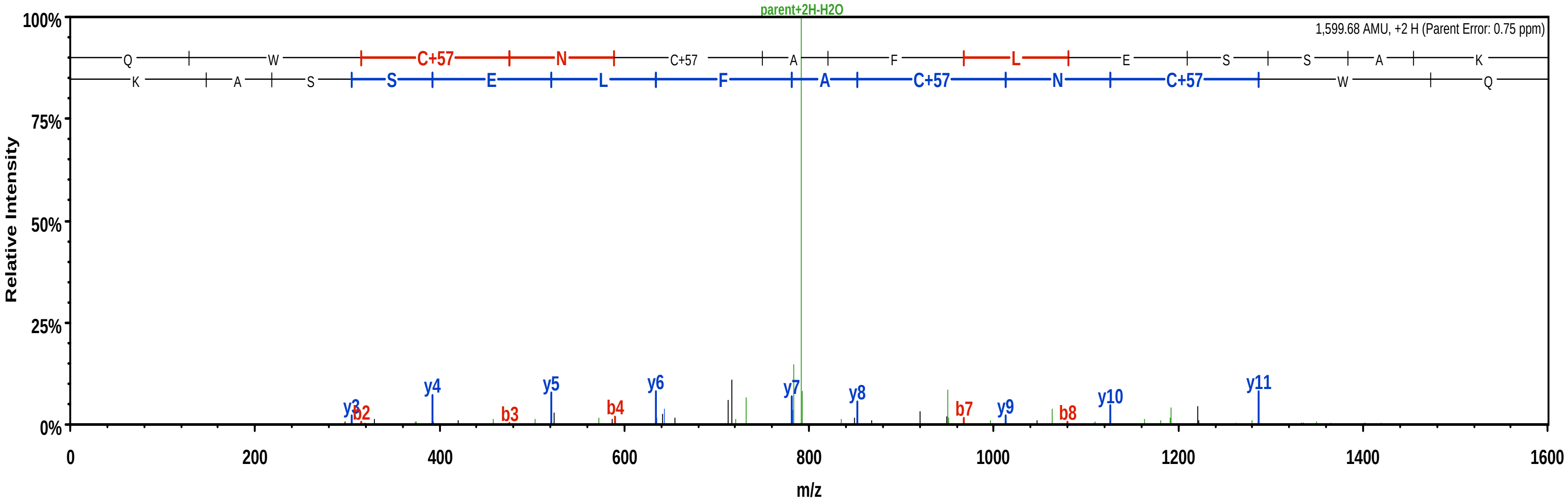


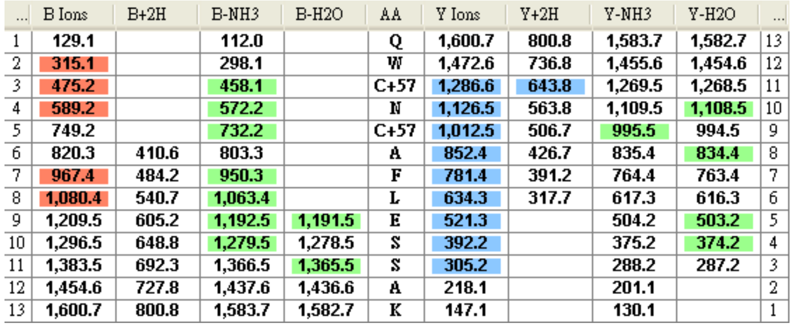


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	2,874.4	1,437.7	2,857.4	2,856.4	26
2	129.1				G	2,803.4	1,402.2	2,786.4	2,785.4	25
3	242.1				L	2,746.4	1,373.7	2,729.3	2,728.4	24
4	355.2				L	2,633.3	1,317.1	2,616.3	2,615.3	23
5	426.3				A	2,520.2	1,260.6	2,503.2	2,502.2	22
6	539.4	270.2			L	2,449.2	1,225.1	2,432.1	2,431.2	21
7	626.4	313.7		608.4	S	2,336.1	1,168.5	2,319.1	2,318.1	20
8	697.4	349.2		679.4	A	2,249.1	1,125.0	2,232.0	2,231.0	19
9	810.5	405.8		792.5	L	2,178.0	1,089.5	2,161.0	2,160.0	18
10	911.6	456.3		893.5	T	2,064.9	1,033.0	2,047.9	2,046.9	17
11	1,058.6	529.8		1,040.6	F	1,963.9	982.4	1,946.9	1,945.9	16
12	1,129.7	565.3		1,111.7	A	1,816.8	908.9	1,799.8	1,798.8	15
13	1,186.7	593.8		1,168.7	G	1,745.8	873.4	1,728.8	1,727.8	14
14	1,299.8	650.4		1,281.8	L	1,688.8	844.9	1,671.7	1,670.7	13
15	1,459.8	730.4		1,441.8	C+57	1,575.7	788.3	1,558.6	1,557.7	12
16	1,622.9	811.9		1,604.9	Y	1,415.6	708.3	1,398.6	1,397.6	11
17	1,769.9	885.5		1,751.9	F	1,252.6	626.8	1,235.6	1,234.6	10
18	1,884.0	942.5	1,866.9	1,866.0	N	1,105.5	553.3	1,088.5	1,087.5	9
19	2,047.0	1,024.0	2,030.0	2,029.0	Y	991.5	496.2	974.4	973.5	8
20	2,184.1	1,092.6	2,167.1	2,166.1	H	828.4	414.7	811.4	810.4	7
21	2,299.1	1,150.1	2,282.1	2,281.1	D	691.3	346.2	674.3	673.3	6
22	2,398.2	1,199.6	2,381.2	2,380.2	V	576.3		559.3		5
23	2,455.2	1,228.1	2,438.2	2,437.2	G	477.2		460.2		4
24	2,568.3	1,284.7	2,551.3	2,550.3	I	420.2		403.2		3
25	2,728.3	1,364.7	2,711.3	2,710.3	C+57	307.1		290.1		2
26	2,874.4	1,437.7	2,857.4	2,856.4	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-95	sp|P62834|RAP1A_HUMAN	QWCNCAFLESSAK	48.95	Unmodified	Light	2	800.84777

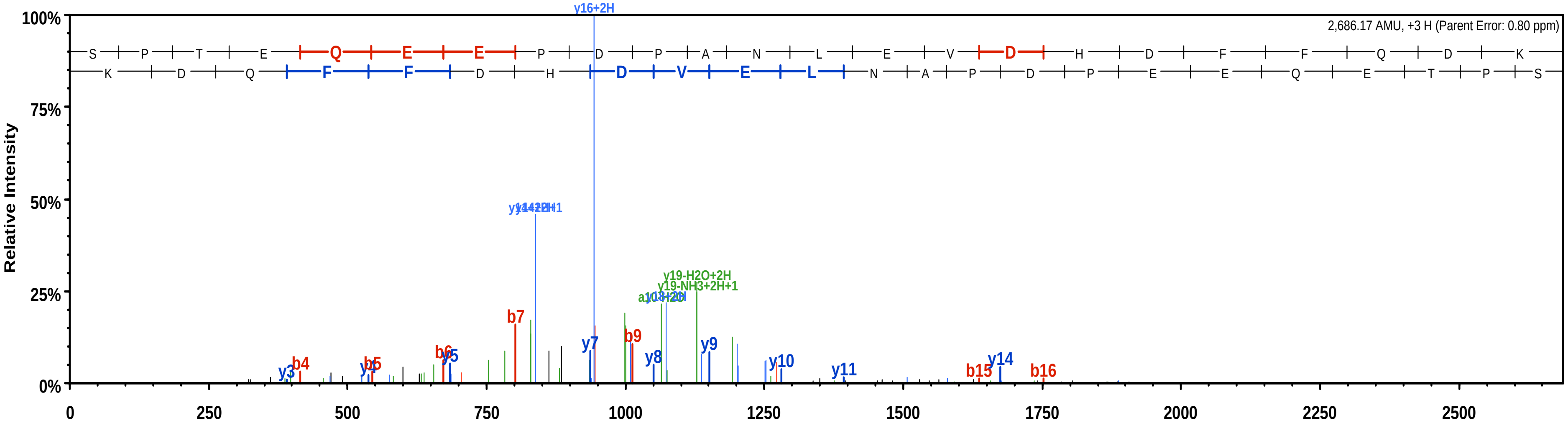


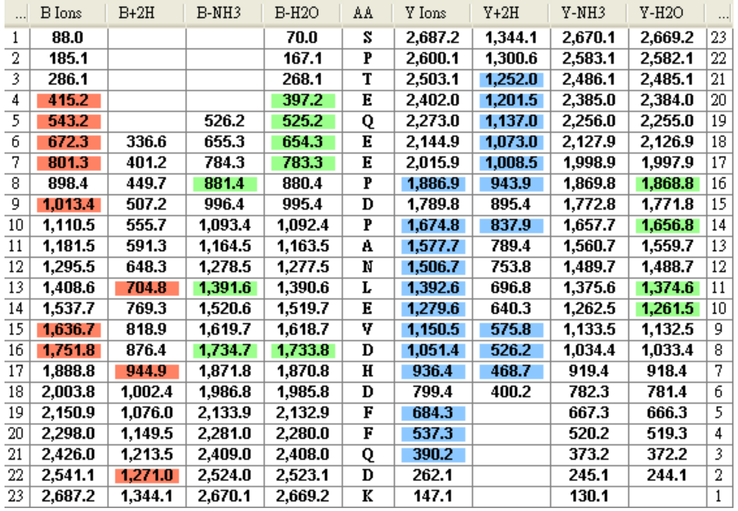


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	129.1		112.0		Q	1,600.7	800.8	1,583.7	1,582.7	13
2	315.1		298.1		W	1,472.6	736.8	1,455.6	1,454.6	12
3	475.2		458.1		C+57	1,286.6	643.8	1,269.5	1,268.5	11
4	589.2		572.2		N	1,126.5	563.8	1,109.5	1,108.5	10
5	749.2		732.2		C+57	1,012.5	506.7	995.5	994.5	9
6	820.3	410.6	803.3		A	852.4	426.7	835.4	834.4	8
7	967.4	484.2	950.3		F	781.4	391.2	764.4	763.4	7
8	1,080.4	540.7	1,063.4		L	634.3	317.7	617.3	616.3	6
9	1,209.5	605.2	1,192.5	1,191.5	E	521.3		504.2	503.2	5
10	1,296.5	648.8	1,279.5	1,278.5	S	392.2		375.2	374.2	4
11	1,383.5	692.3	1,366.5	1,365.5	S	305.2		288.2	287.2	3
12	1,454.6	727.8	1,437.6	1,436.6	A	218.1		201.1		2
13	1,600.7	800.8	1,583.7	1,582.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-96	sp|Q96CU9|FXRD1_HUMAN	SPTEQEEPDPANLEVDHDFFQDK	48.94	Unmodified	Light	3	896.3963

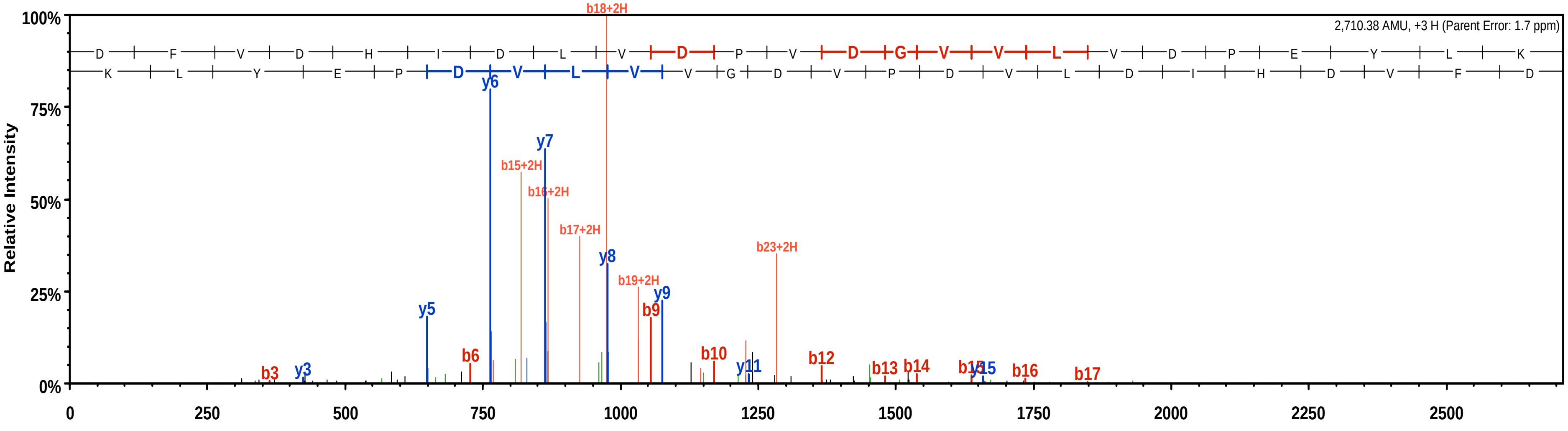


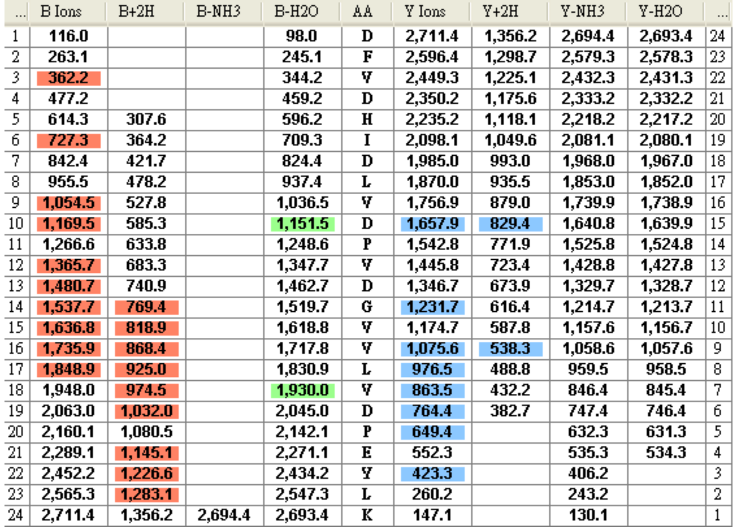


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	2,687.2	1,344.1	2,670.1	2,669.2	23
2	185.1			167.1	P	2,600.1	1,300.6	2,583.1	2,582.1	22
3	286.1			268.1	T	2,503.1	1,252.0	2,486.1	2,485.1	21
4	415.2			397.2	E	2,402.0	1,201.5	2,385.0	2,384.0	20
5	543.2		526.2	525.2	Q	2,273.0	1,137.0	2,256.0	2,255.0	19
6	672.3	336.6	655.3	654.3	E	2,144.9	1,073.0	2,127.9	2,126.9	18
7	801.3	401.2	784.3	783.3	E	2,015.9	1,008.5	1,998.9	1,997.9	17
8	898.4	449.7	881.4	880.4	P	1,886.9	943.9	1,869.8	1,868.8	16
9	1,013.4	507.2	996.4	995.4	D	1,789.8	895.4	1,772.8	1,771.8	15
10	1,110.5	555.7	1,093.4	1,092.4	P	1,674.8	837.9	1,657.7	1,656.8	14
11	1,181.5	591.3	1,164.5	1,163.5	A	1,577.7	789.4	1,560.7	1,559.7	13
12	1,295.5	648.3	1,278.5	1,277.5	N	1,506.7	753.8	1,489.7	1,488.7	12
13	1,408.6	704.8	1,391.6	1,390.6	L	1,392.6	696.8	1,375.6	1,374.6	11
14	1,537.7	769.3	1,520.6	1,519.7	E	1,279.6	640.3	1,262.5	1,261.5	10
15	1,636.7	818.9	1,619.7	1,618.7	V	1,150.5	575.8	1,133.5	1,132.5	9
16	1,751.8	876.4	1,734.7	1,733.8	D	1,051.4	526.2	1,034.4	1,033.4	8
17	1,888.8	944.9	1,871.8	1,870.8	H	936.4	468.7	919.4	918.4	7
18	2,003.8	1,002.4	1,986.8	1,985.8	D	799.4	400.2	782.3	781.4	6
19	2,150.9	1,076.0	2,133.9	2,132.9	F	684.3		667.3	666.3	5
20	2,298.0	1,149.5	2,281.0	2,280.0	F	537.3		520.2	519.3	4
21	2,426.0	1,213.5	2,409.0	2,408.0	Q	390.2		373.2	372.2	3
22	2,541.1	1,271.0	2,524.0	2,523.1	D	262.1		245.1	244.1	2
23	2,687.2	1,344.1	2,670.1	2,669.2	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-97	sp|P49407|ARRB1_HUMAN	DFVDHIDLVDPVDGVVLVDPEYLK	47.1	Unmodified	Light	3	904.46533

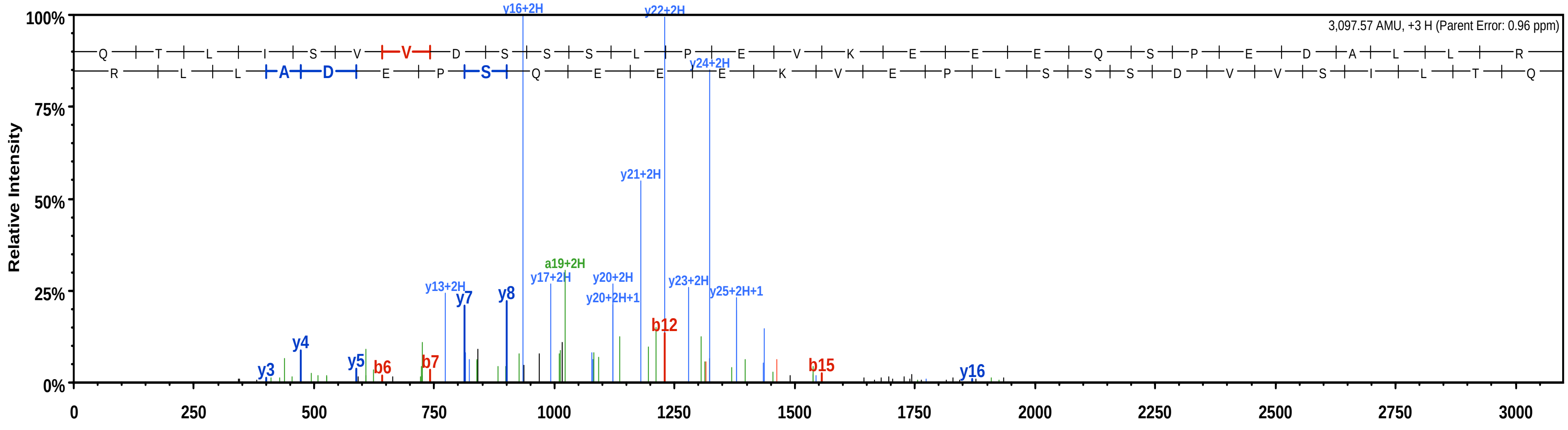


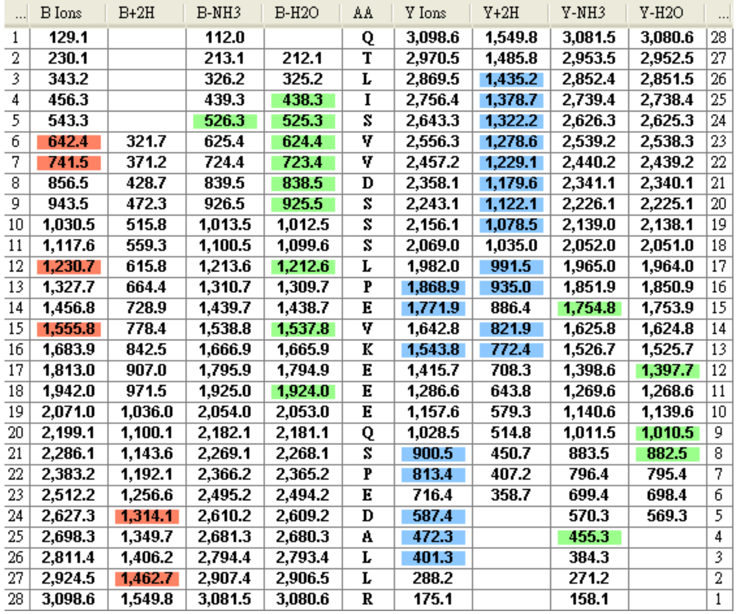


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	2,711.4	1,356.2	2,694.4	2,693.4	24
2	263.1			245.1	F	2,596.4	1,298.7	2,579.3	2,578.3	23
3	362.2			344.2	V	2,449.3	1,225.1	2,432.3	2,431.3	22
4	477.2			459.2	D	2,350.2	1,175.6	2,333.2	2,332.2	21
5	614.3	307.6		596.2	H	2,235.2	1,118.1	2,218.2	2,217.2	20
6	727.3	364.2		709.3	I	2,098.1	1,049.6	2,081.1	2,080.1	19
7	842.4	421.7		824.4	D	1,985.0	993.0	1,968.0	1,967.0	18
8	955.5	478.2		937.4	L	1,870.0	935.5	1,853.0	1,852.0	17
9	1,054.5	527.8		1,036.5	V	1,756.9	879.0	1,739.9	1,738.9	16
10	1,169.5	585.3		1,151.5	D	1,657.9	829.4	1,640.8	1,639.9	15
11	1,266.6	633.8		1,248.6	P	1,542.8	771.9	1,525.8	1,524.8	14
12	1,365.7	683.3		1,347.7	V	1,445.8	723.4	1,428.8	1,427.8	13
13	1,480.7	740.9		1,462.7	D	1,346.7	673.9	1,329.7	1,328.7	12
14	1,537.7	769.4		1,519.7	G	1,231.7	616.4	1,214.7	1,213.7	11
15	1,636.8	818.9		1,618.8	V	1,174.7	587.8	1,157.6	1,156.7	10
16	1,735.9	868.4		1,717.8	V	1,075.6	538.3	1,058.6	1,057.6	9
17	1,848.9	925.0		1,830.9	L	976.5	488.8	959.5	958.5	8
18	1,948.0	974.5		1,930.0	V	863.5	432.2	846.4	845.4	7
19	2,063.0	1,032.0		2,045.0	D	764.4	382.7	747.4	746.4	6
20	2,160.1	1,080.5		2,142.1	P	649.4		632.3	631.3	5
21	2,289.1	1,145.1		2,271.1	E	552.3		535.3	534.3	4
22	2,452.2	1,226.6		2,434.2	Y	423.3		406.2		3
23	2,565.3	1,283.1		2,547.3	L	260.2		243.2		2
24	2,711.4	1,356.2	2,694.4	2,693.4	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-98	sp|Q9UBS9|CA009_HUMAN	QTLISVVDSSSLPEVKEEEQSPEDALLR	46.92	Unmodified	Light	3	1033.5295

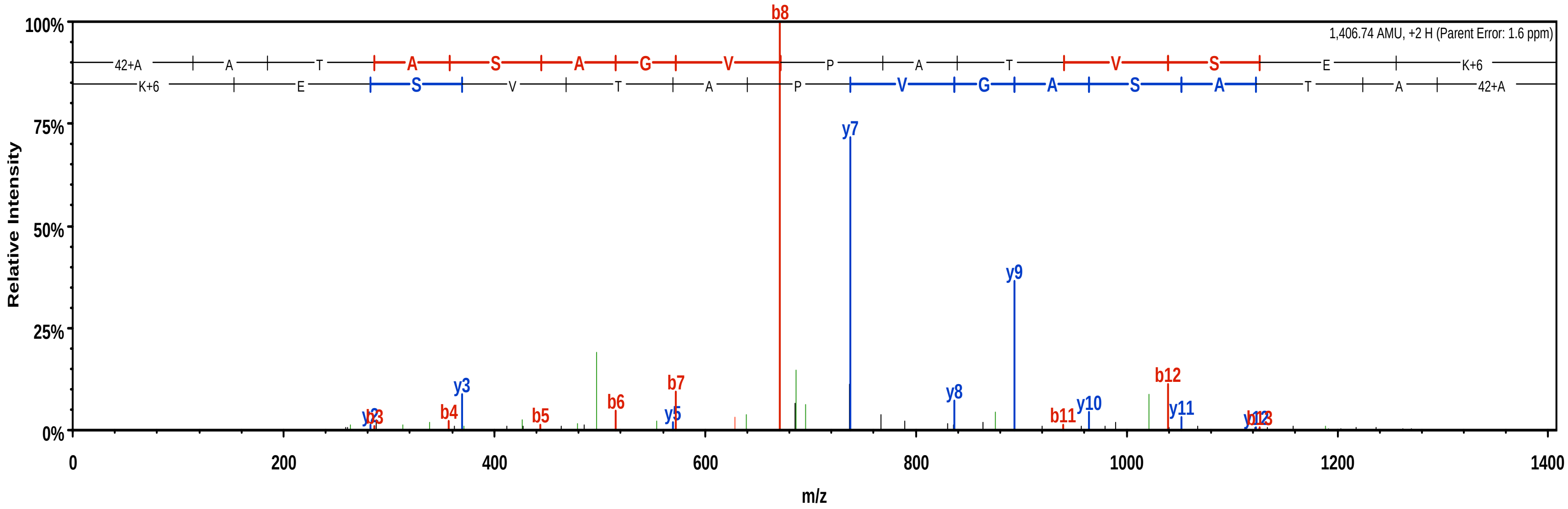


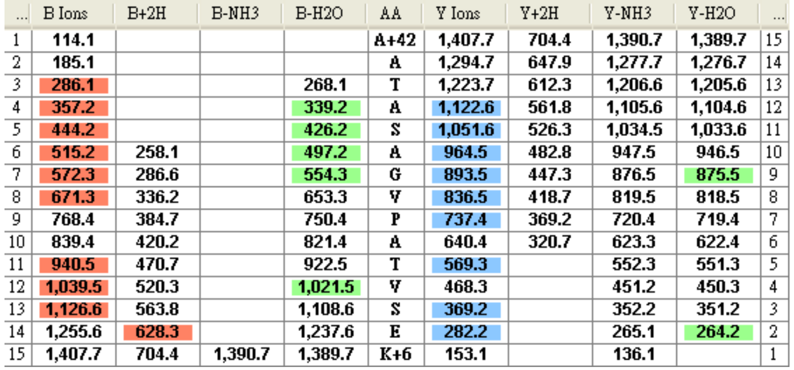


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	129.1		112.0		Q	3,098.6	1,549.8	3,081.5	3,080.6	28
2	230.1		213.1	212.1	T	2,970.5	1,485.8	2,953.5	2,952.5	27
3	343.2		326.2	325.2	L	2,869.5	1,435.2	2,852.4	2,851.5	26
4	456.3		439.3	438.3	I	2,756.4	1,378.7	2,739.4	2,738.4	25
5	543.3		526.3	525.3	S	2,643.3	1,322.2	2,626.3	2,625.3	24
6	642.4	321.7	625.4	624.4	V	2,556.3	1,278.6	2,539.2	2,538.3	23
7	741.5	371.2	724.4	723.4	V	2,457.2	1,229.1	2,440.2	2,439.2	22
8	856.5	428.7	839.5	838.5	D	2,358.1	1,179.6	2,341.1	2,340.1	21
9	943.5	472.3	926.5	925.5	S	2,243.1	1,122.1	2,226.1	2,225.1	20
10	1,030.5	515.8	1,013.5	1,012.5	S	2,156.1	1,078.5	2,139.0	2,138.1	19
11	1,117.6	559.3	1,100.5	1,099.6	S	2,069.0	1,035.0	2,052.0	2,051.0	18
12	1,230.7	615.8	1,213.6	1,212.6	L	1,982.0	991.5	1,965.0	1,964.0	17
13	1,327.7	664.4	1,310.7	1,309.7	P	1,868.9	935.0	1,851.9	1,850.9	16
14	1,456.8	728.9	1,439.7	1,438.7	E	1,771.9	886.4	1,754.8	1,753.9	15
15	1,555.8	778.4	1,538.8	1,537.8	V	1,642.8	821.9	1,625.8	1,624.8	14
16	1,683.9	842.5	1,666.9	1,665.9	K	1,543.8	772.4	1,526.7	1,525.7	13
17	1,813.0	907.0	1,795.9	1,794.9	E	1,415.7	708.3	1,398.6	1,397.7	12
18	1,942.0	971.5	1,925.0	1,924.0	E	1,286.6	643.8	1,269.6	1,268.6	11
19	2,071.0	1,036.0	2,054.0	2,053.0	E	1,157.6	579.3	1,140.6	1,139.6	10
20	2,199.1	1,100.1	2,182.1	2,181.1	Q	1,028.5	514.8	1,011.5	1,010.5	9
21	2,286.1	1,143.6	2,269.1	2,268.1	S	900.5	450.7	883.5	882.5	8
22	2,383.2	1,192.1	2,366.2	2,365.2	P	813.4	407.2	796.4	795.4	7
23	2,512.2	1,256.6	2,495.2	2,494.2	E	716.4	358.7	699.4	698.4	6
24	2,627.3	1,314.1	2,610.2	2,609.2	D	587.4		570.3	569.3	5
25	2,698.3	1,349.7	2,681.3	2,680.3	A	472.3		455.3		4
26	2,811.4	1,406.2	2,794.4	2,793.4	L	401.3		384.3		3
27	2,924.5	1,462.7	2,907.4	2,906.5	L	288.2		271.2		2
28	3,098.6	1,549.8	3,081.5	3,080.6	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-99	sp|O60518|RNBP6_HUMAN	AATASAGVPATVSEK	45.75	Acetyl (Protein N-term)	Heavy	2	701.36464

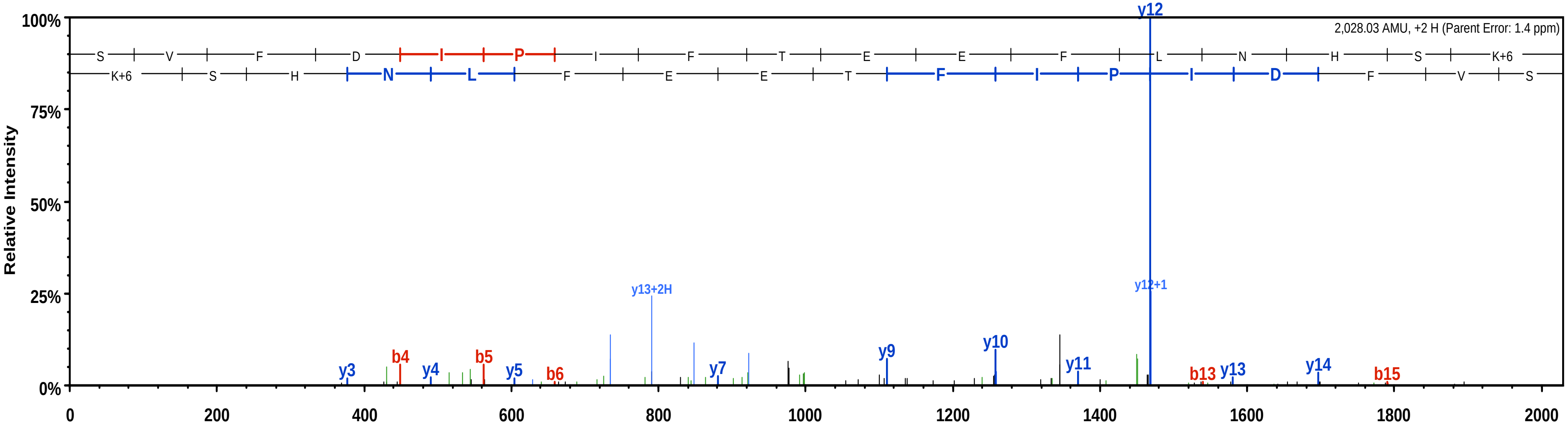


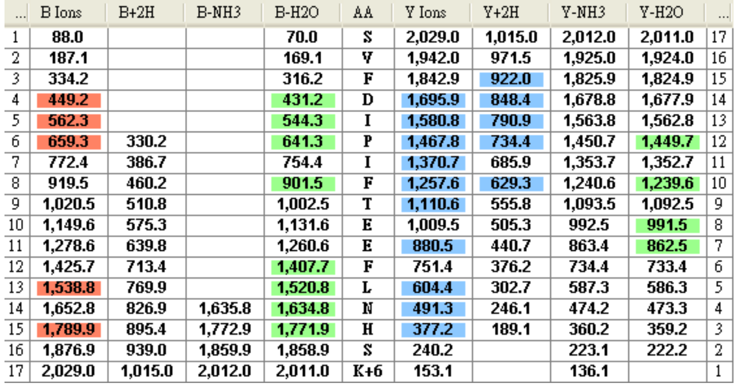


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	1,407.7	704.4	1,390.7	1,389.7	15
2	185.1				A	1,294.7	647.9	1,277.7	1,276.7	14
3	286.1			268.1	T	1,223.7	612.3	1,206.6	1,205.6	13
4	357.2			339.2	A	1,122.6	561.8	1,105.6	1,104.6	12
5	444.2			426.2	S	1,051.6	526.3	1,034.5	1,033.6	11
6	515.2	258.1		497.2	A	964.5	482.8	947.5	946.5	10
7	572.3	286.6		554.3	G	893.5	447.3	876.5	875.5	9
8	671.3	336.2		653.3	V	836.5	418.7	819.5	818.5	8
9	768.4	384.7		750.4	P	737.4	369.2	720.4	719.4	7
10	839.4	420.2		821.4	A	640.4	320.7	623.3	622.4	6
11	940.5	470.7		922.5	T	569.3		552.3	551.3	5
12	1,039.5	520.3		1,021.5	V	468.3		451.2	450.3	4
13	1,126.6	563.8		1,108.6	S	369.2		352.2	351.2	3
14	1,255.6	628.3		1,237.6	E	282.2		265.1	264.2	2
15	1,407.7	704.4	1,390.7	1,389.7	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-100	sp|Q9NP66|HM20A_HUMAN	SVFDIPIFTEEFLNHSK	45.48	Unmodified	Heavy	2	1012.0122

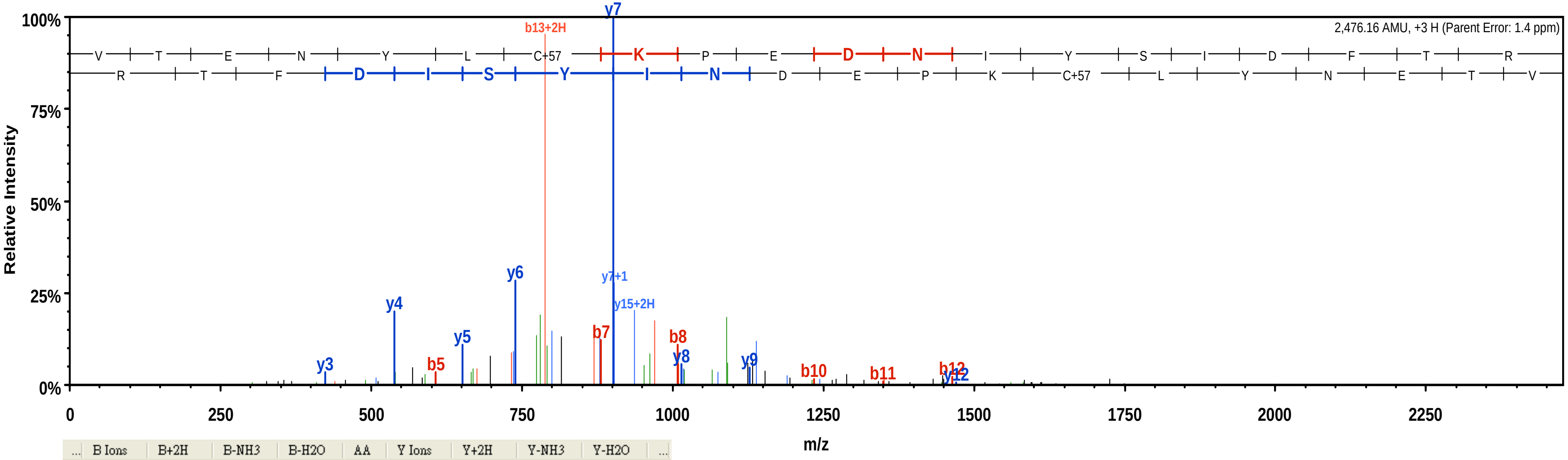


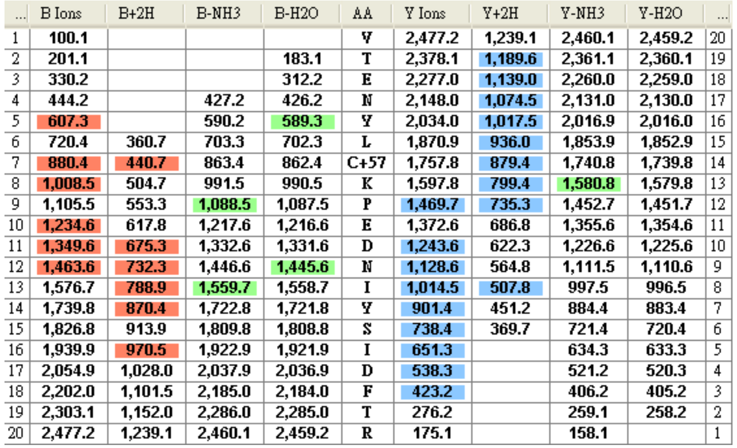


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	2,029.0	1,015.0	2,012.0	2,011.0	17
2	187.1			169.1	V	1,942.0	971.5	1,925.0	1,924.0	16
3	334.2			316.2	F	1,842.9	922.0	1,825.9	1,824.9	15
4	449.2			431.2	D	1,695.9	848.4	1,678.8	1,677.9	14
5	562.3			544.3	I	1,580.8	790.9	1,563.8	1,562.8	13
6	659.3	330.2		641.3	P	1,467.8	734.4	1,450.7	1,449.7	12
7	772.4	386.7		754.4	I	1,370.7	685.9	1,353.7	1,352.7	11
8	919.5	460.2		901.5	F	1,257.6	629.3	1,240.6	1,239.6	10
9	1,020.5	510.8		1,002.5	T	1,110.6	555.8	1,093.5	1,092.5	9
10	1,149.6	575.3		1,131.6	E	1,009.5	505.3	992.5	991.5	8
11	1,278.6	639.8		1,260.6	E	880.5	440.7	863.4	862.5	7
12	1,425.7	713.4		1,407.7	F	751.4	376.2	734.4	733.4	6
13	1,538.8	769.9		1,520.8	L	604.4	302.7	587.3	586.3	5
14	1,652.8	826.9	1,635.8	1,634.8	N	491.3	246.1	474.2	473.3	4
15	1,789.9	895.4	1,772.9	1,771.9	H	377.2	189.1	360.2	359.2	3
16	1,876.9	939.0	1,859.9	1,858.9	S	240.2		223.1	222.2	2
17	2,029.0	1,015.0	2,012.0	2,011.0	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-101	splA6NIH7lU119B_HUMAN	VTENYLCKPEDNIYSIDFTR	44.48	Unmodified	Light	3	826.39329

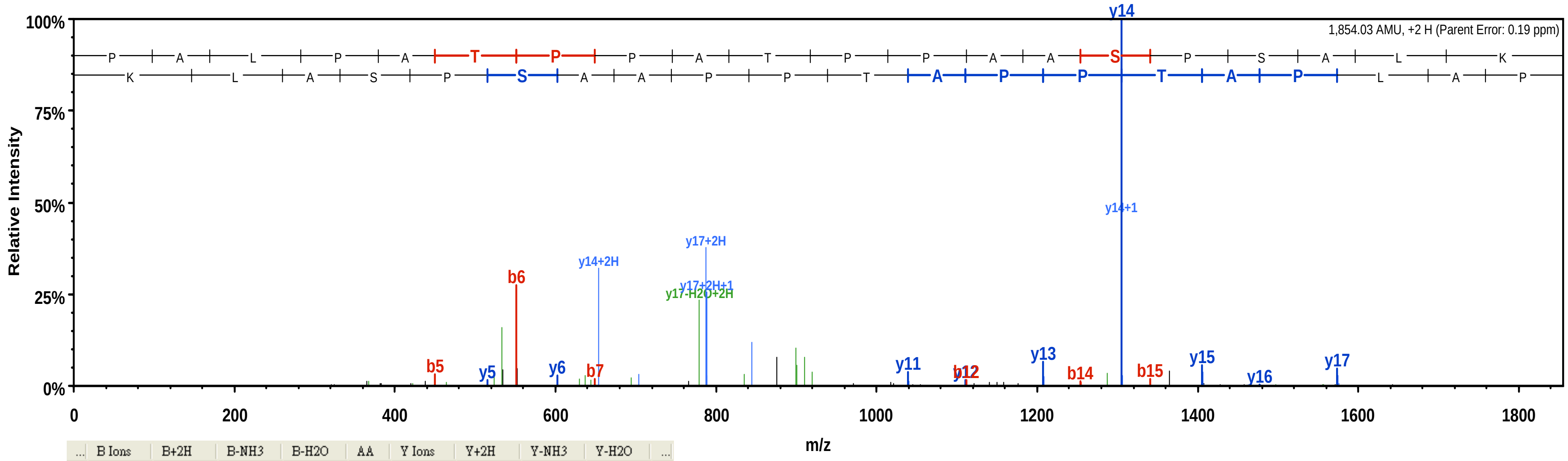


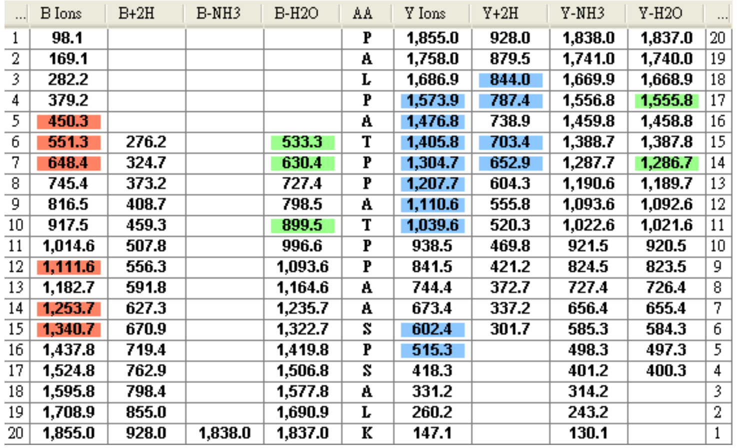


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	2,477.2	1,239.1	2,460.1	2,459.2	20
2	201.1			183.1	T	2,378.1	1,189.6	2,361.1	2,360.1	19
3	330.2			312.2	E	2,277.0	1,139.0	2,260.0	2,259.0	18
4	444.2		427.2	426.2	N	2,148.0	1,074.5	2,131.0	2,130.0	17
5	607.3		590.2	589.3	Y	2,034.0	1,017.5	2,016.9	2,016.0	16
6	720.4	360.7	703.3	702.3	L	1,870.9	936.0	1,853.9	1,852.9	15
7	880.4	440.7	863.4	862.4	C+57	1,757.8	879.4	1,740.8	1,739.8	14
8	1,008.5	504.7	991.5	990.5	K	1,597.8	799.4	1,580.8	1,579.8	13
9	1,105.5	553.3	1,088.5	1,087.5	P	1,469.7	735.3	1,452.7	1,451.7	12
10	1,234.6	617.8	1,217.6	1,216.6	E	1,372.6	686.8	1,355.6	1,354.6	11
11	1,349.6	675.3	1,332.6	1,331.6	D	1,243.6	622.3	1,226.6	1,225.6	10
12	1,463.6	732.3	1,446.6	1,445.6	N	1,128.6	564.8	1,111.5	1,110.6	9
13	1,576.7	788.9	1,559.7	1,558.7	I	1,014.5	507.8	997.5	996.5	8
14	1,739.8	870.4	1,722.8	1,721.8	Y	901.4	451.2	884.4	883.4	7
15	1,826.8	913.9	1,809.8	1,808.8	S	738.4	369.7	721.4	720.4	6
16	1,939.9	970.5	1,922.9	1,921.9	I	651.3		634.3	633.3	5
17	2,054.9	1,028.0	2,037.9	2,036.9	D	538.3		521.2	520.3	4
18	2,202.0	1,101.5	2,185.0	2,184.0	F	423.2		406.2	405.2	3
19	2,303.1	1,152.0	2,286.0	2,285.0	T	276.2		259.1	258.2	2
20	2,477.2	1,239.1	2,460.1	2,459.2	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-102	sp|Q9H211|CDT1_HUMAN	PALPATPPATPPAASPSALK	44.16	Unmodified	Light	2	928.01983

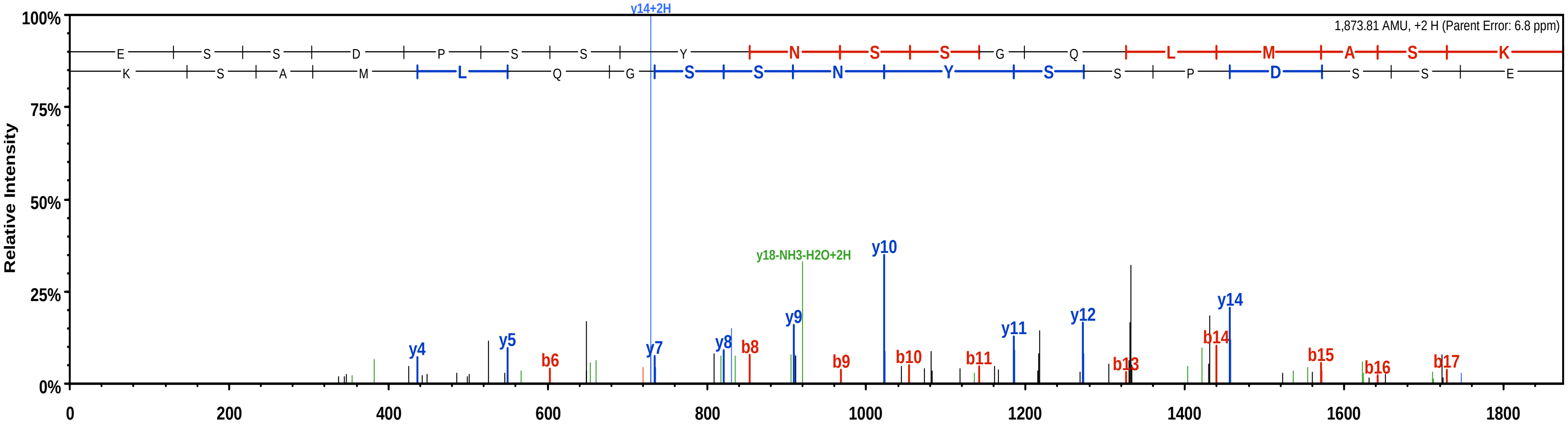


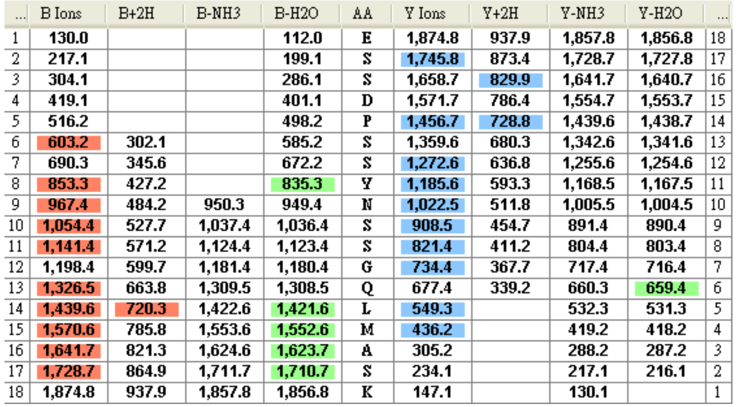


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	98.1				P	1,855.0	928.0	1,838.0	1,837.0	20
2	169.1				A	1,758.0	879.5	1,741.0	1,740.0	19
3	282.2				L	1,686.9	844.0	1,669.9	1,668.9	18
4	379.2				P	1,573.9	787.4	1,556.8	1,555.8	17
5	450.3				A	1,476.8	738.9	1,459.8	1,458.8	16
6	551.3	276.2		533.3	T	1,405.8	703.4	1,388.7	1,387.8	15
7	648.4	324.7		630.4	P	1,304.7	652.9	1,287.7	1,286.7	14
8	745.4	373.2		727.4	P	1,207.7	604.3	1,190.6	1,189.7	13
9	816.5	408.7		798.5	A	1,110.6	555.8	1,093.6	1,092.6	12
10	917.5	459.3		899.5	T	1,039.6	520.3	1,022.6	1,021.6	11
11	1,014.6	507.8		996.6	P	938.5	469.8	921.5	920.5	10
12	1,111.6	556.3		1,093.6	P	841.5	421.2	824.5	823.5	9
13	1,182.7	591.8		1,164.6	A	744.4	372.7	727.4	726.4	8
14	1,253.7	627.3		1,235.7	A	673.4	337.2	656.4	655.4	7
15	1,340.7	670.9		1,322.7	S	602.4	301.7	585.3	584.3	6
16	1,437.8	719.4		1,419.8	P	515.3		498.3	497.3	5
17	1,524.8	762.9		1,506.8	S	418.3		401.2	400.3	4
18	1,595.8	798.4		1,577.8	A	331.2		314.2		3
19	1,708.9	855.0		1,690.9	L	260.2		243.2		2
20	1,855.0	928.0	1,838.0	1,837.0	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-103	sp|P25116|PAR1_HUMAN	ESSDPSSYNSSGQLMASK	43.13	Unmodified	Light	2	937.90727

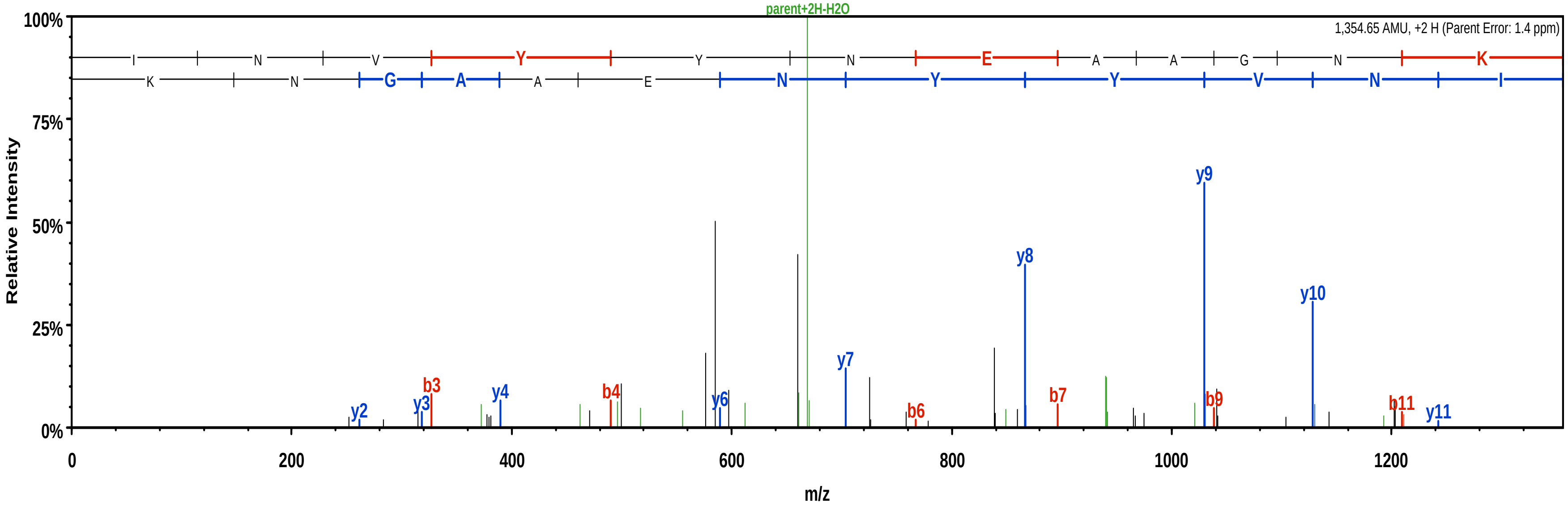


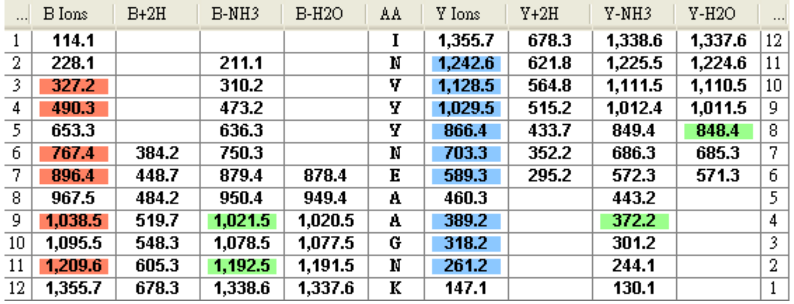


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	1,874.8	937.9	1,857.8	1,856.8	18
2	217.1			199.1	S	1,745.8	873.4	1,728.7	1,727.8	17
3	304.1			286.1	S	1,658.7	829.9	1,641.7	1,640.7	16
4	419.1			401.1	D	1,571.7	786.4	1,554.7	1,553.7	15
5	516.2			498.2	P	1,456.7	728.8	1,439.6	1,438.7	14
6	603.2	302.1		585.2	S	1,359.6	680.3	1,342.6	1,341.6	13
7	690.3	345.6		672.2	S	1,272.6	636.8	1,255.6	1,254.6	12
8	853.3	427.2		835.3	Y	1,185.6	593.3	1,168.5	1,167.5	11
9	967.4	484.2	950.3	949.4	N	1,022.5	511.8	1,005.5	1,004.5	10
10	1,054.4	527.7	1,037.4	1,036.4	S	908.5	454.7	891.4	890.4	9
11	1,141.4	571.2	1,124.4	1,123.4	S	821.4	411.2	804.4	803.4	8
12	1,198.4	599.7	1,181.4	1,180.4	G	734.4	367.7	717.4	716.4	7
13	1,326.5	663.8	1,309.5	1,308.5	Q	677.4	339.2	660.3	659.4	6
14	1,439.6	720.3	1,422.6	1,421.6	L	549.3		532.3	531.3	5
15	1,570.6	785.8	1,553.6	1,552.6	M	436.2		419.2	418.2	4
16	1,641.7	821.3	1,624.6	1,623.7	A	305.2		288.2	287.2	3
17	1,728.7	864.9	1,711.7	1,710.7	S	234.1		217.1	216.1	2
18	1,874.8	937.9	1,857.8	1,856.8	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-104	sp|Q13885|TBB2A_HUMAN	INVYYNEAAGNK	42.93	Unmodified	Light	2	678.33314

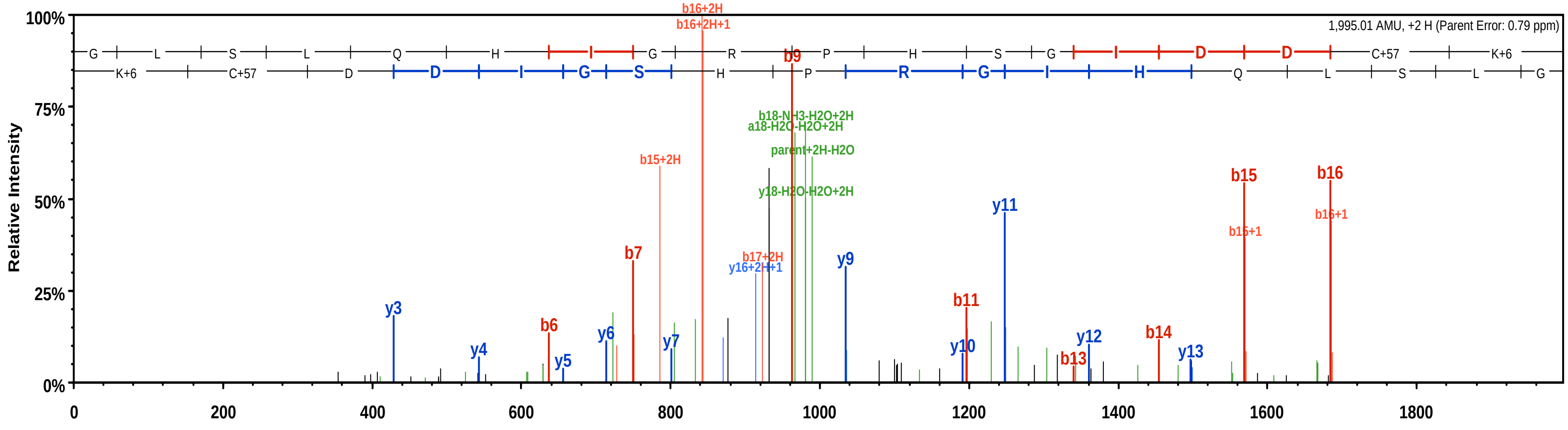


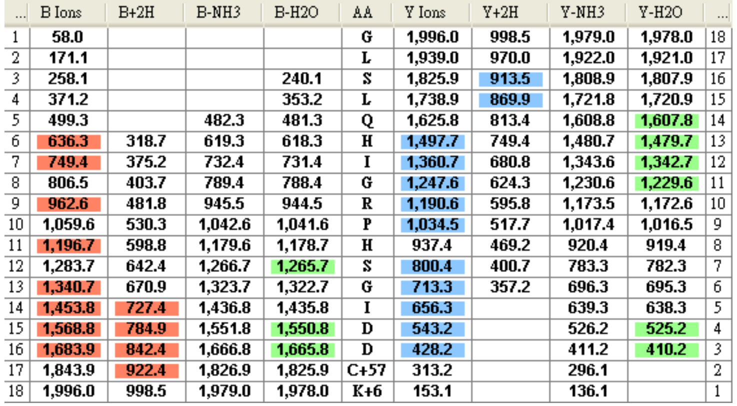


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	1,355.7	678.3	1,338.6	1,337.6	12
2	228.1		211.1		N	1,242.6	621.8	1,225.5	1,224.6	11
3	327.2		310.2		V	1,128.5	564.8	1,111.5	1,110.5	10
4	490.3		473.2		Y	1,029.5	515.2	1,012.4	1,011.5	9
5	653.3		636.3		Y	866.4	433.7	849.4	848.4	8
6	767.4	384.2	750.3		N	703.3	352.2	686.3	685.3	7
7	896.4	448.7	879.4	878.4	E	589.3	295.2	572.3	571.3	6
8	967.5	484.2	950.4	949.4	A	460.3		443.2		5
9	1,038.5	519.7	1,021.5	1,020.5	A	389.2		372.2		4
10	1,095.5	548.3	1,078.5	1,077.5	G	318.2		301.2		3
11	1,209.6	605.3	1,192.5	1,191.5	N	261.2		244.1		2
12	1,355.7	678.3	1,338.6	1,337.6	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-105	sp|O43414|PRNIP_HUMAN	GLSLQHIGRPHSGIDDCK	42.54	Unmodified	Heavy	2	995.4998

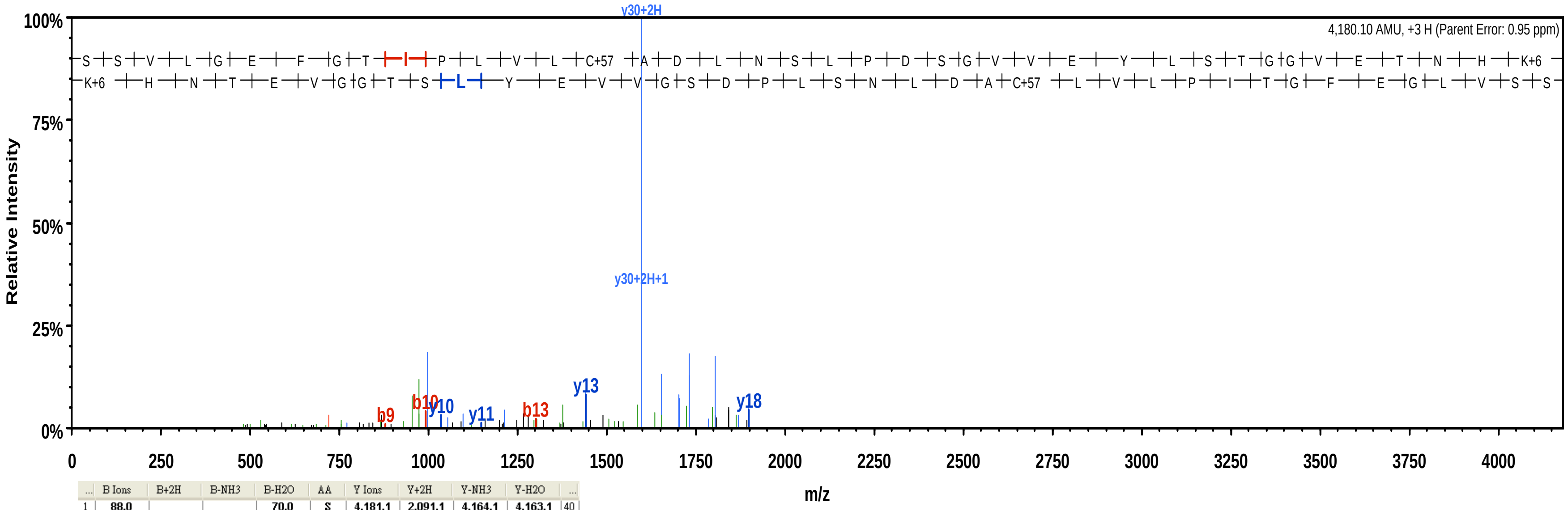


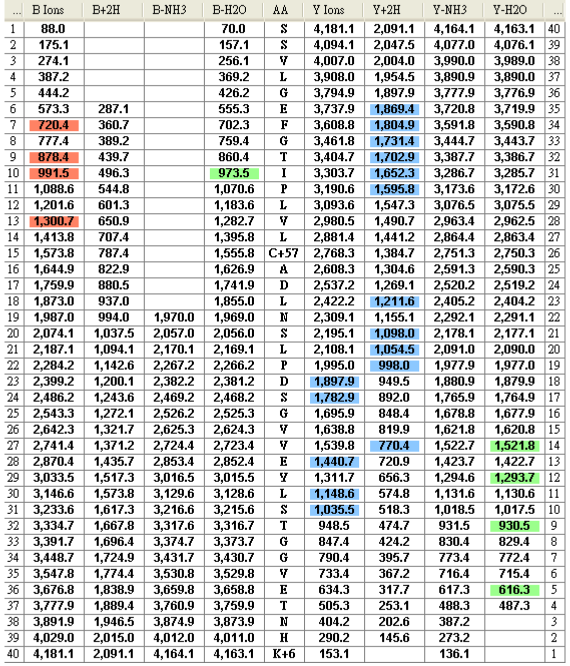


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	1,996.0	998.5	1,979.0	1,978.0	18
2	171.1				L	1,939.0	970.0	1,922.0	1,921.0	17
3	258.1			240.1	S	1,825.9	913.5	1,808.9	1,807.9	16
4	371.2			353.2	L	1,738.9	869.9	1,721.8	1,720.9	15
5	499.3		482.3	481.3	Q	1,625.8	813.4	1,608.8	1,607.8	14
6	636.3	318.7	619.3	618.3	H	1,497.7	749.4	1,480.7	1,479.7	13
7	749.4	375.2	732.4	731.4	I	1,360.7	680.8	1,343.6	1,342.7	12
8	806.5	403.7	789.4	788.4	G	1,247.6	624.3	1,230.6	1,229.6	11
9	962.6	481.8	945.5	944.5	R	1,190.6	595.8	1,173.5	1,172.6	10
10	1,059.6	530.3	1,042.6	1,041.6	P	1,034.5	517.7	1,017.4	1,016.5	9
11	1,196.7	598.8	1,179.6	1,178.7	H	937.4	469.2	920.4	919.4	8
12	1,283.7	642.4	1,266.7	1,265.7	S	800.4	400.7	783.3	782.3	7
13	1,340.7	670.9	1,323.7	1,322.7	G	713.3	357.2	696.3	695.3	6
14	1,453.8	727.4	1,436.8	1,435.8	I	656.3		639.3	638.3	5
15	1,568.8	784.9	1,551.8	1,550.8	D	543.2		526.2	525.2	4
16	1,683.9	842.4	1,666.8	1,665.8	D	428.2		411.2	410.2	3
17	1,843.9	922.4	1,826.9	1,825.9	C+57	313.2		296.1		2
18	1,996.0	998.5	1,979.0	1,978.0	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-106	sp|Q9ULM6|CNOT6_HUMAN	SSVLGEFGTIPLVLCADLNSLPDSGVVEYLSTGGVETNHK	42.49	Unmodified	Heavy	3	1392.3666

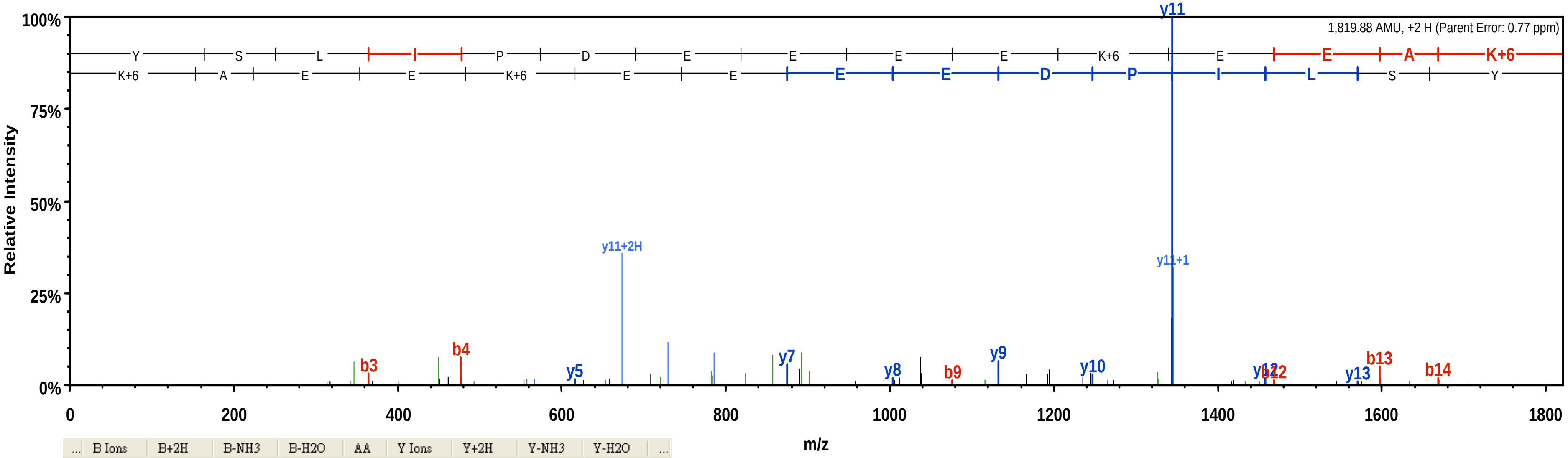


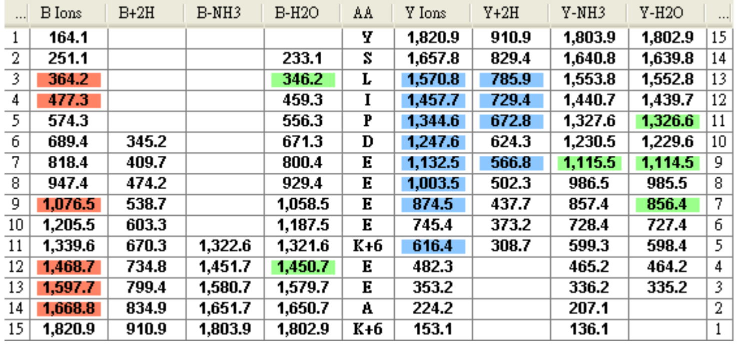


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	4,181.1	2,091.1	4,164.1	4,163.1	40
2	175.1			157.1	S	4,094.1	2,047.5	4,077.0	4,076.1	39
3	274.1			256.1	V	4,007.0	2,004.0	3,990.0	3,989.0	38
4	387.2			369.2	L	3,908.0	1,954.5	3,890.9	3,890.0	37
5	444.2			426.2	G	3,794.9	1,897.9	3,777.9	3,776.9	36
6	573.3	287.1		555.3	E	3,737.9	1,869.4	3,720.8	3,719.9	35
7	720.4	360.7		702.3	F	3,608.8	1,804.9	3,591.8	3,590.8	34
8	777.4	389.2		759.4	G	3,461.8	1,731.4	3,444.7	3,443.7	33
9	878.4	439.7		860.4	T	3,404.7	1,702.9	3,387.7	3,386.7	32
10	991.5	496.3		973.5	I	3,303.7	1,652.3	3,286.7	3,285.7	31
11	1,088.6	544.8		1,070.6	P	3,190.6	1,595.8	3,173.6	3,172.6	30
12	1,201.6	601.3		1,183.6	L	3,093.6	1,547.3	3,076.5	3,075.5	29
13	1,300.7	650.9		1,282.7	V	2,980.5	1,490.7	2,963.4	2,962.5	28
14	1,413.8	707.4		1,395.8	L	2,881.4	1,441.2	2,864.4	2,863.4	27
15	1,573.8	787.4		1,555.8	C+57	2,768.3	1,384.7	2,751.3	2,750.3	26
16	1,644.9	822.9		1,626.9	A	2,608.3	1,304.6	2,591.3	2,590.3	25
17	1,759.9	880.5		1,741.9	D	2,537.2	1,269.1	2,520.2	2,519.2	24
18	1,873.0	937.0		1,855.0	L	2,422.2	1,211.6	2,405.2	2,404.2	23
19	1,987.0	994.0	1,970.0	1,969.0	N	2,309.1	1,155.1	2,292.1	2,291.1	22
20	2,074.1	1,037.5	2,057.0	2,056.0	S	2,195.1	1,098.0	2,178.1	2,177.1	21
21	2,187.1	1,094.1	2,170.1	2,169.1	L	2,108.1	1,054.5	2,091.0	2,090.0	20
22	2,284.2	1,142.6	2,267.2	2,266.2	P	1,995.0	998.0	1,977.9	1,977.0	19
23	2,399.2	1,200.1	2,382.2	2,381.2	D	1,897.9	949.5	1,880.9	1,879.9	18
24	2,486.2	1,243.6	2,469.2	2,468.2	S	1,782.9	892.0	1,765.9	1,764.9	17
25	2,543.3	1,272.1	2,526.2	2,525.3	G	1,695.9	848.4	1,678.8	1,677.9	16
26	2,642.3	1,321.7	2,625.3	2,624.3	V	1,638.8	819.9	1,621.8	1,620.8	15
27	2,741.4	1,371.2	2,724.4	2,723.4	V	1,539.8	770.4	1,522.7	1,521.8	14
28	2,870.4	1,435.7	2,853.4	2,852.4	E	1,440.7	720.9	1,423.7	1,422.7	13
29	3,033.5	1,517.3	3,016.5	3,015.5	Y	1,311.7	656.3	1,294.6	1,293.7	12
30	3,146.6	1,573.8	3,129.6	3,128.6	L	1,148.6	574.8	1,131.6	1,130.6	11
31	3,233.6	1,617.3	3,216.6	3,215.6	S	1,035.5	518.3	1,018.5	1,017.5	10
32	3,334.7	1,667.8	3,317.6	3,316.7	T	948.5	474.7	931.5	930.5	9
33	3,391.7	1,696.4	3,374.7	3,373.7	G	847.4	424.2	830.4	829.4	8
34	3,448.7	1,724.9	3,431.7	3,430.7	G	790.4	395.7	773.4	772.4	7
35	3,547.8	1,774.4	3,530.8	3,529.8	V	733.4	367.2	716.4	715.4	6
36	3,676.8	1,838.9	3,659.8	3,658.8	E	634.3	317.7	617.3	616.3	5
37	3,777.9	1,889.4	3,760.9	3,759.9	T	505.3	253.1	488.3	487.3	4
38	3,891.9	1,946.5	3,874.9	3,873.9	N	404.2	202.6	387.2		3
39	4,029.0	2,015.0	4,012.0	4,011.0	H	290.2	145.6	273.2		2
40	4,181.1	2,091.1	4,164.1	4,163.1	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-107	sp|Q9NP64|NO40_HUMAN	YSLIPDEEEEKEEAK	42.17	Unmodified	Heavy	2	904.92545

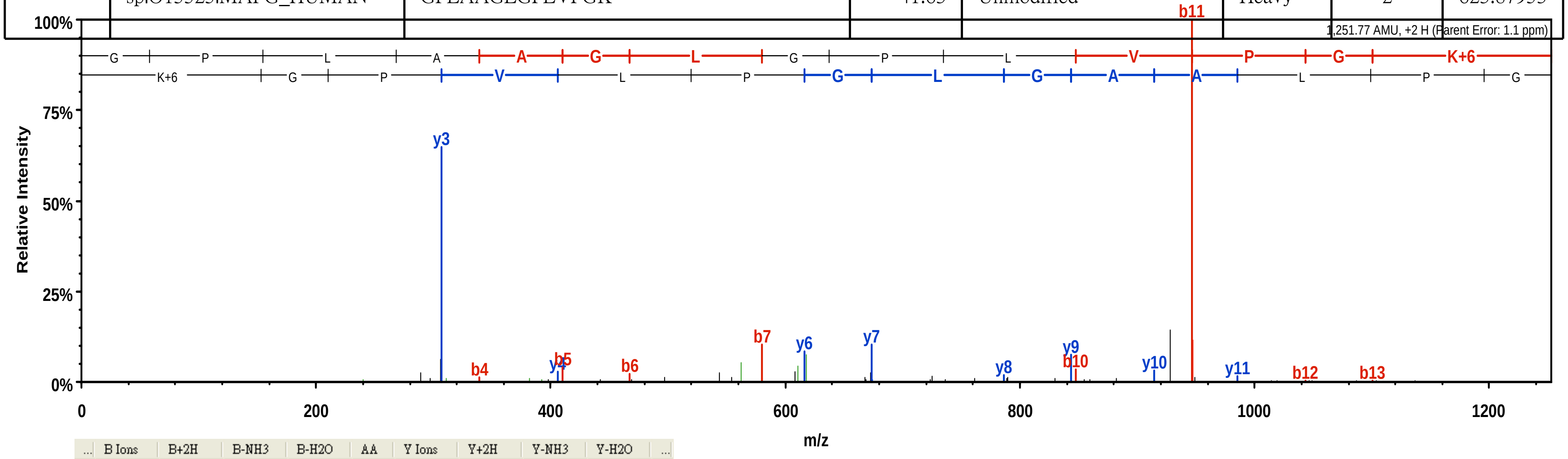


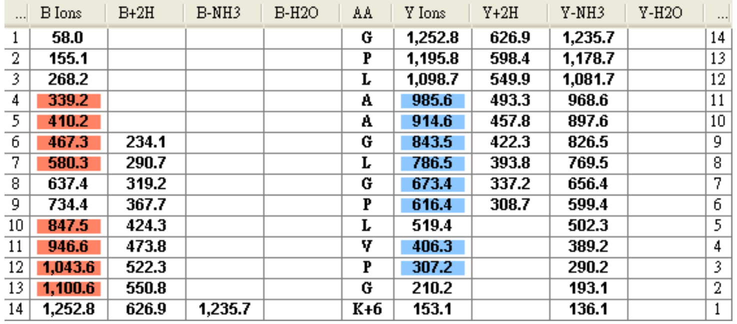


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	164.1				Y	1,820.9	910.9	1,803.9	1,802.9	15
2	251.1			233.1	S	1,657.8	829.4	1,640.8	1,639.8	14
3	364.2			346.2	L	1,570.8	785.9	1,553.8	1,552.8	13
4	477.3			459.3	I	1,457.7	729.4	1,440.7	1,439.7	12
5	574.3			556.3	P	1,344.6	672.8	1,327.6	1,326.6	11
6	689.4	345.2		671.3	D	1,247.6	624.3	1,230.5	1,229.6	10
7	818.4	409.7		800.4	E	1,132.5	566.8	1,115.5	1,114.5	9
8	947.4	474.2		929.4	E	1,003.5	502.3	986.5	985.5	8
9	1,076.5	538.7		1,058.5	E	874.5	437.7	857.4	856.4	7
10	1,205.5	603.3		1,187.5	E	745.4	373.2	728.4	727.4	6
11	1,339.6	670.3	1,322.6	1,321.6	K+6	616.4	308.7	599.3	598.4	5
12	1,468.7	734.8	1,451.7	1,450.7	E	482.3		465.2	464.2	4
13	1,597.7	799.4	1,580.7	1,579.7	E	353.2		336.2	335.2	3
14	1,668.8	834.9	1,651.7	1,650.7	A	224.2		207.1		2
15	1,820.9	910.9	1,803.9	1,802.9	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-108	sp|O15525|MAFG_HUMAN	GPLAAGLGPLVPGK	41.63	Unmodified	Heavy	2	623.87953

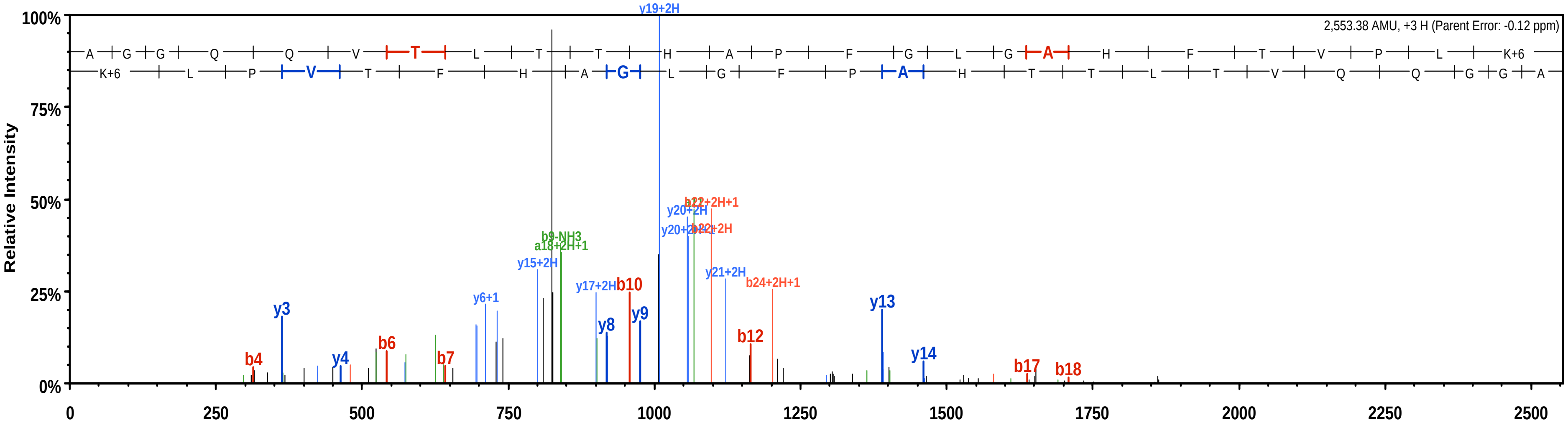


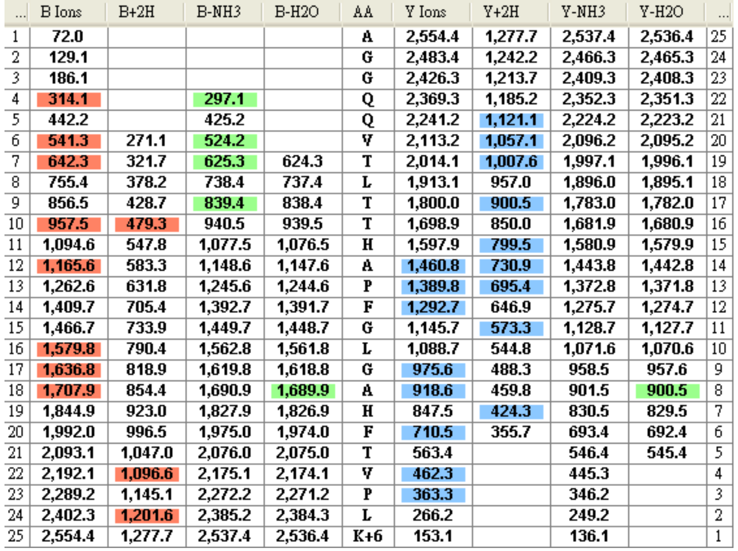


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	1,252.8	626.9	1,235.7		14
2	155.1				P	1,195.8	598.4	1,178.7		13
3	268.2				L	1,098.7	549.9	1,081.7		12
4	**339.2**				A	**985.6**	493.3	968.6		11
5	**410.2**				A	**914.6**	457.8	897.6		10
6	**467.3**	234.1			G	**843.5**	422.3	826.5		9
7	**580.3**	290.7			L	**786.5**	393.8	769.5		8
8	637.4	319.2			G	**673.4**	337.2	656.4		7
9	734.4	367.7			P	**616.4**	308.7	599.4		6
10	**847.5**	424.3			L	519.4		502.3		5
11	**946.6**	473.8			V	**406.3**		389.2		4
12	**1,043.6**	522.3			P	**307.2**		290.2		3
13	**1,100.6**	550.8			G	210.2		193.1		2
14	1,252.8	626.9	1,235.7		K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-109	sp|A0PJW6|YK008_HUMAN	AGGQQVTLTTHAPFGLGAHFTVPLK	40.5	Unmodified	Heavy	3	850.12721

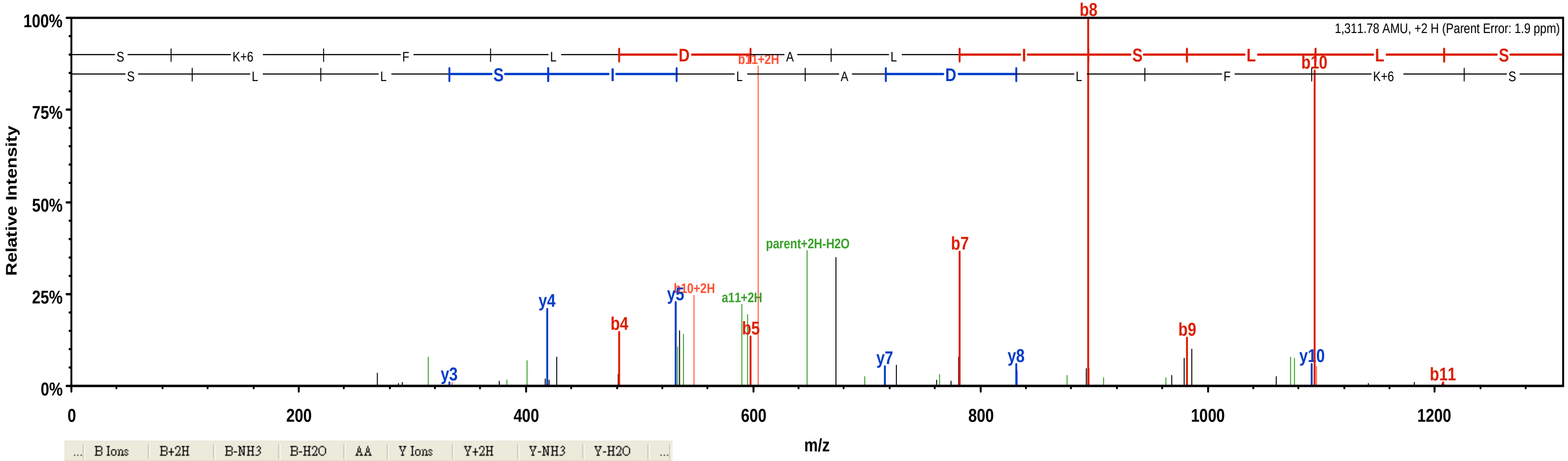


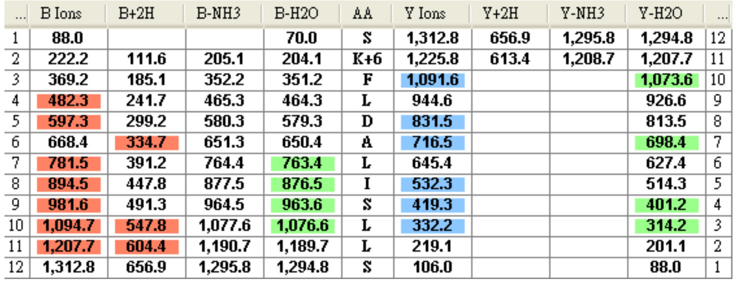


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	2,554.4	1,277.7	2,537.4	2,536.4	25
2	129.1				G	2,483.4	1,242.2	2,466.3	2,465.3	24
3	186.1				G	2,426.3	1,213.7	2,409.3	2,408.3	23
4	314.1		297.1		Q	2,369.3	1,185.2	2,352.3	2,351.3	22
5	442.2		425.2		Q	2,241.2	1,121.1	2,224.2	2,223.2	21
6	541.3	271.1	524.2		V	2,113.2	1,057.1	2,096.2	2,095.2	20
7	642.3	321.7	625.3	624.3	T	2,014.1	1,007.6	1,997.1	1,996.1	19
8	755.4	378.2	738.4	737.4	L	1,913.1	957.0	1,896.0	1,895.1	18
9	856.5	428.7	839.4	838.4	T	1,800.0	900.5	1,783.0	1,782.0	17
10	957.5	479.3	940.5	939.5	T	1,698.9	850.0	1,681.9	1,680.9	16
11	1,094.6	547.8	1,077.5	1,076.5	H	1,597.9	799.5	1,580.9	1,579.9	15
12	1,165.6	583.3	1,148.6	1,147.6	A	1,460.8	730.9	1,443.8	1,442.8	14
13	1,262.6	631.8	1,245.6	1,244.6	P	1,389.8	695.4	1,372.8	1,371.8	13
14	1,409.7	705.4	1,392.7	1,391.7	F	1,292.7	646.9	1,275.7	1,274.7	12
15	1,466.7	733.9	1,449.7	1,448.7	G	1,145.7	573.3	1,128.7	1,127.7	11
16	1,579.8	790.4	1,562.8	1,561.8	L	1,088.7	544.8	1,071.6	1,070.6	10
17	1,636.8	818.9	1,619.8	1,618.8	G	975.6	488.3	958.5	957.6	9
18	1,707.9	854.4	1,690.9	1,689.9	A	918.6	459.8	901.5	900.5	8
19	1,844.9	923.0	1,827.9	1,826.9	H	847.5	424.3	830.5	829.5	7
20	1,992.0	996.5	1,975.0	1,974.0	F	710.5	355.7	693.4	692.4	6
21	2,093.1	1,047.0	2,076.0	2,075.0	T	563.4		546.4	545.4	5
22	2,192.1	1,096.6	2,175.1	2,174.1	V	462.3		445.3		4
23	2,289.2	1,145.1	2,272.2	2,271.2	P	363.3		346.2		3
24	2,402.3	1,201.6	2,385.2	2,384.3	L	266.2		249.2		2
25	2,554.4	1,277.7	2,537.4	2,536.4	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-110	sp|O75419|CC45L_HUMAN	SKFLDALISLLS	40.41	Unmodified	Heavy	2	653.88448

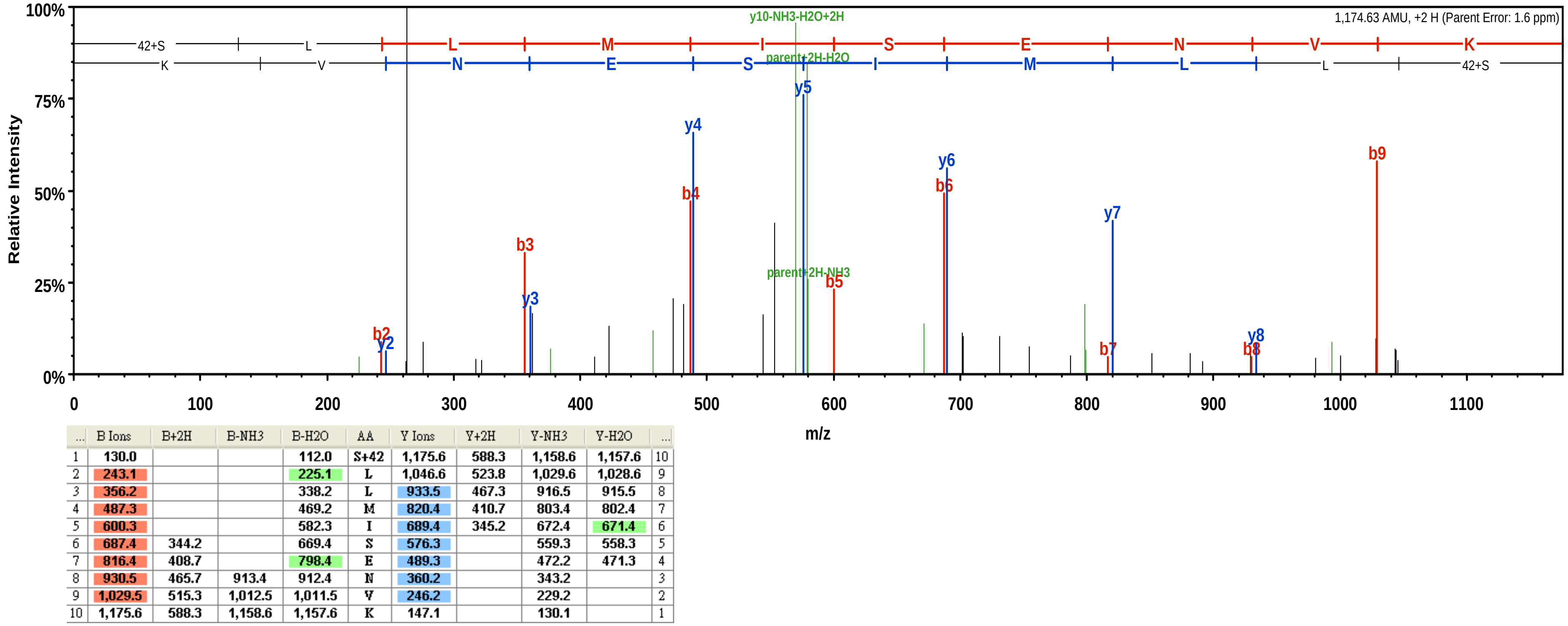




...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	1,312.8	656.9	1,295.8	1,294.8	12
2	222.2	111.6	205.1	204.1	K+6	1,225.8	613.4	1,208.7	1,207.7	11
3	369.2	185.1	352.2	351.2	F	1,091.6			1,073.6	10
4	482.3	241.7	465.3	464.3	L	944.6			926.6	9
5	597.3	299.2	580.3	579.3	D	831.5			813.5	8
6	668.4	334.7	651.3	650.4	A	716.5			698.4	7
7	781.5	391.2	764.4	763.4	L	645.4			627.4	6
8	894.5	447.8	877.5	876.5	I	532.3			514.3	5
9	981.6	491.3	964.5	963.6	S	419.3			401.2	4
10	1,094.7	547.8	1,077.6	1,076.6	L	332.2			314.2	3
11	1,207.7	604.4	1,190.7	1,189.7	L	219.1			201.1	2
12	1,312.8	656.9	1,295.8	1,294.8	S	106.0			88.0	1

Whole proteome

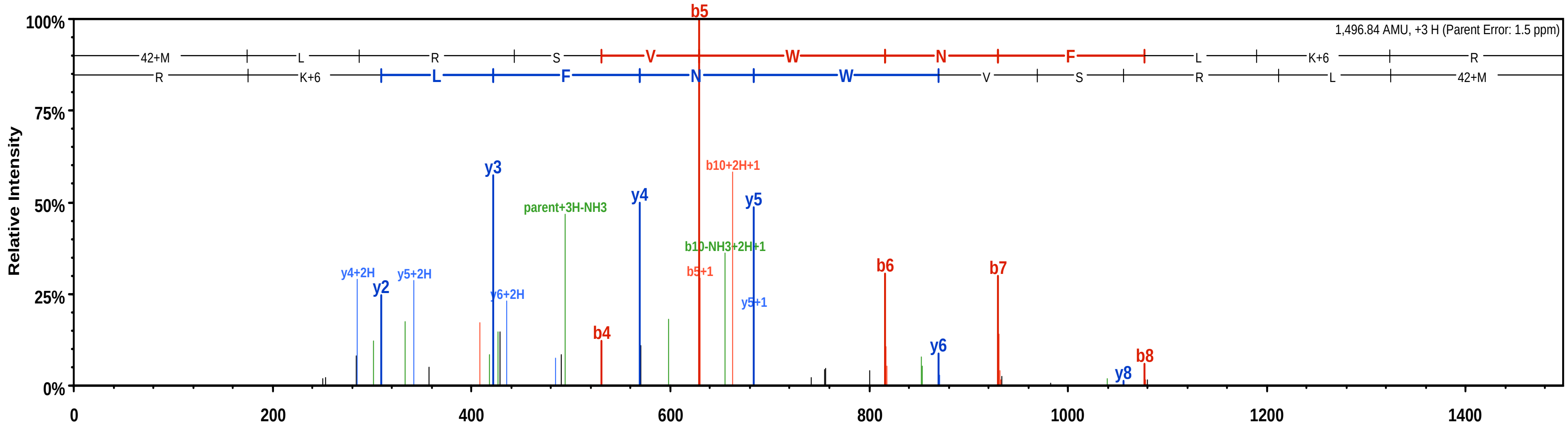
Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-111	sp|O75449|KTNA1_HUMAN	SLLMISENVK	39.9	Acetyl (Protein N-term)	Light	2	588.32066

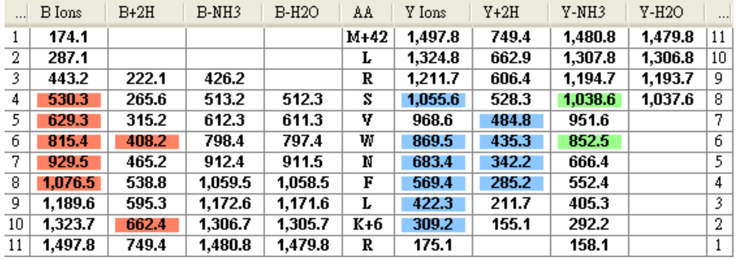


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	S+42	1,175.6	588.3	1,158.6	1,157.6	10
2	243.1			225.1	L	1,046.6	523.8	1,029.6	1,028.6	9
3	356.2			338.2	L	933.5	467.3	916.5	915.5	8
4	487.3			469.2	M	820.4	410.7	803.4	802.4	7
5	600.3			582.3	I	689.4	345.2	672.4	671.4	6
6	687.4	344.2		669.4	S	576.3		559.3	558.3	5
7	816.4	408.7		798.4	E	489.3		472.2	471.3	4
8	930.5	465.7	913.4	912.4	N	360.2		343.2		3
9	1,029.5	515.3	1,012.5	1,011.5	V	246.2		229.2		2
10	1,175.6	588.3	1,158.6	1,157.6	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-112	sp|P56589|PEX3_HUMAN	MLRSVWNFLKR	38.22	Acetyl (Protein N-term)	Heavy	3	497.94662

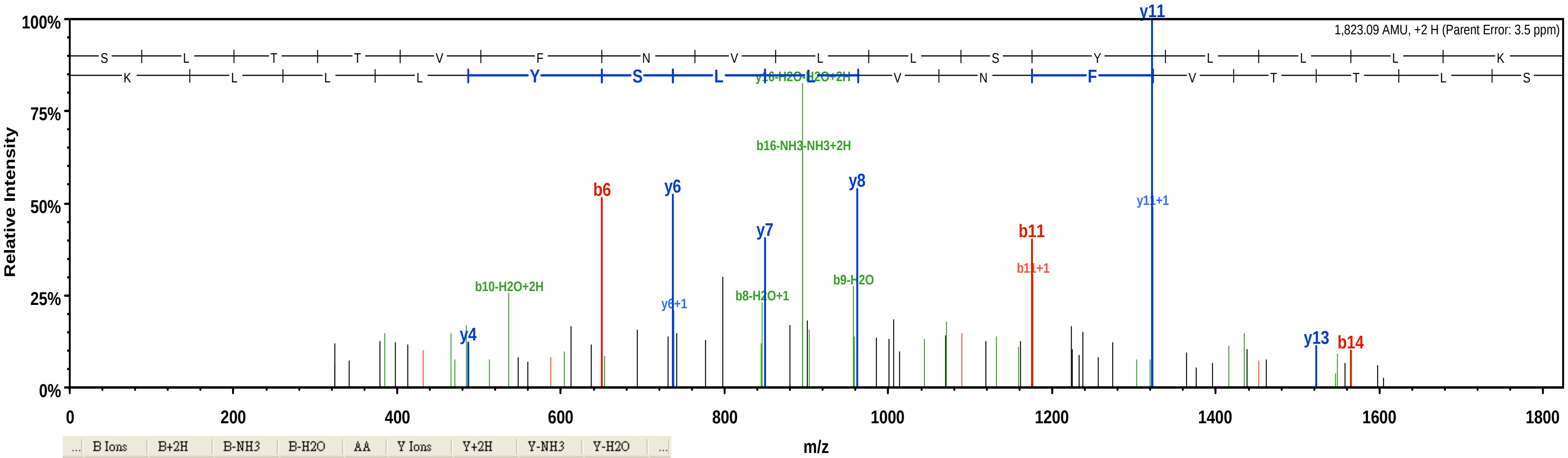


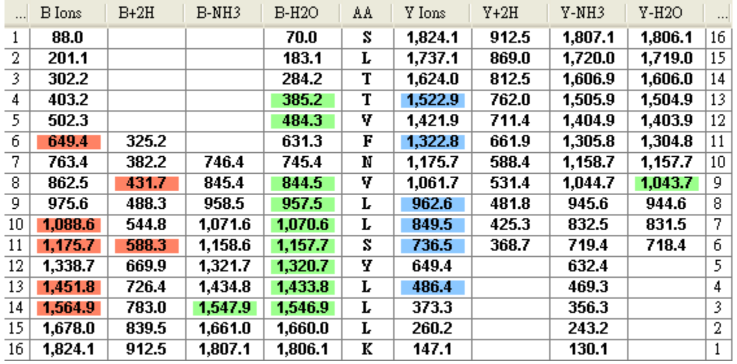


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	174.1				M+42	1,497.8	749.4	1,480.8	1,479.8	11
2	287.1				L	1,324.8	662.9	1,307.8	1,306.8	10
3	443.2	222.1	426.2		R	1,211.7	606.4	1,194.7	1,193.7	9
4	530.3	265.6	513.2	512.3	S	1,055.6	528.3	1,038.6	1,037.6	8
5	629.3	315.2	612.3	611.3	V	968.6	484.8	951.6		7
6	815.4	408.2	798.4	797.4	W	869.5	435.3	852.5		6
7	929.5	465.2	912.4	911.5	N	683.4	342.2	666.4		5
8	1,076.5	538.8	1,059.5	1,058.5	F	569.4	285.2	552.4		4
9	1,189.6	595.3	1,172.6	1,171.6	L	422.3	211.7	405.3		3
10	1,323.7	662.4	1,306.7	1,305.7	K+6	309.2	155.1	292.2		2
11	1,497.8	749.4	1,480.8	1,479.8	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-113	splQ96A29lFUCT1_HUMAN	SLTTVFNVLLSYLLLK	37.89	Unmodified	Light	2	912.54769

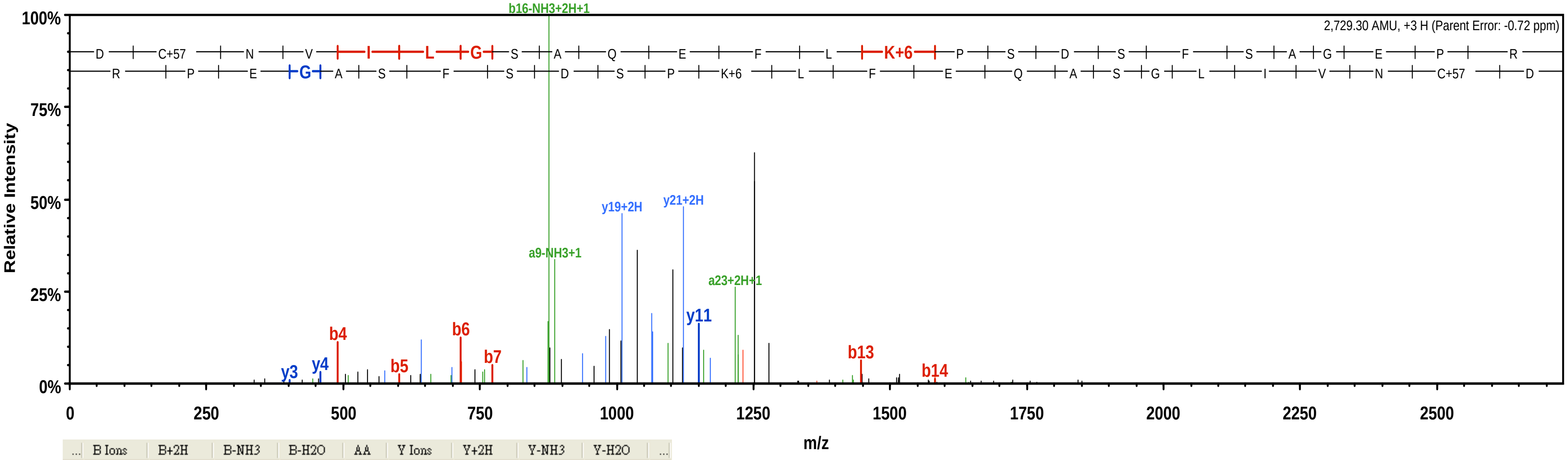


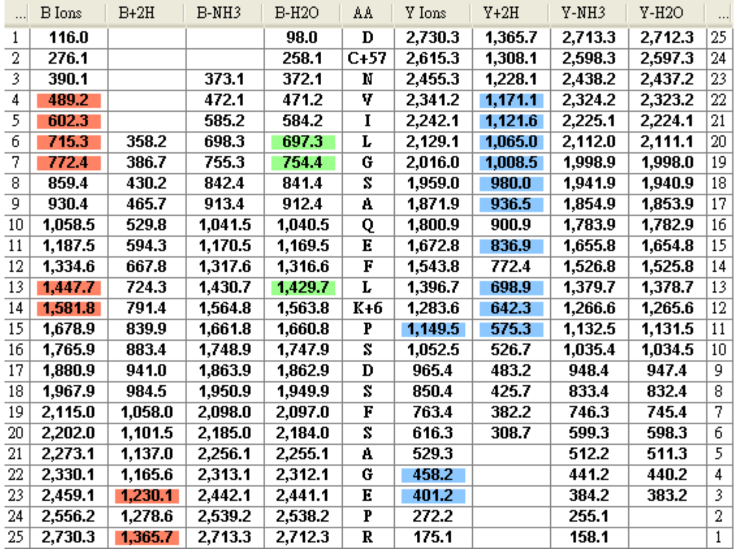


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	1,824.1	912.5	1,807.1	1,806.1	16
2	201.1			183.1	L	1,737.1	869.0	1,720.0	1,719.0	15
3	302.2			284.2	T	1,624.0	812.5	1,606.9	1,606.0	14
4	403.2			385.2	T	1,522.9	762.0	1,505.9	1,504.9	13
5	502.3			484.3	V	1,421.9	711.4	1,404.9	1,403.9	12
6	649.4	325.2		631.3	F	1,322.8	661.9	1,305.8	1,304.8	11
7	763.4	382.2	746.4	745.4	N	1,175.7	588.4	1,158.7	1,157.7	10
8	862.5	431.7	845.4	844.5	V	1,061.7	531.4	1,044.7	1,043.7	9
9	975.6	488.3	958.5	957.5	L	962.6	481.8	945.6	944.6	8
10	1,088.6	544.8	1,071.6	1,070.6	L	849.5	425.3	832.5	831.5	7
11	1,175.7	588.3	1,158.6	1,157.7	S	736.5	368.7	719.4	718.4	6
12	1,338.7	669.9	1,321.7	1,320.7	Y	649.4		632.4		5
13	1,451.8	726.4	1,434.8	1,433.8	L	486.4		469.3		4
14	1,564.9	783.0	1,547.9	1,546.9	L	373.3		356.3		3
15	1,678.0	839.5	1,661.0	1,660.0	L	260.2		243.2		2
16	1,824.1	912.5	1,807.1	1,806.1	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-114	sp|Q9BRA0|LSMD1_HUMAN	DCNVILGSAQEFLKPSDSFSAGEPR	36.86	Unmodified	Light	2	1362.6503

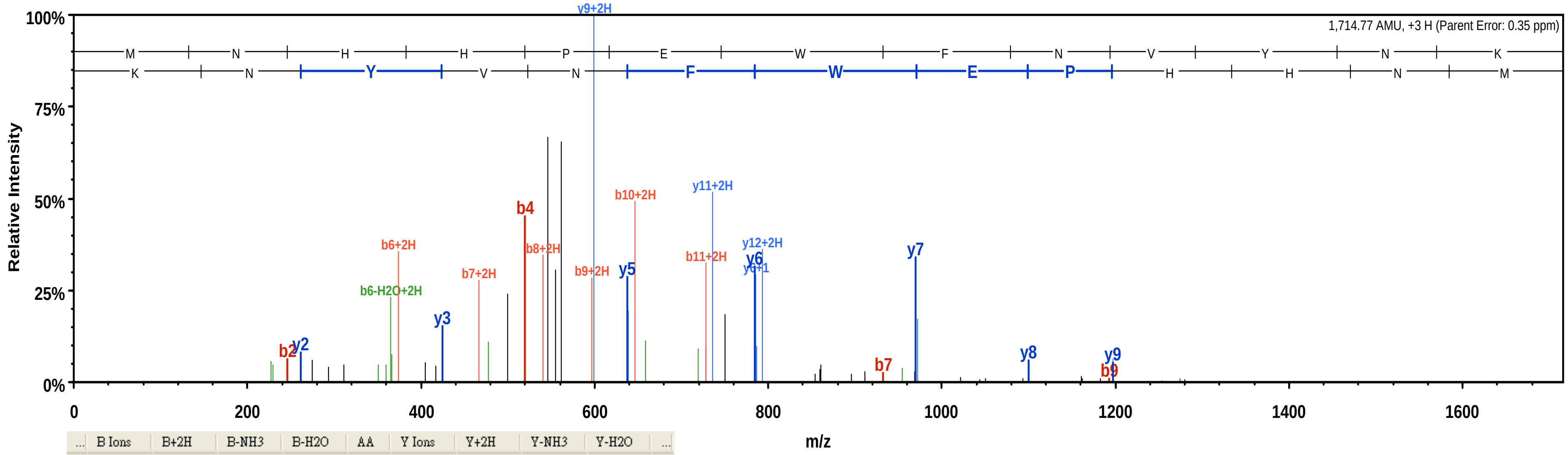


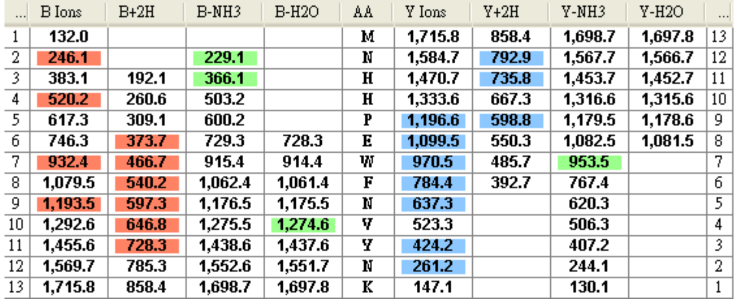


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	2,730.3	1,365.7	2,713.3	2,712.3	25
2	276.1			258.1	C+57	2,615.3	1,308.1	2,598.3	2,597.3	24
3	390.1		373.1	372.1	N	2,455.3	1,228.1	2,438.2	2,437.2	23
4	489.2		472.1	471.2	V	2,341.2	1,171.1	2,324.2	2,323.2	22
5	602.3		585.2	584.2	I	2,242.1	1,121.6	2,225.1	2,224.1	21
6	715.3	358.2	698.3	697.3	L	2,129.1	1,065.0	2,112.0	2,111.1	20
7	772.4	386.7	755.3	754.4	G	2,016.0	1,008.5	1,998.9	1,998.0	19
8	859.4	430.2	842.4	841.4	S	1,959.0	980.0	1,941.9	1,940.9	18
9	930.4	465.7	913.4	912.4	A	1,871.9	936.5	1,854.9	1,853.9	17
10	1,058.5	529.8	1,041.5	1,040.5	Q	1,800.9	900.9	1,783.9	1,782.9	16
11	1,187.5	594.3	1,170.5	1,169.5	E	1,672.8	836.9	1,655.8	1,654.8	15
12	1,334.6	667.8	1,317.6	1,316.6	F	1,543.8	772.4	1,526.8	1,525.8	14
13	1,447.7	724.3	1,430.7	1,429.7	L	1,396.7	698.9	1,379.7	1,378.7	13
14	1,581.8	791.4	1,564.8	1,563.8	K+6	1,283.6	642.3	1,266.6	1,265.6	12
15	1,678.9	839.9	1,661.8	1,660.8	P	1,149.5	575.3	1,132.5	1,131.5	11
16	1,765.9	883.4	1,748.9	1,747.9	S	1,052.5	526.7	1,035.4	1,034.5	10
17	1,880.9	941.0	1,863.9	1,862.9	D	965.4	483.2	948.4	947.4	9
18	1,967.9	984.5	1,950.9	1,949.9	S	850.4	425.7	833.4	832.4	8
19	2,115.0	1,058.0	2,098.0	2,097.0	F	763.4	382.2	746.3	745.4	7
20	2,202.0	1,101.5	2,185.0	2,184.0	S	616.3	308.7	599.3	598.3	6
21	2,273.1	1,137.0	2,256.1	2,255.1	A	529.3		512.2	511.3	5
22	2,330.1	1,165.6	2,313.1	2,312.1	G	458.2		441.2	440.2	4
23	2,459.1	1,230.1	2,442.1	2,441.1	E	401.2		384.2	383.2	3
24	2,556.2	1,278.6	2,539.2	2,538.2	P	272.2		255.1		2
25	2,730.3	1,365.7	2,713.3	2,712.3	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-115	splQ9H0N5lPHS2_HUMAN	MNHHPEWFNVYNK	36.77	Unmodified	Light	3	572.59642

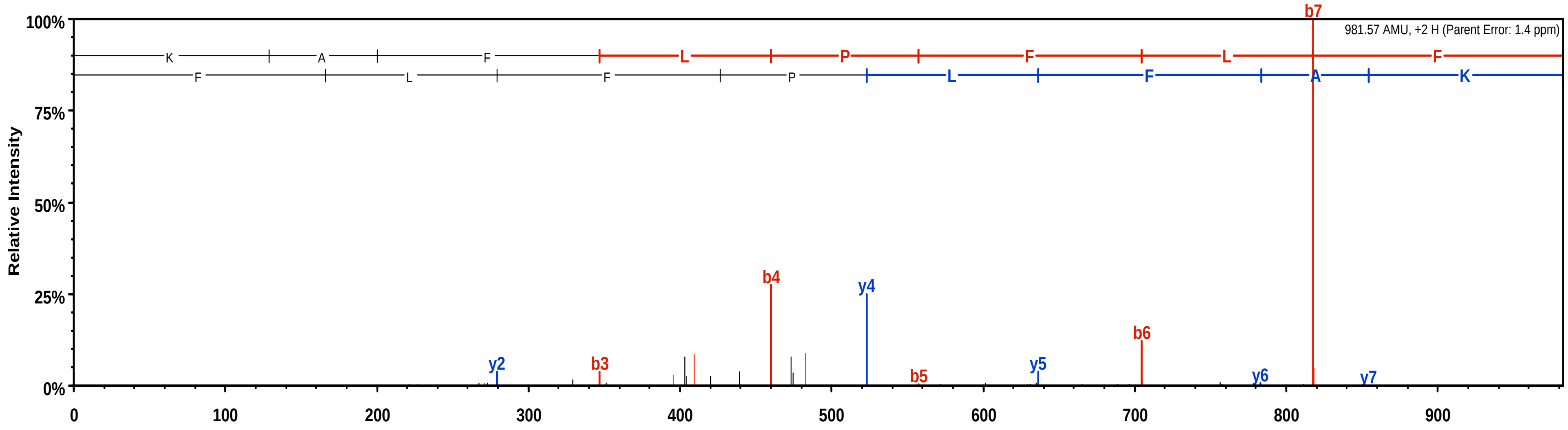


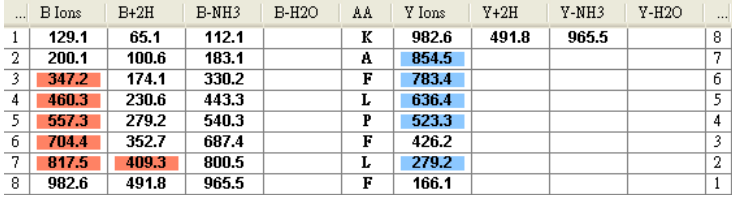


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	132.0				M	1,715.8	858.4	1,698.7	1,697.8	13
2	246.1		229.1		N	1,584.7	792.9	1,567.7	1,566.7	12
3	383.1	192.1	366.1		H	1,470.7	735.8	1,453.7	1,452.7	11
4	520.2	260.6	503.2		H	1,333.6	667.3	1,316.6	1,315.6	10
5	617.3	309.1	600.2		P	1,196.6	598.8	1,179.5	1,178.6	9
6	746.3	373.7	729.3	728.3	E	1,099.5	550.3	1,082.5	1,081.5	8
7	932.4	466.7	915.4	914.4	W	970.5	485.7	953.5		7
8	1,079.5	540.2	1,062.4	1,061.4	F	784.4	392.7	767.4		6
9	1,193.5	597.3	1,176.5	1,175.5	N	637.3		620.3		5
10	1,292.6	646.8	1,275.5	1,274.6	V	523.3		506.3		4
11	1,455.6	728.3	1,438.6	1,437.6	Y	424.2		407.2		3
12	1,569.7	785.3	1,552.6	1,551.7	N	261.2		244.1		2
13	1,715.8	858.4	1,698.7	1,697.8	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-116	splQ9H8P0lS5A3_HUMAN	KAFLPFLF	36.25	Unmodified	Light	2	491.79166

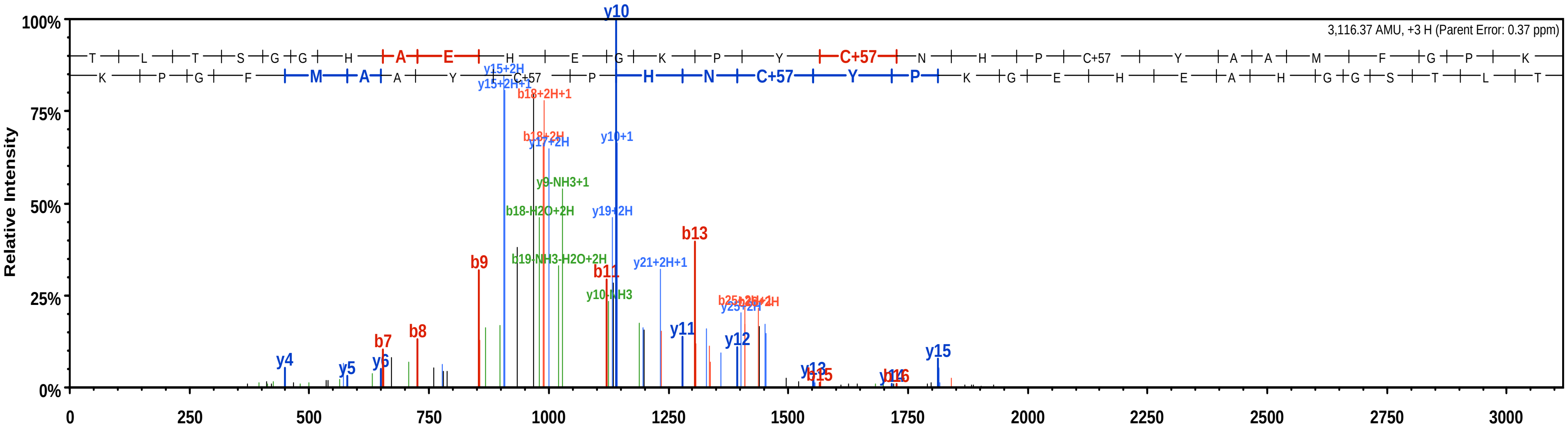


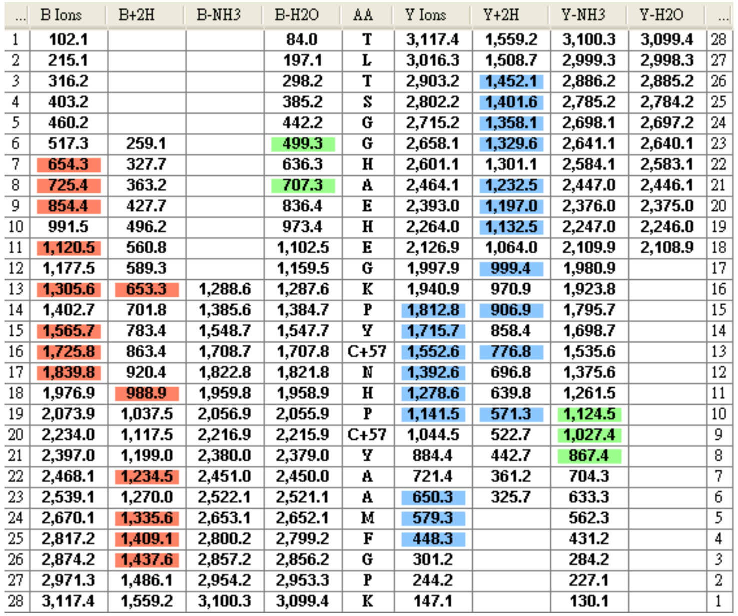


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	129.1	65.1	112.1		K	982.6	491.8	965.5		8
2	200.1	100.6	183.1		A	854.5				7
3	347.2	174.1	330.2		F	783.4				6
4	460.3	230.6	443.3		L	636.4				5
5	557.3	279.2	540.3		P	523.3				4
6	704.4	352.7	687.4		F	426.2				3
7	817.5	409.3	800.5		L	279.2				2
8	982.6	491.8	965.5		F	166.1				1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-117	splP50238lCRIP1_HUMAN	TLTSGGHAEHEGKPYCNHPCYAAMFGPK	36.08	Unmodified	Light	3	1039.797

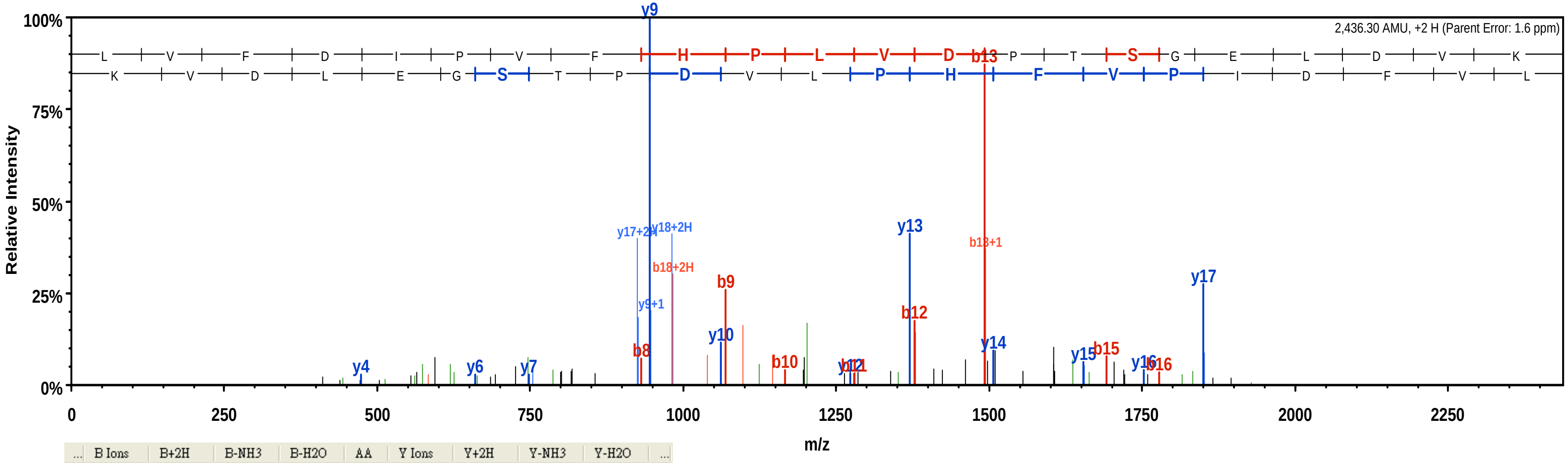


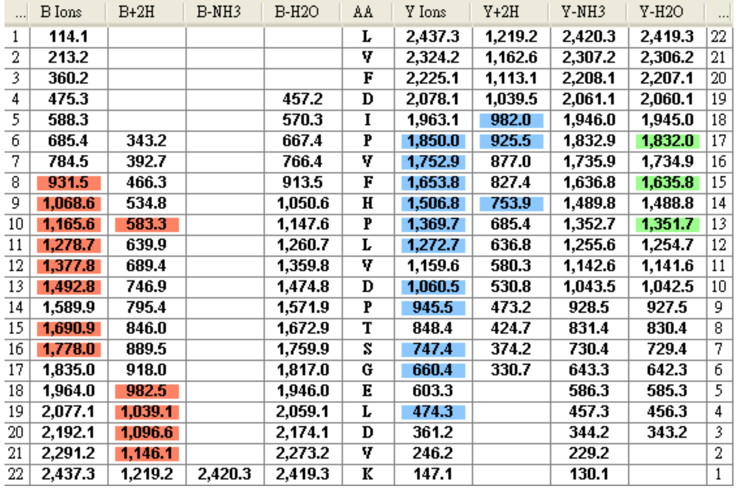


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	102.1			84.0	T	3,117.4	1,559.2	3,100.3	3,099.4	28
2	215.1			197.1	L	3,016.3	1,508.7	2,999.3	2,998.3	27
3	316.2			298.2	T	2,903.2	1,452.1	2,886.2	2,885.2	26
4	403.2			385.2	S	2,802.2	1,401.6	2,785.2	2,784.2	25
5	460.2			442.2	G	2,715.2	1,358.1	2,698.1	2,697.2	24
6	517.3	259.1		499.3	G	2,658.1	1,329.6	2,641.1	2,640.1	23
7	654.3	327.7		636.3	H	2,601.1	1,301.1	2,584.1	2,583.1	22
8	725.4	363.2		707.3	A	2,464.1	1,232.5	2,447.0	2,446.1	21
9	854.4	427.7		836.4	E	2,393.0	1,197.0	2,376.0	2,375.0	20
10	991.5	496.2		973.4	H	2,264.0	1,132.5	2,247.0	2,246.0	19
11	1,120.5	560.8		1,102.5	E	2,126.9	1,064.0	2,109.9	2,108.9	18
12	1,177.5	589.3		1,159.5	G	1,997.9	999.4	1,980.9		17
13	1,305.6	653.3	1,288.6	1,287.6	K	1,940.9	970.9	1,923.8		16
14	1,402.7	701.8	1,385.6	1,384.7	P	1,812.8	906.9	1,795.7		15
15	1,565.7	783.4	1,548.7	1,547.7	Y	1,715.7	858.4	1,698.7		14
16	1,725.8	863.4	1,708.7	1,707.8	C+57	1,552.6	776.8	1,535.6		13
17	1,839.8	920.4	1,822.8	1,821.8	N	1,392.6	696.8	1,375.6		12
18	1,976.9	988.9	1,959.8	1,958.9	H	1,278.6	639.8	1,261.5		11
19	2,073.9	1,037.5	2,056.9	2,055.9	P	1,141.5	571.3	1,124.5		10
20	2,234.0	1,117.5	2,216.9	2,215.9	C+57	1,044.5	522.7	1,027.4		9
21	2,397.0	1,199.0	2,380.0	2,379.0	Y	884.4	442.7	867.4		8
22	2,468.1	1,234.5	2,451.0	2,450.0	A	721.4	361.2	704.3		7
23	2,539.1	1,270.0	2,522.1	2,521.1	A	650.3	325.7	633.3		6
24	2,670.1	1,335.6	2,653.1	2,652.1	M	579.3		562.3		5
25	2,817.2	1,409.1	2,800.2	2,799.2	F	448.3		431.2		4
26	2,874.2	1,437.6	2,857.2	2,856.2	G	301.2		284.2		3
27	2,971.3	1,486.1	2,954.2	2,953.3	P	244.2		227.1		2
28	3,117.4	1,559.2	3,100.3	3,099.4	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-118	sp|Q9H8T0|AKTIP_HUMAN	LVFDIPVFHPLVDPTSGELDVK	35.85	Unmodified	Light	2	1219.1543

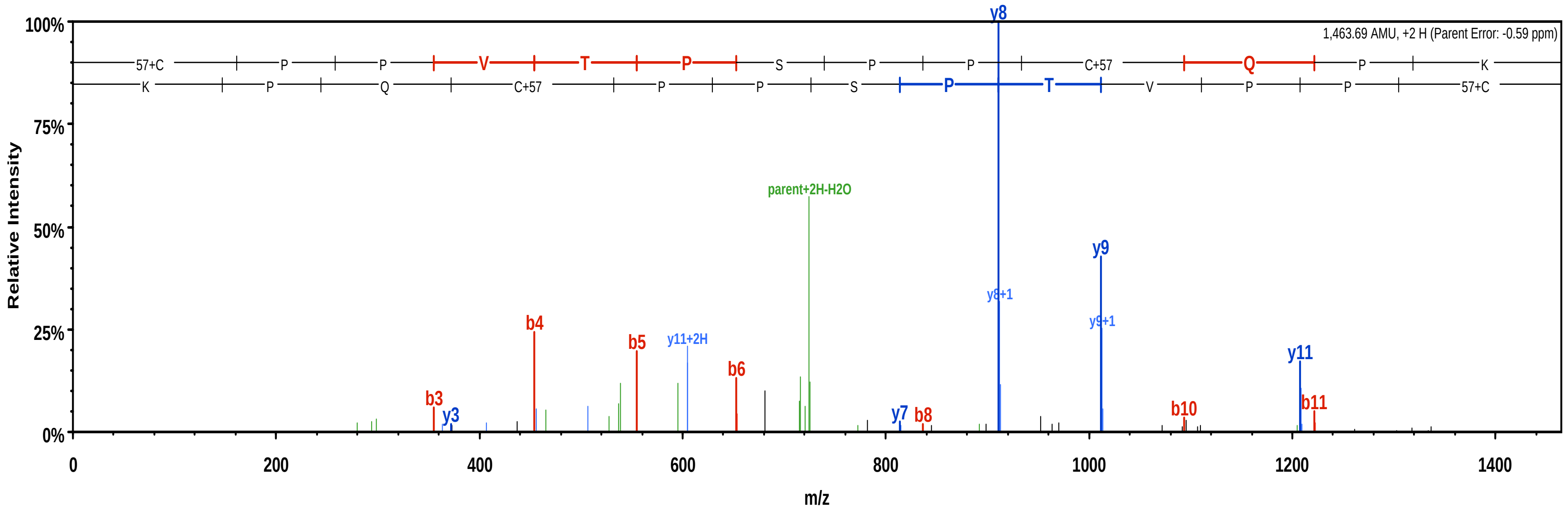


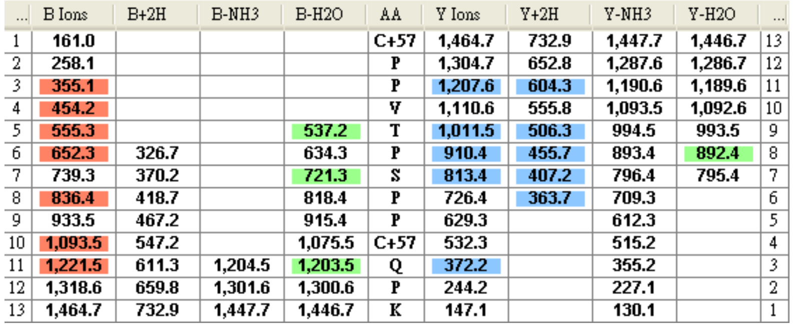


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	2,437.3	1,219.2	2,420.3	2,419.3	22
2	213.2				V	2,324.2	1,162.6	2,307.2	2,306.2	21
3	360.2				F	2,225.1	1,113.1	2,208.1	2,207.1	20
4	475.3			457.2	D	2,078.1	1,039.5	2,061.1	2,060.1	19
5	588.3			570.3	I	1,963.1	982.0	1,946.0	1,945.0	18
6	685.4	343.2		667.4	P	1,850.0	925.5	1,832.9	1,832.0	17
7	784.5	392.7		766.4	V	1,752.9	877.0	1,735.9	1,734.9	16
8	931.5	466.3		913.5	F	1,653.8	827.4	1,636.8	1,635.8	15
9	1,068.6	534.8		1,050.6	H	1,506.8	753.9	1,489.8	1,488.8	14
10	1,165.6	583.3		1,147.6	P	1,369.7	685.4	1,352.7	1,351.7	13
11	1,278.7	639.9		1,260.7	L	1,272.7	636.8	1,255.6	1,254.7	12
12	1,377.8	689.4		1,359.8	V	1,159.6	580.3	1,142.6	1,141.6	11
13	1,492.8	746.9		1,474.8	D	1,060.5	530.8	1,043.5	1,042.5	10
14	1,589.9	795.4		1,571.9	P	945.5	473.2	928.5	927.5	9
15	1,690.9	846.0		1,672.9	T	848.4	424.7	831.4	830.4	8
16	1,778.0	889.5		1,759.9	S	747.4	374.2	730.4	729.4	7
17	1,835.0	918.0		1,817.0	G	660.4	330.7	643.3	642.3	6
18	1,964.0	982.5		1,946.0	E	603.3		586.3	585.3	5
19	2,077.1	1,039.1		2,059.1	L	474.3		457.3	456.3	4
20	2,192.1	1,096.6		2,174.1	D	361.2		344.2	343.2	3
21	2,291.2	1,146.1		2,273.2	V	246.2		229.2		2
22	2,437.3	1,219.2	2,420.3	2,419.3	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-119	sp|P22531|SPR2E_HUMAN	CPPVTPSPPCQPK	35.51	Unmodified	Light	2	732.85232

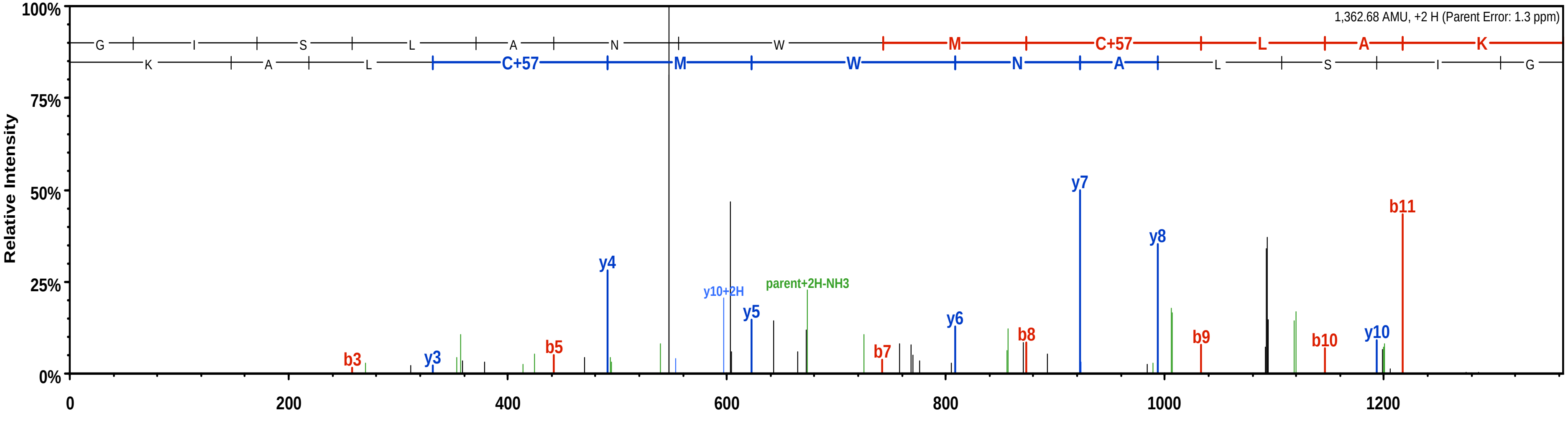


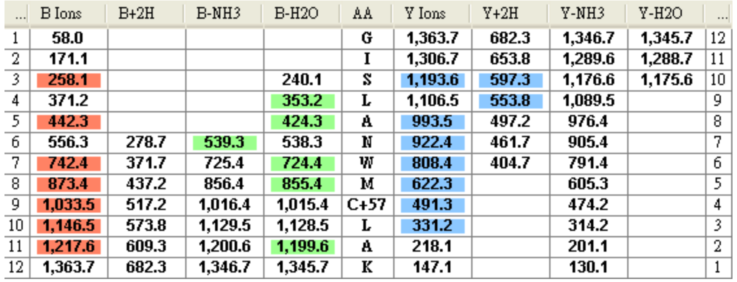


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	161.0				C+57	1,464.7	732.9	1,447.7	1,446.7	13
2	258.1				P	1,304.7	652.8	1,287.6	1,286.7	12
3	355.1				P	1,207.6	604.3	1,190.6	1,189.6	11
4	454.2				V	1,110.6	555.8	1,093.5	1,092.6	10
5	555.3			537.2	T	1,011.5	506.3	994.5	993.5	9
6	652.3	326.7		634.3	P	910.4	455.7	893.4	892.4	8
7	739.3	370.2		721.3	S	813.4	407.2	796.4	795.4	7
8	836.4	418.7		818.4	P	726.4	363.7	709.3		6
9	933.5	467.2		915.4	P	629.3		612.3		5
10	1,093.5	547.2		1,075.5	C+57	532.3		515.2		4
11	1,221.5	611.3	1,204.5	1,203.5	Q	372.2		355.2		3
12	1,318.6	659.8	1,301.6	1,300.6	P	244.2		227.1		2
13	1,464.7	732.9	1,447.7	1,446.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-120	sp|P61626|LYSC_HUMAN	GISLANWMCLAK	34.86	Unmodified	Light	2	682.34668

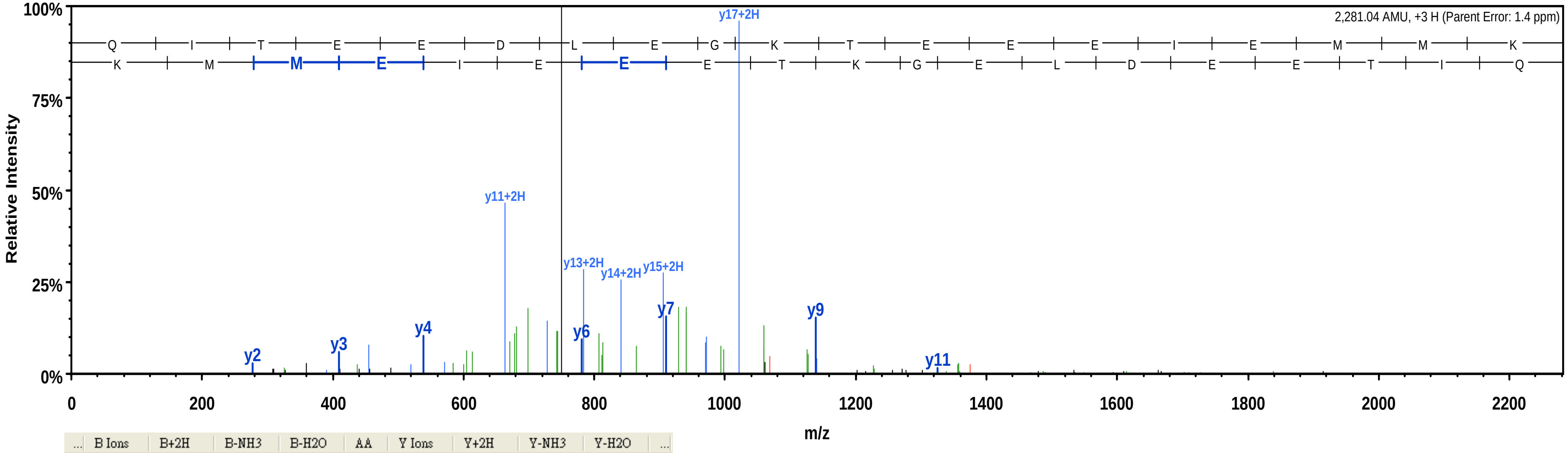


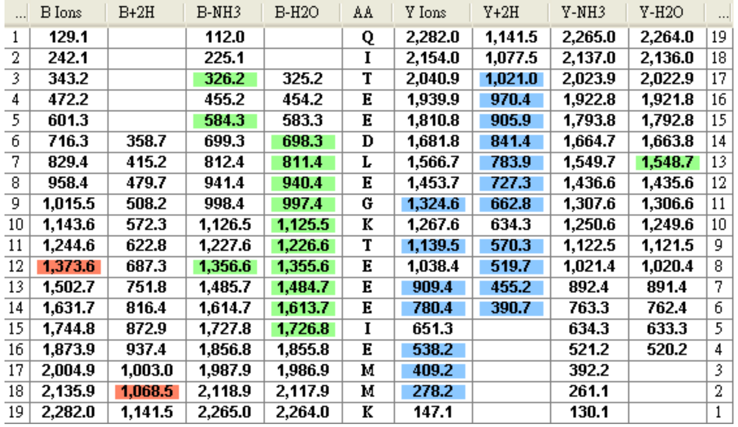


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	1,363.7	682.3	1,346.7	1,345.7	12
2	171.1				I	1,306.7	653.8	1,289.6	1,288.7	11
3	258.1			240.1	S	1,193.6	597.3	1,176.6	1,175.6	10
4	371.2			353.2	L	1,106.5	553.8	1,089.5		9
5	442.3			424.3	A	993.5	497.2	976.4		8
6	556.3	278.7	539.3	538.3	N	922.4	461.7	905.4		7
7	742.4	371.7	725.4	724.4	W	808.4	404.7	791.4		6
8	873.4	437.2	856.4	855.4	M	622.3		605.3		5
9	1,033.5	517.2	1,016.4	1,015.4	C+57	491.3		474.2		4
10	1,146.5	573.8	1,129.5	1,128.5	L	331.2		314.2		3
11	1,217.6	609.3	1,200.6	1,199.6	A	218.1		201.1		2
12	1,363.7	682.3	1,346.7	1,345.7	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-121	sp|Q8WVK2|SNR27_HUMAN	QITEEDLEGKTEEEIEMMK	33.42	Unmodified	Light	3	761.35199

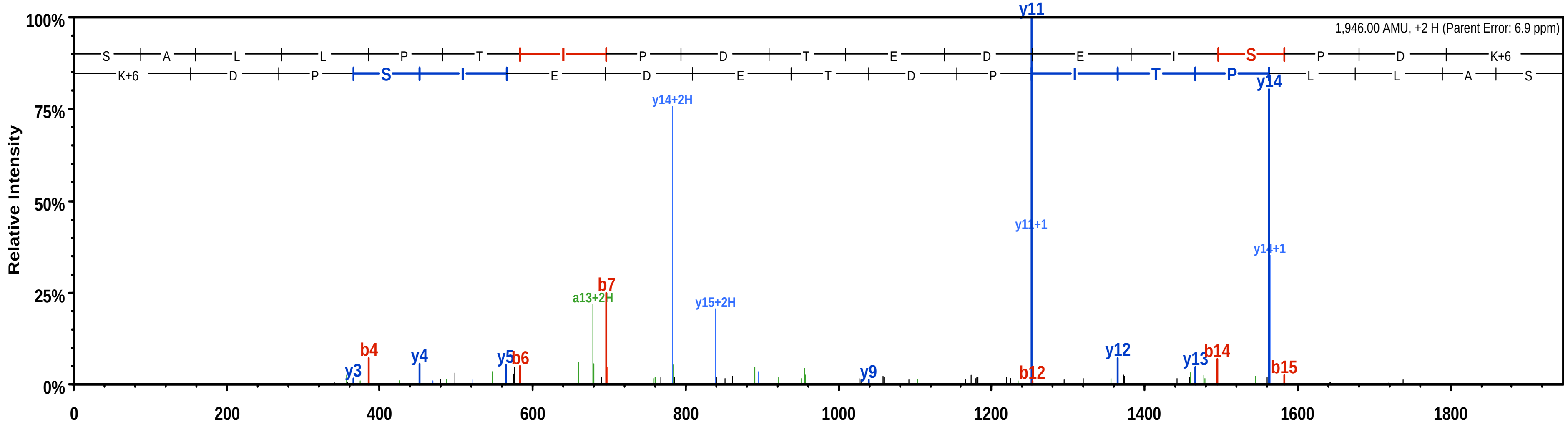


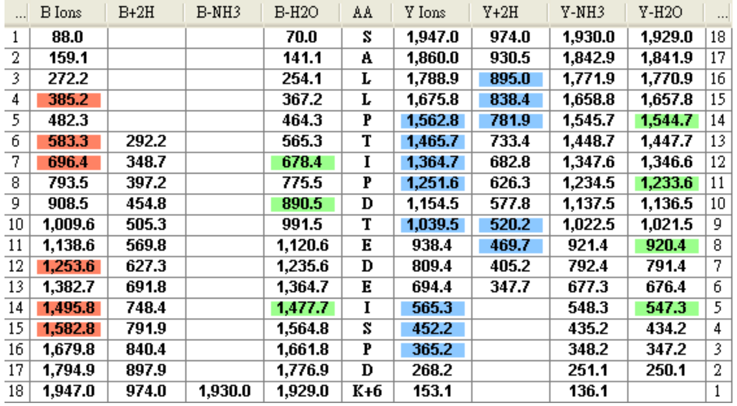


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	129.1		112.0		Q	2,282.0	1,141.5	2,265.0	2,264.0	19
2	242.1		225.1		I	2,154.0	1,077.5	2,137.0	2,136.0	18
3	343.2		326.2	325.2	T	2,040.9	1,021.0	2,023.9	2,022.9	17
4	472.2		455.2	454.2	E	1,939.9	970.4	1,922.8	1,921.8	16
5	601.3		584.3	583.3	E	1,810.8	905.9	1,793.8	1,792.8	15
6	716.3	358.7	699.3	698.3	D	1,681.8	841.4	1,664.7	1,663.8	14
7	829.4	415.2	812.4	811.4	L	1,566.7	783.9	1,549.7	1,548.7	13
8	958.4	479.7	941.4	940.4	E	1,453.7	727.3	1,436.6	1,435.6	12
9	1,015.5	508.2	998.4	997.4	G	1,324.6	662.8	1,307.6	1,306.6	11
10	1,143.6	572.3	1,126.5	1,125.5	K	1,267.6	634.3	1,250.6	1,249.6	10
11	1,244.6	622.8	1,227.6	1,226.6	T	1,139.5	570.3	1,122.5	1,121.5	9
12	1,373.6	687.3	1,356.6	1,355.6	E	1,038.4	519.7	1,021.4	1,020.4	8
13	1,502.7	751.8	1,485.7	1,484.7	E	909.4	455.2	892.4	891.4	7
14	1,631.7	816.4	1,614.7	1,613.7	E	780.4	390.7	763.3	762.4	6
15	1,744.8	872.9	1,727.8	1,726.8	I	651.3		634.3	633.3	5
16	1,873.9	937.4	1,856.8	1,855.8	E	538.2		521.2	520.2	4
17	2,004.9	1,003.0	1,987.9	1,986.9	M	409.2		392.2		3
18	2,135.9	1,068.5	2,118.9	2,117.9	M	278.2		261.1		2
19	2,282.0	1,141.5	2,265.0	2,264.0	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-122	sp|Q96SW2|CRBN_HUMAN	SALLPTIPDTEDEISPDK	33.06	Unmodified	Heavy	2	970.98859

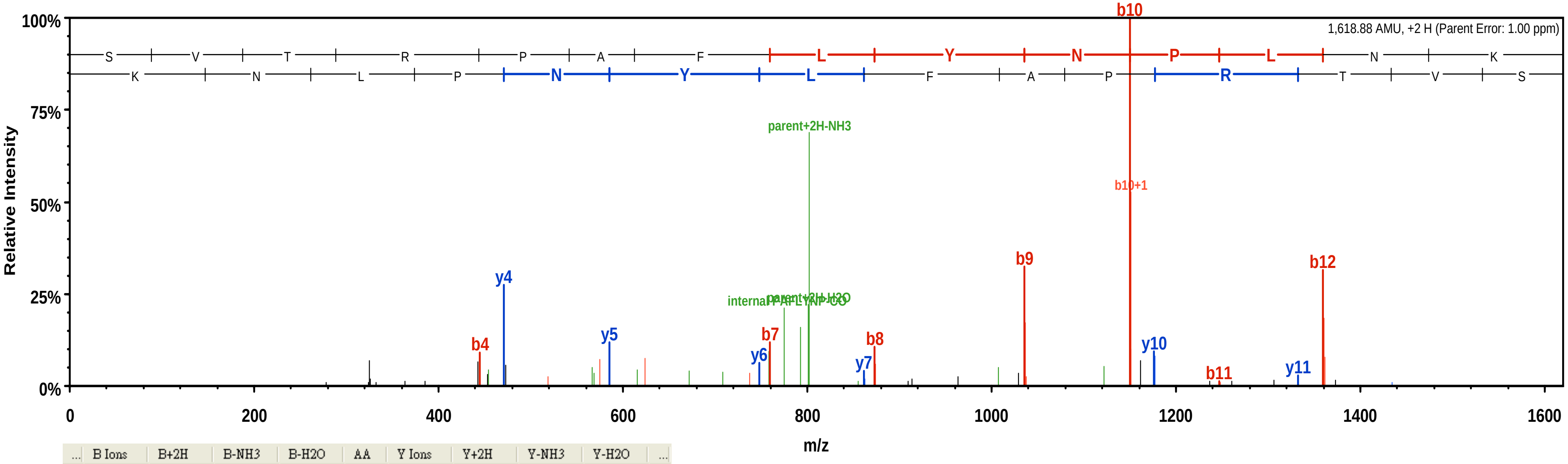


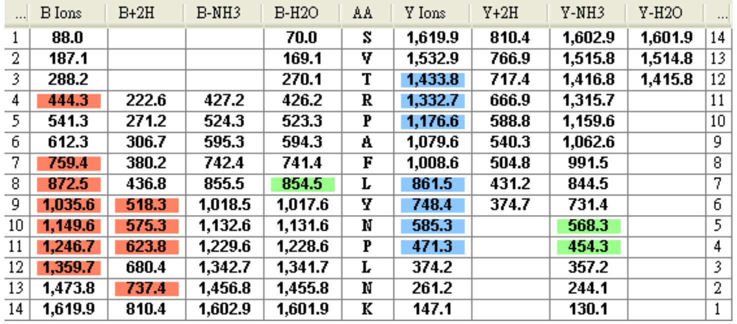


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	1,947.0	974.0	1,930.0	1,929.0	18
2	159.1			141.1	A	1,860.0	930.5	1,842.9	1,841.9	17
3	272.2			254.1	L	1,788.9	895.0	1,771.9	1,770.9	16
4	385.2			367.2	L	1,675.8	838.4	1,658.8	1,657.8	15
5	482.3			464.3	P	1,562.8	781.9	1,545.7	1,544.7	14
6	583.3	292.2		565.3	T	1,465.7	733.4	1,448.7	1,447.7	13
7	696.4	348.7		678.4	I	1,364.7	682.8	1,347.6	1,346.6	12
8	793.5	397.2		775.5	P	1,251.6	626.3	1,234.5	1,233.6	11
9	908.5	454.8		890.5	D	1,154.5	577.8	1,137.5	1,136.5	10
10	1,009.6	505.3		991.5	T	1,039.5	520.2	1,022.5	1,021.5	9
11	1,138.6	569.8		1,120.6	E	938.4	469.7	921.4	920.4	8
12	1,253.6	627.3		1,235.6	D	809.4	405.2	792.4	791.4	7
13	1,382.7	691.8		1,364.7	E	694.4	347.7	677.3	676.4	6
14	1,495.8	748.4		1,477.7	I	565.3		548.3	547.3	5
15	1,582.8	791.9		1,564.8	S	452.2		435.2	434.2	4
16	1,679.8	840.4		1,661.8	P	365.2		348.2	347.2	3
17	1,794.9	897.9		1,776.9	D	268.2		251.1	250.1	2
18	1,947.0	974.0	1,930.0	1,929.0	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-123	sp|Q8N6N3|CA052_HUMAN	SVTRPAFLYNPLNK	32.38	Unmodified	Light	2	810.44884

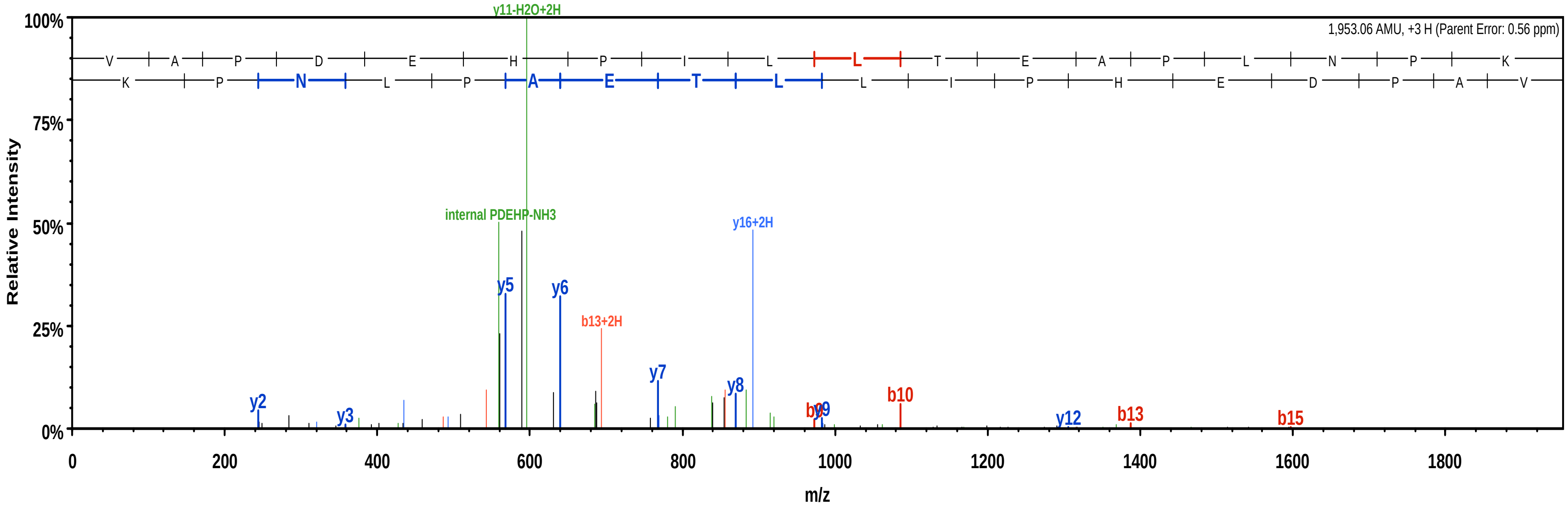


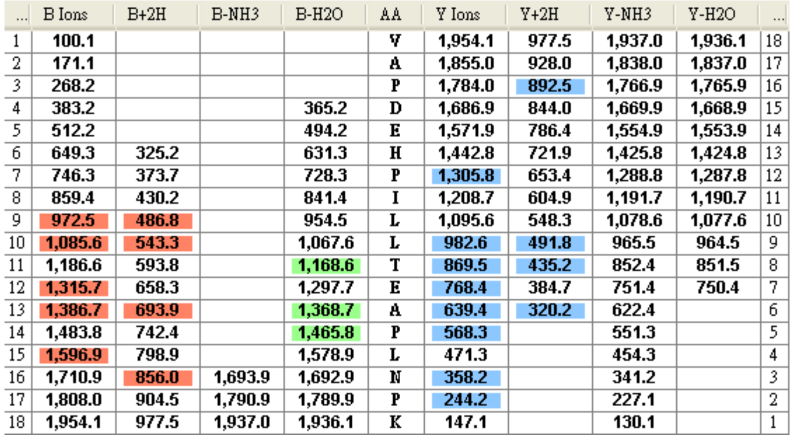


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	1,619.9	810.4	1,602.9	1,601.9	14
2	187.1			169.1	V	1,532.9	766.9	1,515.8	1,514.8	13
3	288.2			270.1	T	1,433.8	717.4	1,416.8	1,415.8	12
4	444.3	222.6	427.2	426.2	R	1,332.7	666.9	1,315.7		11
5	541.3	271.2	524.3	523.3	P	1,176.6	588.8	1,159.6		10
6	612.3	306.7	595.3	594.3	A	1,079.6	540.3	1,062.6		9
7	759.4	380.2	742.4	741.4	F	1,008.6	504.8	991.5		8
8	872.5	436.8	855.5	854.5	L	861.5	431.2	844.5		7
9	1,035.6	518.3	1,018.5	1,017.6	Y	748.4	374.7	731.4		6
10	1,149.6	575.3	1,132.6	1,131.6	N	585.3		568.3		5
11	1,246.7	623.8	1,229.6	1,228.6	P	471.3		454.3		4
12	1,359.7	680.4	1,342.7	1,341.7	L	374.2		357.2		3
13	1,473.8	737.4	1,456.8	1,455.8	N	261.2		244.1		2
14	1,619.9	810.4	1,602.9	1,601.9	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-124	sp|Q562R1|ACTBL_HUMAN	VAPDEHPILLTEAPLNPK	27.28	Unmodified	Light	3	652.02632

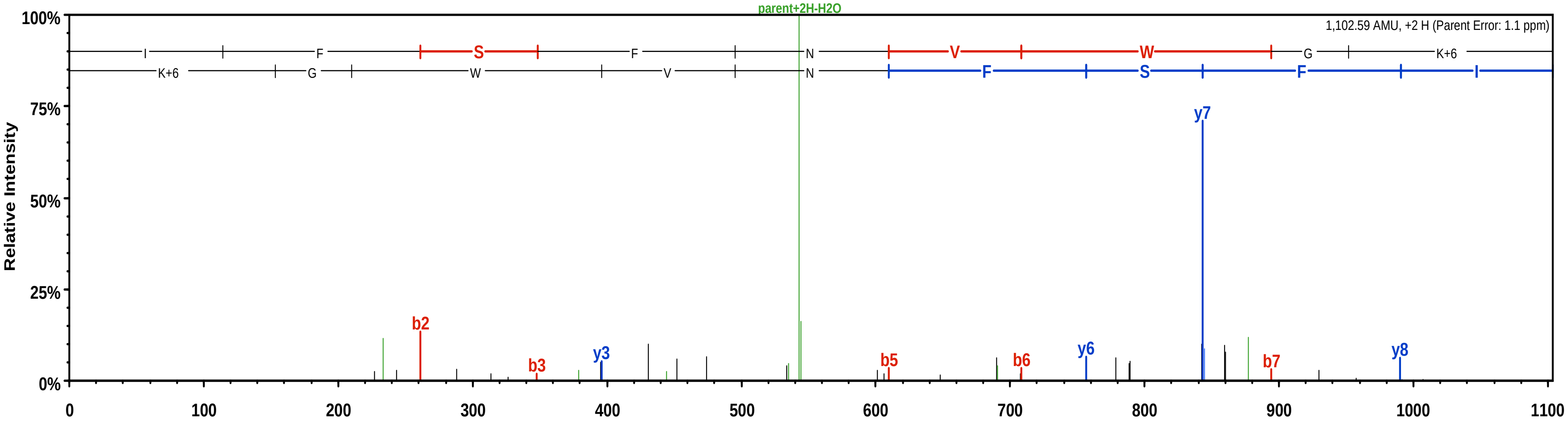


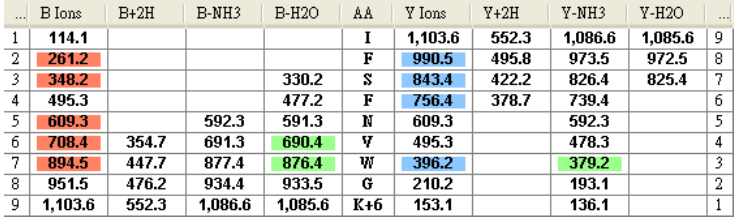


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	1,954.1	977.5	1,937.0	1,936.1	18
2	171.1				A	1,855.0	928.0	1,838.0	1,837.0	17
3	268.2				P	1,784.0	892.5	1,766.9	1,765.9	16
4	383.2			365.2	D	1,686.9	844.0	1,669.9	1,668.9	15
5	512.2			494.2	E	1,571.9	786.4	1,554.9	1,553.9	14
6	649.3	325.2		631.3	H	1,442.8	721.9	1,425.8	1,424.8	13
7	746.3	373.7		728.3	P	1,305.8	653.4	1,288.8	1,287.8	12
8	859.4	430.2		841.4	I	1,208.7	604.9	1,191.7	1,190.7	11
9	972.5	486.8		954.5	L	1,095.6	548.3	1,078.6	1,077.6	10
10	1,085.6	543.3		1,067.6	L	982.6	491.8	965.5	964.5	9
11	1,186.6	593.8		1,168.6	T	869.5	435.2	852.4	851.5	8
12	1,315.7	658.3		1,297.7	E	768.4	384.7	751.4	750.4	7
13	1,386.7	693.9		1,368.7	A	639.4	320.2	622.4		6
14	1,483.8	742.4		1,465.8	P	568.3		551.3		5
15	1,596.9	798.9		1,578.9	L	471.3		454.3		4
16	1,710.9	856.0	1,693.9	1,692.9	N	358.2		341.2		3
17	1,808.0	904.5	1,790.9	1,789.9	P	244.2		227.1		2
18	1,954.1	977.5	1,937.0	1,936.1	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-125	sp|Q9UHQ4|BAP29_HUMAN	IFSFNVWGK	27.04	Unmodified	Heavy	2	549.29256

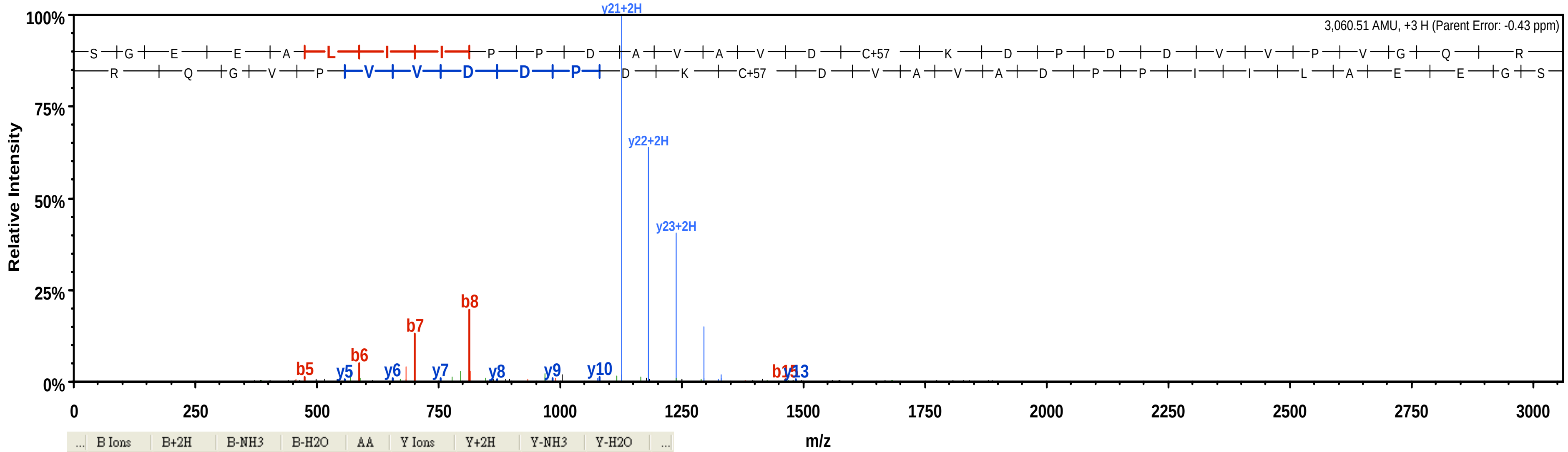


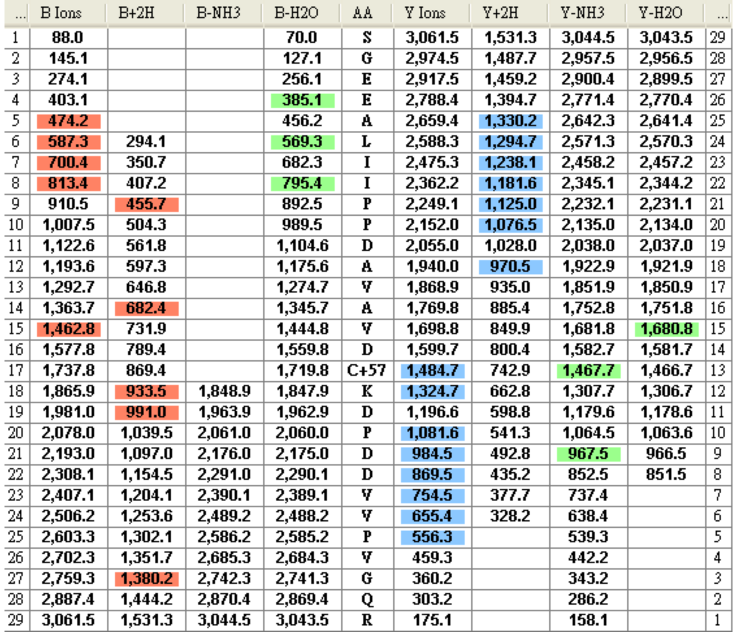


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	1,103.6	552.3	1,086.6	1,085.6	9
2	261.2				F	990.5	495.8	973.5	972.5	8
3	348.2			330.2	S	843.4	422.2	826.4	825.4	7
4	495.3			477.2	F	756.4	378.7	739.4		6
5	609.3		592.3	591.3	N	609.3		592.3		5
6	708.4	354.7	691.3	690.4	V	495.3		478.3		4
7	894.5	447.7	877.4	876.4	W	396.2		379.2		3
8	951.5	476.2	934.4	933.5	G	210.2		193.1		2
9	1,103.6	552.3	1,086.6	1,085.6	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-126	splQ9Y287lITM2B_HUMAN	SGEEALIIPPDAVAVDCKDPDDVVPVGQR	26.31	Unmodified	Light	3	1021.1764

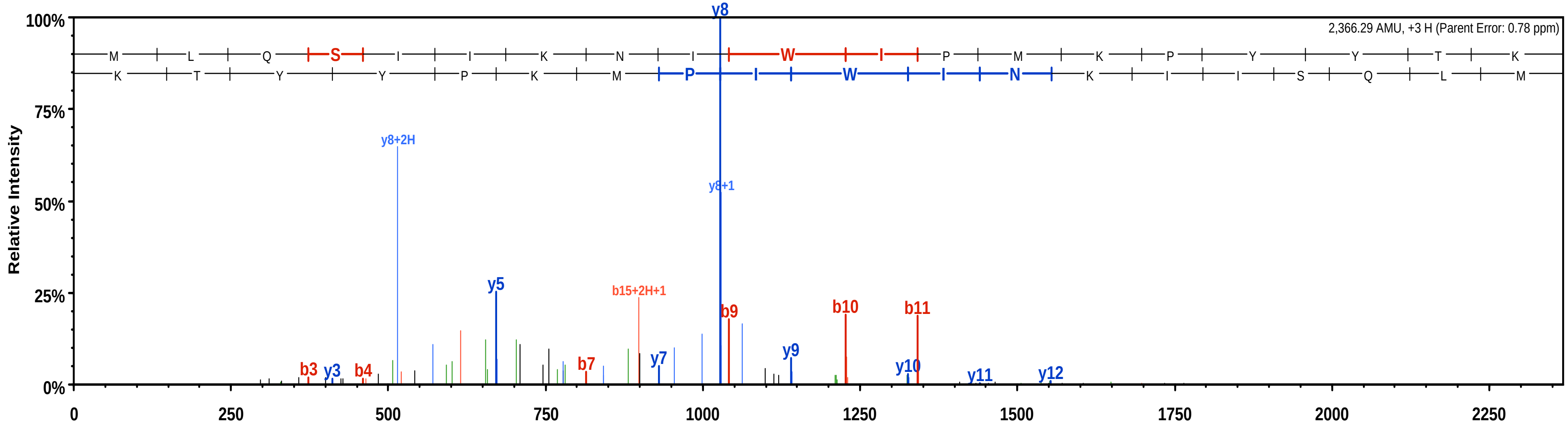


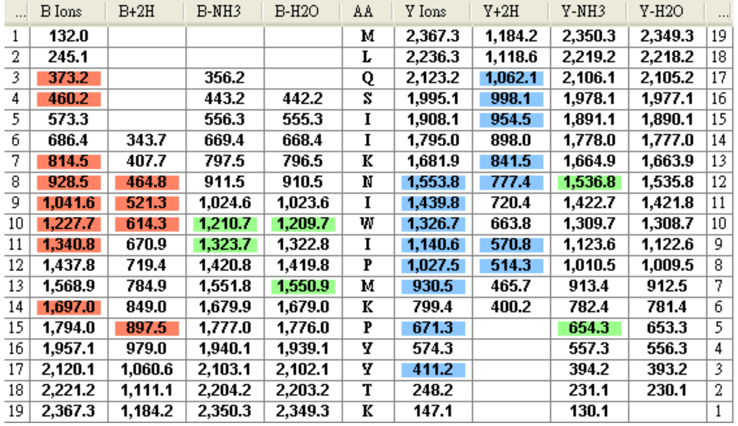


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	3,061.5	1,531.3	3,044.5	3,043.5	29
2	145.1			127.1	G	2,974.5	1,487.7	2,957.5	2,956.5	28
3	274.1			256.1	E	2,917.5	1,459.2	2,900.4	2,899.5	27
4	403.1			385.1	E	2,788.4	1,394.7	2,771.4	2,770.4	26
5	474.2			456.2	A	2,659.4	1,330.2	2,642.3	2,641.4	25
6	587.3	294.1		569.3	L	2,588.3	1,294.7	2,571.3	2,570.3	24
7	700.4	350.7		682.3	I	2,475.3	1,238.1	2,458.2	2,457.2	23
8	813.4	407.2		795.4	I	2,362.2	1,181.6	2,345.1	2,344.2	22
9	910.5	455.7		892.5	P	2,249.1	1,125.0	2,232.1	2,231.1	21
10	1,007.5	504.3		989.5	P	2,152.0	1,076.5	2,135.0	2,134.0	20
11	1,122.6	561.8		1,104.6	D	2,055.0	1,028.0	2,038.0	2,037.0	19
12	1,193.6	597.3		1,175.6	A	1,940.0	970.5	1,922.9	1,921.9	18
13	1,292.7	646.8		1,274.7	V	1,868.9	935.0	1,851.9	1,850.9	17
14	1,363.7	682.4		1,345.7	A	1,769.8	885.4	1,752.8	1,751.8	16
15	1,462.8	731.9		1,444.8	V	1,698.8	849.9	1,681.8	1,680.8	15
16	1,577.8	789.4		1,559.8	D	1,599.7	800.4	1,582.7	1,581.7	14
17	1,737.8	869.4		1,719.8	C+57	1,484.7	742.9	1,467.7	1,466.7	13
18	1,865.9	933.5	1,848.9	1,847.9	K	1,324.7	662.8	1,307.7	1,306.7	12
19	1,981.0	991.0	1,963.9	1,962.9	D	1,196.6	598.8	1,179.6	1,178.6	11
20	2,078.0	1,039.5	2,061.0	2,060.0	P	1,081.6	541.3	1,064.5	1,063.6	10
21	2,193.0	1,097.0	2,176.0	2,175.0	D	984.5	492.8	967.5	966.5	9
22	2,308.1	1,154.5	2,291.0	2,290.1	D	869.5	435.2	852.5	851.5	8
23	2,407.1	1,204.1	2,390.1	2,389.1	V	754.5	377.7	737.4		7
24	2,506.2	1,253.6	2,489.2	2,488.2	V	655.4	328.2	638.4		6
25	2,603.3	1,302.1	2,586.2	2,585.2	P	556.3		539.3		5
26	2,702.3	1,351.7	2,685.3	2,684.3	V	459.3		442.2		4
27	2,759.3	1,380.2	2,742.3	2,741.3	G	360.2		343.2		3
28	2,887.4	1,444.2	2,870.4	2,869.4	Q	303.2		286.2		2
29	3,061.5	1,531.3	3,044.5	3,043.5	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-127	sp|P56378|68MP_HUMAN	MLQSIIKNIWIPMKPYYTK	26.11	Unmodified	Light	3	789.77043

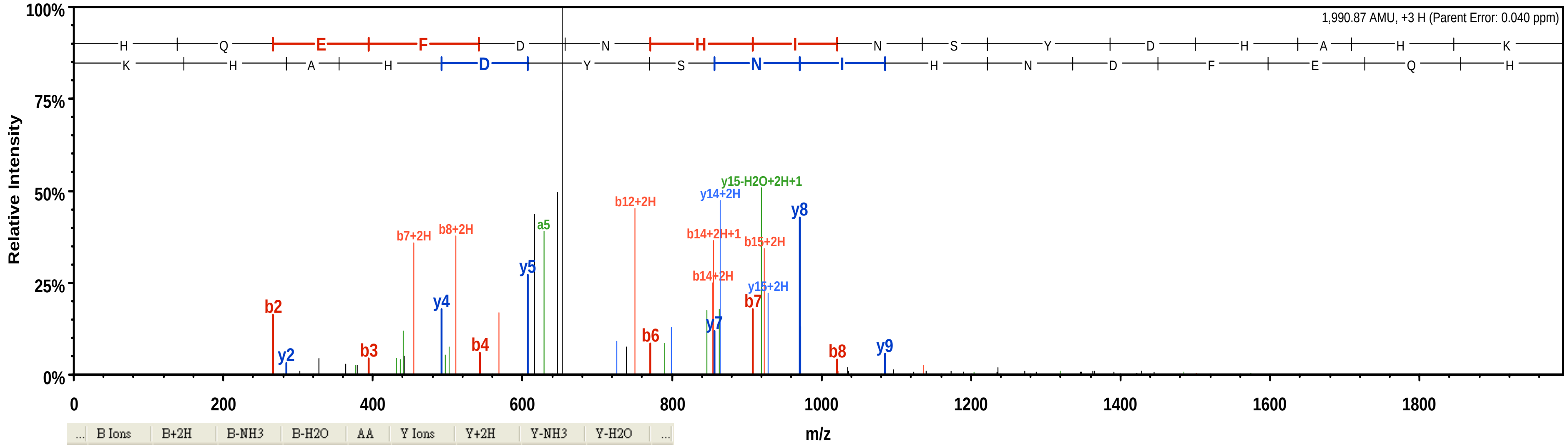


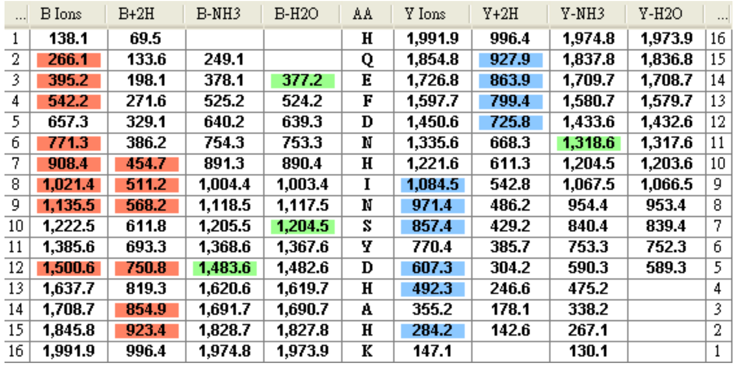


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	132.0				M	2,367.3	1,184.2	2,350.3	2,349.3	19
2	245.1				L	2,236.3	1,118.6	2,219.2	2,218.2	18
3	373.2		356.2		Q	2,123.2	1,062.1	2,106.1	2,105.2	17
4	460.2		443.2	442.2	S	1,995.1	998.1	1,978.1	1,977.1	16
5	573.3		556.3	555.3	I	1,908.1	954.5	1,891.1	1,890.1	15
6	686.4	343.7	669.4	668.4	I	1,795.0	898.0	1,778.0	1,777.0	14
7	814.5	407.7	797.5	796.5	K	1,681.9	841.5	1,664.9	1,663.9	13
8	928.5	464.8	911.5	910.5	N	1,553.8	777.4	1,536.8	1,535.8	12
9	1,041.6	521.3	1,024.6	1,023.6	I	1,439.8	720.4	1,422.7	1,421.8	11
10	1,227.7	614.3	1,210.7	1,209.7	W	1,326.7	663.8	1,309.7	1,308.7	10
11	1,340.8	670.9	1,323.7	1,322.8	I	1,140.6	570.8	1,123.6	1,122.6	9
12	1,437.8	719.4	1,420.8	1,419.8	P	1,027.5	514.3	1,010.5	1,009.5	8
13	1,568.9	784.9	1,551.8	1,550.9	M	930.5	465.7	913.4	912.5	7
14	1,697.0	849.0	1,679.9	1,679.0	K	799.4	400.2	782.4	781.4	6
15	1,794.0	897.5	1,777.0	1,776.0	P	671.3		654.3	653.3	5
16	1,957.1	979.0	1,940.1	1,939.1	Y	574.3		557.3	556.3	4
17	2,120.1	1,060.6	2,103.1	2,102.1	Y	411.2		394.2	393.2	3
18	2,221.2	1,111.1	2,204.2	2,203.2	T	248.2		231.1	230.1	2
19	2,367.3	1,184.2	2,350.3	2,349.3	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-128	splA4D1E1lZ804B_HUMAN	HQEFDNHINSYDHAHK	25.54	Unmodified	Light	3	664.62962

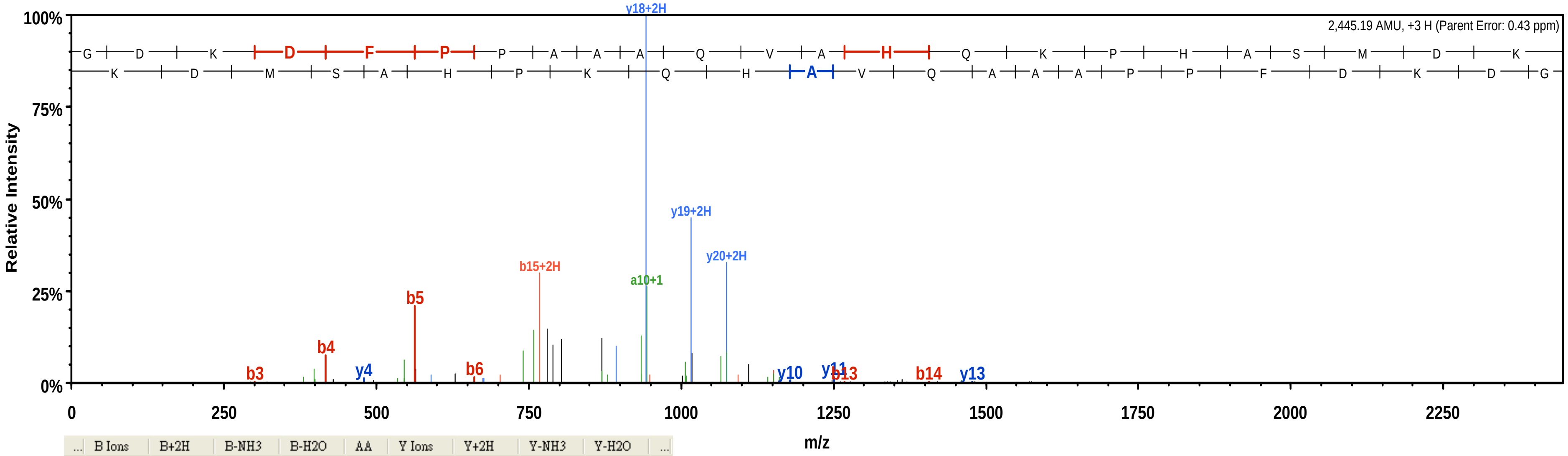


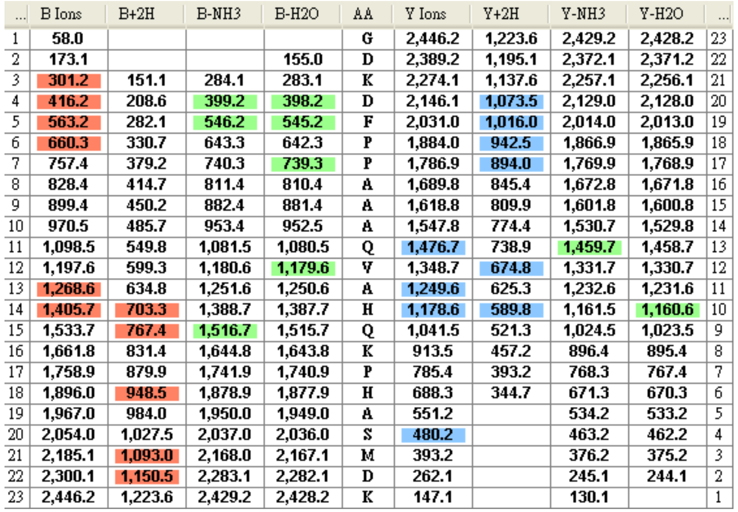


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	138.1	69.5			H	1,991.9	996.4	1,974.8	1,973.9	16
2	266.1	133.6	249.1		Q	1,854.8	927.9	1,837.8	1,836.8	15
3	395.2	198.1	378.1	377.2	E	1,726.8	863.9	1,709.7	1,708.7	14
4	542.2	271.6	525.2	524.2	F	1,597.7	799.4	1,580.7	1,579.7	13
5	657.3	329.1	640.2	639.3	D	1,450.6	725.8	1,433.6	1,432.6	12
6	771.3	386.2	754.3	753.3	N	1,335.6	668.3	1,318.6	1,317.6	11
7	908.4	454.7	891.3	890.4	H	1,221.6	611.3	1,204.5	1,203.6	10
8	1,021.4	511.2	1,004.4	1,003.4	I	1,084.5	542.8	1,067.5	1,066.5	9
9	1,135.5	568.2	1,118.5	1,117.5	N	971.4	486.2	954.4	953.4	8
10	1,222.5	611.8	1,205.5	1,204.5	S	857.4	429.2	840.4	839.4	7
11	1,385.6	693.3	1,368.6	1,367.6	Y	770.4	385.7	753.3	752.3	6
12	1,500.6	750.8	1,483.6	1,482.6	D	607.3	304.2	590.3	589.3	5
13	1,637.7	819.3	1,620.6	1,619.7	H	492.3	246.6	475.2		4
14	1,708.7	854.9	1,691.7	1,690.7	A	355.2	178.1	338.2		3
15	1,845.8	923.4	1,828.7	1,827.8	H	284.2	142.6	267.1		2
16	1,991.9	996.4	1,974.8	1,973.9	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-129	splP51397lDAP1_HUMAN	GDKDFPPAAAQVAHQKPHASMDK	24.99	Unmodified	Light	3	816.06925

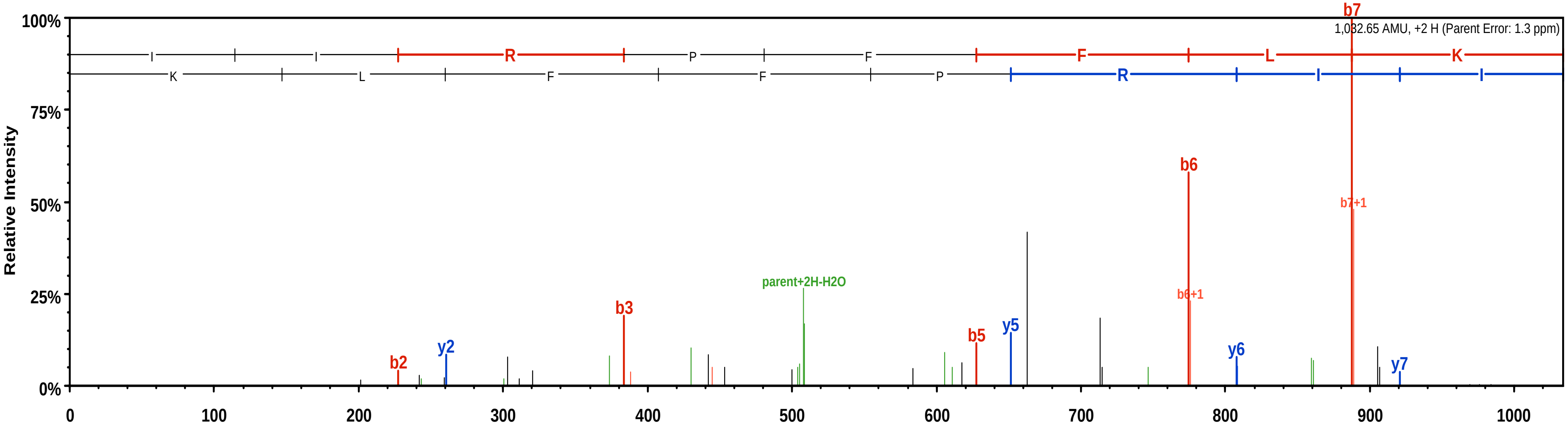


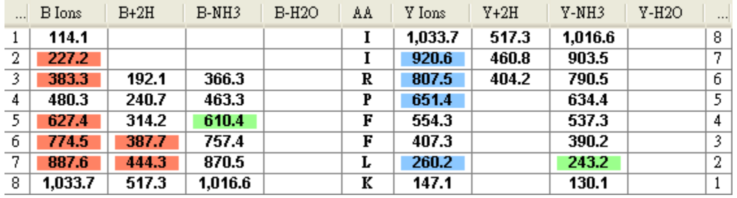


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	2,446.2	1,223.6	2,429.2	2,428.2	23
2	173.1			155.0	D	2,389.2	1,195.1	2,372.1	2,371.2	22
3	301.2	151.1	284.1	283.1	K	2,274.1	1,137.6	2,257.1	2,256.1	21
4	416.2	208.6	399.2	398.2	D	2,146.1	1,073.5	2,129.0	2,128.0	20
5	563.2	282.1	546.2	545.2	F	2,031.0	1,016.0	2,014.0	2,013.0	19
6	660.3	330.7	643.3	642.3	P	1,884.0	942.5	1,866.9	1,865.9	18
7	757.4	379.2	740.3	739.3	P	1,786.9	894.0	1,769.9	1,768.9	17
8	828.4	414.7	811.4	810.4	A	1,689.8	845.4	1,672.8	1,671.8	16
9	899.4	450.2	882.4	881.4	A	1,618.8	809.9	1,601.8	1,600.8	15
10	970.5	485.7	953.4	952.5	A	1,547.8	774.4	1,530.7	1,529.8	14
11	1,098.5	549.8	1,081.5	1,080.5	Q	1,476.7	738.9	1,459.7	1,458.7	13
12	1,197.6	599.3	1,180.6	1,179.6	V	1,348.7	674.8	1,331.7	1,330.7	12
13	1,268.6	634.8	1,251.6	1,250.6	A	1,249.6	625.3	1,232.6	1,231.6	11
14	1,405.7	703.3	1,388.7	1,387.7	H	1,178.6	589.8	1,161.5	1,160.6	10
15	1,533.7	767.4	1,516.7	1,515.7	Q	1,041.5	521.3	1,024.5	1,023.5	9
16	1,661.8	831.4	1,644.8	1,643.8	K	913.5	457.2	896.4	895.4	8
17	1,758.9	879.9	1,741.9	1,740.9	P	785.4	393.2	768.3	767.4	7
18	1,896.0	948.5	1,878.9	1,877.9	H	688.3	344.7	671.3	670.3	6
19	1,967.0	984.0	1,950.0	1,949.0	A	551.2		534.2	533.2	5
20	2,054.0	1,027.5	2,037.0	2,036.0	S	480.2		463.2	462.2	4
21	2,185.1	1,093.0	2,168.0	2,167.1	M	393.2		376.2	375.2	3
22	2,300.1	1,150.5	2,283.1	2,282.1	D	262.1		245.1	244.1	2
23	2,446.2	1,223.6	2,429.2	2,428.2	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-130	sp|Q00765|REEP5_HUMAN	IIRPFFLK	23.94	Unmodified	Light	2	517.33149

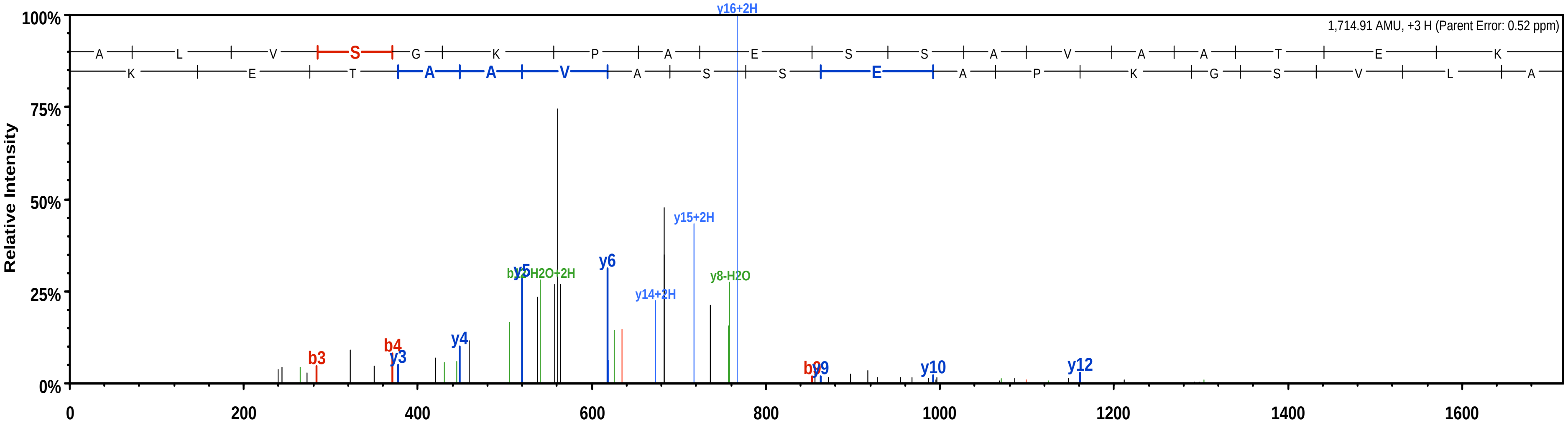


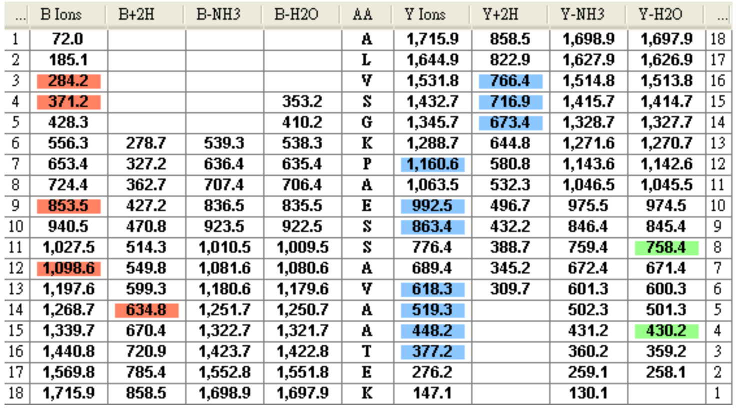


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	1,033.7	517.3	1,016.6		8
2	227.2				I	920.6	460.8	903.5		7
3	383.3	192.1	366.3		R	807.5	404.2	790.5		6
4	480.3	240.7	463.3		P	651.4		634.4		5
5	627.4	314.2	610.4		F	554.3		537.3		4
6	774.5	387.7	757.4		F	407.3		390.2		3
7	887.6	444.3	870.5		L	260.2		243.2		2
8	1,033.7	517.3	1,016.6		K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-131	sp|O95182|NDUA7_HUMAN	ALVSGKPAESSAVAATEK	23.34	Unmodified	Light	3	572.64399

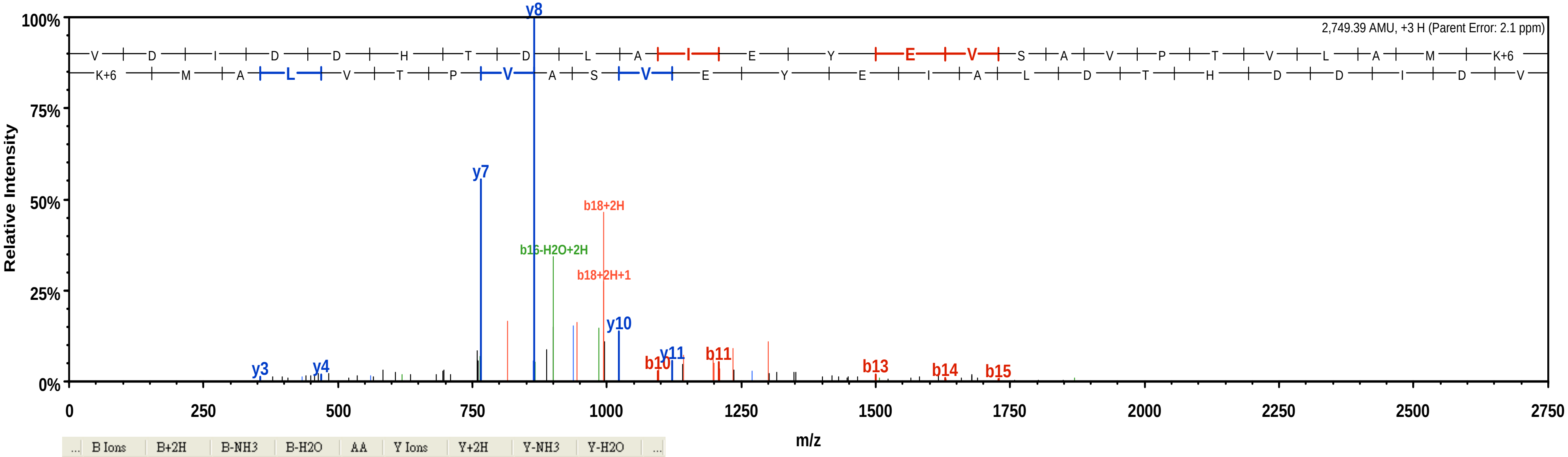


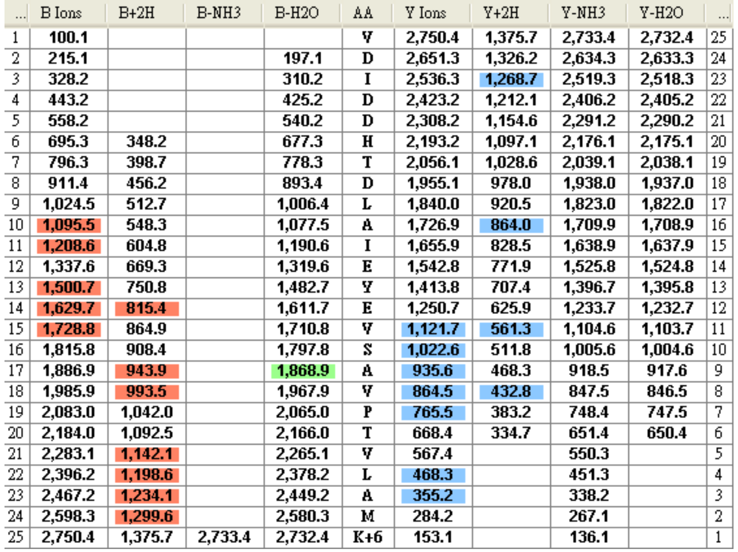


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	1,715.9	858.5	1,698.9	1,697.9	18
2	185.1				L	1,644.9	822.9	1,627.9	1,626.9	17
3	284.2				V	1,531.8	766.4	1,514.8	1,513.8	16
4	371.2			353.2	S	1,432.7	716.9	1,415.7	1,414.7	15
5	428.3			410.2	G	1,345.7	673.4	1,328.7	1,327.7	14
6	556.3	278.7	539.3	538.3	K	1,288.7	644.8	1,271.6	1,270.7	13
7	653.4	327.2	636.4	635.4	P	1,160.6	580.8	1,143.6	1,142.6	12
8	724.4	362.7	707.4	706.4	A	1,063.5	532.3	1,046.5	1,045.5	11
9	853.5	427.2	836.5	835.5	E	992.5	496.7	975.5	974.5	10
10	940.5	470.8	923.5	922.5	S	863.4	432.2	846.4	845.4	9
11	1,027.5	514.3	1,010.5	1,009.5	S	776.4	388.7	759.4	758.4	8
12	1,098.6	549.8	1,081.6	1,080.6	A	689.4	345.2	672.4	671.4	7
13	1,197.6	599.3	1,180.6	1,179.6	V	618.3	309.7	601.3	600.3	6
14	1,268.7	634.8	1,251.7	1,250.7	A	519.3		502.3	501.3	5
15	1,339.7	670.4	1,322.7	1,321.7	A	448.2		431.2	430.2	4
16	1,440.8	720.9	1,423.7	1,422.8	T	377.2		360.2	359.2	3
17	1,569.8	785.4	1,552.8	1,551.8	E	276.2		259.1	258.1	2
18	1,715.9	858.5	1,698.9	1,697.9	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-132	sp|Q99757|THIOM_HUMAN	VDIDDHTDLAIEYEVSAVPTVLAMK	19.46	Unmodified	Heavy	3	915.46148

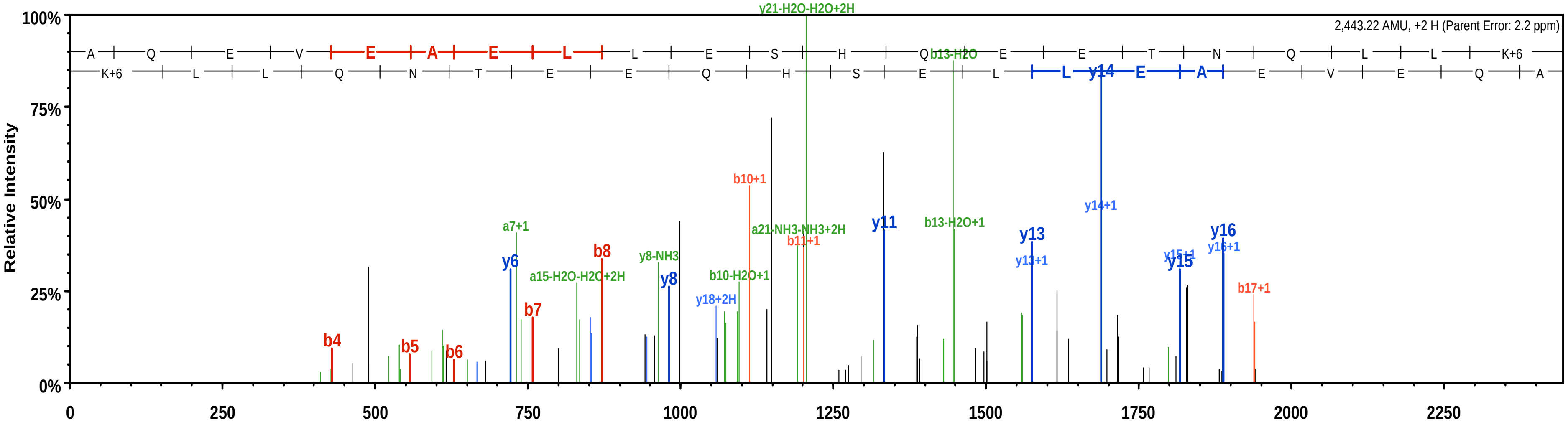


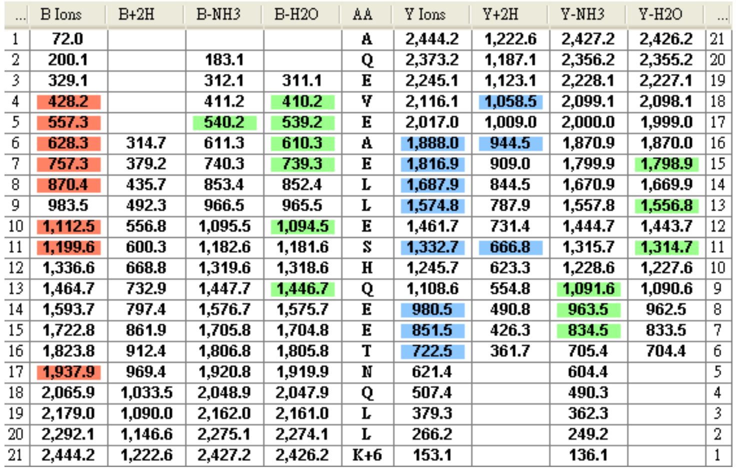


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	2,750.4	1,375.7	2,733.4	2,732.4	25
2	215.1			197.1	D	2,651.3	1,326.2	2,634.3	2,633.3	24
3	328.2			310.2	I	2,536.3	1,268.7	2,519.3	2,518.3	23
4	443.2			425.2	D	2,423.2	1,212.1	2,406.2	2,405.2	22
5	558.2			540.2	D	2,308.2	1,154.6	2,291.2	2,290.2	21
6	695.3	348.2		677.3	H	2,193.2	1,097.1	2,176.1	2,175.1	20
7	796.3	398.7		778.3	T	2,056.1	1,028.6	2,039.1	2,038.1	19
8	911.4	456.2		893.4	D	1,955.1	978.0	1,938.0	1,937.0	18
9	1,024.5	512.7		1,006.4	L	1,840.0	920.5	1,823.0	1,822.0	17
10	1,095.5	548.3		1,077.5	A	1,726.9	864.0	1,709.9	1,708.9	16
11	1,208.6	604.8		1,190.6	I	1,655.9	828.5	1,638.9	1,637.9	15
12	1,337.6	669.3		1,319.6	E	1,542.8	771.9	1,525.8	1,524.8	14
13	1,500.7	750.8		1,482.7	Y	1,413.8	707.4	1,396.7	1,395.8	13
14	1,629.7	815.4		1,611.7	E	1,250.7	625.9	1,233.7	1,232.7	12
15	1,728.8	864.9		1,710.8	V	1,121.7	561.3	1,104.6	1,103.7	11
16	1,815.8	908.4		1,797.8	S	1,022.6	511.8	1,005.6	1,004.6	10
17	1,886.9	943.9		1,868.9	A	935.6	468.3	918.5	917.6	9
18	1,985.9	993.5		1,967.9	V	864.5	432.8	847.5	846.5	8
19	2,083.0	1,042.0		2,065.0	P	765.5	383.2	748.4	747.5	7
20	2,184.0	1,092.5		2,166.0	T	668.4	334.7	651.4	650.4	6
21	2,283.1	1,142.1		2,265.1	V	567.4		550.3		5
22	2,396.2	1,198.6		2,378.2	L	468.3		451.3		4
23	2,467.2	1,234.1		2,449.2	A	355.2		338.2		3
24	2,598.3	1,299.6		2,580.3	M	284.2		267.1		2
25	2,750.4	1,375.7	2,733.4	2,732.4	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-133	sp|Q13439|GOGA4_HUMAN	AQEVEAELLESHQEETNQLLK	17.25	Unmodified	Heavy	2	1219.6059

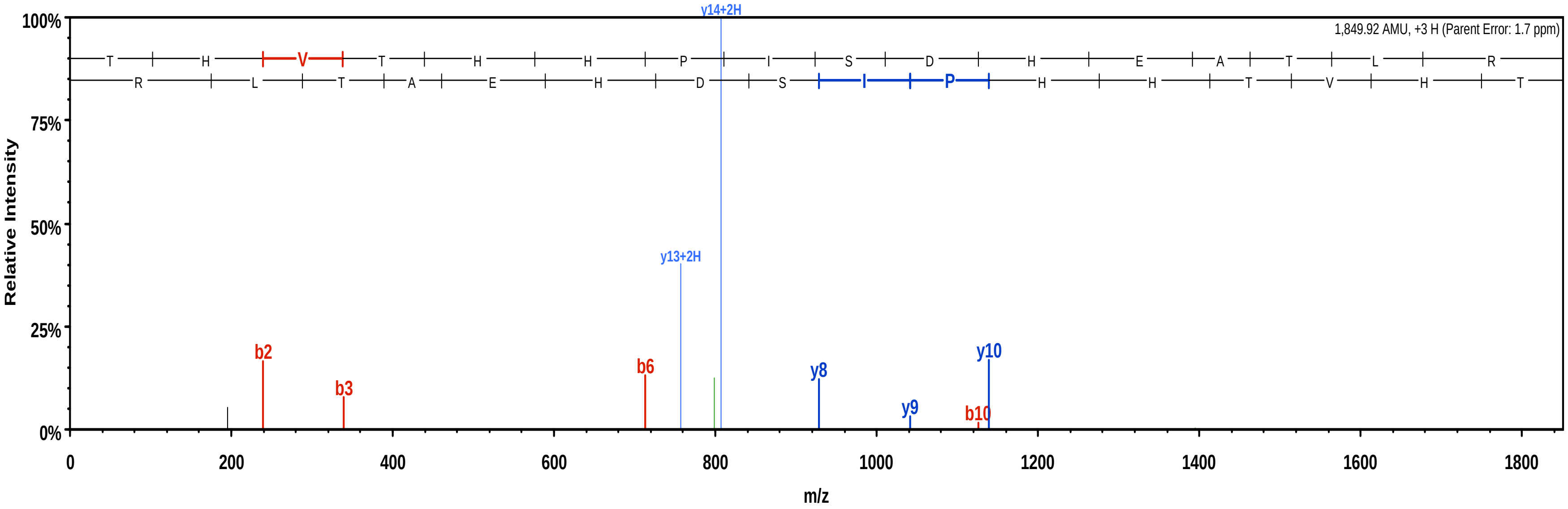


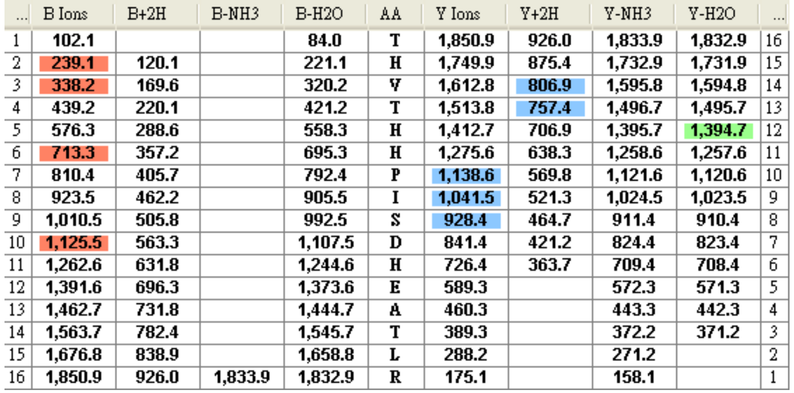


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	2,444.2	1,222.6	2,427.2	2,426.2	21
2	200.1		183.1		Q	2,373.2	1,187.1	2,356.2	2,355.2	20
3	329.1		312.1	311.1	E	2,245.1	1,123.1	2,228.1	2,227.1	19
4	428.2		411.2	410.2	V	2,116.1	1,058.5	2,099.1	2,098.1	18
5	557.3		540.2	539.2	E	2,017.0	1,009.0	2,000.0	1,999.0	17
6	628.3	314.7	611.3	610.3	A	1,888.0	944.5	1,870.9	1,870.0	16
7	757.3	379.2	740.3	739.3	E	1,816.9	909.0	1,799.9	1,798.9	15
8	870.4	435.7	853.4	852.4	L	1,687.9	844.5	1,670.9	1,669.9	14
9	983.5	492.3	966.5	965.5	L	1,574.8	787.9	1,557.8	1,556.8	13
10	1,112.5	556.8	1,095.5	1,094.5	E	1,461.7	731.4	1,444.7	1,443.7	12
11	1,199.6	600.3	1,182.6	1,181.6	S	1,332.7	666.8	1,315.7	1,314.7	11
12	1,336.6	668.8	1,319.6	1,318.6	H	1,245.7	623.3	1,228.6	1,227.6	10
13	1,464.7	732.9	1,447.7	1,446.7	Q	1,108.6	554.8	1,091.6	1,090.6	9
14	1,593.7	797.4	1,576.7	1,575.7	E	980.5	490.8	963.5	962.5	8
15	1,722.8	861.9	1,705.8	1,704.8	E	851.5	426.3	834.5	833.5	7
16	1,823.8	912.4	1,806.8	1,805.8	T	722.5	361.7	705.4	704.4	6
17	1,937.9	969.4	1,920.8	1,919.9	N	621.4		604.4		5
18	2,065.9	1,033.5	2,048.9	2,047.9	Q	507.4		490.3		4
19	2,179.0	1,090.0	2,162.0	2,161.0	L	379.3		362.3		3
20	2,292.1	1,146.6	2,275.1	2,274.1	L	266.2		249.2		2
21	2,444.2	1,222.6	2,427.2	2,426.2	K+6	153.1		136.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-134	sp|P10321|1C07_HUMAN	THVTHHPLSDHEATLR	12.61	Unmodified		3	617.64672

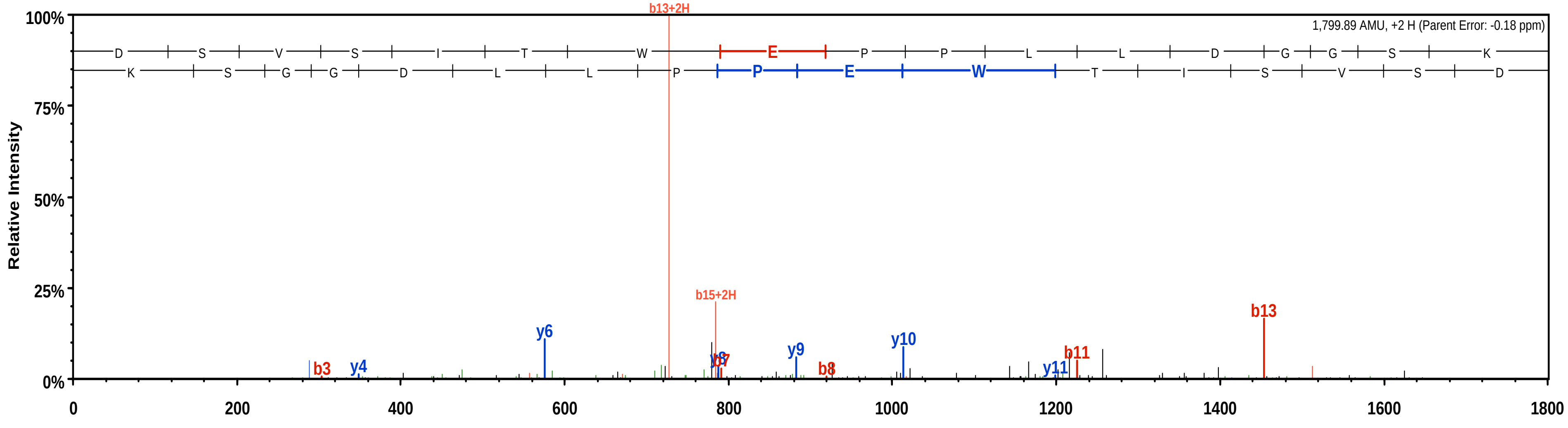


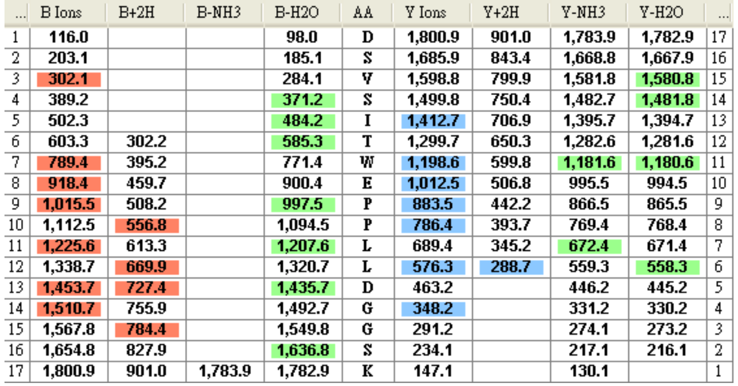


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	102.1			84.0	T	1,850.9	926.0	1,833.9	1,832.9	16
2	239.1	120.1		221.1	H	1,749.9	875.4	1,732.9	1,731.9	15
3	338.2	169.6		320.2	V	1,612.8	806.9	1,595.8	1,594.8	14
4	439.2	220.1		421.2	T	1,513.8	757.4	1,496.7	1,495.7	13
5	576.3	288.6		558.3	H	1,412.7	706.9	1,395.7	1,394.7	12
6	713.3	357.2		695.3	H	1,275.6	638.3	1,258.6	1,257.6	11
7	810.4	405.7		792.4	P	1,138.6	569.8	1,121.6	1,120.6	10
8	923.5	462.2		905.5	I	1,041.5	521.3	1,024.5	1,023.5	9
9	1,010.5	505.8		992.5	S	928.4	464.7	911.4	910.4	8
10	1,125.5	563.3		1,107.5	D	841.4	421.2	824.4	823.4	7
11	1,262.6	631.8		1,244.6	H	726.4	363.7	709.4	708.4	6
12	1,391.6	696.3		1,373.6	E	589.3		572.3	571.3	5
13	1,462.7	731.8		1,444.7	A	460.3		443.3	442.3	4
14	1,563.7	782.4		1,545.7	T	389.3		372.2	371.2	3
15	1,676.8	838.9		1,658.8	L	288.2		271.2		2
16	1,850.9	926.0	1,833.9	1,832.9	R	175.1		158.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-135	sp|Q8WZ42|TITIN_HUMAN	DSVSITWEPPLLDGGSK	11.33	Unmodified	Light	2	900.95435

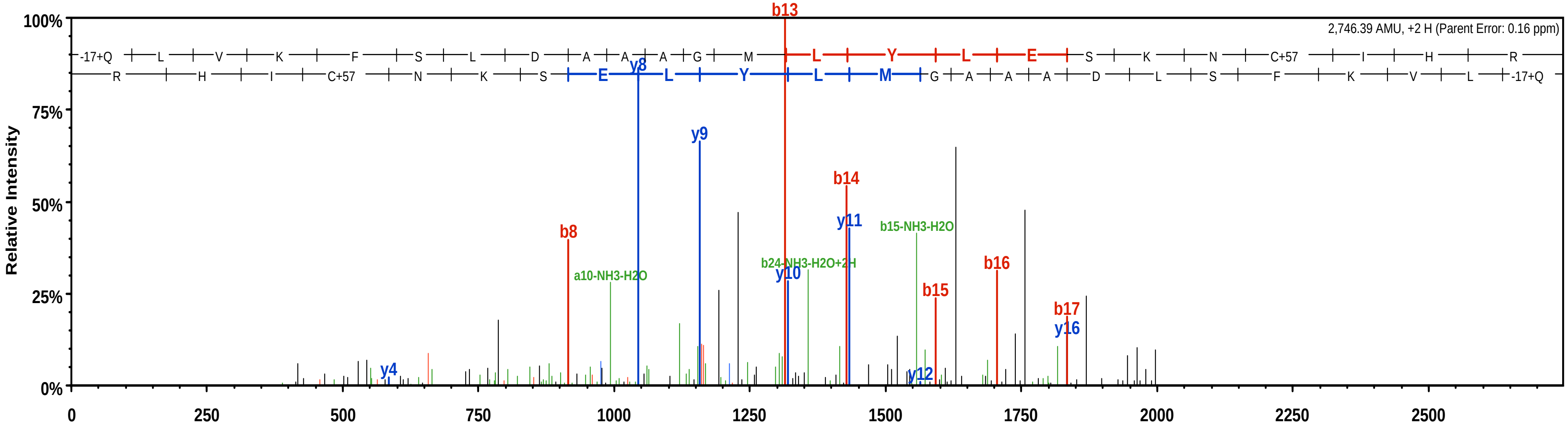


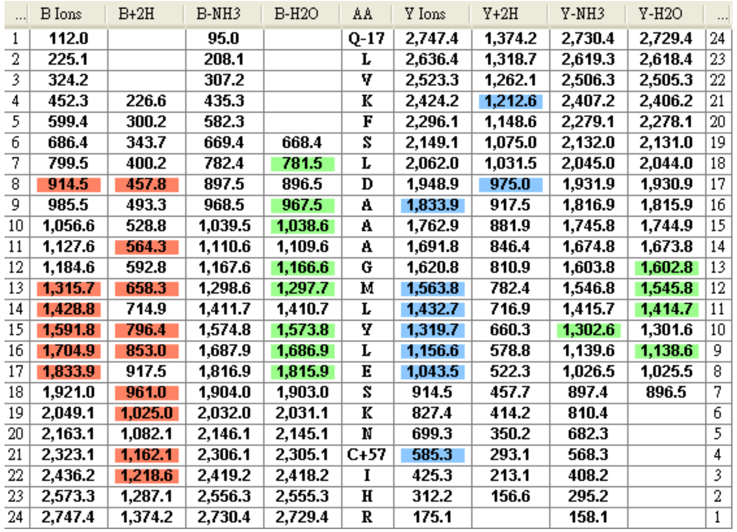


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	1,800.9	901.0	1,783.9	1,782.9	17
2	203.1			185.1	S	1,685.9	843.4	1,668.8	1,667.9	16
3	302.1			284.1	V	1,598.8	799.9	1,581.8	1,580.8	15
4	389.2			371.2	S	1,499.8	750.4	1,482.7	1,481.8	14
5	502.3			484.2	I	1,412.7	706.9	1,395.7	1,394.7	13
6	603.3	302.2		585.3	T	1,299.7	650.3	1,282.6	1,281.6	12
7	789.4	395.2		771.4	W	1,198.6	599.8	1,181.6	1,180.6	11
8	918.4	459.7		900.4	E	1,012.5	506.8	995.5	994.5	10
9	1,015.5	508.2		997.5	P	883.5	442.2	866.5	865.5	9
10	1,112.5	556.8		1,094.5	P	786.4	393.7	769.4	768.4	8
11	1,225.6	613.3		1,207.6	L	689.4	345.2	672.4	671.4	7
12	1,338.7	669.9		1,320.7	L	576.3	288.7	559.3	558.3	6
13	1,453.7	727.4		1,435.7	D	463.2		446.2	445.2	5
14	1,510.7	755.9		1,492.7	G	348.2		331.2	330.2	4
15	1,567.8	784.4		1,549.8	G	291.2		274.1	273.2	3
16	1,654.8	827.9		1,636.8	S	234.1		217.1	216.1	2
17	1,800.9	901.0	1,783.9	1,782.9	K	147.1		130.1		1

Whole proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
W-136	sp|P16591|FER_HUMAN	QLVKFSLDAAAGMLYLESKNCIHR	5.55	Gln->pyro-Glu (N-term Q)	Light	2	1374.204

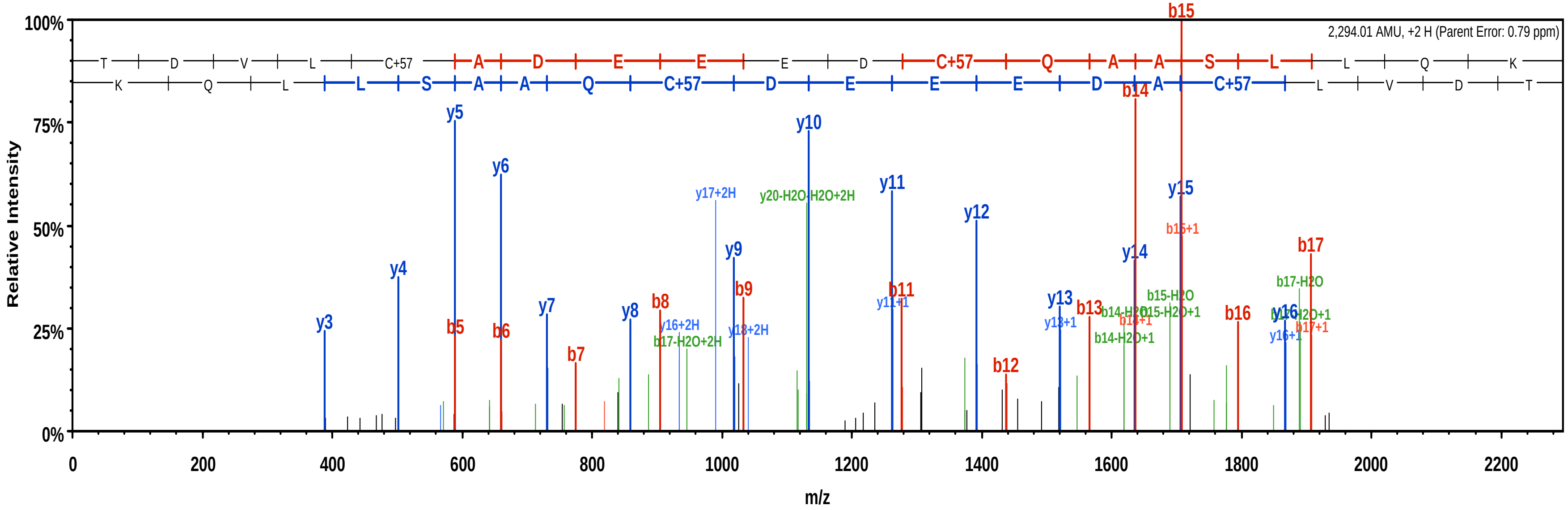


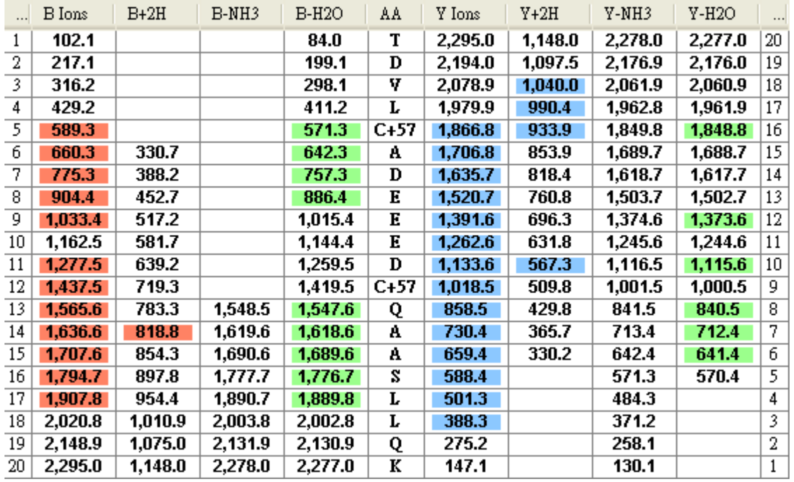


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	2,747.4	1,374.2	2,730.4	2,729.4	24
2	225.1		208.1		L	2,636.4	1,318.7	2,619.3	2,618.4	23
3	324.2		307.2		V	2,523.3	1,262.1	2,506.3	2,505.3	22
4	452.3	226.6	435.3		K	2,424.2	1,212.6	2,407.2	2,406.2	21
5	599.4	300.2	582.3		F	2,296.1	1,148.6	2,279.1	2,278.1	20
6	686.4	343.7	669.4	668.4	S	2,149.1	1,075.0	2,132.0	2,131.0	19
7	799.5	400.2	782.4	781.5	L	2,062.0	1,031.5	2,045.0	2,044.0	18
8	914.5	457.8	897.5	896.5	D	1,948.9	975.0	1,931.9	1,930.9	17
9	985.5	493.3	968.5	967.5	A	1,833.9	917.5	1,816.9	1,815.9	16
10	1,056.6	528.8	1,039.5	1,038.6	A	1,762.9	881.9	1,745.8	1,744.9	15
11	1,127.6	564.3	1,110.6	1,109.6	A	1,691.8	846.4	1,674.8	1,673.8	14
12	1,184.6	592.8	1,167.6	1,166.6	G	1,620.8	810.9	1,603.8	1,602.8	13
13	1,315.7	658.3	1,298.6	1,297.7	M	1,563.8	782.4	1,546.8	1,545.8	12
14	1,428.8	714.9	1,411.7	1,410.7	L	1,432.7	716.9	1,415.7	1,414.7	11
15	1,591.8	796.4	1,574.8	1,573.8	Y	1,319.7	660.3	1,302.6	1,301.6	10
16	1,704.9	853.0	1,687.9	1,686.9	L	1,156.6	578.8	1,139.6	1,138.6	9
17	1,833.9	917.5	1,816.9	1,815.9	E	1,043.5	522.3	1,026.5	1,025.5	8
18	1,921.0	961.0	1,904.0	1,903.0	S	914.5	457.7	897.4	896.5	7
19	2,049.1	1,025.0	2,032.0	2,031.1	K	827.4	414.2	810.4		6
20	2,163.1	1,082.1	2,146.1	2,145.1	N	699.3	350.2	682.3		5
21	2,323.1	1,162.1	2,306.1	2,305.1	C+57	585.3	293.1	568.3		4
22	2,436.2	1,218.6	2,419.2	2,418.2	I	425.3	213.1	408.2		3
23	2,573.3	1,287.1	2,556.3	2,555.3	H	312.2	156.6	295.2		2
24	2,747.4	1,374.2	2,730.4	2,729.4	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-1	sp|Q6W2J9|BCOR_HUMAN	TDVLCADEEEDCQAASLLQK	137.51	Unmodified	Light	2	1148.0094

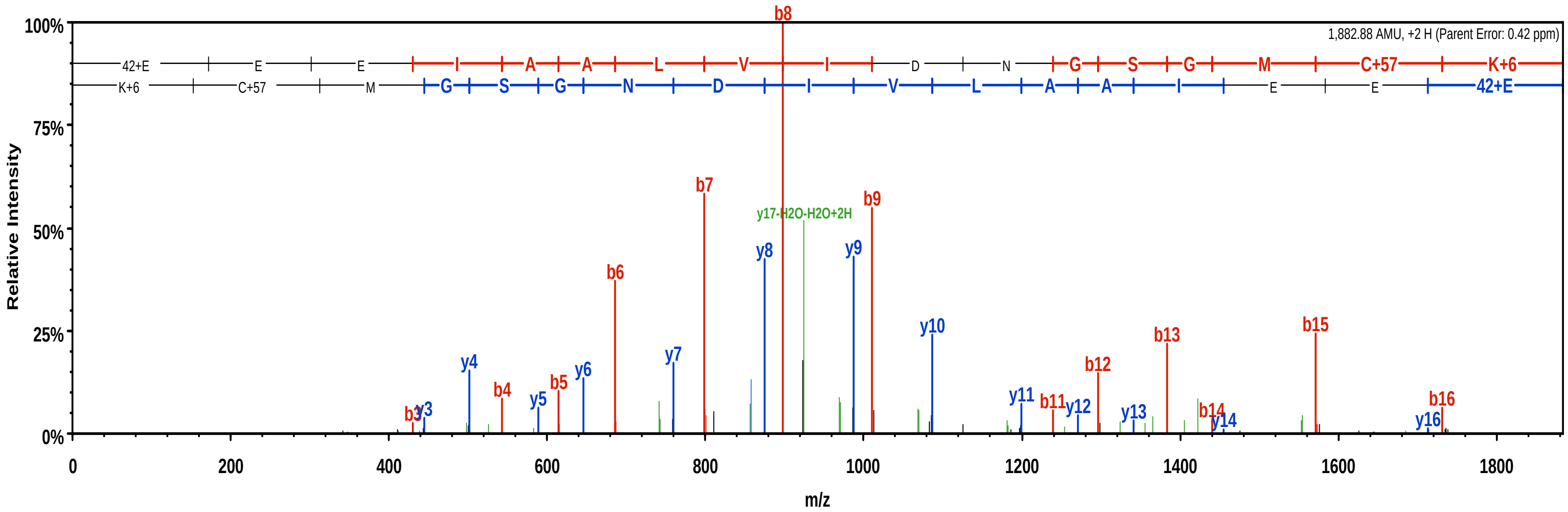


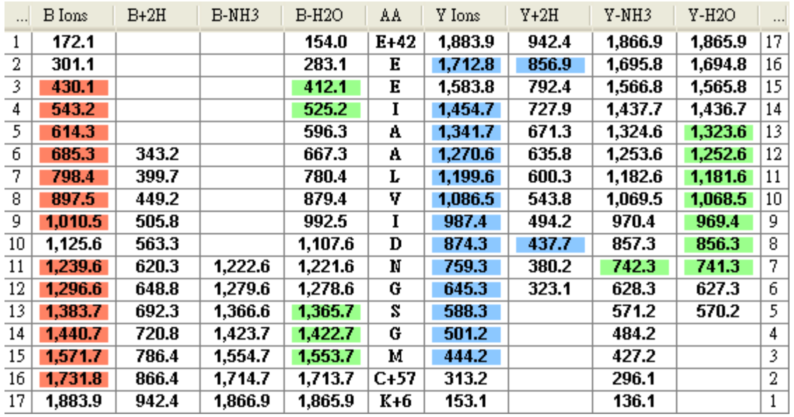


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	102.1			84.0	T	2,295.0	1,148.0	2,278.0	2,277.0	20
2	217.1			199.1	D	2,194.0	1,097.5	2,176.9	2,176.0	19
3	316.2			298.1	V	2,078.9	1,040.0	2,061.9	2,060.9	18
4	429.2			411.2	L	1,979.9	990.4	1,962.8	1,961.9	17
5	589.3			571.3	C+57	1,866.8	933.9	1,849.8	1,848.8	16
6	660.3	330.7		642.3	A	1,706.8	853.9	1,689.7	1,688.7	15
7	775.3	388.2		757.3	D	1,635.7	818.4	1,618.7	1,617.7	14
8	904.4	452.7		886.4	E	1,520.7	760.8	1,503.7	1,502.7	13
9	1,033.4	517.2		1,015.4	E	1,391.6	696.3	1,374.6	1,373.6	12
10	1,162.5	581.7		1,144.4	E	1,262.6	631.8	1,245.6	1,244.6	11
11	1,277.5	639.2		1,259.5	D	1,133.6	567.3	1,116.5	1,115.6	10
12	1,437.5	719.3		1,419.5	C+57	1,018.5	509.8	1,001.5	1,000.5	9
13	1,565.6	783.3	1,548.5	1,547.6	Q	858.5	429.8	841.5	840.5	8
14	1,636.6	818.8	1,619.6	1,618.6	A	730.4	365.7	713.4	712.4	7
15	1,707.6	854.3	1,690.6	1,689.6	A	659.4	330.2	642.4	641.4	6
16	1,794.7	897.8	1,777.7	1,776.7	S	588.4		571.3	570.4	5
17	1,907.8	954.4	1,890.7	1,889.8	L	501.3		484.3		4
18	2,020.8	1,010.9	2,003.8	2,002.8	L	388.3		371.2		3
19	2,148.9	1,075.0	2,131.9	2,130.9	Q	275.2		258.1		2
20	2,295.0	1,148.0	2,278.0	2,277.0	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-2	sp|P63261|ACTG_HUMAN	EEEIAALVIDNGSGMCK	137.14	Acetyl (Protein N-term)	Heavy	2	939.43461

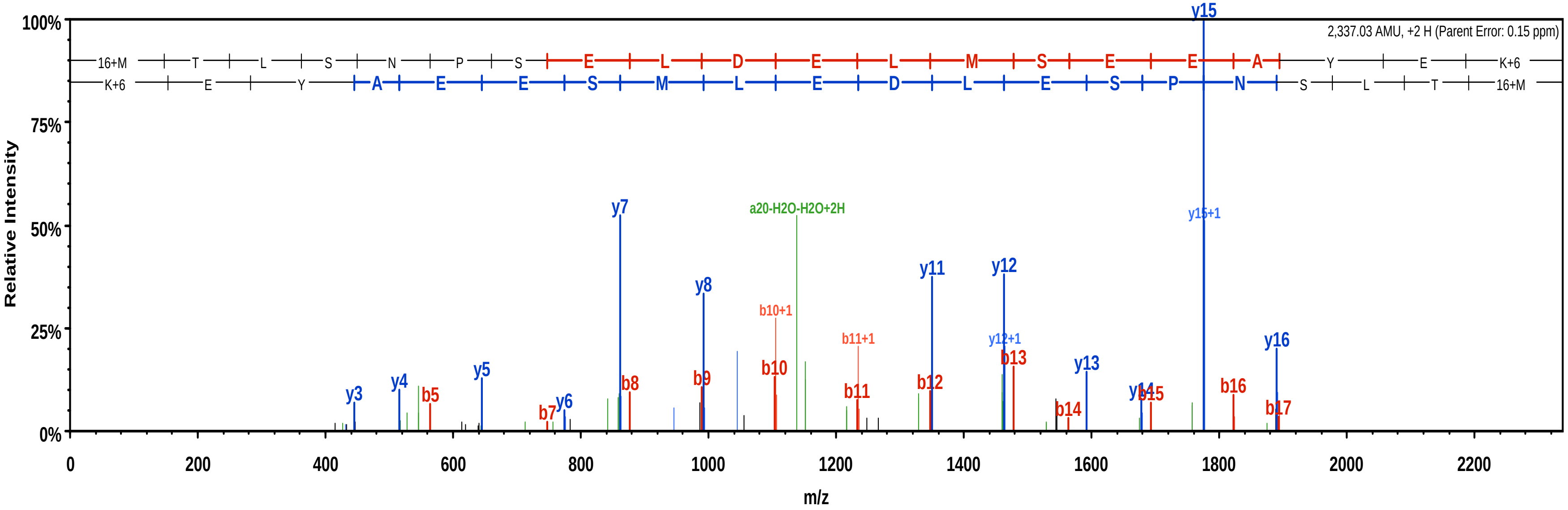


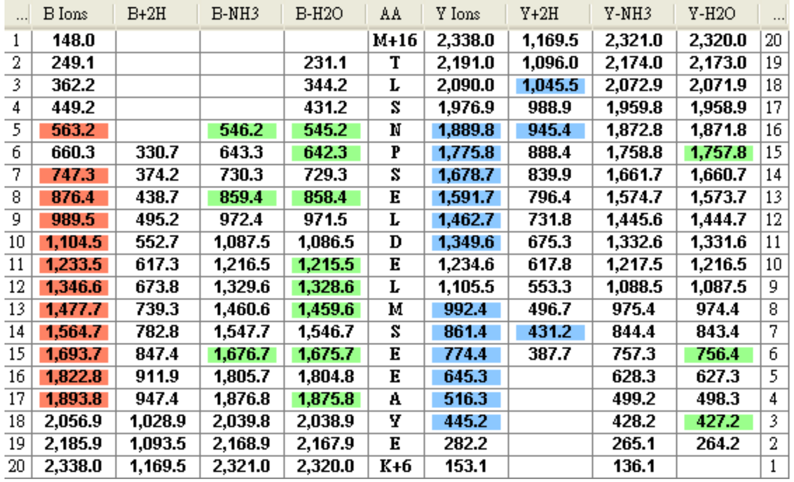


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	172.1			154.0	E+42	1,883.9	942.4	1,866.9	1,865.9	17
2	301.1			283.1	E	1,712.8	856.9	1,695.8	1,694.8	16
3	430.1			412.1	E	1,583.8	792.4	1,566.8	1,565.8	15
4	543.2			525.2	I	1,454.7	727.9	1,437.7	1,436.7	14
5	614.3			596.3	A	1,341.7	671.3	1,324.6	1,323.6	13
6	685.3	343.2		667.3	A	1,270.6	635.8	1,253.6	1,252.6	12
7	798.4	399.7		780.4	L	1,199.6	600.3	1,182.6	1,181.6	11
8	897.5	449.2		879.4	V	1,086.5	543.8	1,069.5	1,068.5	10
9	1,010.5	505.8		992.5	I	987.4	494.2	970.4	969.4	9
10	1,125.6	563.3		1,107.6	D	874.3	437.7	857.3	856.3	8
11	1,239.6	620.3	1,222.6	1,221.6	N	759.3	380.2	742.3	741.3	7
12	1,296.6	648.8	1,279.6	1,278.6	G	645.3	323.1	628.3	627.3	6
13	1,383.7	692.3	1,366.6	1,365.7	S	588.3		571.2	570.2	5
14	1,440.7	720.8	1,423.7	1,422.7	G	501.2		484.2		4
15	1,571.7	786.4	1,554.7	1,553.7	M	444.2		427.2		3
16	1,731.8	866.4	1,714.7	1,713.7	C+57	313.2		296.1		2
17	1,883.9	942.4	1,866.9	1,865.9	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-3	sp|P23434|GCSH_HUMAN	MTLSNPSELDELMSEEAYEK	129.93	Oxidation (M)	Heavy	2	1166.514

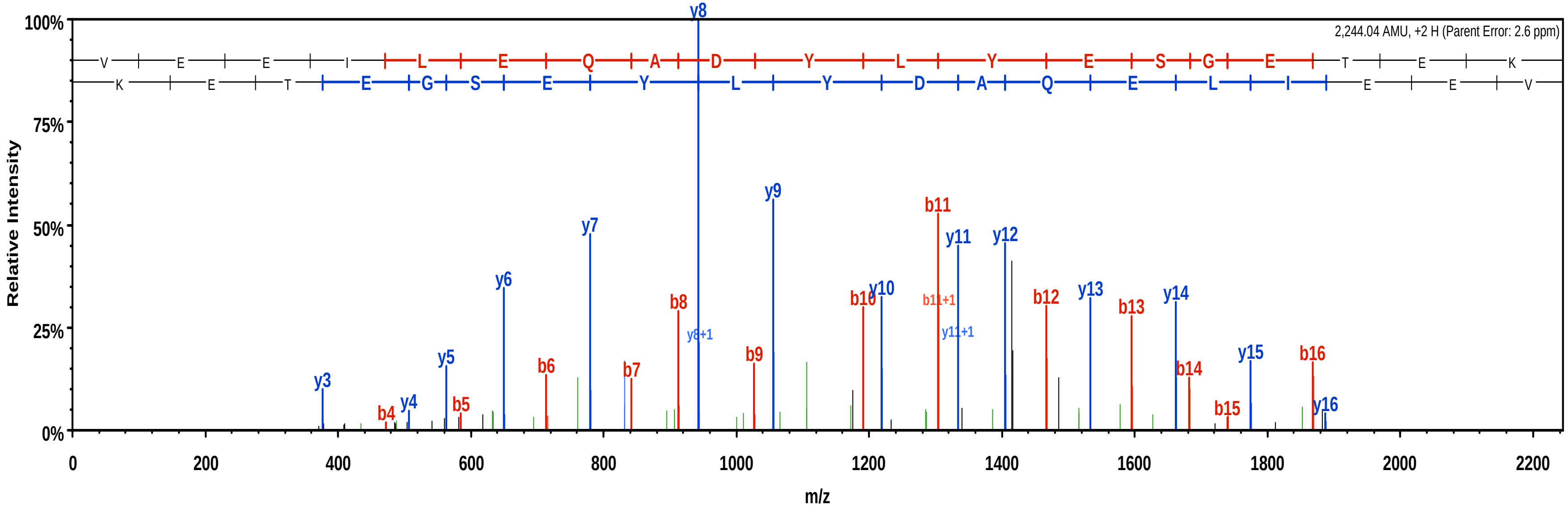


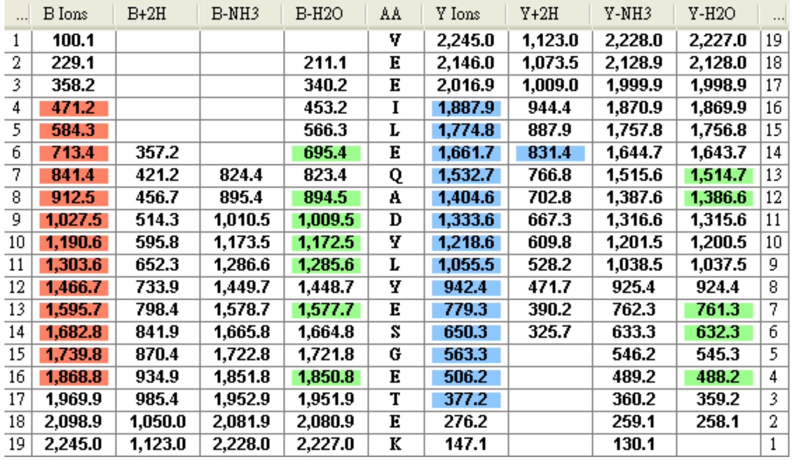


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.0				M+16	2,338.0	1,169.5	2,321.0	2,320.0	20
2	249.1			231.1	T	2,191.0	1,096.0	2,174.0	2,173.0	19
3	362.2			344.2	L	2,090.0	1,045.5	2,072.9	2,071.9	18
4	449.2			431.2	S	1,976.9	988.9	1,959.8	1,958.9	17
5	563.2		546.2	545.2	N	1,889.8	945.4	1,872.8	1,871.8	16
6	660.3	330.7	643.3	642.3	P	1,775.8	888.4	1,758.8	1,757.8	15
7	747.3	374.2	730.3	729.3	S	1,678.7	839.9	1,661.7	1,660.7	14
8	876.4	438.7	859.4	858.4	E	1,591.7	796.4	1,574.7	1,573.7	13
9	989.5	495.2	972.4	971.5	L	1,462.7	731.8	1,445.6	1,444.7	12
10	1,104.5	552.7	1,087.5	1,086.5	D	1,349.6	675.3	1,332.6	1,331.6	11
11	1,233.5	617.3	1,216.5	1,215.5	E	1,234.6	617.8	1,217.5	1,216.5	10
12	1,346.6	673.8	1,329.6	1,328.6	L	1,105.5	553.3	1,088.5	1,087.5	9
13	1,477.7	739.3	1,460.6	1,459.6	M	992.4	496.7	975.4	974.4	8
14	1,564.7	782.8	1,547.7	1,546.7	S	861.4	431.2	844.4	843.4	7
15	1,693.7	847.4	1,676.7	1,675.7	E	774.4	387.7	757.3	756.4	6
16	1,822.8	911.9	1,805.7	1,804.8	E	645.3		628.3	627.3	5
17	1,893.8	947.4	1,876.8	1,875.8	A	516.3		499.2	498.3	4
18	2,056.9	1,028.9	2,039.8	2,038.9	Y	445.2		428.2	427.2	3
19	2,185.9	1,093.5	2,168.9	2,167.9	E	282.2		265.1	264.2	2
20	2,338.0	1,169.5	2,321.0	2,320.0	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-4	sp|Q96DB5|RMD1_HUMAN	VEEILEQADYLYESGETEK	125.77	Unmodified	Light	2	1123.0234

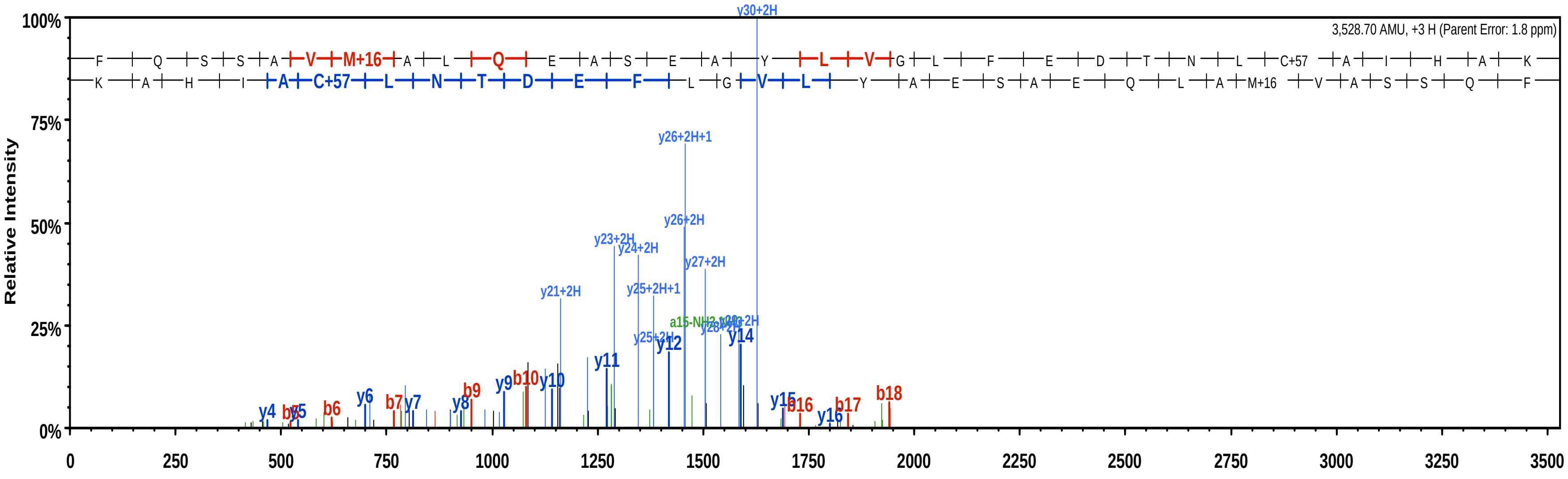


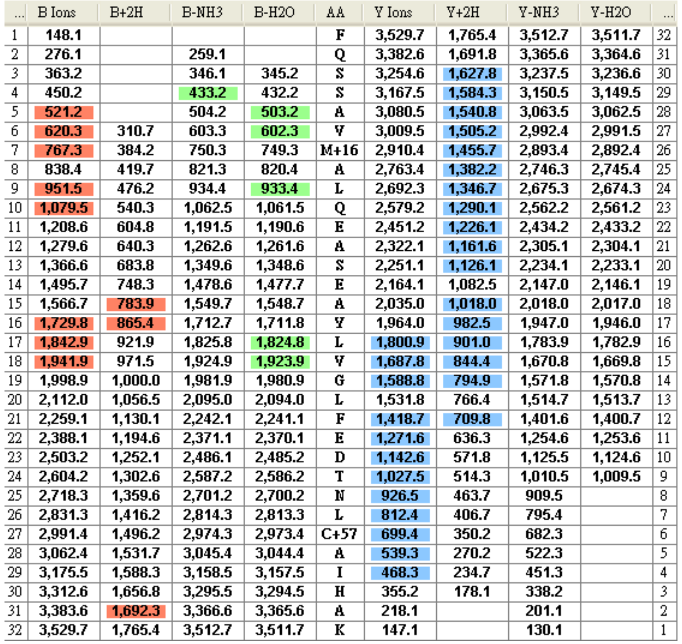


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	2,245.0	1,123.0	2,228.0	2,227.0	19
2	229.1			211.1	E	2,146.0	1,073.5	2,128.9	2,128.0	18
3	358.2			340.2	E	2,016.9	1,009.0	1,999.9	1,998.9	17
4	471.2			453.2	I	1,887.9	944.4	1,870.9	1,869.9	16
5	584.3			566.3	L	1,774.8	887.9	1,757.8	1,756.8	15
6	713.4	357.2		695.4	E	1,661.7	831.4	1,644.7	1,643.7	14
7	841.4	421.2	824.4	823.4	Q	1,532.7	766.8	1,515.6	1,514.7	13
8	912.5	456.7	895.4	894.5	A	1,404.6	702.8	1,387.6	1,386.6	12
9	1,027.5	514.3	1,010.5	1,009.5	D	1,333.6	667.3	1,316.6	1,315.6	11
10	1,190.6	595.8	1,173.5	1,172.5	Y	1,218.6	609.8	1,201.5	1,200.5	10
11	1,303.6	652.3	1,286.6	1,285.6	L	1,055.5	528.2	1,038.5	1,037.5	9
12	1,466.7	733.9	1,449.7	1,448.7	Y	942.4	471.7	925.4	924.4	8
13	1,595.7	798.4	1,578.7	1,577.7	E	779.3	390.2	762.3	761.3	7
14	1,682.8	841.9	1,665.8	1,664.8	S	650.3	325.7	633.3	632.3	6
15	1,739.8	870.4	1,722.8	1,721.8	G	563.3		546.2	545.3	5
16	1,868.8	934.9	1,851.8	1,850.8	E	506.2		489.2	488.2	4
17	1,969.9	985.4	1,952.9	1,951.9	T	377.2		360.2	359.2	3
18	2,098.9	1,050.0	2,081.9	2,080.9	E	276.2		259.1	258.1	2
19	2,245.0	1,123.0	2,228.0	2,227.0	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-5	sp|Q71DI3|H32_HUMAN	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	119.54	Oxidation (M)	Light	3	1177.2374

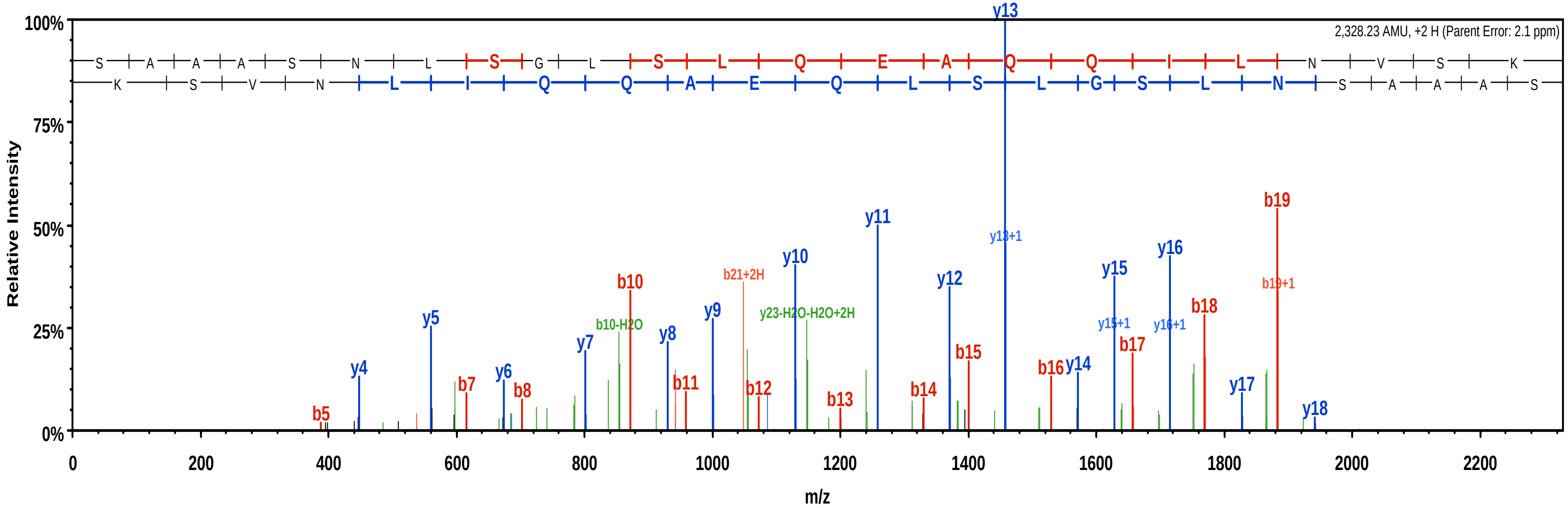


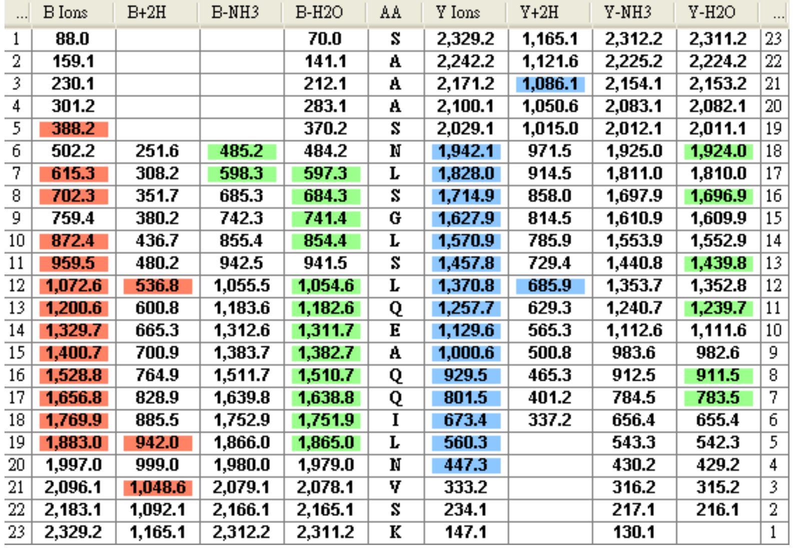


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.1				F	3,529.7	1,765.4	3,512.7	3,511.7	32
2	276.1		259.1		Q	3,382.6	1,691.8	3,365.6	3,364.6	31
3	363.2		346.1	345.2	S	3,254.6	1,627.8	3,237.5	3,236.6	30
4	450.2		433.2	432.2	S	3,167.5	1,584.3	3,150.5	3,149.5	29
5	521.2		504.2	503.2	A	3,080.5	1,540.8	3,063.5	3,062.5	28
6	620.3	310.7	603.3	602.3	V	3,009.5	1,505.2	2,992.4	2,991.5	27
7	767.3	384.2	750.3	749.3	M+16	2,910.4	1,455.7	2,893.4	2,892.4	26
8	838.4	419.7	821.3	820.4	A	2,763.4	1,382.2	2,746.3	2,745.4	25
9	951.5	476.2	934.4	933.4	L	2,692.3	1,346.7	2,675.3	2,674.3	24
10	1,079.5	540.3	1,062.5	1,061.5	Q	2,579.2	1,290.1	2,562.2	2,561.2	23
11	1,208.6	604.8	1,191.5	1,190.6	E	2,451.2	1,226.1	2,434.2	2,433.2	22
12	1,279.6	640.3	1,262.6	1,261.6	A	2,322.1	1,161.6	2,305.1	2,304.1	21
13	1,366.6	683.8	1,349.6	1,348.6	S	2,251.1	1,126.1	2,234.1	2,233.1	20
14	1,495.7	748.3	1,478.6	1,477.7	E	2,164.1	1,082.5	2,147.0	2,146.1	19
15	1,566.7	783.9	1,549.7	1,548.7	A	2,035.0	1,018.0	2,018.0	2,017.0	18
16	1,729.8	865.4	1,712.7	1,711.8	Y	1,964.0	982.5	1,947.0	1,946.0	17
17	1,842.9	921.9	1,825.8	1,824.8	L	1,800.9	901.0	1,783.9	1,782.9	16
18	1,941.9	971.5	1,924.9	1,923.9	V	1,687.8	844.4	1,670.8	1,669.8	15
19	1,998.9	1,000.0	1,981.9	1,980.9	G	1,588.8	794.9	1,571.8	1,570.8	14
20	2,112.0	1,056.5	2,095.0	2,094.0	L	1,531.8	766.4	1,514.7	1,513.7	13
21	2,259.1	1,130.1	2,242.1	2,241.1	F	1,418.7	709.8	1,401.6	1,400.7	12
22	2,388.1	1,194.6	2,371.1	2,370.1	E	1,271.6	636.3	1,254.6	1,253.6	11
23	2,503.2	1,252.1	2,486.1	2,485.2	D	1,142.6	571.8	1,125.5	1,124.6	10
24	2,604.2	1,302.6	2,587.2	2,586.2	T	1,027.5	514.3	1,010.5	1,009.5	9
25	2,718.3	1,359.6	2,701.2	2,700.2	N	926.5	463.7	909.5		8
26	2,831.3	1,416.2	2,814.3	2,813.3	L	812.4	406.7	795.4		7
27	2,991.4	1,496.2	2,974.3	2,973.4	C+57	699.4	350.2	682.3		6
28	3,062.4	1,531.7	3,045.4	3,044.4	A	539.3	270.2	522.3		5
29	3,175.5	1,588.3	3,158.5	3,157.5	I	468.3	234.7	451.3		4
30	3,312.6	1,656.8	3,295.5	3,294.5	H	355.2	178.1	338.2		3
31	3,383.6	1,692.3	3,366.6	3,365.6	A	218.1		201.1		2
32	3,529.7	1,765.4	3,512.7	3,511.7	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-6	sp|Q9Y3D7|TIM16_HUMAN	SAAASNLSGLSLQEAQQILNVSK	114.78	Unmodified	Light	2	1165.1215

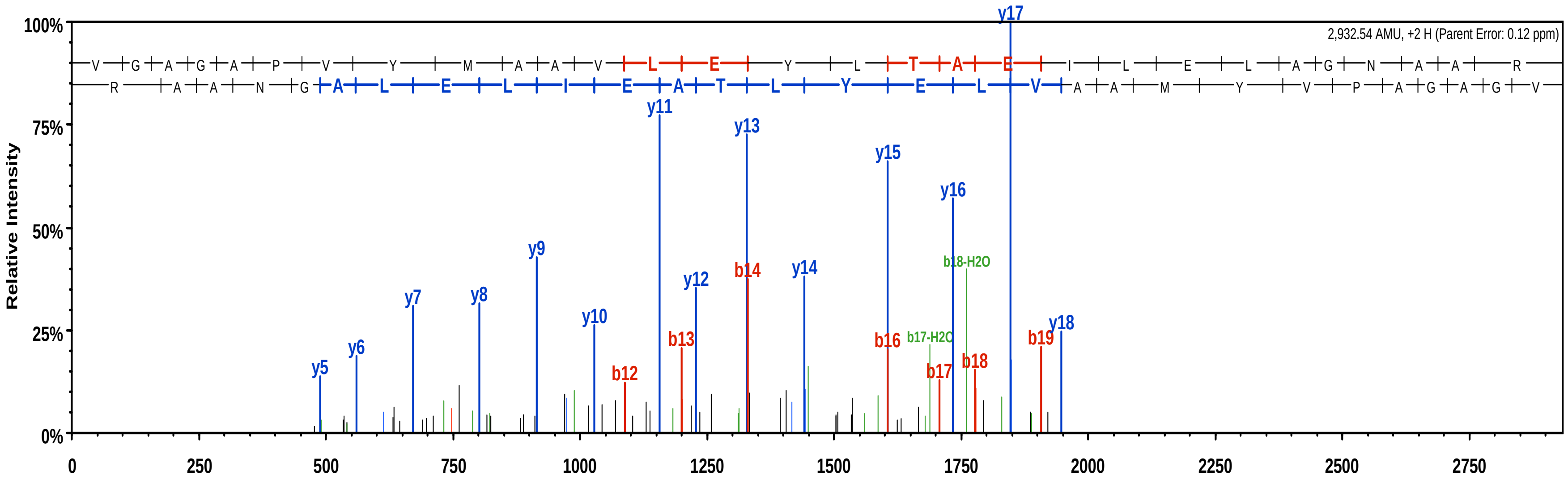


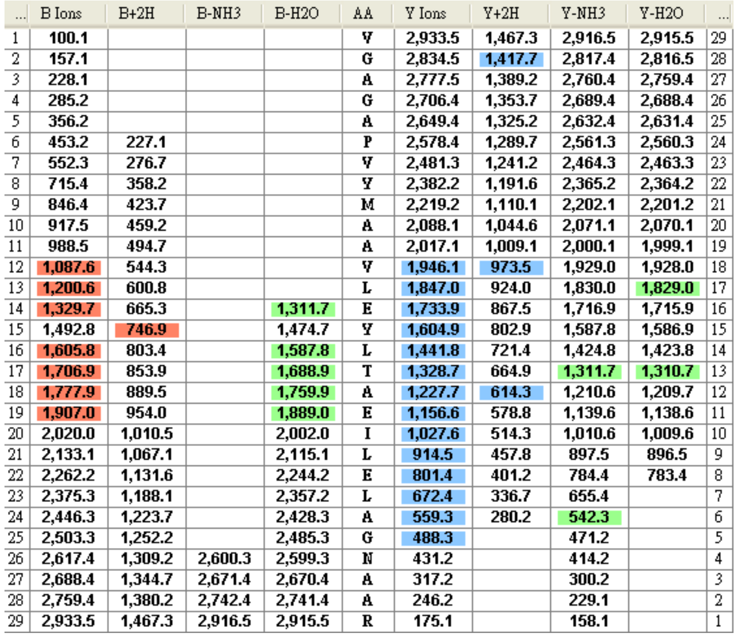


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	2,329.2	1,165.1	2,312.2	2,311.2	23
2	159.1			141.1	A	2,242.2	1,121.6	2,225.2	2,224.2	22
3	230.1			212.1	A	2,171.2	1,086.1	2,154.1	2,153.2	21
4	301.2			283.1	A	2,100.1	1,050.6	2,083.1	2,082.1	20
5	388.2			370.2	S	2,029.1	1,015.0	2,012.1	2,011.1	19
6	502.2	251.6	485.2	484.2	N	1,942.1	971.5	1,925.0	1,924.0	18
7	615.3	308.2	598.3	597.3	L	1,828.0	914.5	1,811.0	1,810.0	17
8	702.3	351.7	685.3	684.3	S	1,714.9	858.0	1,697.9	1,696.9	16
9	759.4	380.2	742.3	741.4	G	1,627.9	814.5	1,610.9	1,609.9	15
10	872.4	436.7	855.4	854.4	L	1,570.9	785.9	1,553.9	1,552.9	14
11	959.5	480.2	942.5	941.5	S	1,457.8	729.4	1,440.8	1,439.8	13
12	1,072.6	536.8	1,055.5	1,054.6	L	1,370.8	685.9	1,353.7	1,352.8	12
13	1,200.6	600.8	1,183.6	1,182.6	Q	1,257.7	629.3	1,240.7	1,239.7	11
14	1,329.7	665.3	1,312.6	1,311.7	E	1,129.6	565.3	1,112.6	1,111.6	10
15	1,400.7	700.9	1,383.7	1,382.7	A	1,000.6	500.8	983.6	982.6	9
16	1,528.8	764.9	1,511.7	1,510.7	Q	929.5	465.3	912.5	911.5	8
17	1,656.8	828.9	1,639.8	1,638.8	Q	801.5	401.2	784.5	783.5	7
18	1,769.9	885.5	1,752.9	1,751.9	I	673.4	337.2	656.4	655.4	6
19	1,883.0	942.0	1,866.0	1,865.0	L	560.3		543.3	542.3	5
20	1,997.0	999.0	1,980.0	1,979.0	N	447.3		430.2	429.2	4
21	2,096.1	1,048.6	2,079.1	2,078.1	V	333.2		316.2	315.2	3
22	2,183.1	1,092.1	2,166.1	2,165.1	S	234.1		217.1	216.1	2
23	2,329.2	1,165.1	2,312.2	2,311.2	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-7	sp|Q6FI13|H2A2A_HUMAN	VGAGAPVYMAAVLEYLTAEILELAGNAAR	114.18	Unmodified		2	1467.2757

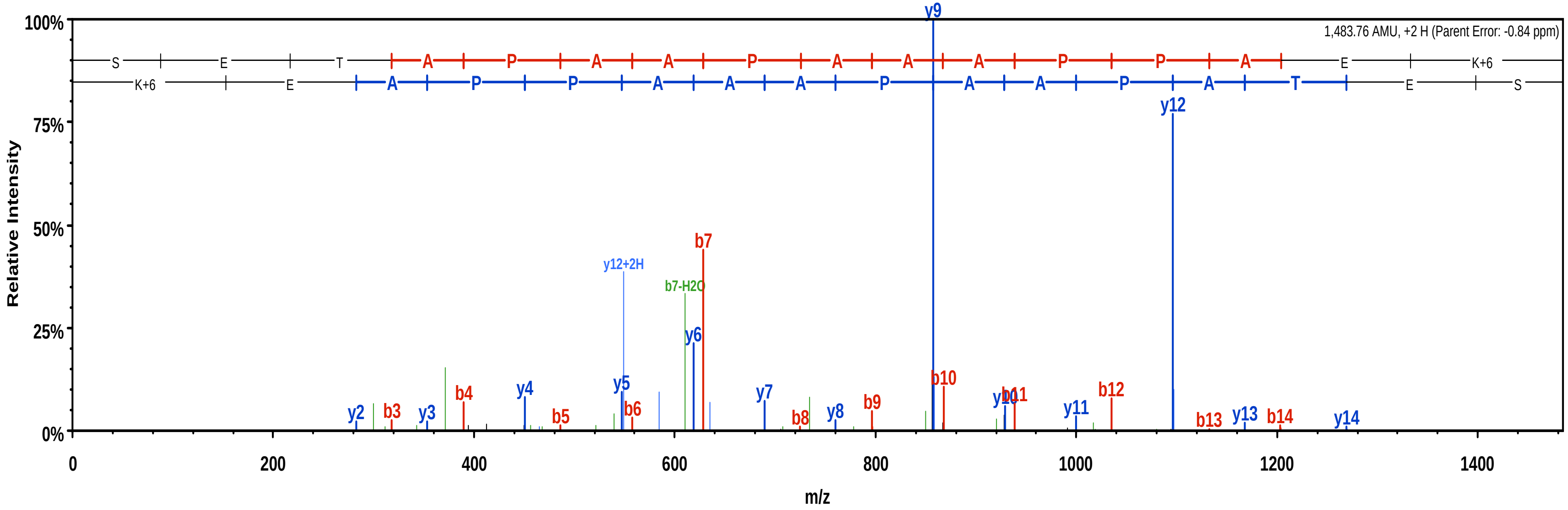


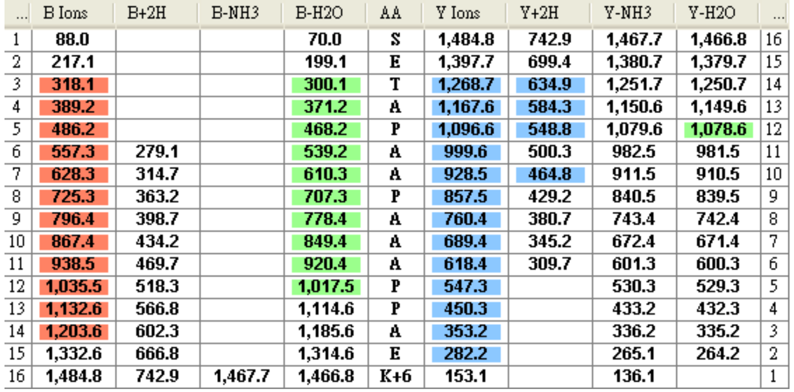


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	2,933.5	1,467.3	2,916.5	2,915.5	29
2	157.1				G	2,834.5	1,417.7	2,817.4	2,816.5	28
3	228.1				A	2,777.5	1,389.2	2,760.4	2,759.4	27
4	285.2				G	2,706.4	1,353.7	2,689.4	2,688.4	26
5	356.2				A	2,649.4	1,325.2	2,632.4	2,631.4	25
6	453.2	227.1			P	2,578.4	1,289.7	2,561.3	2,560.3	24
7	552.3	276.7			V	2,481.3	1,241.2	2,464.3	2,463.3	23
8	715.4	358.2			Y	2,382.2	1,191.6	2,365.2	2,364.2	22
9	846.4	423.7			M	2,219.2	1,110.1	2,202.1	2,201.2	21
10	917.5	459.2			A	2,088.1	1,044.6	2,071.1	2,070.1	20
11	988.5	494.7			A	2,017.1	1,009.1	2,000.1	1,999.1	19
12	1,087.6	544.3			V	1,946.1	973.5	1,929.0	1,928.0	18
13	1,200.6	600.8			L	1,847.0	924.0	1,830.0	1,829.0	17
14	1,329.7	665.3		1,311.7	E	1,733.9	867.5	1,716.9	1,715.9	16
15	1,492.8	746.9		1,474.7	Y	1,604.9	802.9	1,587.8	1,586.9	15
16	1,605.8	803.4		1,587.8	L	1,441.8	721.4	1,424.8	1,423.8	14
17	1,706.9	853.9		1,688.9	T	1,328.7	664.9	1,311.7	1,310.7	13
18	1,777.9	889.5		1,759.9	A	1,227.7	614.3	1,210.6	1,209.7	12
19	1,907.0	954.0		1,889.0	E	1,156.6	578.8	1,139.6	1,138.6	11
20	2,020.0	1,010.5		2,002.0	I	1,027.6	514.3	1,010.6	1,009.6	10
21	2,133.1	1,067.1		2,115.1	L	914.5	457.8	897.5	896.5	9
22	2,262.2	1,131.6		2,244.2	E	801.4	401.2	784.4	783.4	8
23	2,375.3	1,188.1		2,357.2	L	672.4	336.7	655.4		7
24	2,446.3	1,223.7		2,428.3	A	559.3	280.2	542.3		6
25	2,503.3	1,252.2		2,485.3	G	488.3		471.2		5
26	2,617.4	1,309.2	2,600.3	2,599.3	N	431.2		414.2		4
27	2,688.4	1,344.7	2,671.4	2,670.4	A	317.2		300.2		3
28	2,759.4	1,380.2	2,742.4	2,741.4	A	246.2		229.1		2
29	2,933.5	1,467.3	2,916.5	2,915.5	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-8	sp|P16403|H12_HUMAN	SETAPAAPAAAPPAEK	110.15	Unmodified	Heavy	2	739.87791

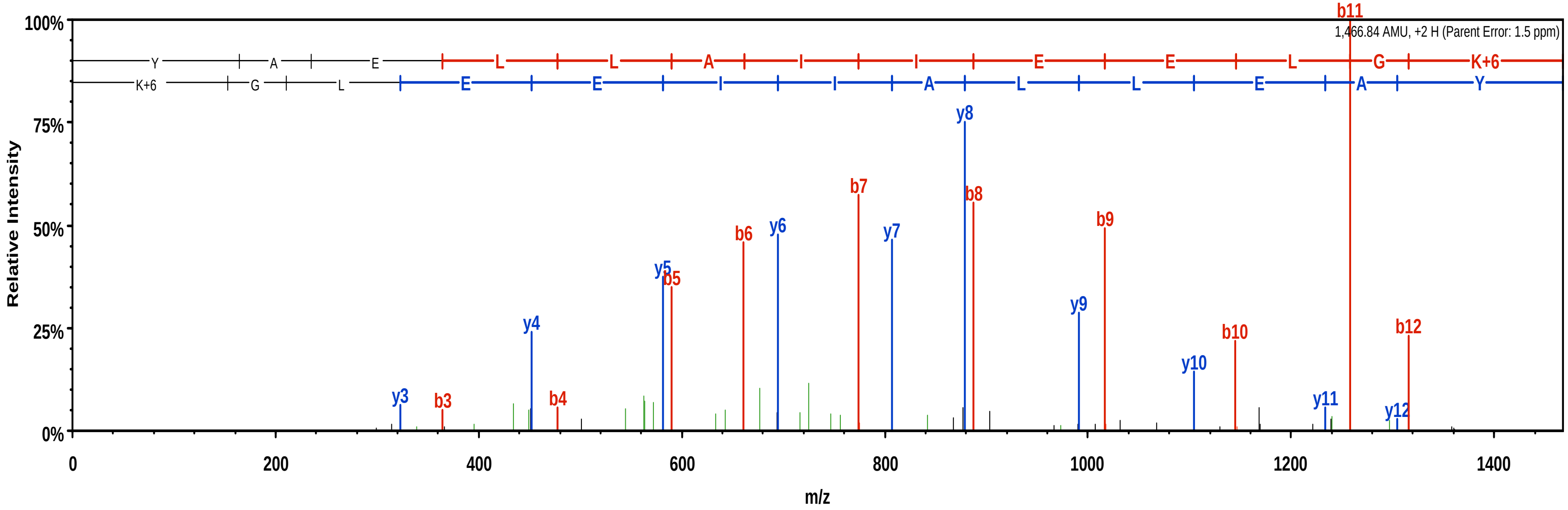


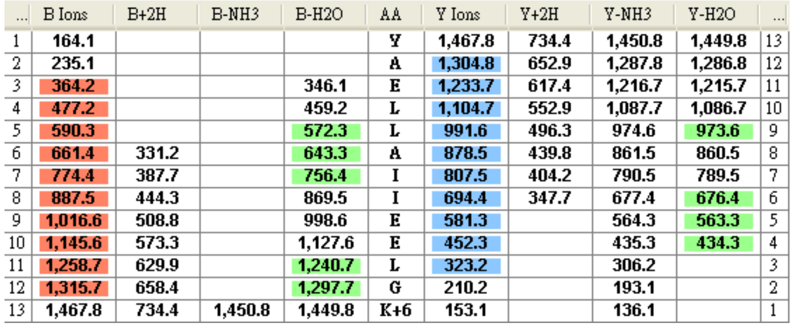


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	1,484.8	742.9	1,467.7	1,466.8	16
2	217.1			199.1	E	1,397.7	699.4	1,380.7	1,379.7	15
3	318.1			300.1	T	1,268.7	634.9	1,251.7	1,250.7	14
4	389.2			371.2	A	1,167.6	584.3	1,150.6	1,149.6	13
5	486.2			468.2	P	1,096.6	548.8	1,079.6	1,078.6	12
6	557.3	279.1		539.2	A	999.6	500.3	982.5	981.5	11
7	628.3	314.7		610.3	A	928.5	464.8	911.5	910.5	10
8	725.3	363.2		707.3	P	857.5	429.2	840.5	839.5	9
9	796.4	398.7		778.4	A	760.4	380.7	743.4	742.4	8
10	867.4	434.2		849.4	A	689.4	345.2	672.4	671.4	7
11	938.5	469.7		920.4	A	618.4	309.7	601.3	600.3	6
12	1,035.5	518.3		1,017.5	P	547.3		530.3	529.3	5
13	1,132.6	566.8		1,114.6	P	450.3		433.2	432.3	4
14	1,203.6	602.3		1,185.6	A	353.2		336.2	335.2	3
15	1,332.6	666.8		1,314.6	E	282.2		265.1	264.2	2
16	1,484.8	742.9	1,467.7	1,466.8	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-9	sp|O14519|CDKA1_HUMAN	YAELLAIIEELGK	108.99	Unmodified	Heavy	2	731.4136

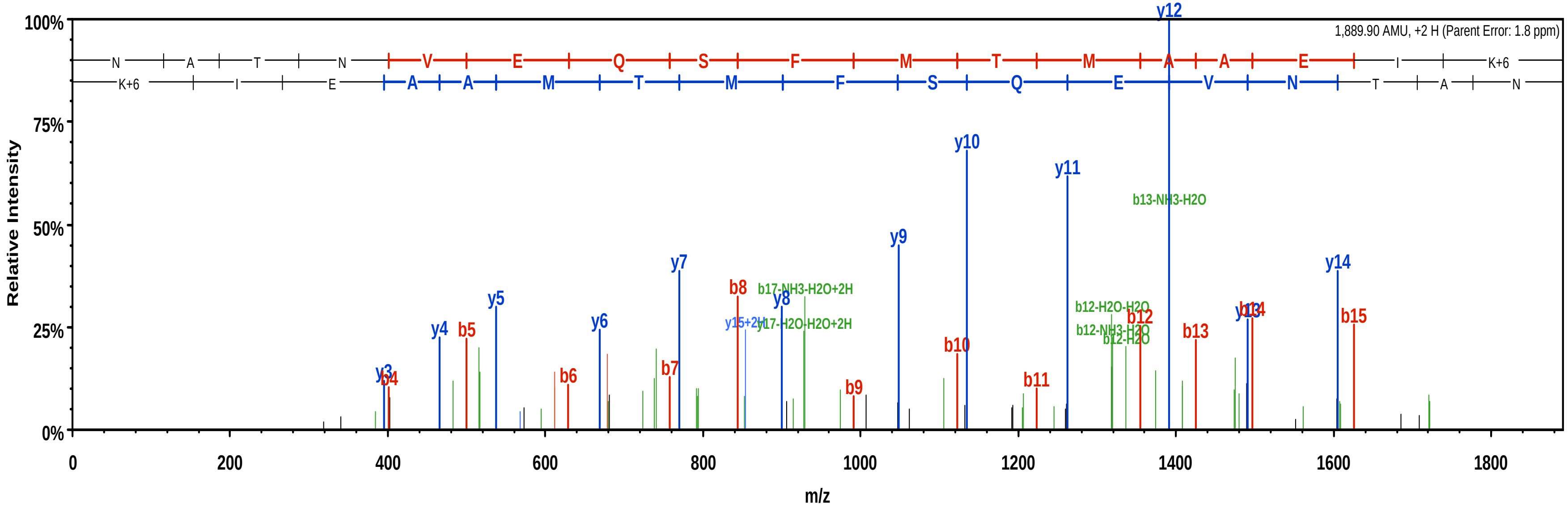


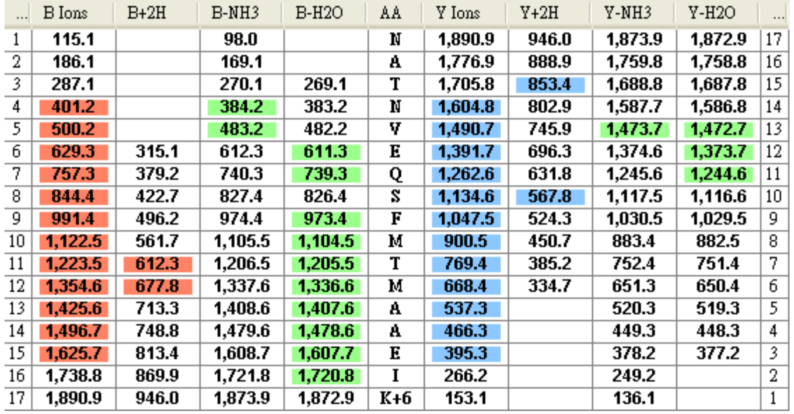


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	164.1				Y	1,467.8	734.4	1,450.8	1,449.8	13
2	235.1				A	1,304.8	652.9	1,287.8	1,286.8	12
3	364.2			346.1	E	1,233.7	617.4	1,216.7	1,215.7	11
4	477.2			459.2	L	1,104.7	552.9	1,087.7	1,086.7	10
5	590.3			572.3	L	991.6	496.3	974.6	973.6	9
6	661.4	331.2		643.3	A	878.5	439.8	861.5	860.5	8
7	774.4	387.7		756.4	I	807.5	404.2	790.5	789.5	7
8	887.5	444.3		869.5	I	694.4	347.7	677.4	676.4	6
9	1,016.6	508.8		998.6	E	581.3		564.3	563.3	5
10	1,145.6	573.3		1,127.6	E	452.3		435.3	434.3	4
11	1,258.7	629.9		1,240.7	L	323.2		306.2		3
12	1,315.7	658.4		1,297.7	G	210.2		193.1		2
13	1,467.8	734.4	1,450.8	1,449.8	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-10	sp|P62820|RAB1A_HUMAN	NATNVEQSFMTMAAEIK	108.84	Unmodified	Heavy	2	942.94514

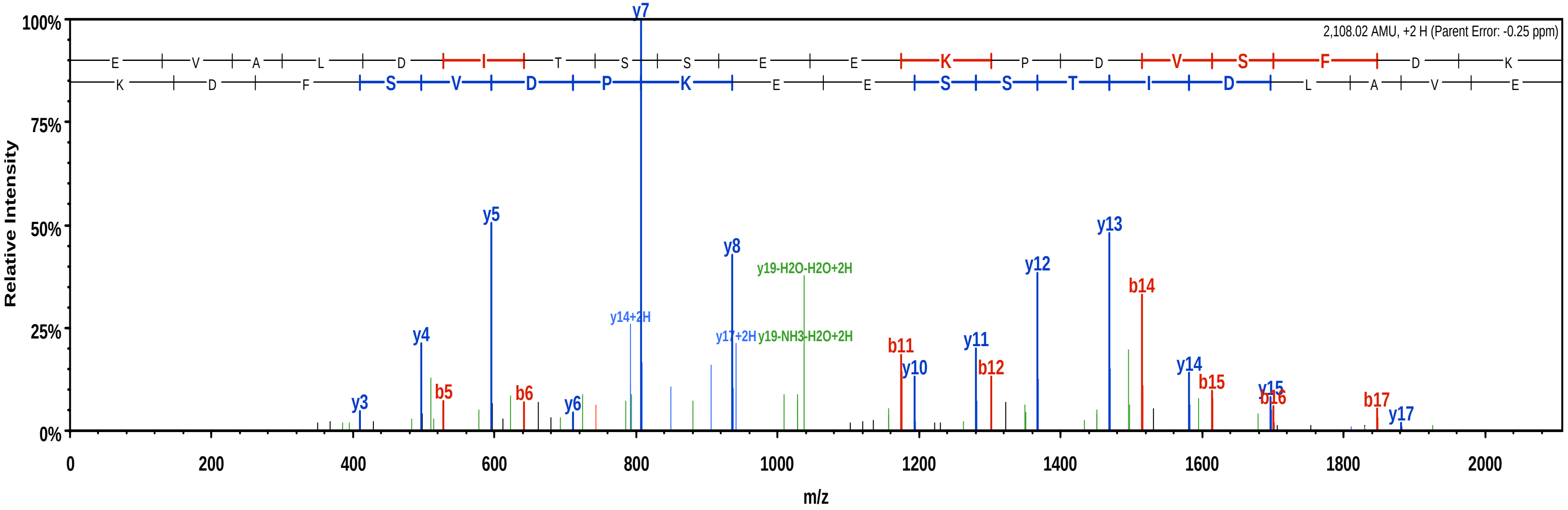


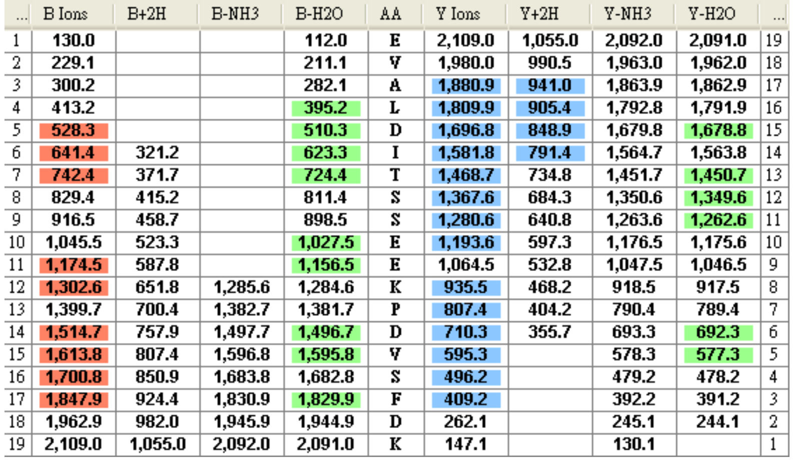


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	115.1		98.0		N	1,890.9	946.0	1,873.9	1,872.9	17
2	186.1		169.1		A	1,776.9	888.9	1,759.8	1,758.8	16
3	287.1		270.1	269.1	T	1,705.8	853.4	1,688.8	1,687.8	15
4	401.2		384.2	383.2	N	1,604.8	802.9	1,587.7	1,586.8	14
5	500.2		483.2	482.2	V	1,490.7	745.9	1,473.7	1,472.7	13
6	629.3	315.1	612.3	611.3	E	1,391.7	696.3	1,374.6	1,373.7	12
7	757.3	379.2	740.3	739.3	Q	1,262.6	631.8	1,245.6	1,244.6	11
8	844.4	422.7	827.4	826.4	S	1,134.6	567.8	1,117.5	1,116.6	10
9	991.4	496.2	974.4	973.4	F	1,047.5	524.3	1,030.5	1,029.5	9
10	1,122.5	561.7	1,105.5	1,104.5	M	900.5	450.7	883.4	882.5	8
11	1,223.5	612.3	1,206.5	1,205.5	T	769.4	385.2	752.4	751.4	7
12	1,354.6	677.8	1,337.6	1,336.6	M	668.4	334.7	651.3	650.4	6
13	1,425.6	713.3	1,408.6	1,407.6	A	537.3		520.3	519.3	5
14	1,496.7	748.8	1,479.6	1,478.6	A	466.3		449.3	448.3	4
15	1,625.7	813.4	1,608.7	1,607.7	E	395.3		378.2	377.2	3
16	1,738.8	869.9	1,721.8	1,720.8	I	266.2		249.2		2
17	1,890.9	946.0	1,873.9	1,872.9	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-11	sp|Q9Y375|CIA30_HUMAN	EVALDITSSEEKPDVSFDK	108.49	Unmodified	Light	2	1055.0153

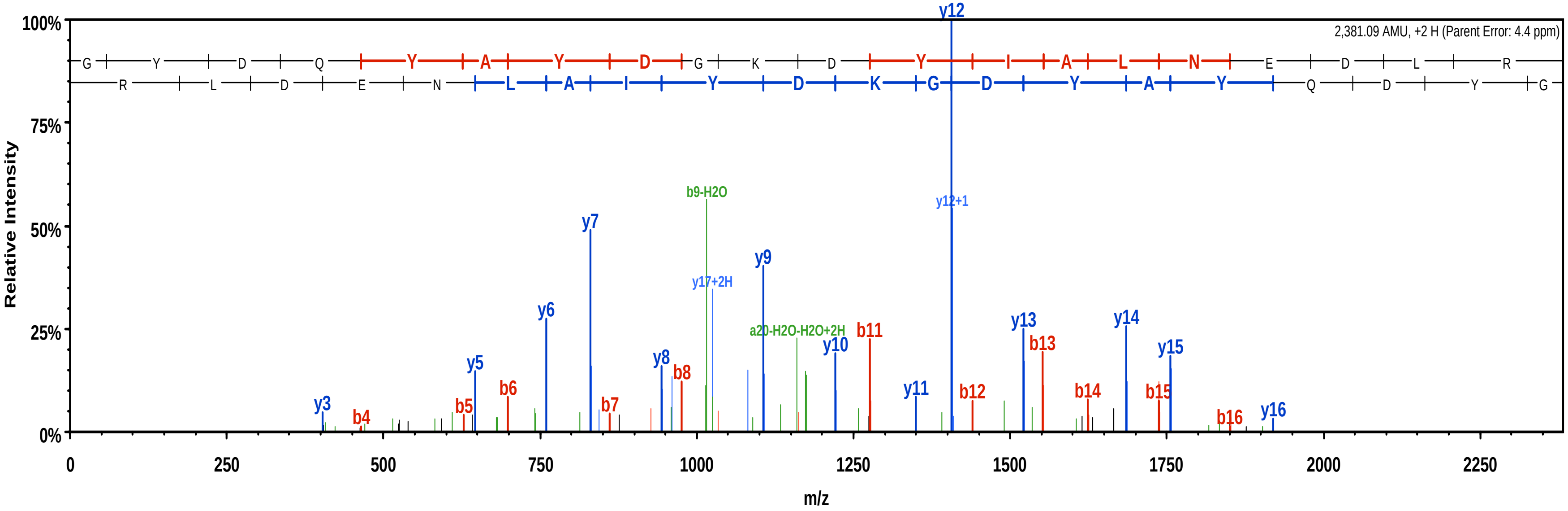


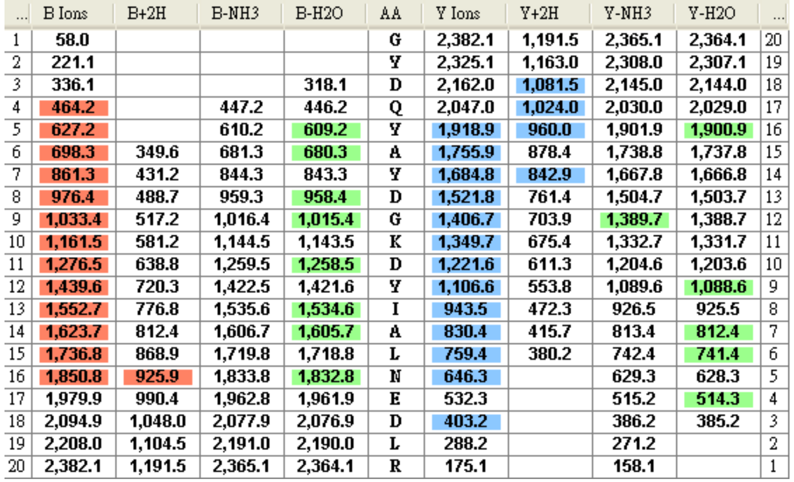


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	2,109.0	1,055.0	2,092.0	2,091.0	19
2	229.1			211.1	V	1,980.0	990.5	1,963.0	1,962.0	18
3	300.2			282.1	A	1,880.9	941.0	1,863.9	1,862.9	17
4	413.2			395.2	L	1,809.9	905.4	1,792.8	1,791.9	16
5	528.3			510.3	D	1,696.8	848.9	1,679.8	1,678.8	15
6	641.4	321.2		623.3	I	1,581.8	791.4	1,564.7	1,563.8	14
7	742.4	371.7		724.4	T	1,468.7	734.8	1,451.7	1,450.7	13
8	829.4	415.2		811.4	S	1,367.6	684.3	1,350.6	1,349.6	12
9	916.5	458.7		898.5	S	1,280.6	640.8	1,263.6	1,262.6	11
10	1,045.5	523.3		1,027.5	E	1,193.6	597.3	1,176.5	1,175.6	10
11	1,174.5	587.8		1,156.5	E	1,064.5	532.8	1,047.5	1,046.5	9
12	1,302.6	651.8	1,285.6	1,284.6	K	935.5	468.2	918.5	917.5	8
13	1,399.7	700.4	1,382.7	1,381.7	P	807.4	404.2	790.4	789.4	7
14	1,514.7	757.9	1,497.7	1,496.7	D	710.3	355.7	693.3	692.3	6
15	1,613.8	807.4	1,596.8	1,595.8	V	595.3		578.3	577.3	5
16	1,700.8	850.9	1,683.8	1,682.8	S	496.2		479.2	478.2	4
17	1,847.9	924.4	1,830.9	1,829.9	F	409.2		392.2	391.2	3
18	1,962.9	982.0	1,945.9	1,944.9	D	262.1		245.1	244.1	2
19	2,109.0	1,055.0	2,092.0	2,091.0	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-12	sp|P30499|1C01_HUMAN	GYDQYAYDGKDYIALNEDLR	105.42	Unmodified	Light	2	1191.5479

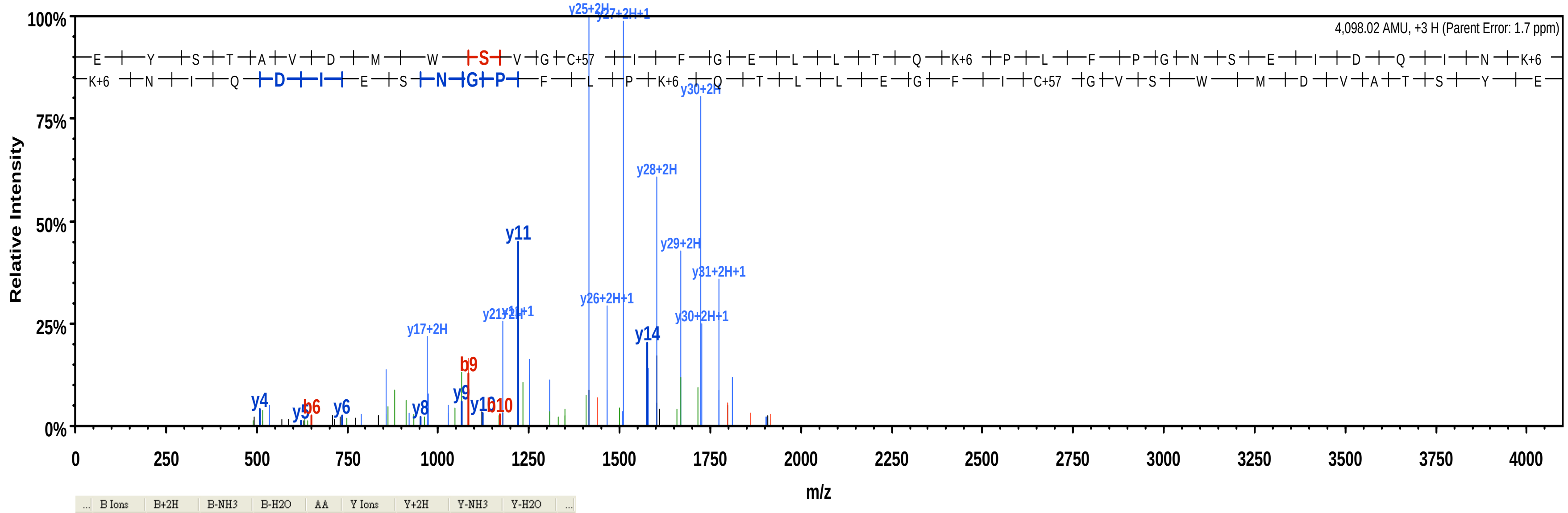


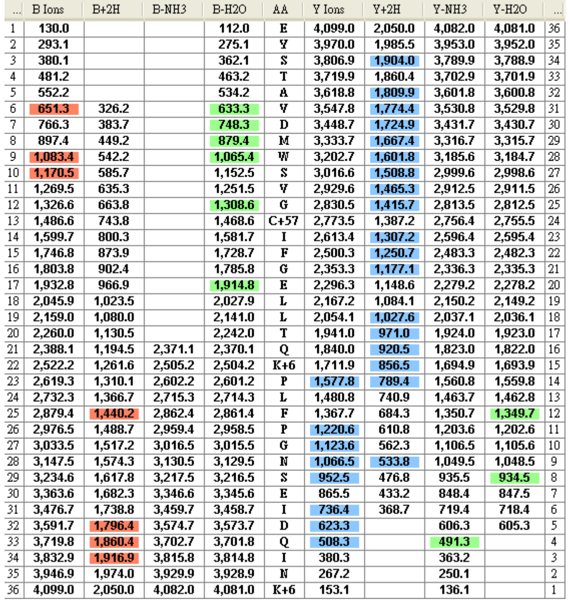


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	2,382.1	1,191.5	2,365.1	2,364.1	20
2	221.1				Y	2,325.1	1,163.0	2,308.0	2,307.1	19
3	336.1			318.1	D	2,162.0	1,081.5	2,145.0	2,144.0	18
4	464.2		447.2	446.2	Q	2,047.0	1,024.0	2,030.0	2,029.0	17
5	627.2		610.2	609.2	Y	1,918.9	960.0	1,901.9	1,900.9	16
6	698.3	349.6	681.3	680.3	A	1,755.9	878.4	1,738.8	1,737.8	15
7	861.3	431.2	844.3	843.3	Y	1,684.8	842.9	1,667.8	1,666.8	14
8	976.4	488.7	959.3	958.4	D	1,521.8	761.4	1,504.7	1,503.7	13
9	1,033.4	517.2	1,016.4	1,015.4	G	1,406.7	703.9	1,389.7	1,388.7	12
10	1,161.5	581.2	1,144.5	1,143.5	K	1,349.7	675.4	1,332.7	1,331.7	11
11	1,276.5	638.8	1,259.5	1,258.5	D	1,221.6	611.3	1,204.6	1,203.6	10
12	1,439.6	720.3	1,422.5	1,421.6	Y	1,106.6	553.8	1,089.6	1,088.6	9
13	1,552.7	776.8	1,535.6	1,534.6	I	943.5	472.3	926.5	925.5	8
14	1,623.7	812.4	1,606.7	1,605.7	A	830.4	415.7	813.4	812.4	7
15	1,736.8	868.9	1,719.8	1,718.8	L	759.4	380.2	742.4	741.4	6
16	1,850.8	925.9	1,833.8	1,832.8	N	646.3		629.3	628.3	5
17	1,979.9	990.4	1,962.8	1,961.9	E	532.3		515.2	514.3	4
18	2,094.9	1,048.0	2,077.9	2,076.9	D	403.2		386.2	385.2	3
19	2,208.0	1,104.5	2,191.0	2,190.0	L	288.2		271.2		2
20	2,382.1	1,191.5	2,365.1	2,364.1	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-13	sp|Q9UQ88|CD2L2_HUMAN	EYSTAVDMWSVGCIFGELLTQKPLFPGNSEIDQINK	98.7	Unmodified	Heavy	3	1362.9991

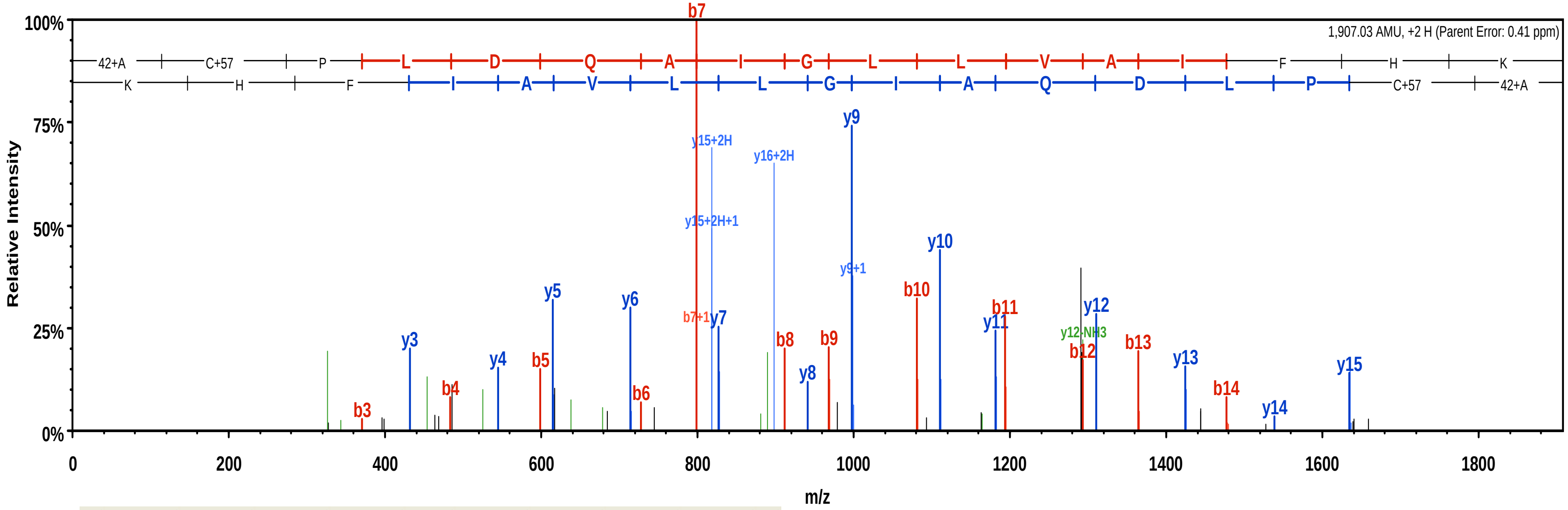


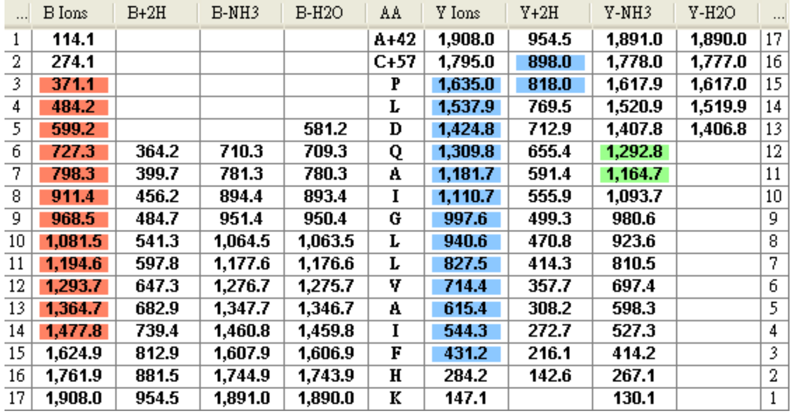


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	4,099.0	2,050.0	4,082.0	4,081.0	36
2	293.1			275.1	Y	3,970.0	1,985.5	3,953.0	3,952.0	35
3	380.1			362.1	S	3,806.9	1,904.0	3,789.9	3,788.9	34
4	481.2			463.2	T	3,719.9	1,860.4	3,702.9	3,701.9	33
5	552.2			534.2	A	3,618.8	1,809.9	3,601.8	3,600.8	32
6	651.3	326.2		633.3	V	3,547.8	1,774.4	3,530.8	3,529.8	31
7	766.3	383.7		748.3	D	3,448.7	1,724.9	3,431.7	3,430.7	30
8	897.4	449.2		879.4	M	3,333.7	1,667.4	3,316.7	3,315.7	29
9	1,083.4	542.2		1,065.4	W	3,202.7	1,601.8	3,185.6	3,184.7	28
10	1,170.5	585.7		1,152.5	S	3,016.6	1,508.8	2,999.6	2,998.6	27
11	1,269.5	635.3		1,251.5	V	2,929.6	1,465.3	2,912.5	2,911.5	26
12	1,326.6	663.8		1,308.6	G	2,830.5	1,415.7	2,813.5	2,812.5	25
13	1,486.6	743.8		1,468.6	C+57	2,773.5	1,387.2	2,756.4	2,755.5	24
14	1,599.7	800.3		1,581.7	I	2,613.4	1,307.2	2,596.4	2,595.4	23
15	1,746.8	873.9		1,728.7	F	2,500.3	1,250.7	2,483.3	2,482.3	22
16	1,803.8	902.4		1,785.8	G	2,353.3	1,177.1	2,336.3	2,335.3	21
17	1,932.8	966.9		1,914.8	E	2,296.3	1,148.6	2,279.2	2,278.2	20
18	2,045.9	1,023.5		2,027.9	L	2,167.2	1,084.1	2,150.2	2,149.2	19
19	2,159.0	1,080.0		2,141.0	L	2,054.1	1,027.6	2,037.1	2,036.1	18
20	2,260.0	1,130.5		2,242.0	T	1,941.0	971.0	1,924.0	1,923.0	17
21	2,388.1	1,194.5	2,371.1	2,370.1	Q	1,840.0	920.5	1,823.0	1,822.0	16
22	2,522.2	1,261.6	2,505.2	2,504.2	K+6	1,711.9	856.5	1,694.9	1,693.9	15
23	2,619.3	1,310.1	2,602.2	2,601.2	P	1,577.8	789.4	1,560.8	1,559.8	14
24	2,732.3	1,366.7	2,715.3	2,714.3	L	1,480.8	740.9	1,463.7	1,462.8	13
25	2,879.4	1,440.2	2,862.4	2,861.4	F	1,367.7	684.3	1,350.7	1,349.7	12
26	2,976.5	1,488.7	2,959.4	2,958.5	P	1,220.6	610.8	1,203.6	1,202.6	11
27	3,033.5	1,517.2	3,016.5	3,015.5	G	1,123.6	562.3	1,106.5	1,105.6	10
28	3,147.5	1,574.3	3,130.5	3,129.5	N	1,066.5	533.8	1,049.5	1,048.5	9
29	3,234.6	1,617.8	3,217.5	3,216.5	S	952.5	476.8	935.5	934.5	8
30	3,363.6	1,682.3	3,346.6	3,345.6	E	865.5	433.2	848.4	847.5	7
31	3,476.7	1,738.8	3,459.7	3,458.7	I	736.4	368.7	719.4	718.4	6
32	3,591.7	1,796.4	3,574.7	3,573.7	D	623.3		606.3	605.3	5
33	3,719.8	1,860.4	3,702.7	3,701.8	Q	508.3		491.3		4
34	3,832.9	1,916.9	3,815.8	3,814.8	I	380.3		363.2		3
35	3,946.9	1,974.0	3,929.9	3,928.9	N	267.2		250.1		2
36	4,099.0	2,050.0	4,082.0	4,081.0	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-14	splP06703lS10A6_HUMAN	ACPLDQAIGLLVAIFHK	98.61	Acetyl (Protein N-term)	Light	2	954.52422

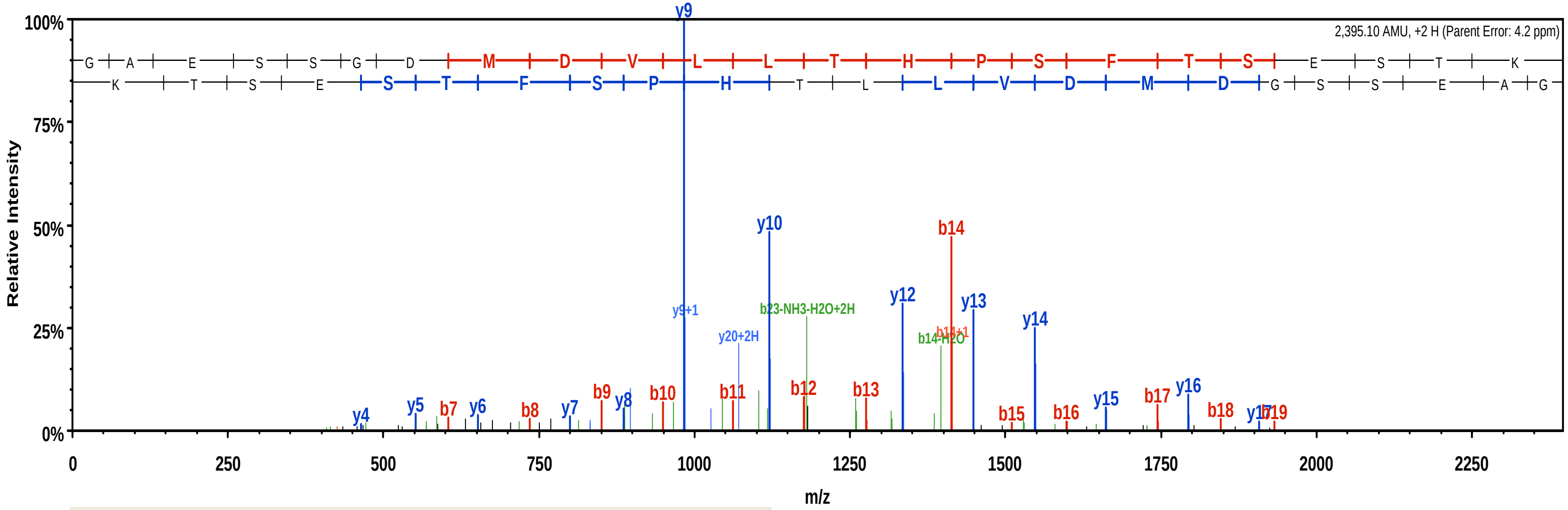


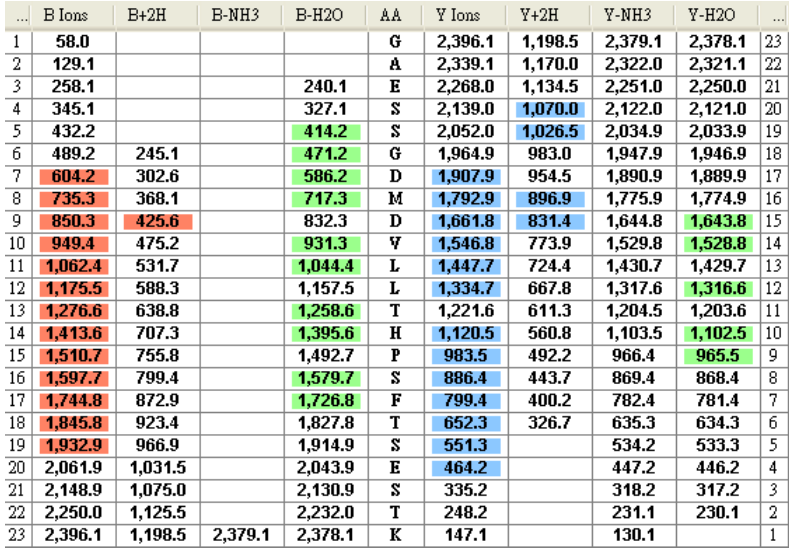


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	1,908.0	954.5	1,891.0	1,890.0	17
2	274.1				C+57	1,795.0	898.0	1,778.0	1,777.0	16
3	371.1				P	1,635.0	818.0	1,617.9	1,617.0	15
4	484.2				L	1,537.9	769.5	1,520.9	1,519.9	14
5	599.2			581.2	D	1,424.8	712.9	1,407.8	1,406.8	13
6	727.3	364.2	710.3	709.3	Q	1,309.8	655.4	1,292.8		12
7	798.3	399.7	781.3	780.3	A	1,181.7	591.4	1,164.7		11
8	911.4	456.2	894.4	893.4	I	1,110.7	555.9	1,093.7		10
9	968.5	484.7	951.4	950.4	G	997.6	499.3	980.6		9
10	1,081.5	541.3	1,064.5	1,063.5	L	940.6	470.8	923.6		8
11	1,194.6	597.8	1,177.6	1,176.6	L	827.5	414.3	810.5		7
12	1,293.7	647.3	1,276.7	1,275.7	V	714.4	357.7	697.4		6
13	1,364.7	682.9	1,347.7	1,346.7	A	615.4	308.2	598.3		5
14	1,477.8	739.4	1,460.8	1,459.8	I	544.3	272.7	527.3		4
15	1,624.9	812.9	1,607.9	1,606.9	F	431.2	216.1	414.2		3
16	1,761.9	881.5	1,744.9	1,743.9	H	284.2	142.6	267.1		2
17	1,908.0	954.5	1,891.0	1,890.0	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-15	sp|P06746|DPOLB_HUMAN	GAESSGDMDVLLTHPSFTSESTK	97.77	Unmodified	Light	2	1198.5497

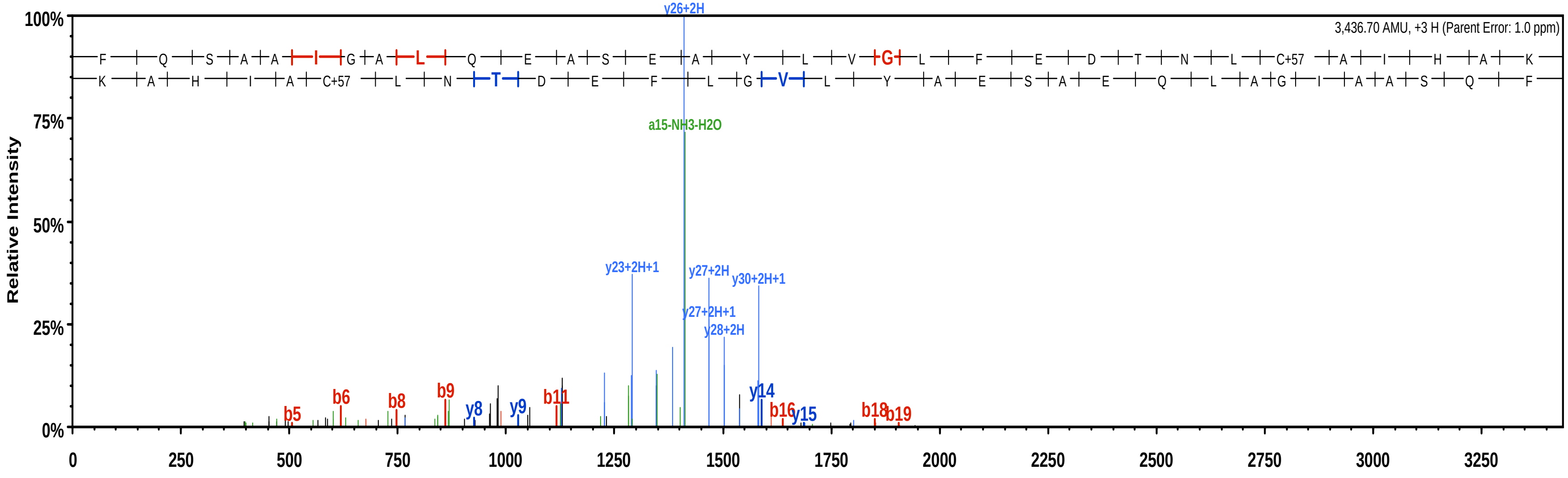


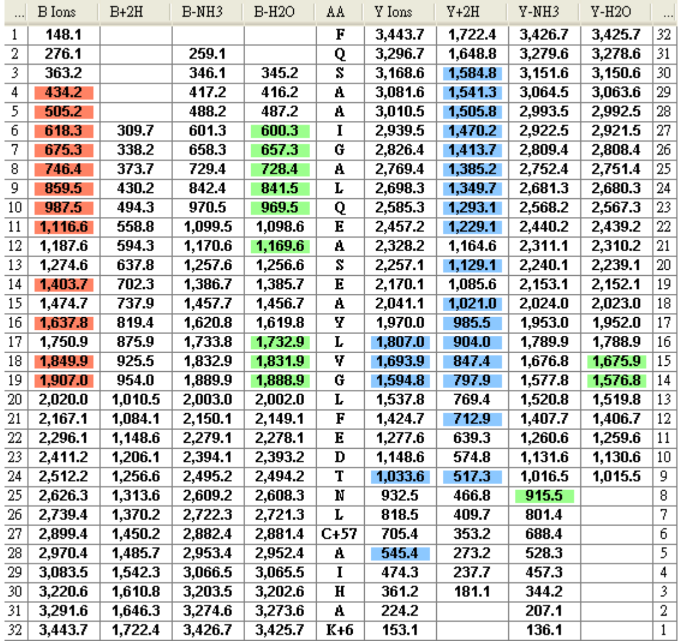


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	2,396.1	1,198.5	2,379.1	2,378.1	23
2	129.1				A	2,339.1	1,170.0	2,322.0	2,321.1	22
3	258.1			240.1	E	2,268.0	1,134.5	2,251.0	2,250.0	21
4	345.1			327.1	S	2,139.0	1,070.0	2,122.0	2,121.0	20
5	432.2			414.2	S	2,052.0	1,026.5	2,034.9	2,033.9	19
6	489.2	245.1		471.2	G	1,964.9	983.0	1,947.9	1,946.9	18
7	604.2	302.6		586.2	D	1,907.9	954.5	1,890.9	1,889.9	17
8	735.3	368.1		717.3	M	1,792.9	896.9	1,775.9	1,774.9	16
9	850.3	425.6		832.3	D	1,661.8	831.4	1,644.8	1,643.8	15
10	949.4	475.2		931.3	V	1,546.8	773.9	1,529.8	1,528.8	14
11	1,062.4	531.7		1,044.4	L	1,447.7	724.4	1,430.7	1,429.7	13
12	1,175.5	588.3		1,157.5	L	1,334.7	667.8	1,317.6	1,316.6	12
13	1,276.6	638.8		1,258.6	T	1,221.6	611.3	1,204.5	1,203.6	11
14	1,413.6	707.3		1,395.6	H	1,120.5	560.8	1,103.5	1,102.5	10
15	1,510.7	755.8		1,492.7	P	983.5	492.2	966.4	965.5	9
16	1,597.7	799.4		1,579.7	S	886.4	443.7	869.4	868.4	8
17	1,744.8	872.9		1,726.8	F	799.4	400.2	782.4	781.4	7
18	1,845.8	923.4		1,827.8	T	652.3	326.7	635.3	634.3	6
19	1,932.9	966.9		1,914.9	S	551.3		534.2	533.3	5
20	2,061.9	1,031.5		2,043.9	E	464.2		447.2	446.2	4
21	2,148.9	1,075.0		2,130.9	S	335.2		318.2	317.2	3
22	2,250.0	1,125.5		2,232.0	T	248.2		231.1	230.1	2
23	2,396.1	1,198.5	2,379.1	2,378.1	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-16	sp|P84243|H33_HUMAN	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	97.26	Unmodified	Heavy	3	1146.573

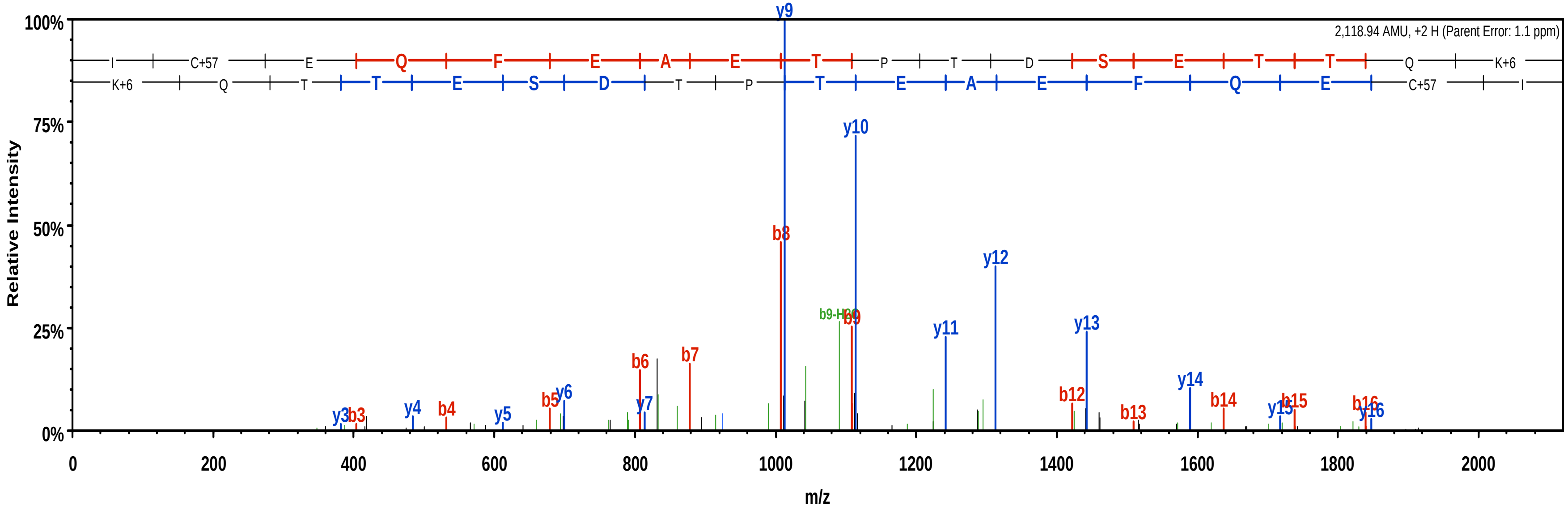


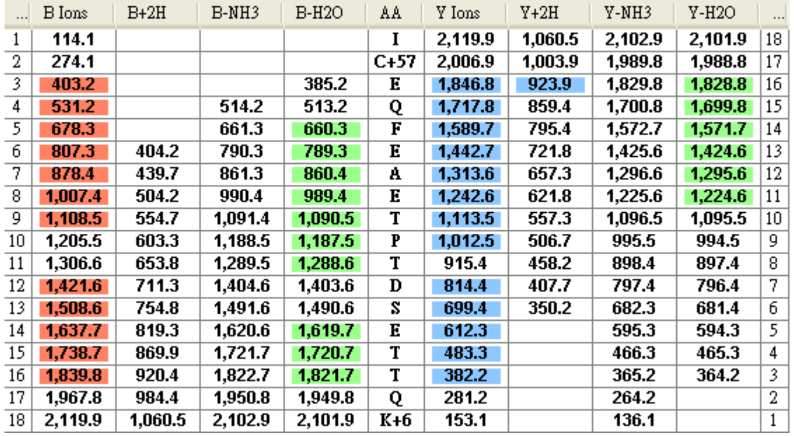


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.1				F	3,443.7	1,722.4	3,426.7	3,425.7	32
2	276.1		259.1		Q	3,296.7	1,648.8	3,279.6	3,278.6	31
3	363.2		346.1	345.2	S	3,168.6	1,584.8	3,151.6	3,150.6	30
4	434.2		417.2	416.2	A	3,081.6	1,541.3	3,064.5	3,063.6	29
5	505.2		488.2	487.2	A	3,010.5	1,505.8	2,993.5	2,992.5	28
6	618.3	309.7	601.3	600.3	I	2,939.5	1,470.2	2,922.5	2,921.5	27
7	675.3	338.2	658.3	657.3	G	2,826.4	1,413.7	2,809.4	2,808.4	26
8	746.4	373.7	729.4	728.4	A	2,769.4	1,385.2	2,752.4	2,751.4	25
9	859.5	430.2	842.4	841.5	L	2,698.3	1,349.7	2,681.3	2,680.3	24
10	987.5	494.3	970.5	969.5	Q	2,585.3	1,293.1	2,568.2	2,567.3	23
11	1,116.6	558.8	1,099.5	1,098.6	E	2,457.2	1,229.1	2,440.2	2,439.2	22
12	1,187.6	594.3	1,170.6	1,169.6	A	2,328.2	1,164.6	2,311.1	2,310.2	21
13	1,274.6	637.8	1,257.6	1,256.6	S	2,257.1	1,129.1	2,240.1	2,239.1	20
14	1,403.7	702.3	1,386.7	1,385.7	E	2,170.1	1,085.6	2,153.1	2,152.1	19
15	1,474.7	737.9	1,457.7	1,456.7	A	2,041.1	1,021.0	2,024.0	2,023.0	18
16	1,637.8	819.4	1,620.8	1,619.8	Y	1,970.0	985.5	1,953.0	1,952.0	17
17	1,750.9	875.9	1,733.8	1,732.9	L	1,807.0	904.0	1,789.9	1,788.9	16
18	1,849.9	925.5	1,832.9	1,831.9	V	1,693.9	847.4	1,676.8	1,675.9	15
19	1,907.0	954.0	1,889.9	1,888.9	G	1,594.8	797.9	1,577.8	1,576.8	14
20	2,020.0	1,010.5	2,003.0	2,002.0	L	1,537.8	769.4	1,520.8	1,519.8	13
21	2,167.1	1,084.1	2,150.1	2,149.1	F	1,424.7	712.9	1,407.7	1,406.7	12
22	2,296.1	1,148.6	2,279.1	2,278.1	E	1,277.6	639.3	1,260.6	1,259.6	11
23	2,411.2	1,206.1	2,394.1	2,393.2	D	1,148.6	574.8	1,131.6	1,130.6	10
24	2,512.2	1,256.6	2,495.2	2,494.2	T	1,033.6	517.3	1,016.5	1,015.5	9
25	2,626.3	1,313.6	2,609.2	2,608.3	N	932.5	466.8	915.5		8
26	2,739.4	1,370.2	2,722.3	2,721.3	L	818.5	409.7	801.4		7
27	2,899.4	1,450.2	2,882.4	2,881.4	C+57	705.4	353.2	688.4		6
28	2,970.4	1,485.7	2,953.4	2,952.4	A	545.4	273.2	528.3		5
29	3,083.5	1,542.3	3,066.5	3,065.5	I	474.3	237.7	457.3		4
30	3,220.6	1,610.8	3,203.5	3,202.6	H	361.2	181.1	344.2		3
31	3,291.6	1,646.3	3,274.6	3,273.6	A	224.2		207.1		2
32	3,443.7	1,722.4	3,426.7	3,425.7	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-17	sp|P40855|PEX19_HUMAN	ICEQFEAETPTDSETTQK	96.34	Unmodified	Heavy	2	1057.4651

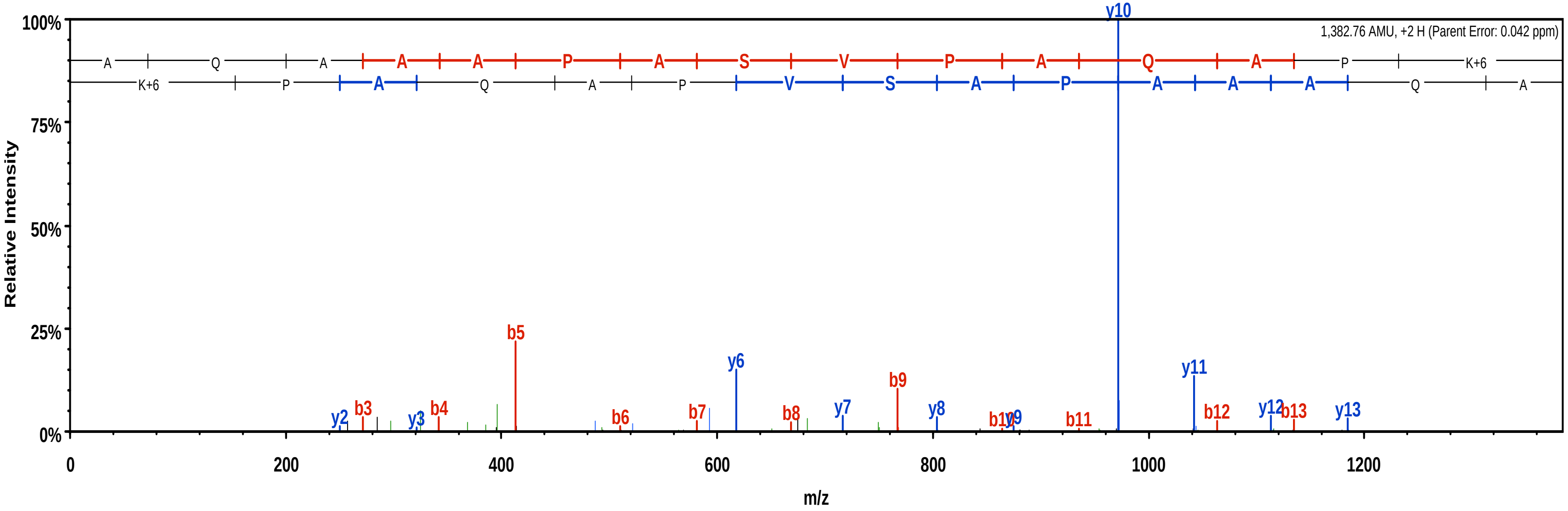


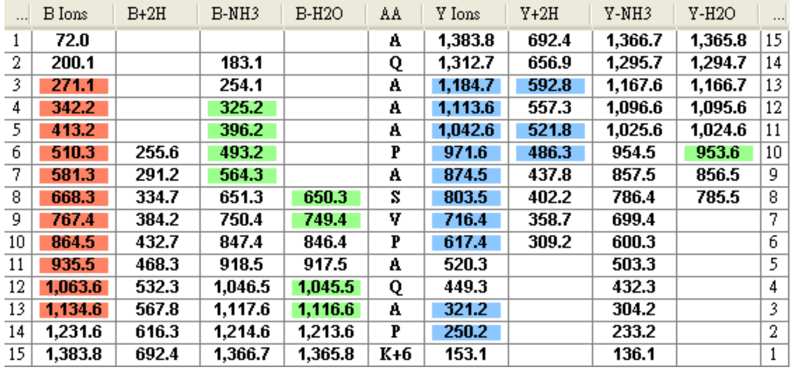


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	2,119.9	1,060.5	2,102.9	2,101.9	18
2	274.1				C+57	2,006.9	1,003.9	1,989.8	1,988.8	17
3	403.2			385.2	E	1,846.8	923.9	1,829.8	1,828.8	16
4	531.2		514.2	513.2	Q	1,717.8	859.4	1,700.8	1,699.8	15
5	678.3		661.3	660.3	F	1,589.7	795.4	1,572.7	1,571.7	14
6	807.3	404.2	790.3	789.3	E	1,442.7	721.8	1,425.6	1,424.6	13
7	878.4	439.7	861.3	860.4	A	1,313.6	657.3	1,296.6	1,295.6	12
8	1,007.4	504.2	990.4	989.4	E	1,242.6	621.8	1,225.6	1,224.6	11
9	1,108.5	554.7	1,091.4	1,090.5	T	1,113.5	557.3	1,096.5	1,095.5	10
10	1,205.5	603.3	1,188.5	1,187.5	P	1,012.5	506.7	995.5	994.5	9
11	1,306.6	653.8	1,289.5	1,288.6	T	915.4	458.2	898.4	897.4	8
12	1,421.6	711.3	1,404.6	1,403.6	D	814.4	407.7	797.4	796.4	7
13	1,508.6	754.8	1,491.6	1,490.6	S	699.4	350.2	682.3	681.4	6
14	1,637.7	819.3	1,620.6	1,619.7	E	612.3		595.3	594.3	5
15	1,738.7	869.9	1,721.7	1,720.7	T	483.3		466.3	465.3	4
16	1,839.8	920.4	1,822.7	1,821.7	T	382.2		365.2	364.2	3
17	1,967.8	984.4	1,950.8	1,949.8	Q	281.2		264.2		2
18	2,119.9	1,060.5	2,102.9	2,101.9	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-18	splP47914lRL29_HUMAN	AQAAAPASVPAQAPK	95.7	Unmodified	Heavy	2	689.37788

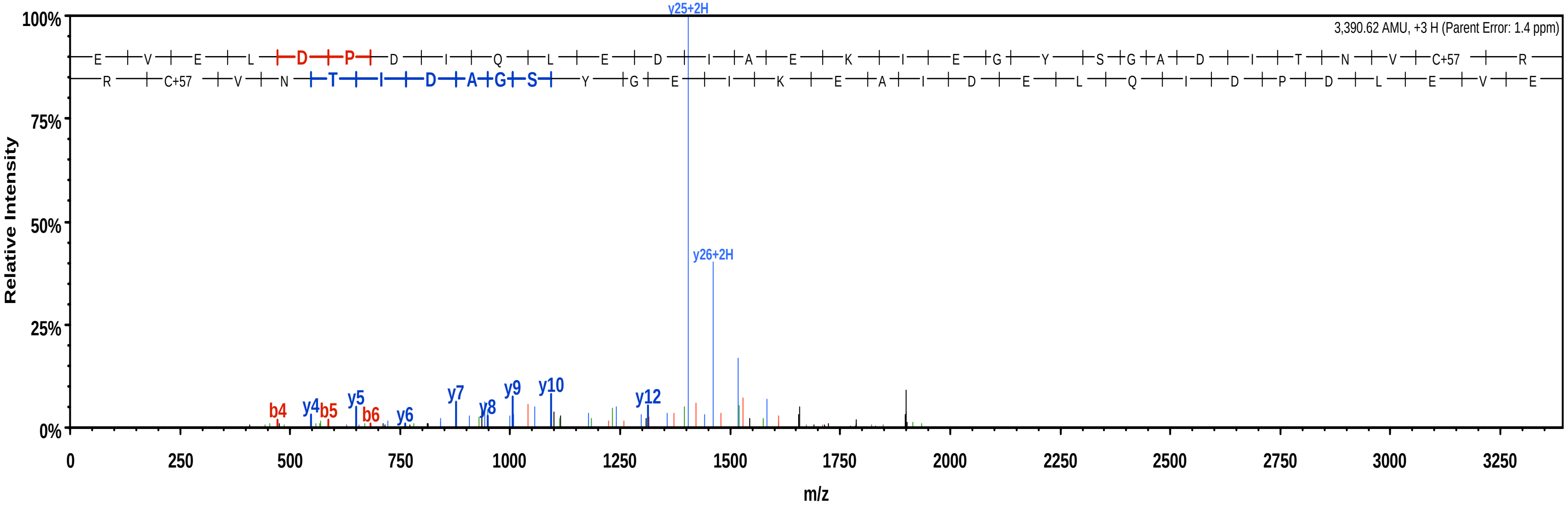


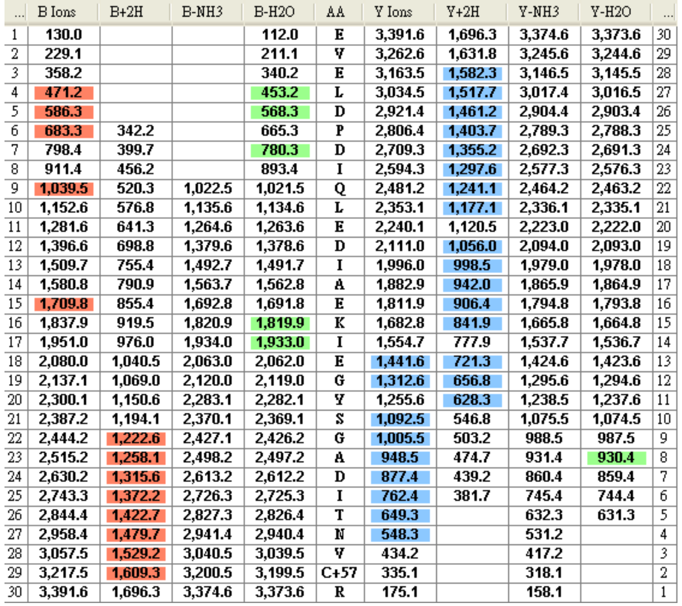


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	1,383.8	692.4	1,366.7	1,365.8	15
2	200.1		183.1		Q	1,312.7	656.9	1,295.7	1,294.7	14
3	271.1		254.1		A	1,184.7	592.8	1,167.6	1,166.7	13
4	342.2		325.2		A	1,113.6	557.3	1,096.6	1,095.6	12
5	413.2		396.2		A	1,042.6	521.8	1,025.6	1,024.6	11
6	510.3	255.6	493.2		P	971.6	486.3	954.5	953.6	10
7	581.3	291.2	564.3		A	874.5	437.8	857.5	856.5	9
8	668.3	334.7	651.3	650.3	S	803.5	402.2	786.4	785.5	8
9	767.4	384.2	750.4	749.4	V	716.4	358.7	699.4		7
10	864.5	432.7	847.4	846.4	P	617.4	309.2	600.3		6
11	935.5	468.3	918.5	917.5	A	520.3		503.3		5
12	1,063.6	532.3	1,046.5	1,045.5	Q	449.3		432.3		4
13	1,134.6	567.8	1,117.6	1,116.6	A	321.2		304.2		3
14	1,231.6	616.3	1,214.6	1,213.6	P	250.2		233.2		2
15	1,383.8	692.4	1,366.7	1,365.8	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-19	sp|Q9BW62|KATL1_HUMAN	EVELDPDIQLEDIAEKIEGYSGADITNVCR	94.96	Unmodified	Light	3	1131.2118

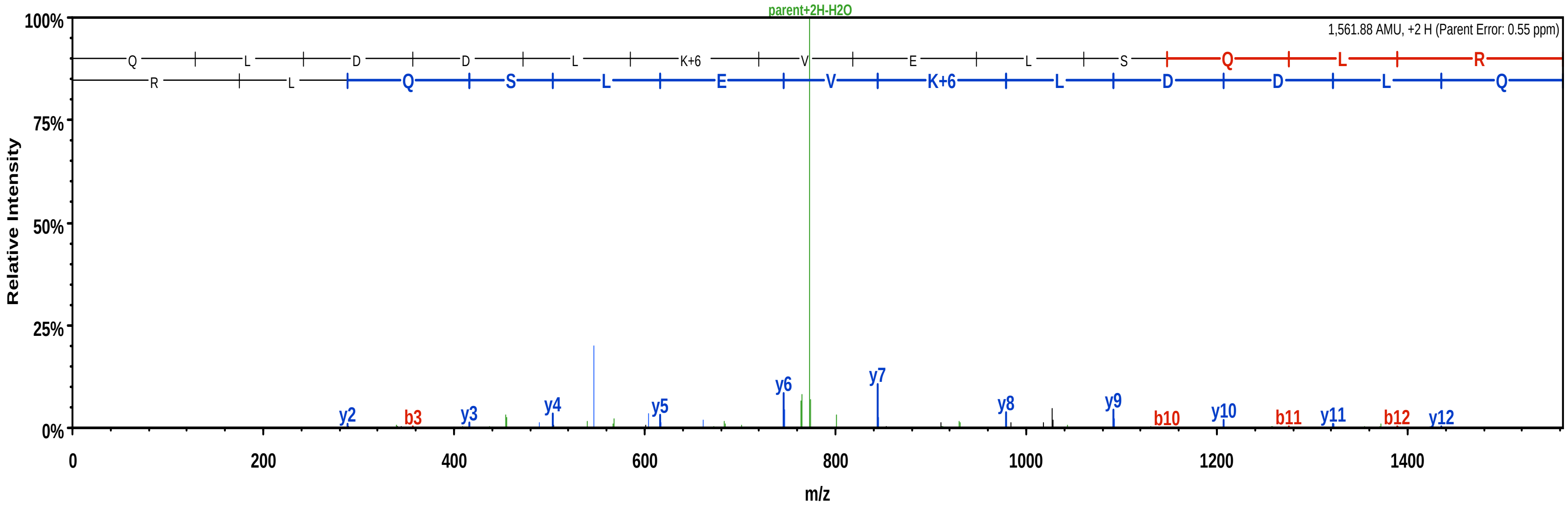


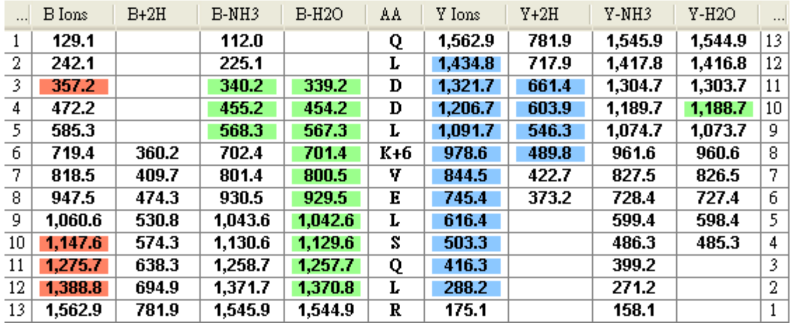


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	3,391.6	1,696.3	3,374.6	3,373.6	30
2	229.1			211.1	V	3,262.6	1,631.8	3,245.6	3,244.6	29
3	358.2			340.2	E	3,163.5	1,582.3	3,146.5	3,145.5	28
4	471.2			453.2	L	3,034.5	1,517.7	3,017.4	3,016.5	27
5	586.3			568.3	D	2,921.4	1,461.2	2,904.4	2,903.4	26
6	683.3	342.2		665.3	P	2,806.4	1,403.7	2,789.3	2,788.3	25
7	798.4	399.7		780.3	D	2,709.3	1,355.2	2,692.3	2,691.3	24
8	911.4	456.2		893.4	I	2,594.3	1,297.6	2,577.3	2,576.3	23
9	1,039.5	520.3	1,022.5	1,021.5	Q	2,481.2	1,241.1	2,464.2	2,463.2	22
10	1,152.6	576.8	1,135.6	1,134.6	L	2,353.1	1,177.1	2,336.1	2,335.1	21
11	1,281.6	641.3	1,264.6	1,263.6	E	2,240.1	1,120.5	2,223.0	2,222.0	20
12	1,396.6	698.8	1,379.6	1,378.6	D	2,111.0	1,056.0	2,094.0	2,093.0	19
13	1,509.7	755.4	1,492.7	1,491.7	I	1,996.0	998.5	1,979.0	1,978.0	18
14	1,580.8	790.9	1,563.7	1,562.8	A	1,882.9	942.0	1,865.9	1,864.9	17
15	1,709.8	855.4	1,692.8	1,691.8	E	1,811.9	906.4	1,794.8	1,793.8	16
16	1,837.9	919.5	1,820.9	1,819.9	K	1,682.8	841.9	1,665.8	1,664.8	15
17	1,951.0	976.0	1,934.0	1,933.0	I	1,554.7	777.9	1,537.7	1,536.7	14
18	2,080.0	1,040.5	2,063.0	2,062.0	E	1,441.6	721.3	1,424.6	1,423.6	13
19	2,137.1	1,069.0	2,120.0	2,119.0	G	1,312.6	656.8	1,295.6	1,294.6	12
20	2,300.1	1,150.6	2,283.1	2,282.1	Y	1,255.6	628.3	1,238.5	1,237.6	11
21	2,387.2	1,194.1	2,370.1	2,369.1	S	1,092.5	546.8	1,075.5	1,074.5	10
22	2,444.2	1,222.6	2,427.1	2,426.2	G	1,005.5	503.2	988.5	987.5	9
23	2,515.2	1,258.1	2,498.2	2,497.2	A	948.5	474.7	931.4	930.4	8
24	2,630.2	1,315.6	2,613.2	2,612.2	D	877.4	439.2	860.4	859.4	7
25	2,743.3	1,372.2	2,726.3	2,725.3	I	762.4	381.7	745.4	744.4	6
26	2,844.4	1,422.7	2,827.3	2,826.4	T	649.3		632.3	631.3	5
27	2,958.4	1,479.7	2,941.4	2,940.4	N	548.3		531.2		4
28	3,057.5	1,529.2	3,040.5	3,039.5	V	434.2		417.2		3
29	3,217.5	1,609.3	3,200.5	3,199.5	C+57	335.1		318.1		2
30	3,391.6	1,696.3	3,374.6	3,373.6	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-20	sp|P42766|RL35_HUMAN	QLDDLKVELSQLR	94.25	Unmodified	Heavy	2	778.93576

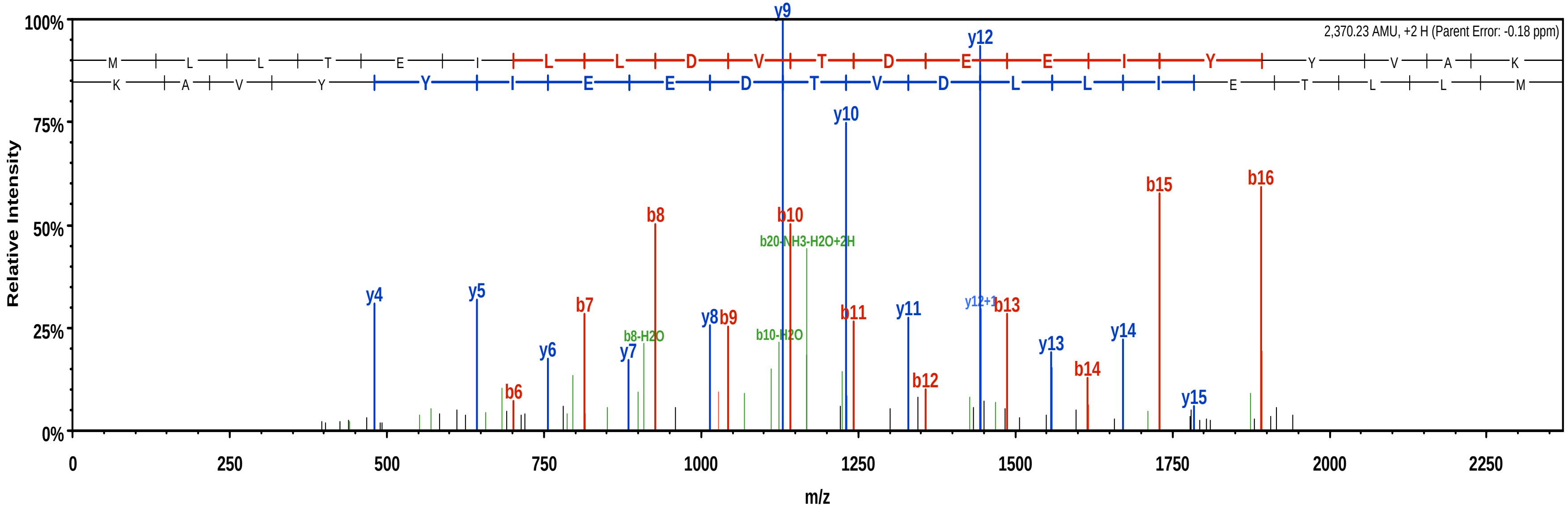


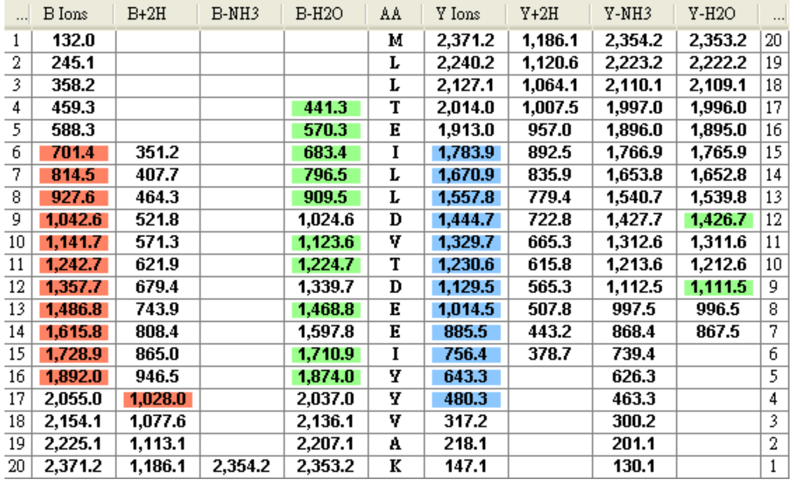


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	129.1		112.0		Q	1,562.9	781.9	1,545.9	1,544.9	13
2	242.1		225.1		L	1,434.8	717.9	1,417.8	1,416.8	12
3	357.2		340.2	339.2	D	1,321.7	661.4	1,304.7	1,303.7	11
4	472.2		455.2	454.2	D	1,206.7	603.9	1,189.7	1,188.7	10
5	585.3		568.3	567.3	L	1,091.7	546.3	1,074.7	1,073.7	9
6	719.4	360.2	702.4	701.4	K+6	978.6	489.8	961.6	960.6	8
7	818.5	409.7	801.4	800.5	V	844.5	422.7	827.5	826.5	7
8	947.5	474.3	930.5	929.5	E	745.4	373.2	728.4	727.4	6
9	1,060.6	530.8	1,043.6	1,042.6	L	616.4		599.4	598.4	5
10	1,147.6	574.3	1,130.6	1,129.6	S	503.3		486.3	485.3	4
11	1,275.7	638.3	1,258.7	1,257.7	Q	416.3		399.2		3
12	1,388.8	694.9	1,371.7	1,370.8	L	288.2		271.2		2
13	1,562.9	781.9	1,545.9	1,544.9	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-21	sp|Q8TF01|SFR18_HUMAN	MLLTEILLDVTDEEIYYVAK	92.1	Unmodified	Light	2	1186.1213

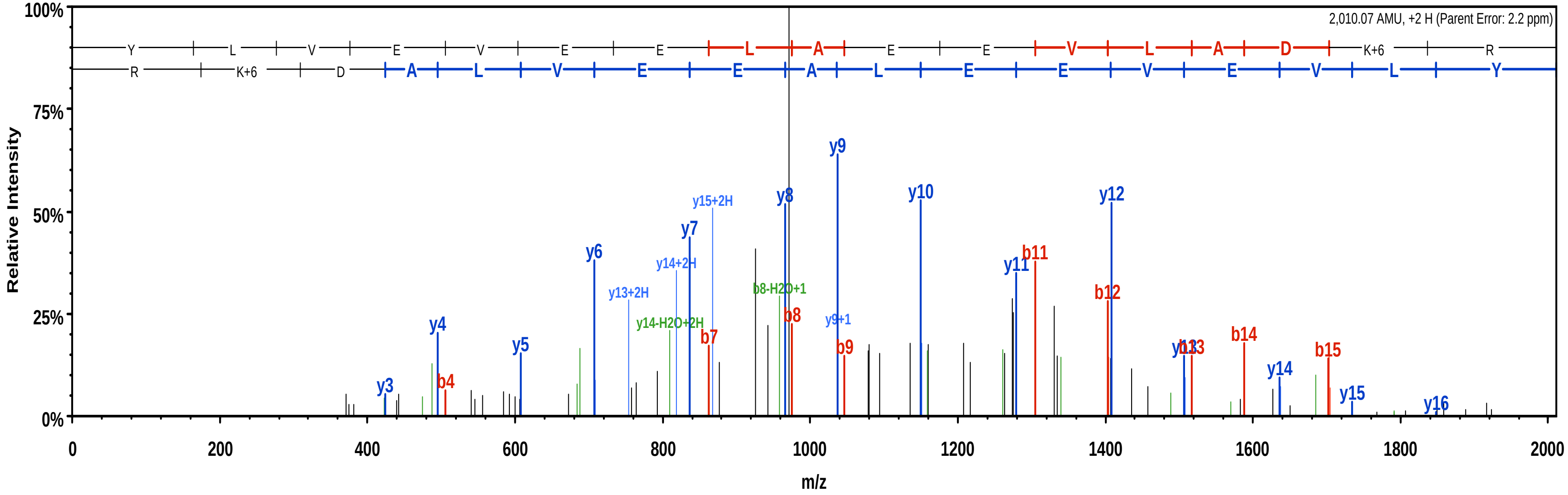


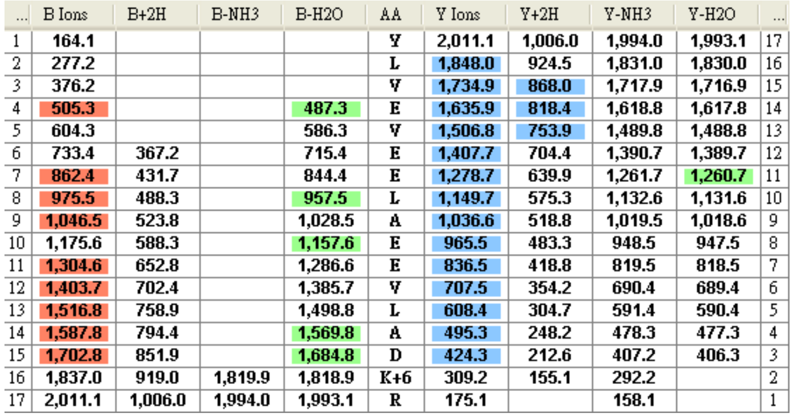


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	132.0				M	2,371.2	1,186.1	2,354.2	2,353.2	20
2	245.1				L	2,240.2	1,120.6	2,223.2	2,222.2	19
3	358.2				L	2,127.1	1,064.1	2,110.1	2,109.1	18
4	459.3			441.3	T	2,014.0	1,007.5	1,997.0	1,996.0	17
5	588.3			570.3	E	1,913.0	957.0	1,896.0	1,895.0	16
6	701.4	351.2		683.4	I	1,783.9	892.5	1,766.9	1,765.9	15
7	814.5	407.7		796.5	L	1,670.9	835.9	1,653.8	1,652.8	14
8	927.6	464.3		909.5	L	1,557.8	779.4	1,540.7	1,539.8	13
9	1,042.6	521.8		1,024.6	D	1,444.7	722.8	1,427.7	1,426.7	12
10	1,141.7	571.3		1,123.6	V	1,329.7	665.3	1,312.6	1,311.6	11
11	1,242.7	621.9		1,224.7	T	1,230.6	615.8	1,213.6	1,212.6	10
12	1,357.7	679.4		1,339.7	D	1,129.5	565.3	1,112.5	1,111.5	9
13	1,486.8	743.9		1,468.8	E	1,014.5	507.8	997.5	996.5	8
14	1,615.8	808.4		1,597.8	E	885.5	443.2	868.4	867.5	7
15	1,728.9	865.0		1,710.9	I	756.4	378.7	739.4		6
16	1,892.0	946.5		1,874.0	Y	643.3		626.3		5
17	2,055.0	1,028.0		2,037.0	Y	480.3		463.3		4
18	2,154.1	1,077.6		2,136.1	V	317.2		300.2		3
19	2,225.1	1,113.1		2,207.1	A	218.1		201.1		2
20	2,371.2	1,186.1	2,354.2	2,353.2	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-22	sp|Q9NUG6|PDRG1_HUMAN	YLVEVEELAEEVLADKR	91.45	Unmodified	Heavy	2	1003.028

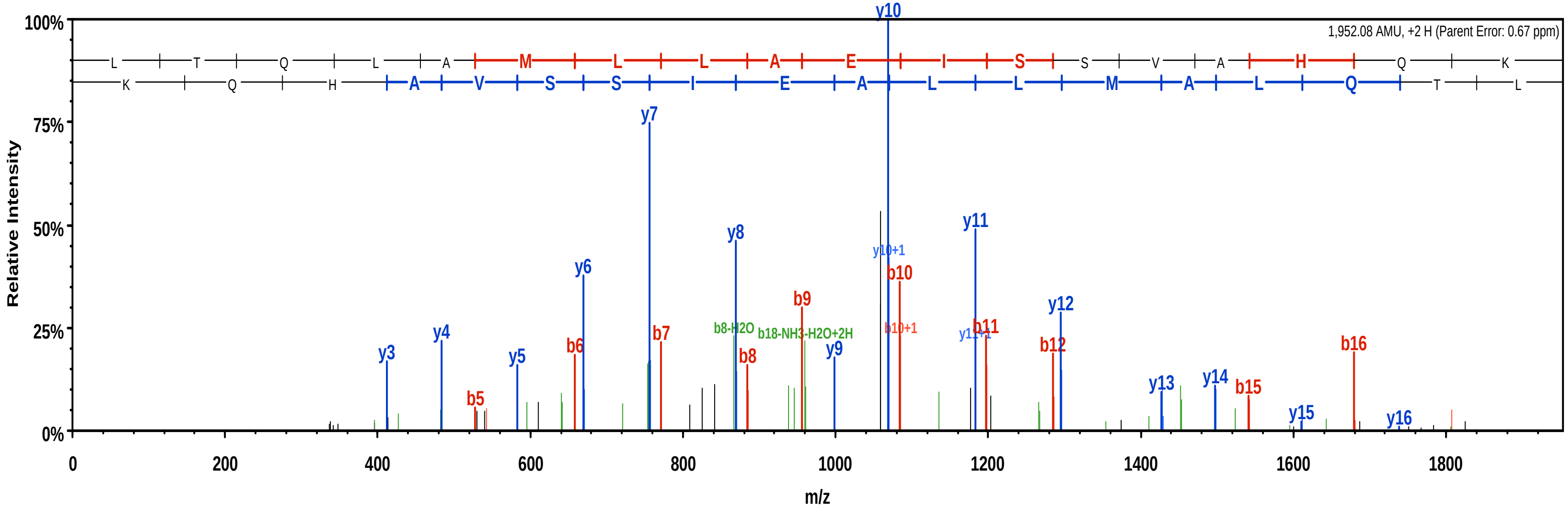


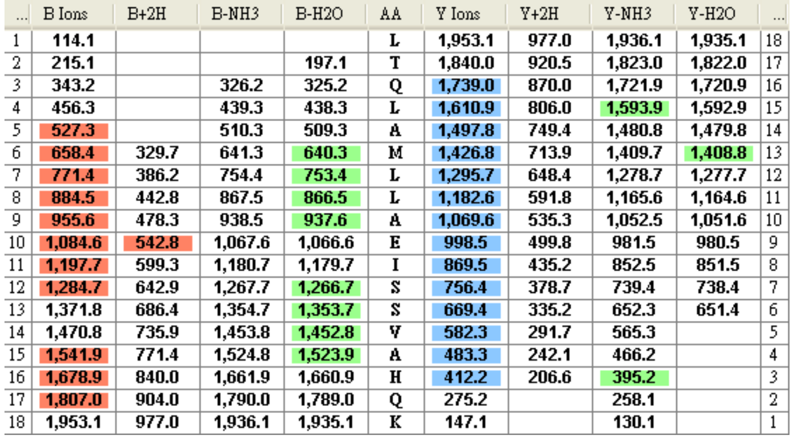


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	164.1				Y	2,011.1	1,006.0	1,994.0	1,993.1	17
2	277.2				L	1,848.0	924.5	1,831.0	1,830.0	16
3	376.2				V	1,734.9	868.0	1,717.9	1,716.9	15
4	505.3			487.3	E	1,635.9	818.4	1,618.8	1,617.8	14
5	604.3			586.3	V	1,506.8	753.9	1,489.8	1,488.8	13
6	733.4	367.2		715.4	E	1,407.7	704.4	1,390.7	1,389.7	12
7	862.4	431.7		844.4	E	1,278.7	639.9	1,261.7	1,260.7	11
8	975.5	488.3		957.5	L	1,149.7	575.3	1,132.6	1,131.6	10
9	1,046.5	523.8		1,028.5	A	1,036.6	518.8	1,019.5	1,018.6	9
10	1,175.6	588.3		1,157.6	E	965.5	483.3	948.5	947.5	8
11	1,304.6	652.8		1,286.6	E	836.5	418.8	819.5	818.5	7
12	1,403.7	702.4		1,385.7	V	707.5	354.2	690.4	689.4	6
13	1,516.8	758.9		1,498.8	L	608.4	304.7	591.4	590.4	5
14	1,587.8	794.4		1,569.8	A	495.3	248.2	478.3	477.3	4
15	1,702.8	851.9		1,684.8	D	424.3	212.6	407.2	406.3	3
16	1,837.0	919.0	1,819.9	1,818.9	K+6	309.2	155.1	292.2		2
17	2,011.1	1,006.0	1,994.0	1,993.1	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-23	sp|Q5VTE6|ANGE2_HUMAN	LTQLAMLLAEISSVAHQK	90.67	Unmodified	Light	2	977.04552

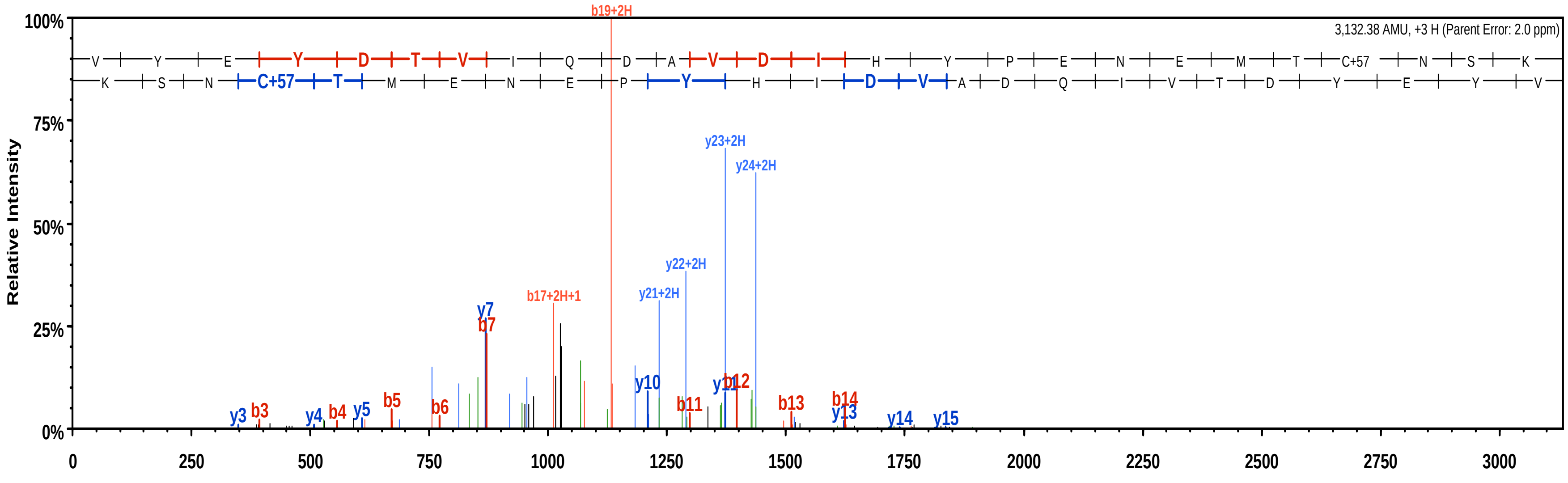


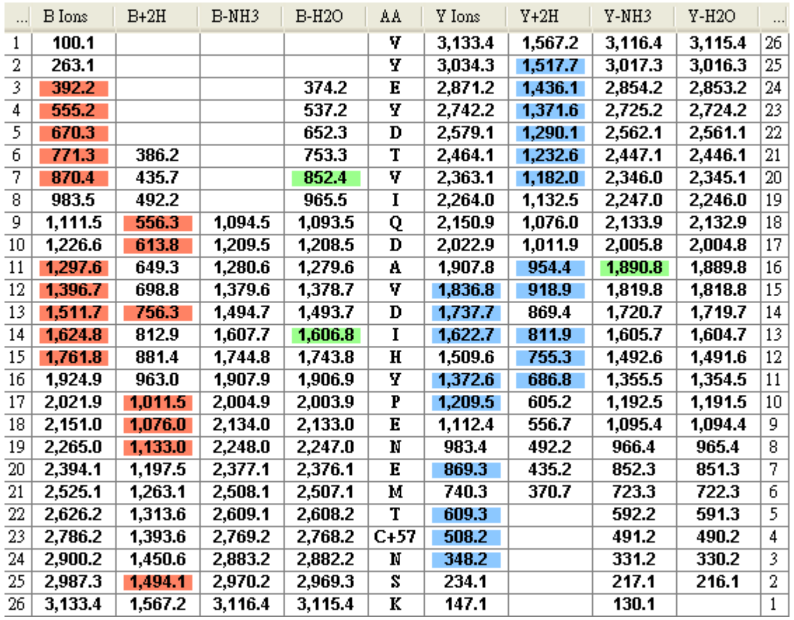


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	1,953.1	977.0	1,936.1	1,935.1	18
2	215.1			197.1	T	1,840.0	920.5	1,823.0	1,822.0	17
3	343.2		326.2	325.2	Q	1,739.0	870.0	1,721.9	1,720.9	16
4	456.3		439.3	438.3	L	1,610.9	806.0	1,593.9	1,592.9	15
5	527.3		510.3	509.3	A	1,497.8	749.4	1,480.8	1,479.8	14
6	658.4	329.7	641.3	640.3	M	1,426.8	713.9	1,409.7	1,408.8	13
7	771.4	386.2	754.4	753.4	L	1,295.7	648.4	1,278.7	1,277.7	12
8	884.5	442.8	867.5	866.5	L	1,182.6	591.8	1,165.6	1,164.6	11
9	955.6	478.3	938.5	937.6	A	1,069.6	535.3	1,052.5	1,051.6	10
10	1,084.6	542.8	1,067.6	1,066.6	E	998.5	499.8	981.5	980.5	9
11	1,197.7	599.3	1,180.7	1,179.7	I	869.5	435.2	852.5	851.5	8
12	1,284.7	642.9	1,267.7	1,266.7	S	756.4	378.7	739.4	738.4	7
13	1,371.8	686.4	1,354.7	1,353.7	S	669.4	335.2	652.3	651.4	6
14	1,470.8	735.9	1,453.8	1,452.8	V	582.3	291.7	565.3		5
15	1,541.9	771.4	1,524.8	1,523.9	A	483.3	242.1	466.2		4
16	1,678.9	840.0	1,661.9	1,660.9	H	412.2	206.6	395.2		3
17	1,807.0	904.0	1,790.0	1,789.0	Q	275.2		258.1		2
18	1,953.1	977.0	1,936.1	1,935.1	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-24	sp|Q8NHY2|RFWD2_HUMAN	VYEYDTVIQDAVDIHYPENEMTCNSK	90.05	Unmodified	Light	3	1045.1304

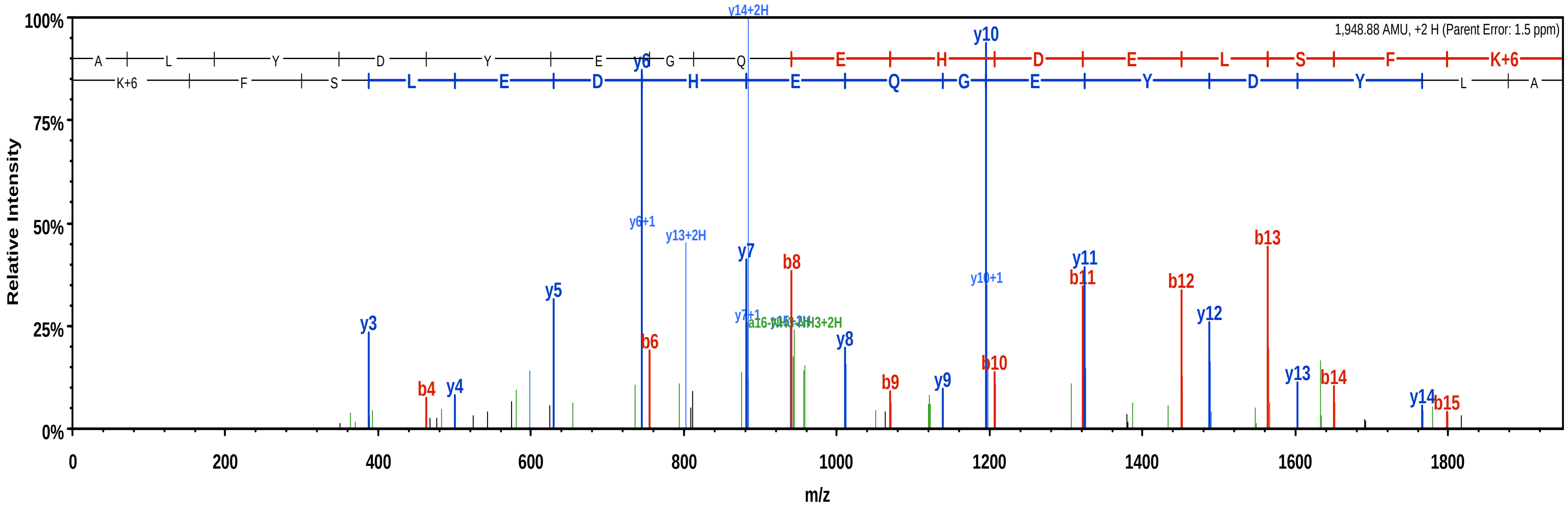


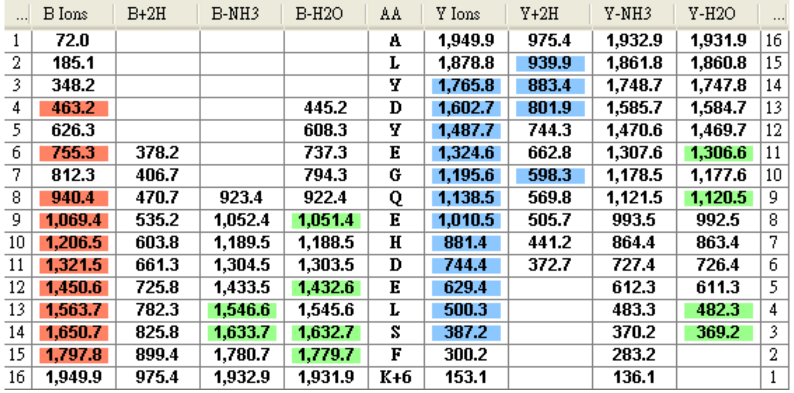


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	3,133.4	1,567.2	3,116.4	3,115.4	26
2	263.1				Y	3,034.3	1,517.7	3,017.3	3,016.3	25
3	392.2			374.2	E	2,871.2	1,436.1	2,854.2	2,853.2	24
4	555.2			537.2	Y	2,742.2	1,371.6	2,725.2	2,724.2	23
5	670.3			652.3	D	2,579.1	1,290.1	2,562.1	2,561.1	22
6	771.3	386.2		753.3	T	2,464.1	1,232.6	2,447.1	2,446.1	21
7	870.4	435.7		852.4	V	2,363.1	1,182.0	2,346.0	2,345.1	20
8	983.5	492.2		965.5	I	2,264.0	1,132.5	2,247.0	2,246.0	19
9	1,111.5	556.3	1,094.5	1,093.5	Q	2,150.9	1,076.0	2,133.9	2,132.9	18
10	1,226.6	613.8	1,209.5	1,208.5	D	2,022.9	1,011.9	2,005.8	2,004.8	17
11	1,297.6	649.3	1,280.6	1,279.6	A	1,907.8	954.4	1,890.8	1,889.8	16
12	1,396.7	698.8	1,379.6	1,378.7	V	1,836.8	918.9	1,819.8	1,818.8	15
13	1,511.7	756.3	1,494.7	1,493.7	D	1,737.7	869.4	1,720.7	1,719.7	14
14	1,624.8	812.9	1,607.7	1,606.8	I	1,622.7	811.9	1,605.7	1,604.7	13
15	1,761.8	881.4	1,744.8	1,743.8	H	1,509.6	755.3	1,492.6	1,491.6	12
16	1,924.9	963.0	1,907.9	1,906.9	Y	1,372.6	686.8	1,355.5	1,354.5	11
17	2,021.9	1,011.5	2,004.9	2,003.9	P	1,209.5	605.2	1,192.5	1,191.5	10
18	2,151.0	1,076.0	2,134.0	2,133.0	E	1,112.4	556.7	1,095.4	1,094.4	9
19	2,265.0	1,133.0	2,248.0	2,247.0	N	983.4	492.2	966.4	965.4	8
20	2,394.1	1,197.5	2,377.1	2,376.1	E	869.3	435.2	852.3	851.3	7
21	2,525.1	1,263.1	2,508.1	2,507.1	M	740.3	370.7	723.3	722.3	6
22	2,626.2	1,313.6	2,609.1	2,608.2	T	609.3		592.2	591.3	5
23	2,786.2	1,393.6	2,769.2	2,768.2	C+57	508.2		491.2	490.2	4
24	2,900.2	1,450.6	2,883.2	2,882.2	N	348.2		331.2	330.2	3
25	2,987.3	1,494.1	2,970.2	2,969.3	S	234.1		217.1	216.1	2
26	3,133.4	1,567.2	3,116.4	3,115.4	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-25	sp|Q9UNF0|PACN2_HUMAN	ALYDYEGQEHDELSFK	89.96	Unmodified	Heavy	2	972.43652

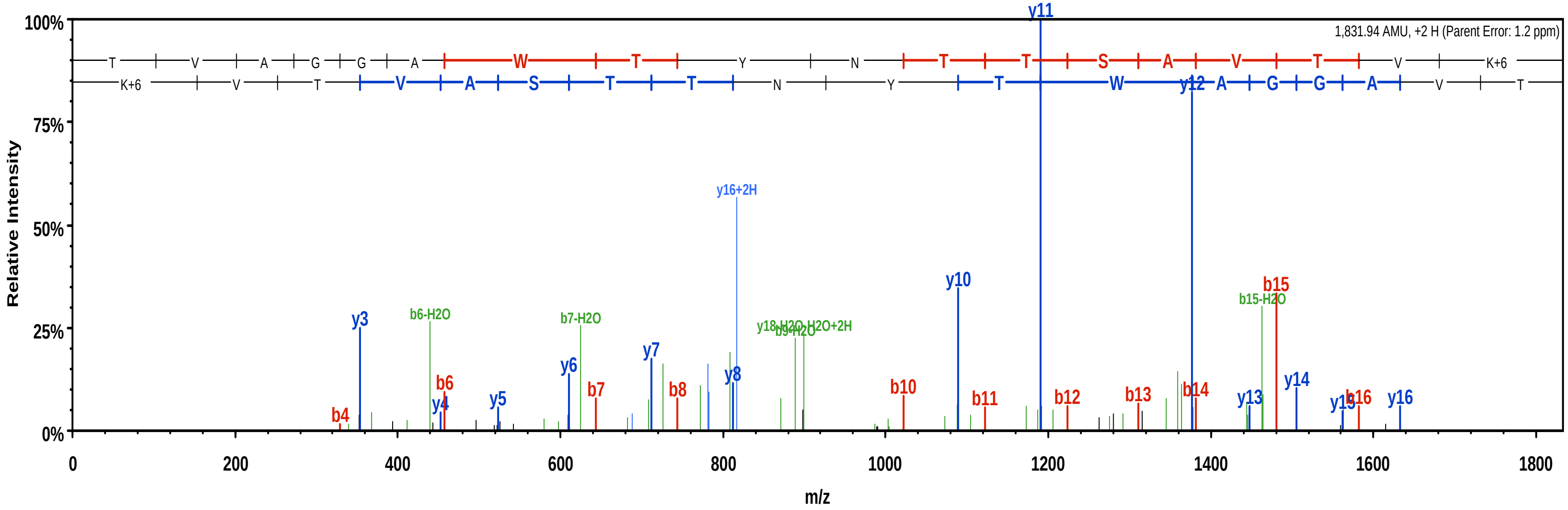


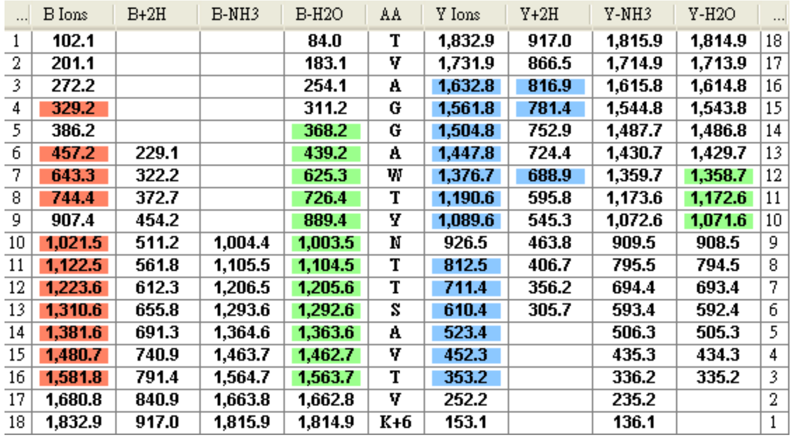


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	1,949.9	975.4	1,932.9	1,931.9	16
2	185.1				L	1,878.8	939.9	1,861.8	1,860.8	15
3	348.2				Y	1,765.8	883.4	1,748.7	1,747.8	14
4	463.2			445.2	D	1,602.7	801.9	1,585.7	1,584.7	13
5	626.3			608.3	Y	1,487.7	744.3	1,470.6	1,469.7	12
6	755.3	378.2		737.3	E	1,324.6	662.8	1,307.6	1,306.6	11
7	812.3	406.7		794.3	G	1,195.6	598.3	1,178.5	1,177.6	10
8	940.4	470.7	923.4	922.4	Q	1,138.5	569.8	1,121.5	1,120.5	9
9	1,069.4	535.2	1,052.4	1,051.4	E	1,010.5	505.7	993.5	992.5	8
10	1,206.5	603.8	1,189.5	1,188.5	H	881.4	441.2	864.4	863.4	7
11	1,321.5	661.3	1,304.5	1,303.5	D	744.4	372.7	727.4	726.4	6
12	1,450.6	725.8	1,433.5	1,432.6	E	629.4		612.3	611.3	5
13	1,563.7	782.3	1,546.6	1,545.6	L	500.3		483.3	482.3	4
14	1,650.7	825.8	1,633.7	1,632.7	S	387.2		370.2	369.2	3
15	1,797.8	899.4	1,780.7	1,779.7	F	300.2		283.2		2
16	1,949.9	975.4	1,932.9	1,931.9	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-26	sp|P61513|RL37A_HUMAN	TVAGGAWTYNTTSAVTVK	88.91	Unmodified	Heavy	2	913.96779

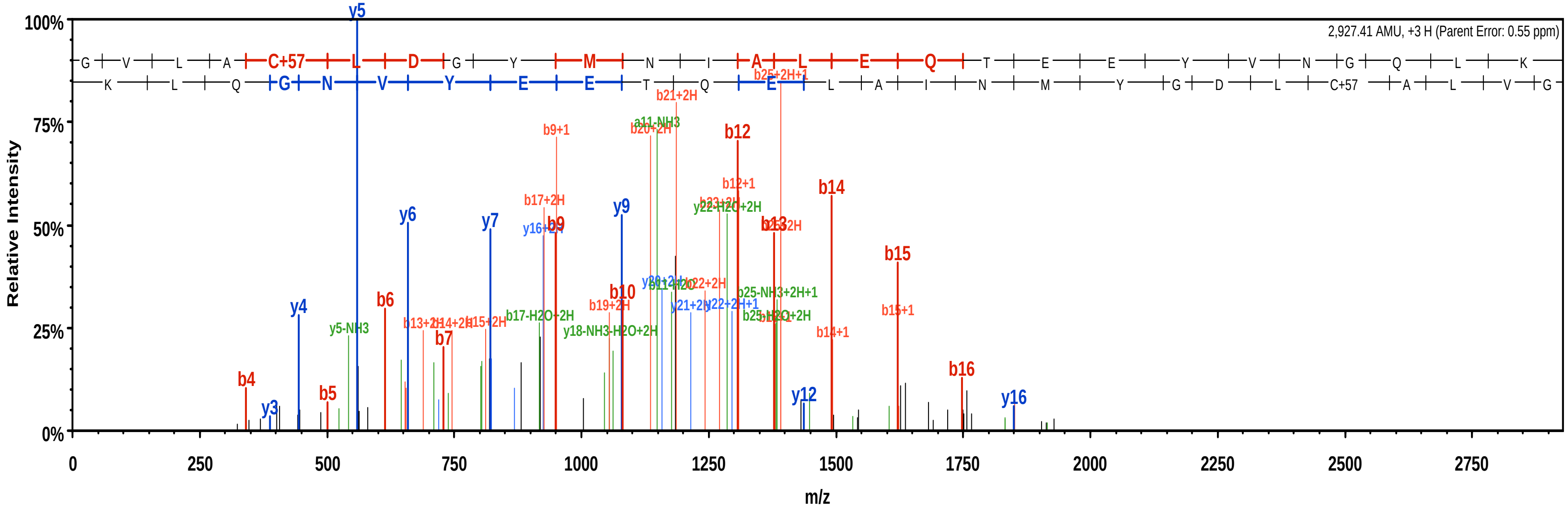


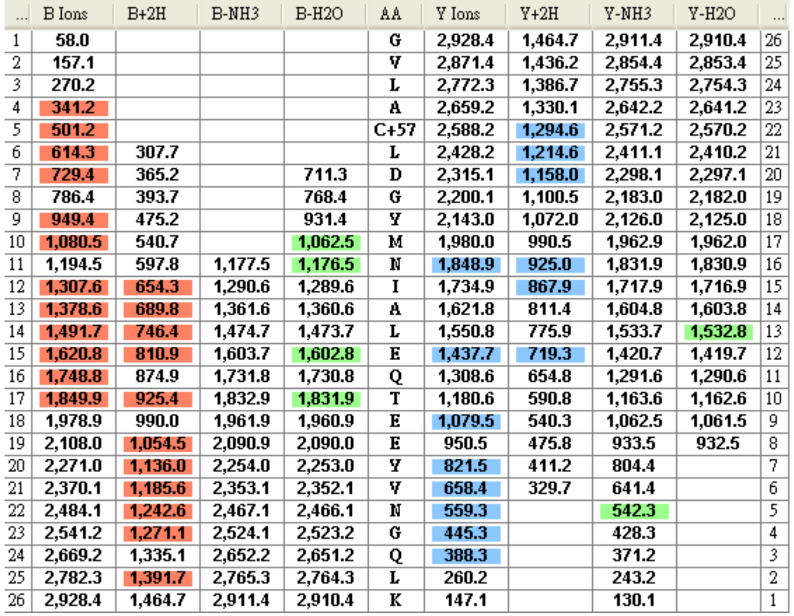


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	102.1			84.0	T	1,832.9	917.0	1,815.9	1,814.9	18
2	201.1			183.1	V	1,731.9	866.5	1,714.9	1,713.9	17
3	272.2			254.1	A	1,632.8	816.9	1,615.8	1,614.8	16
4	329.2			311.2	G	1,561.8	781.4	1,544.8	1,543.8	15
5	386.2			368.2	G	1,504.8	752.9	1,487.7	1,486.8	14
6	457.2	229.1		439.2	A	1,447.8	724.4	1,430.7	1,429.7	13
7	643.3	322.2		625.3	W	1,376.7	688.9	1,359.7	1,358.7	12
8	744.4	372.7		726.4	T	1,190.6	595.8	1,173.6	1,172.6	11
9	907.4	454.2		889.4	Y	1,089.6	545.3	1,072.6	1,071.6	10
10	1,021.5	511.2	1,004.4	1,003.5	N	926.5	463.8	909.5	908.5	9
11	1,122.5	561.8	1,105.5	1,104.5	T	812.5	406.7	795.5	794.5	8
12	1,223.6	612.3	1,206.5	1,205.6	T	711.4	356.2	694.4	693.4	7
13	1,310.6	655.8	1,293.6	1,292.6	S	610.4	305.7	593.4	592.4	6
14	1,381.6	691.3	1,364.6	1,363.6	A	523.4		506.3	505.3	5
15	1,480.7	740.9	1,463.7	1,462.7	V	452.3		435.3	434.3	4
16	1,581.8	791.4	1,564.7	1,563.7	T	353.2		336.2	335.2	3
17	1,680.8	840.9	1,663.8	1,662.8	V	252.2		235.2		2
18	1,832.9	917.0	1,815.9	1,814.9	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-27	sp|P62312|LSM6_HUMAN	GVLACLDGYMNIALEQTEEYVNGQLK	87.47	Unmodified	Light	3	976.80877

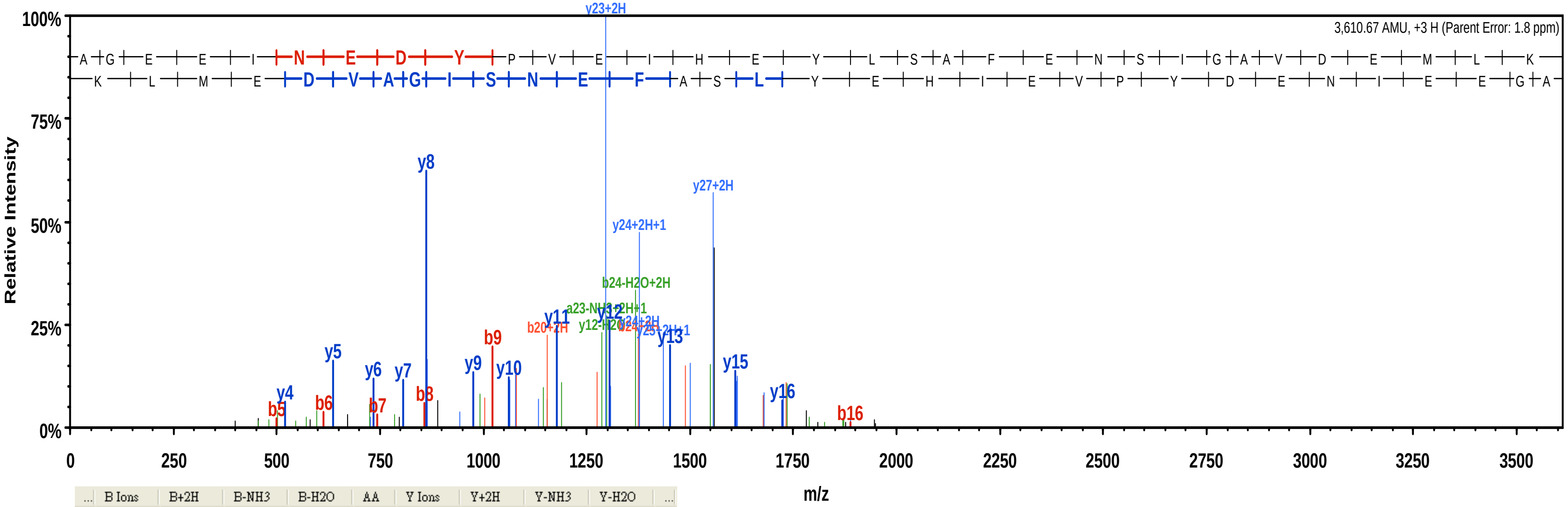


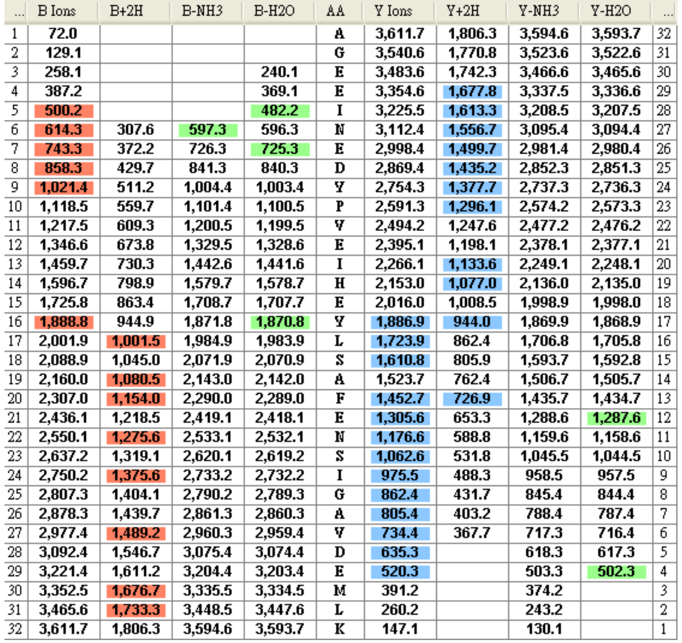


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	2,928.4	1,464.7	2,911.4	2,910.4	26
2	157.1				V	2,871.4	1,436.2	2,854.4	2,853.4	25
3	270.2				L	2,772.3	1,386.7	2,755.3	2,754.3	24
4	341.2				A	2,659.2	1,330.1	2,642.2	2,641.2	23
5	501.2				C+57	2,588.2	1,294.6	2,571.2	2,570.2	22
6	614.3	307.7			L	2,428.2	1,214.6	2,411.1	2,410.2	21
7	729.4	365.2		711.3	D	2,315.1	1,158.0	2,298.1	2,297.1	20
8	786.4	393.7		768.4	G	2,200.1	1,100.5	2,183.0	2,182.0	19
9	949.4	475.2		931.4	Y	2,143.0	1,072.0	2,126.0	2,125.0	18
10	1,080.5	540.7		1,062.5	M	1,980.0	990.5	1,962.9	1,962.0	17
11	1,194.5	597.8	1,177.5	1,176.5	N	1,848.9	925.0	1,831.9	1,830.9	16
12	1,307.6	654.3	1,290.6	1,289.6	I	1,734.9	867.9	1,717.9	1,716.9	15
13	1,378.6	689.8	1,361.6	1,360.6	A	1,621.8	811.4	1,604.8	1,603.8	14
14	1,491.7	746.4	1,474.7	1,473.7	L	1,550.8	775.9	1,533.7	1,532.8	13
15	1,620.8	810.9	1,603.7	1,602.8	E	1,437.7	719.3	1,420.7	1,419.7	12
16	1,748.8	874.9	1,731.8	1,730.8	Q	1,308.6	654.8	1,291.6	1,290.6	11
17	1,849.9	925.4	1,832.9	1,831.9	T	1,180.6	590.8	1,163.6	1,162.6	10
18	1,978.9	990.0	1,961.9	1,960.9	E	1,079.5	540.3	1,062.5	1,061.5	9
19	2,108.0	1,054.5	2,090.9	2,090.0	E	950.5	475.8	933.5	932.5	8
20	2,271.0	1,136.0	2,254.0	2,253.0	Y	821.5	411.2	804.4		7
21	2,370.1	1,185.6	2,353.1	2,352.1	V	658.4	329.7	641.4		6
22	2,484.1	1,242.6	2,467.1	2,466.1	N	559.3		542.3		5
23	2,541.2	1,271.1	2,524.1	2,523.2	G	445.3		428.3		4
24	2,669.2	1,335.1	2,652.2	2,651.2	Q	388.3		371.2		3
25	2,782.3	1,391.7	2,765.3	2,764.3	L	260.2		243.2		2
26	2,928.4	1,464.7	2,911.4	2,910.4	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-28	sp|Q13901|C1D_HUMAN	AGEEINEDYPVEIHEYLSAFENSIGAVDEMLK	85.59	Unmodified	Light	3	1204.5627

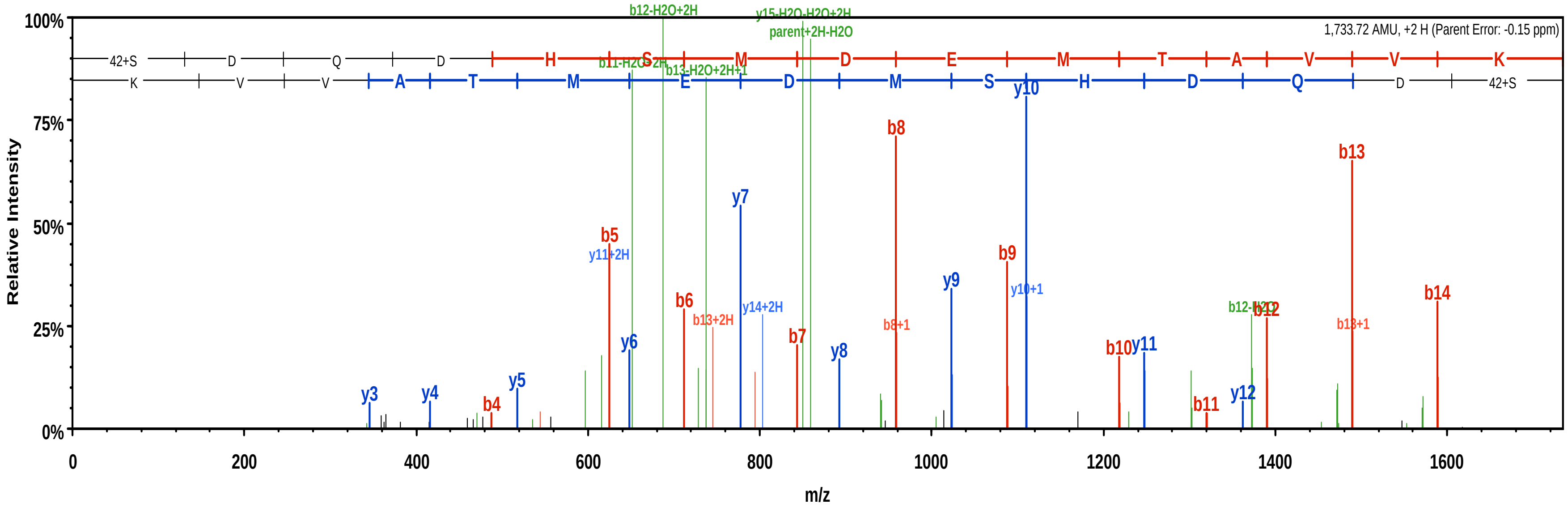


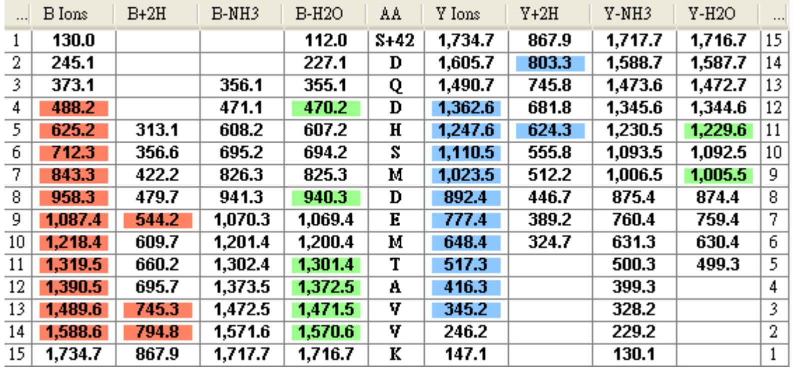


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	3,611.7	1,806.3	3,594.6	3,593.7	32
2	129.1				G	3,540.6	1,770.8	3,523.6	3,522.6	31
3	258.1			240.1	E	3,483.6	1,742.3	3,466.6	3,465.6	30
4	387.2			369.1	E	3,354.6	1,677.8	3,337.5	3,336.6	29
5	500.2			482.2	I	3,225.5	1,613.3	3,208.5	3,207.5	28
6	614.3	307.6	597.3	596.3	N	3,112.4	1,556.7	3,095.4	3,094.4	27
7	743.3	372.2	726.3	725.3	E	2,998.4	1,499.7	2,981.4	2,980.4	26
8	858.3	429.7	841.3	840.3	D	2,869.4	1,435.2	2,852.3	2,851.3	25
9	1,021.4	511.2	1,004.4	1,003.4	Y	2,754.3	1,377.7	2,737.3	2,736.3	24
10	1,118.5	559.7	1,101.4	1,100.5	P	2,591.3	1,296.1	2,574.2	2,573.3	23
11	1,217.5	609.3	1,200.5	1,199.5	V	2,494.2	1,247.6	2,477.2	2,476.2	22
12	1,346.6	673.8	1,329.5	1,328.6	E	2,395.1	1,198.1	2,378.1	2,377.1	21
13	1,459.7	730.3	1,442.6	1,441.6	I	2,266.1	1,133.6	2,249.1	2,248.1	20
14	1,596.7	798.9	1,579.7	1,578.7	H	2,153.0	1,077.0	2,136.0	2,135.0	19
15	1,725.8	863.4	1,708.7	1,707.7	E	2,016.0	1,008.5	1,998.9	1,998.0	18
16	1,888.8	944.9	1,871.8	1,870.8	Y	1,886.9	944.0	1,869.9	1,868.9	17
17	2,001.9	1,001.5	1,984.9	1,983.9	L	1,723.9	862.4	1,706.8	1,705.8	16
18	2,088.9	1,045.0	2,071.9	2,070.9	S	1,610.8	805.9	1,593.7	1,592.8	15
19	2,160.0	1,080.5	2,143.0	2,142.0	A	1,523.7	762.4	1,506.7	1,505.7	14
20	2,307.0	1,154.0	2,290.0	2,289.0	F	1,452.7	726.9	1,435.7	1,434.7	13
21	2,436.1	1,218.5	2,419.1	2,418.1	E	1,305.6	653.3	1,288.6	1,287.6	12
22	2,550.1	1,275.6	2,533.1	2,532.1	N	1,176.6	588.8	1,159.6	1,158.6	11
23	2,637.2	1,319.1	2,620.1	2,619.2	S	1,062.6	531.8	1,045.5	1,044.5	10
24	2,750.2	1,375.6	2,733.2	2,732.2	I	975.5	488.3	958.5	957.5	9
25	2,807.3	1,404.1	2,790.2	2,789.3	G	862.4	431.7	845.4	844.4	8
26	2,878.3	1,439.7	2,861.3	2,860.3	A	805.4	403.2	788.4	787.4	7
27	2,977.4	1,489.2	2,960.3	2,959.4	V	734.4	367.7	717.3	716.4	6
28	3,092.4	1,546.7	3,075.4	3,074.4	D	635.3		618.3	617.3	5
29	3,221.4	1,611.2	3,204.4	3,203.4	E	520.3		503.3	502.3	4
30	3,352.5	1,676.7	3,335.5	3,334.5	M	391.2		374.2		3
31	3,465.6	1,733.3	3,448.5	3,447.6	L	260.2		243.2		2
32	3,611.7	1,806.3	3,594.6	3,593.7	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-29	splP08047lSP1_HUMAN	SDQDHSMDEMTAVVK	84.92	Acetyl (Protein N-term)	Light	2	867.8691

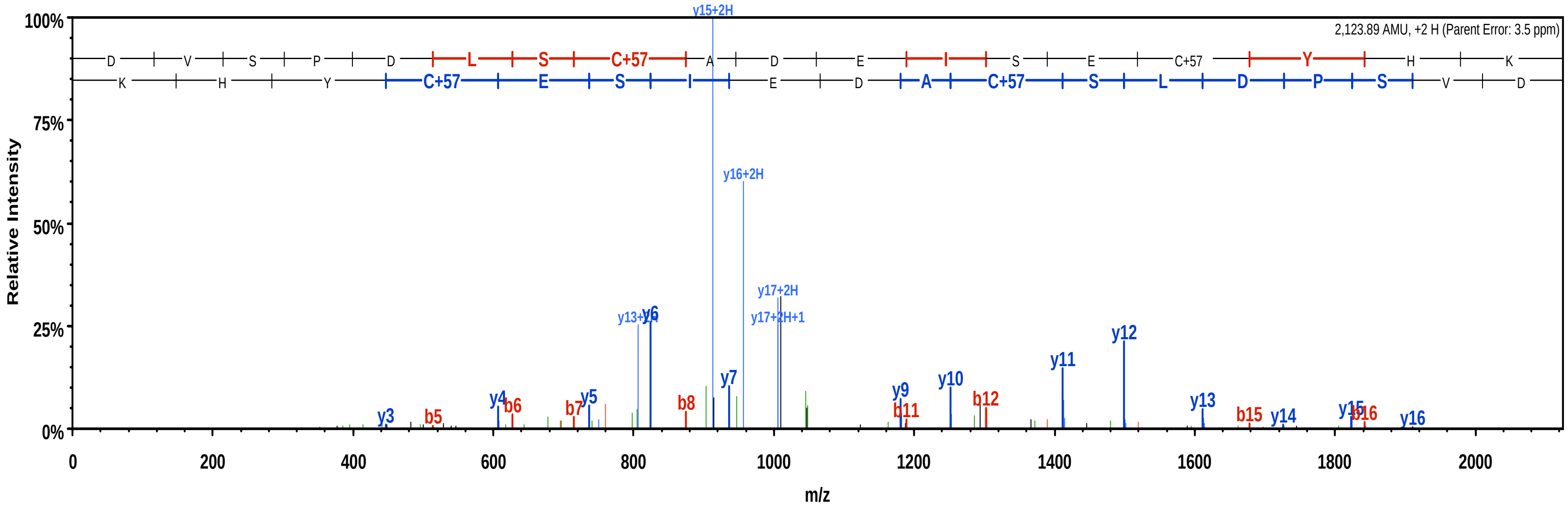


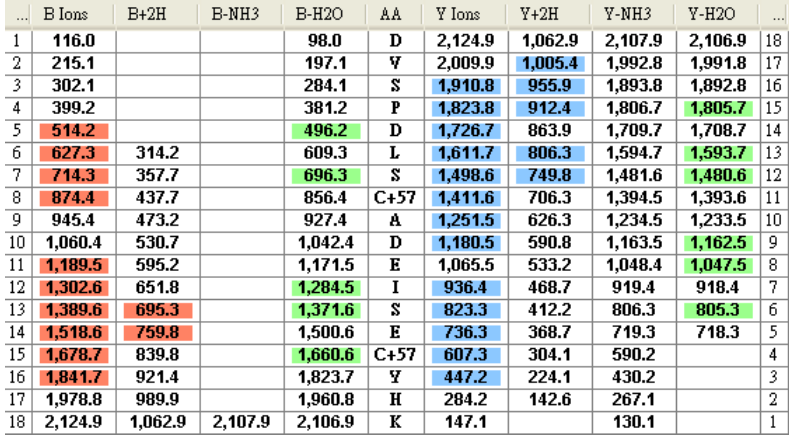


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	S+42	1,734.7	867.9	1,717.7	1,716.7	15
2	245.1			227.1	D	1,605.7	803.3	1,588.7	1,587.7	14
3	373.1		356.1	355.1	Q	1,490.7	745.8	1,473.6	1,472.7	13
4	488.2		471.1	470.2	D	1,362.6	681.8	1,345.6	1,344.6	12
5	625.2	313.1	608.2	607.2	H	1,247.6	624.3	1,230.5	1,229.6	11
6	712.3	356.6	695.2	694.2	S	1,110.5	555.8	1,093.5	1,092.5	10
7	843.3	422.2	826.3	825.3	M	1,023.5	512.2	1,006.5	1,005.5	9
8	958.3	479.7	941.3	940.3	D	892.4	446.7	875.4	874.4	8
9	1,087.4	544.2	1,070.3	1,069.4	E	777.4	389.2	760.4	759.4	7
10	1,218.4	609.7	1,201.4	1,200.4	M	648.4	324.7	631.3	630.4	6
11	1,319.5	660.2	1,302.4	1,301.4	T	517.3		500.3	499.3	5
12	1,390.5	695.7	1,373.5	1,372.5	A	416.3		399.3		4
13	1,489.6	745.3	1,472.5	1,471.5	V	345.2		328.2		3
14	1,588.6	794.8	1,571.6	1,570.6	V	246.2		229.2		2
15	1,734.7	867.9	1,717.7	1,716.7	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-30	sp|Q96S66|CLCC1_HUMAN	DVSPDLSCADEISECYHK	83.52	Unmodified	Light	2	1062.9461

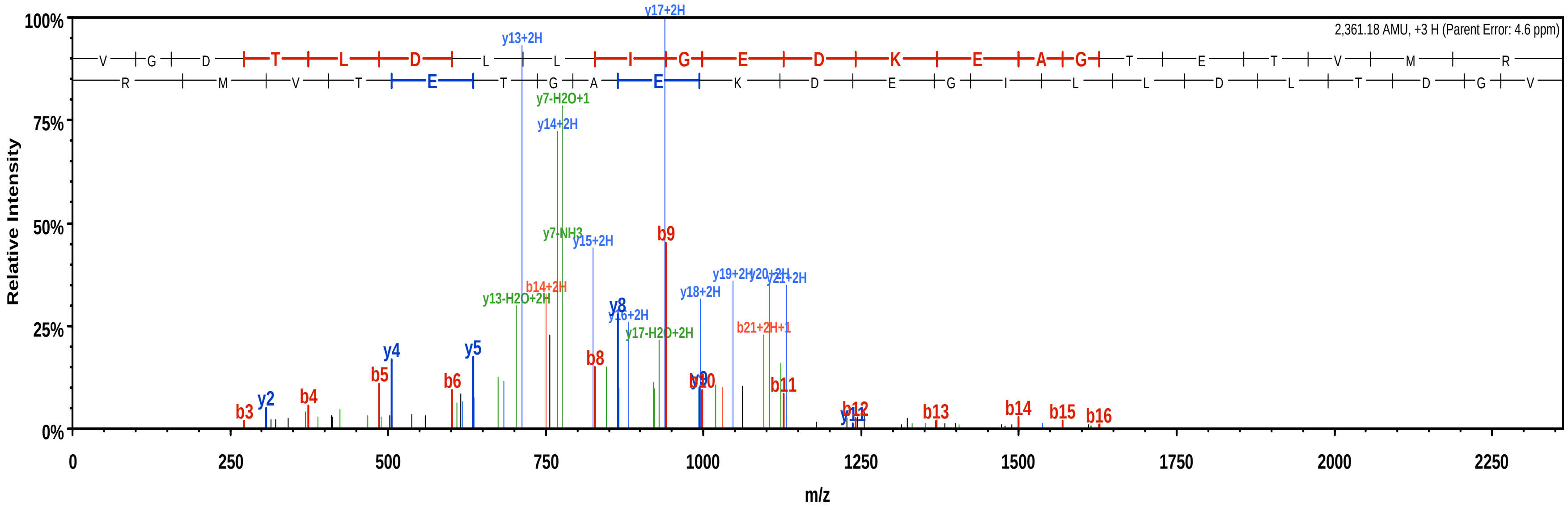


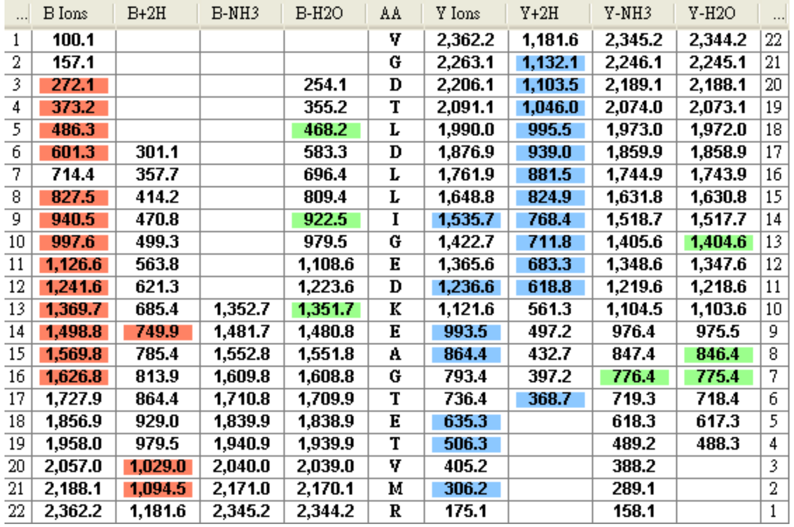


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	2,124.9	1,062.9	2,107.9	2,106.9	18
2	215.1			197.1	V	2,009.9	1,005.4	1,992.8	1,991.8	17
3	302.1			284.1	S	1,910.8	955.9	1,893.8	1,892.8	16
4	399.2			381.2	P	1,823.8	912.4	1,806.7	1,805.7	15
5	514.2			496.2	D	1,726.7	863.9	1,709.7	1,708.7	14
6	627.3	314.2		609.3	L	1,611.7	806.3	1,594.7	1,593.7	13
7	714.3	357.7		696.3	S	1,498.6	749.8	1,481.6	1,480.6	12
8	874.4	437.7		856.4	C+57	1,411.6	706.3	1,394.5	1,393.6	11
9	945.4	473.2		927.4	A	1,251.5	626.3	1,234.5	1,233.5	10
10	1,060.4	530.7		1,042.4	D	1,180.5	590.8	1,163.5	1,162.5	9
11	1,189.5	595.2		1,171.5	E	1,065.5	533.2	1,048.4	1,047.5	8
12	1,302.6	651.8		1,284.5	I	936.4	468.7	919.4	918.4	7
13	1,389.6	695.3		1,371.6	S	823.3	412.2	806.3	805.3	6
14	1,518.6	759.8		1,500.6	E	736.3	368.7	719.3	718.3	5
15	1,678.7	839.8		1,660.6	C+57	607.3	304.1	590.2		4
16	1,841.7	921.4		1,823.7	Y	447.2	224.1	430.2		3
17	1,978.8	989.9		1,960.8	H	284.2	142.6	267.1		2
18	2,124.9	1,062.9	2,107.9	2,106.9	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-31	sp|Q9P0P8|CF203_HUMAN	VGDTLDLLIGEDKEAGTETVMR	82.79	Unmodified	Light	3	788.06506

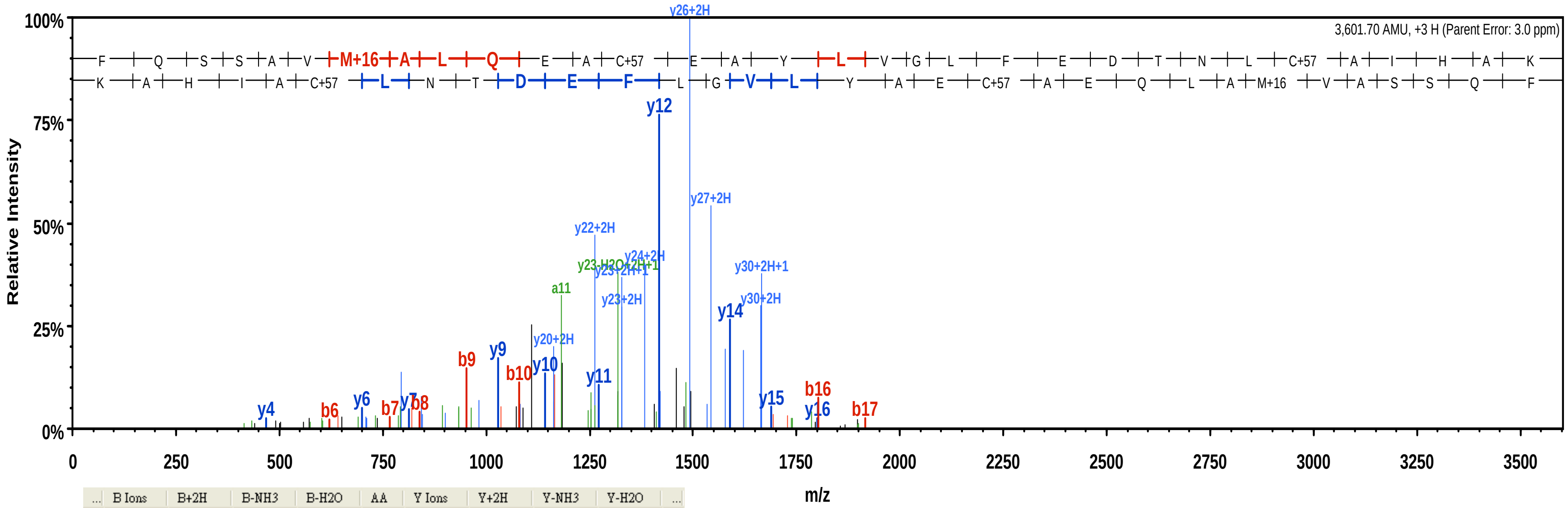


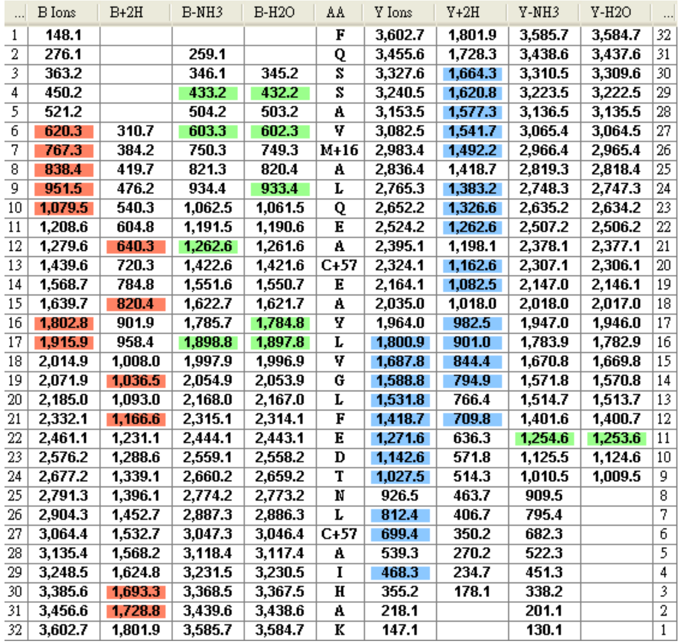


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	2,362.2	1,181.6	2,345.2	2,344.2	22
2	157.1				G	2,263.1	1,132.1	2,246.1	2,245.1	21
3	272.1			254.1	D	2,206.1	1,103.5	2,189.1	2,188.1	20
4	373.2			355.2	T	2,091.1	1,046.0	2,074.0	2,073.1	19
5	486.3			468.2	L	1,990.0	995.5	1,973.0	1,972.0	18
6	601.3	301.1		583.3	D	1,876.9	939.0	1,859.9	1,858.9	17
7	714.4	357.7		696.4	L	1,761.9	881.5	1,744.9	1,743.9	16
8	827.5	414.2		809.4	L	1,648.8	824.9	1,631.8	1,630.8	15
9	940.5	470.8		922.5	I	1,535.7	768.4	1,518.7	1,517.7	14
10	997.6	499.3		979.5	G	1,422.7	711.8	1,405.6	1,404.6	13
11	1,126.6	563.8		1,108.6	E	1,365.6	683.3	1,348.6	1,347.6	12
12	1,241.6	621.3		1,223.6	D	1,236.6	618.8	1,219.6	1,218.6	11
13	1,369.7	685.4	1,352.7	1,351.7	K	1,121.6	561.3	1,104.5	1,103.6	10
14	1,498.8	749.9	1,481.7	1,480.8	E	993.5	497.2	976.4	975.5	9
15	1,569.8	785.4	1,552.8	1,551.8	A	864.4	432.7	847.4	846.4	8
16	1,626.8	813.9	1,609.8	1,608.8	G	793.4	397.2	776.4	775.4	7
17	1,727.9	864.4	1,710.8	1,709.9	T	736.4	368.7	719.3	718.4	6
18	1,856.9	929.0	1,839.9	1,838.9	E	635.3		618.3	617.3	5
19	1,958.0	979.5	1,940.9	1,939.9	T	506.3		489.2	488.3	4
20	2,057.0	1,029.0	2,040.0	2,039.0	V	405.2		388.2		3
21	2,188.1	1,094.5	2,171.0	2,170.1	M	306.2		289.1		2
22	2,362.2	1,181.6	2,345.2	2,344.2	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-32	sp|P68431|H31_HUMAN	FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	80.49	Oxidation (M)	Light	3	1201.5703

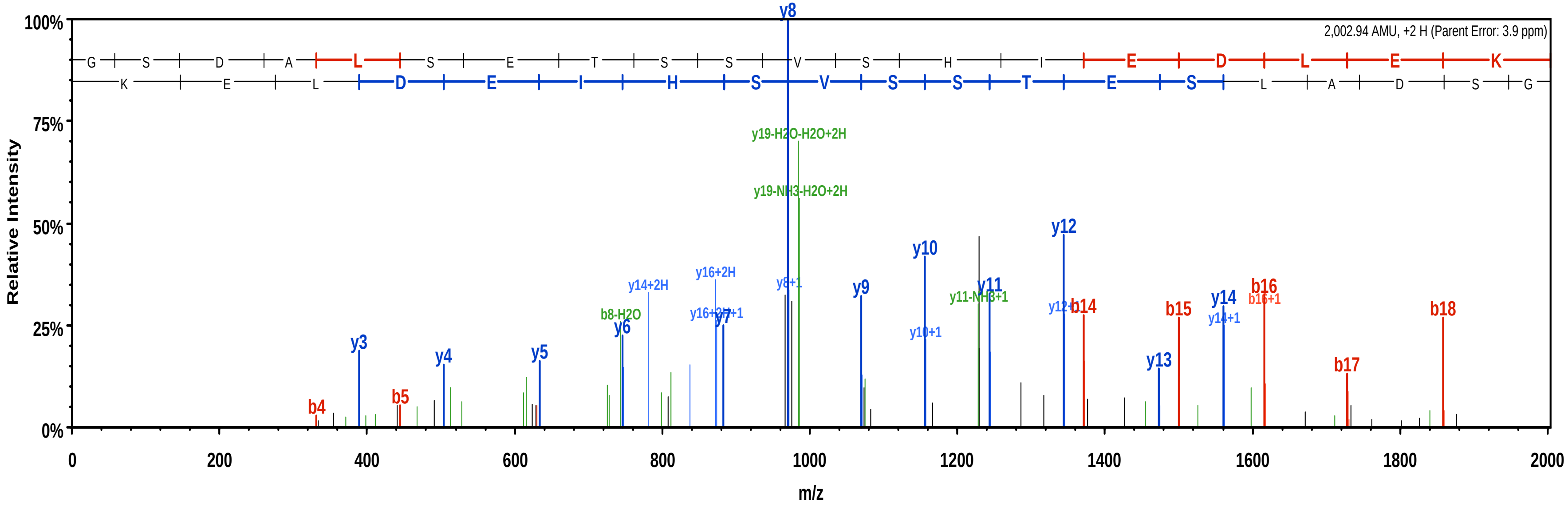


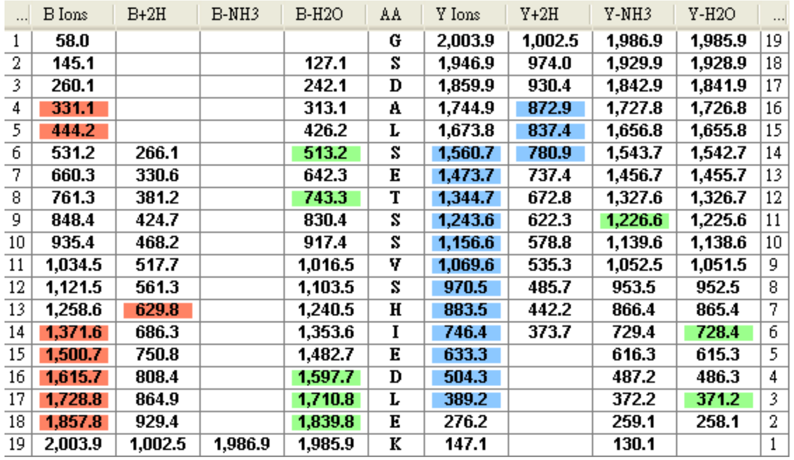


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.1				F	3,602.7	1,801.9	3,585.7	3,584.7	32
2	276.1		259.1		Q	3,455.6	1,728.3	3,438.6	3,437.6	31
3	363.2		346.1	345.2	S	3,327.6	1,664.3	3,310.5	3,309.6	30
4	450.2		433.2	432.2	S	3,240.5	1,620.8	3,223.5	3,222.5	29
5	521.2		504.2	503.2	A	3,153.5	1,577.3	3,136.5	3,135.5	28
6	620.3	310.7	603.3	602.3	V	3,082.5	1,541.7	3,065.4	3,064.5	27
7	767.3	384.2	750.3	749.3	M+16	2,983.4	1,492.2	2,966.4	2,965.4	26
8	838.4	419.7	821.3	820.4	A	2,836.4	1,418.7	2,819.3	2,818.4	25
9	951.5	476.2	934.4	933.4	L	2,765.3	1,383.2	2,748.3	2,747.3	24
10	1,079.5	540.3	1,062.5	1,061.5	Q	2,652.2	1,326.6	2,635.2	2,634.2	23
11	1,208.6	604.8	1,191.5	1,190.6	E	2,524.2	1,262.6	2,507.2	2,506.2	22
12	1,279.6	640.3	1,262.6	1,261.6	A	2,395.1	1,198.1	2,378.1	2,377.1	21
13	1,439.6	720.3	1,422.6	1,421.6	C+57	2,324.1	1,162.6	2,307.1	2,306.1	20
14	1,568.7	784.8	1,551.6	1,550.7	E	2,164.1	1,082.5	2,147.0	2,146.1	19
15	1,639.7	820.4	1,622.7	1,621.7	A	2,035.0	1,018.0	2,018.0	2,017.0	18
16	1,802.8	901.9	1,785.7	1,784.8	Y	1,964.0	982.5	1,947.0	1,946.0	17
17	1,915.9	958.4	1,898.8	1,897.8	L	1,800.9	901.0	1,783.9	1,782.9	16
18	2,014.9	1,008.0	1,997.9	1,996.9	V	1,687.8	844.4	1,670.8	1,669.8	15
19	2,071.9	1,036.5	2,054.9	2,053.9	G	1,588.8	794.9	1,571.8	1,570.8	14
20	2,185.0	1,093.0	2,168.0	2,167.0	L	1,531.8	766.4	1,514.7	1,513.7	13
21	2,332.1	1,166.6	2,315.1	2,314.1	F	1,418.7	709.8	1,401.6	1,400.7	12
22	2,461.1	1,231.1	2,444.1	2,443.1	E	1,271.6	636.3	1,254.6	1,253.6	11
23	2,576.2	1,288.6	2,559.1	2,558.2	D	1,142.6	571.8	1,125.5	1,124.6	10
24	2,677.2	1,339.1	2,660.2	2,659.2	T	1,027.5	514.3	1,010.5	1,009.5	9
25	2,791.3	1,396.1	2,774.2	2,773.2	N	926.5	463.7	909.5		8
26	2,904.3	1,452.7	2,887.3	2,886.3	L	812.4	406.7	795.4		7
27	3,064.4	1,532.7	3,047.3	3,046.4	C+57	699.4	350.2	682.3		6
28	3,135.4	1,568.2	3,118.4	3,117.4	A	539.3	270.2	522.3		5
29	3,248.5	1,624.8	3,231.5	3,230.5	I	468.3	234.7	451.3		4
30	3,385.6	1,693.3	3,368.5	3,367.5	H	355.2	178.1	338.2		3
31	3,456.6	1,728.8	3,439.6	3,438.6	A	218.1		201.1		2
32	3,602.7	1,801.9	3,585.7	3,584.7	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-33	sp|Q6P996|PDXD1_HUMAN	GSDALSETSSVSHIEDLEK	80.08	Unmodified	Light	2	1002.4738

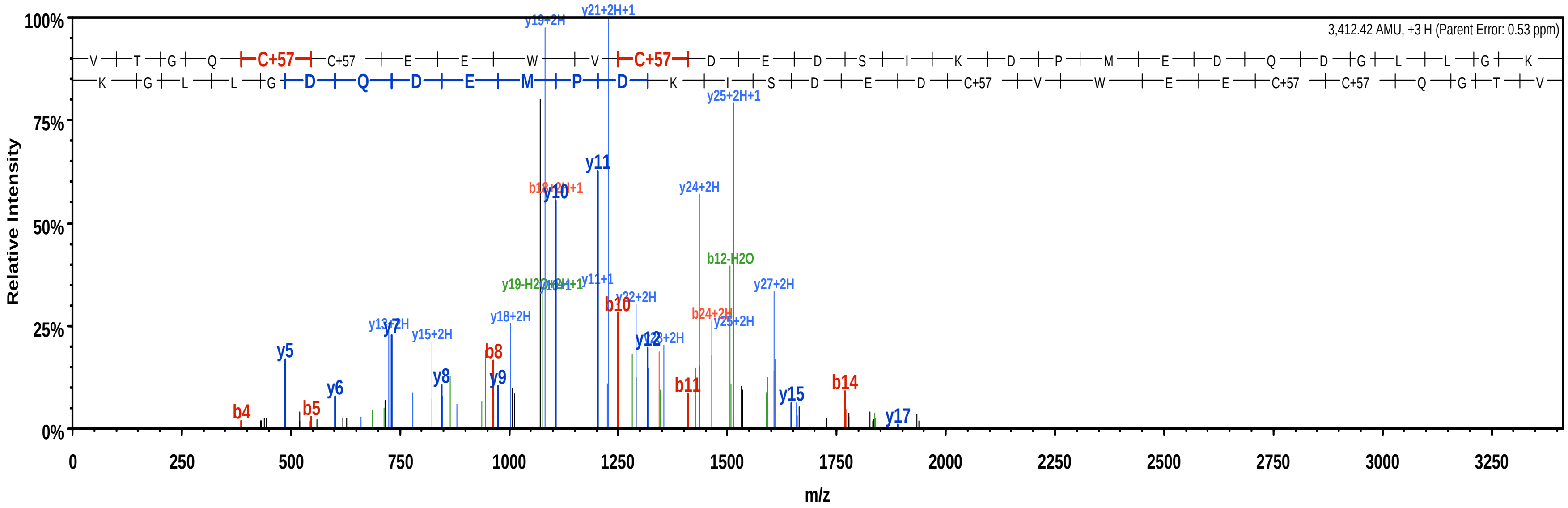


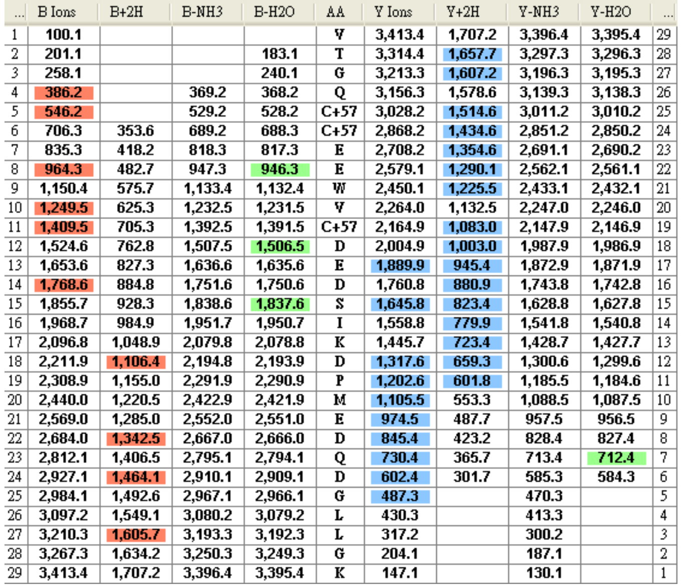


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	2,003.9	1,002.5	1,986.9	1,985.9	19
2	145.1			127.1	S	1,946.9	974.0	1,929.9	1,928.9	18
3	260.1			242.1	D	1,859.9	930.4	1,842.9	1,841.9	17
4	331.1			313.1	A	1,744.9	872.9	1,727.8	1,726.8	16
5	444.2			426.2	L	1,673.8	837.4	1,656.8	1,655.8	15
6	531.2	266.1		513.2	S	1,560.7	780.9	1,543.7	1,542.7	14
7	660.3	330.6		642.3	E	1,473.7	737.4	1,456.7	1,455.7	13
8	761.3	381.2		743.3	T	1,344.7	672.8	1,327.6	1,326.7	12
9	848.4	424.7		830.4	S	1,243.6	622.3	1,226.6	1,225.6	11
10	935.4	468.2		917.4	S	1,156.6	578.8	1,139.6	1,138.6	10
11	1,034.5	517.7		1,016.5	V	1,069.6	535.3	1,052.5	1,051.5	9
12	1,121.5	561.3		1,103.5	S	970.5	485.7	953.5	952.5	8
13	1,258.6	629.8		1,240.5	H	883.5	442.2	866.4	865.4	7
14	1,371.6	686.3		1,353.6	I	746.4	373.7	729.4	728.4	6
15	1,500.7	750.8		1,482.7	E	633.3		616.3	615.3	5
16	1,615.7	808.4		1,597.7	D	504.3		487.2	486.3	4
17	1,728.8	864.9		1,710.8	L	389.2		372.2	371.2	3
18	1,857.8	929.4		1,839.8	E	276.2		259.1	258.1	2
19	2,003.9	1,002.5	1,986.9	1,985.9	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-34	sp|O00622|CYR61_HUMAN	VTGQCCEEWVCDEDSIKDPMEDQDGLLGK	80.02	Unmodified	Light	3	1138.4807

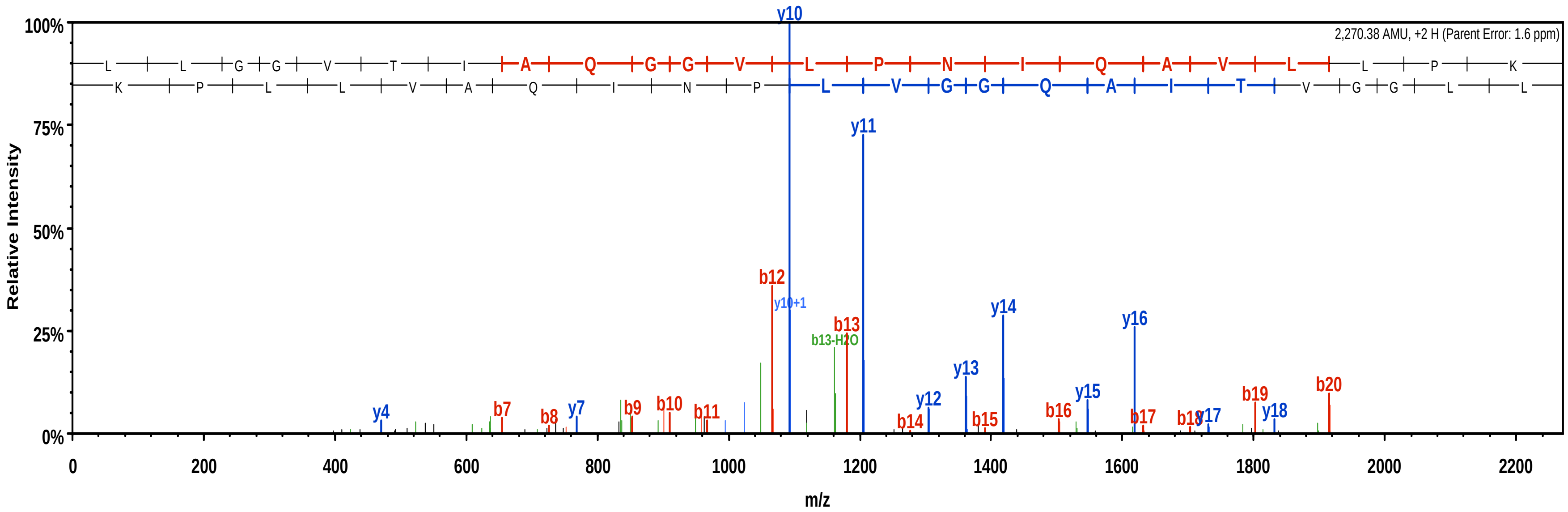


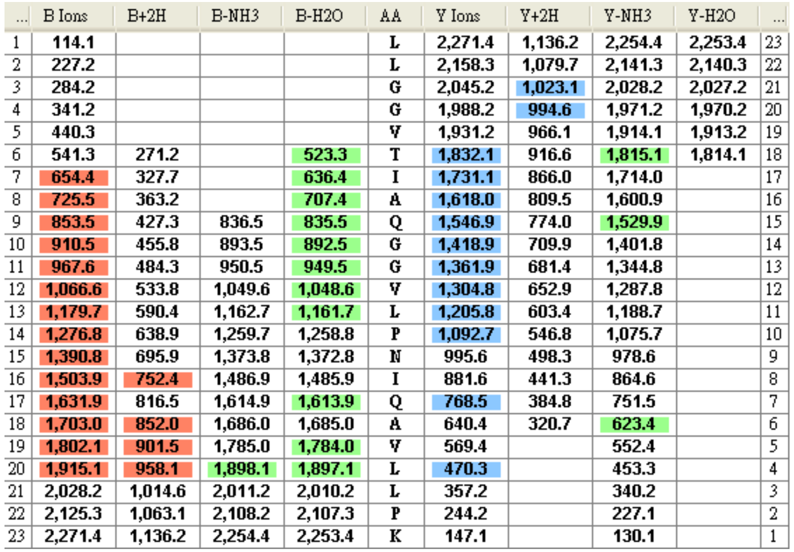


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	3,413.4	1,707.2	3,396.4	3,395.4	29
2	201.1			183.1	T	3,314.4	1,657.7	3,297.3	3,296.3	28
3	258.1			240.1	G	3,213.3	1,607.2	3,196.3	3,195.3	27
4	386.2		369.2	368.2	Q	3,156.3	1,578.6	3,139.3	3,138.3	26
5	546.2		529.2	528.2	C+57	3,028.2	1,514.6	3,011.2	3,010.2	25
6	706.3	353.6	689.2	688.3	C+57	2,868.2	1,434.6	2,851.2	2,850.2	24
7	835.3	418.2	818.3	817.3	E	2,708.2	1,354.6	2,691.1	2,690.2	23
8	964.3	482.7	947.3	946.3	E	2,579.1	1,290.1	2,562.1	2,561.1	22
9	1,150.4	575.7	1,133.4	1,132.4	W	2,450.1	1,225.5	2,433.1	2,432.1	21
10	1,249.5	625.3	1,232.5	1,231.5	V	2,264.0	1,132.5	2,247.0	2,246.0	20
11	1,409.5	705.3	1,392.5	1,391.5	C+57	2,164.9	1,083.0	2,147.9	2,146.9	19
12	1,524.6	762.8	1,507.5	1,506.5	D	2,004.9	1,003.0	1,987.9	1,986.9	18
13	1,653.6	827.3	1,636.6	1,635.6	E	1,889.9	945.4	1,872.9	1,871.9	17
14	1,768.6	884.8	1,751.6	1,750.6	D	1,760.8	880.9	1,743.8	1,742.8	16
15	1,855.7	928.3	1,838.6	1,837.6	S	1,645.8	823.4	1,628.8	1,627.8	15
16	1,968.7	984.9	1,951.7	1,950.7	I	1,558.8	779.9	1,541.8	1,540.8	14
17	2,096.8	1,048.9	2,079.8	2,078.8	K	1,445.7	723.4	1,428.7	1,427.7	13
18	2,211.9	1,106.4	2,194.8	2,193.9	D	1,317.6	659.3	1,300.6	1,299.6	12
19	2,308.9	1,155.0	2,291.9	2,290.9	P	1,202.6	601.8	1,185.5	1,184.6	11
20	2,440.0	1,220.5	2,422.9	2,421.9	M	1,105.5	553.3	1,088.5	1,087.5	10
21	2,569.0	1,285.0	2,552.0	2,551.0	E	974.5	487.7	957.5	956.5	9
22	2,684.0	1,342.5	2,667.0	2,666.0	D	845.4	423.2	828.4	827.4	8
23	2,812.1	1,406.5	2,795.1	2,794.1	Q	730.4	365.7	713.4	712.4	7
24	2,927.1	1,464.1	2,910.1	2,909.1	D	602.4	301.7	585.3	584.3	6
25	2,984.1	1,492.6	2,967.1	2,966.1	G	487.3		470.3		5
26	3,097.2	1,549.1	3,080.2	3,079.2	L	430.3		413.3		4
27	3,210.3	1,605.7	3,193.3	3,192.3	L	317.2		300.2		3
28	3,267.3	1,634.2	3,250.3	3,249.3	G	204.1		187.1		2
29	3,413.4	1,707.2	3,396.4	3,395.4	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-35	sp|P16104|H2AX_HUMAN	LLGGVTIAQGGVLPNIQAVLLPK	79.25	Unmodified	Light	2	1136.1936

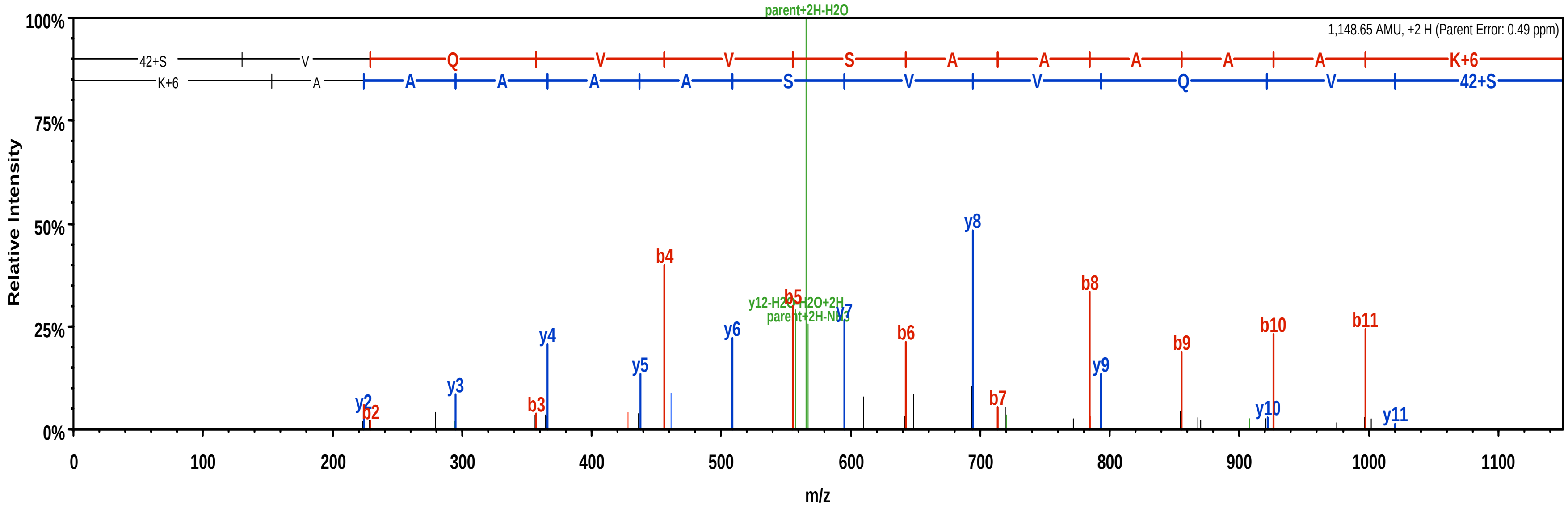


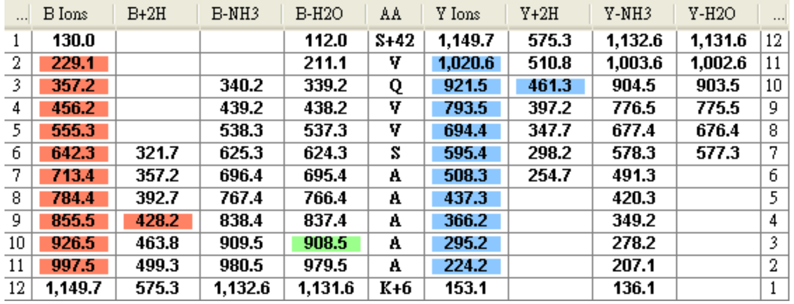


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	2,271.4	1,136.2	2,254.4	2,253.4	23
2	227.2				L	2,158.3	1,079.7	2,141.3	2,140.3	22
3	284.2				G	2,045.2	1,023.1	2,028.2	2,027.2	21
4	341.2				G	1,988.2	994.6	1,971.2	1,970.2	20
5	440.3				V	1,931.2	966.1	1,914.1	1,913.2	19
6	541.3	271.2		523.3	T	1,832.1	916.6	1,815.1	1,814.1	18
7	654.4	327.7		636.4	I	1,731.1	866.0	1,714.0		17
8	725.5	363.2		707.4	A	1,618.0	809.5	1,600.9		16
9	853.5	427.3	836.5	835.5	Q	1,546.9	774.0	1,529.9		15
10	910.5	455.8	893.5	892.5	G	1,418.9	709.9	1,401.8		14
11	967.6	484.3	950.5	949.5	G	1,361.9	681.4	1,344.8		13
12	1,066.6	533.8	1,049.6	1,048.6	V	1,304.8	652.9	1,287.8		12
13	1,179.7	590.4	1,162.7	1,161.7	L	1,205.8	603.4	1,188.7		11
14	1,276.8	638.9	1,259.7	1,258.8	P	1,092.7	546.8	1,075.7		10
15	1,390.8	695.9	1,373.8	1,372.8	N	995.6	498.3	978.6		9
16	1,503.9	752.4	1,486.9	1,485.9	I	881.6	441.3	864.6		8
17	1,631.9	816.5	1,614.9	1,613.9	Q	768.5	384.8	751.5		7
18	1,703.0	852.0	1,686.0	1,685.0	A	640.4	320.7	623.4		6
19	1,802.1	901.5	1,785.0	1,784.0	V	569.4		552.4		5
20	1,915.1	958.1	1,898.1	1,897.1	L	470.3		453.3		4
21	2,028.2	1,014.6	2,011.2	2,010.2	L	357.2		340.2		3
22	2,125.3	1,063.1	2,108.2	2,107.3	P	244.2		227.1		2
23	2,271.4	1,136.2	2,254.4	2,253.4	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-36	sp|Q96HN2|SAHH3_HUMAN	SVQVVSAAAAAK	78.3	Acetyl (Protein N-term)	Heavy	2	572.32205

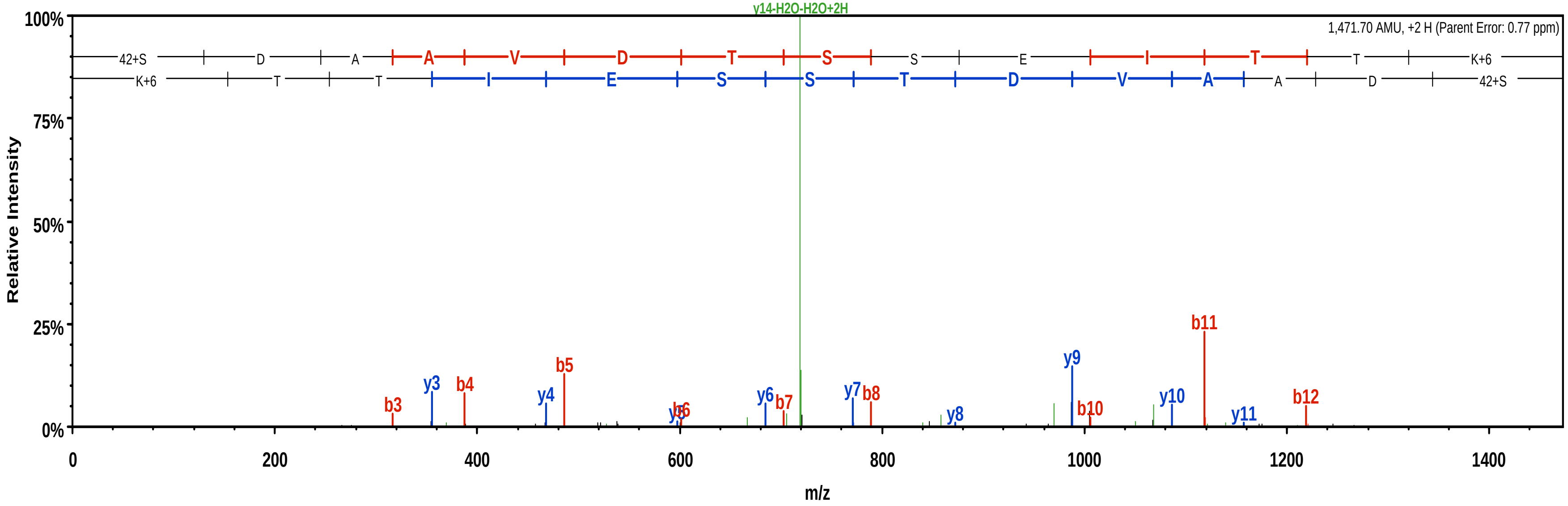


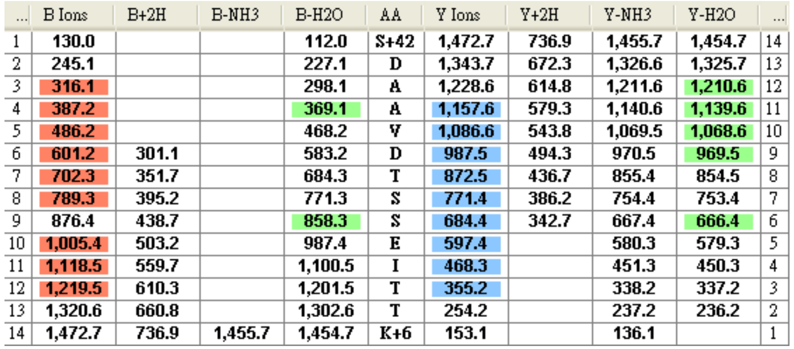


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	S+42	1,149.7	575.3	1,132.6	1,131.6	12
2	229.1			211.1	V	1,020.6	510.8	1,003.6	1,002.6	11
3	357.2		340.2	339.2	Q	921.5	461.3	904.5	903.5	10
4	456.2		439.2	438.2	V	793.5	397.2	776.5	775.5	9
5	555.3		538.3	537.3	V	694.4	347.7	677.4	676.4	8
6	642.3	321.7	625.3	624.3	S	595.4	298.2	578.3	577.3	7
7	713.4	357.2	696.4	695.4	A	508.3	254.7	491.3		6
8	784.4	392.7	767.4	766.4	A	437.3		420.3		5
9	855.5	428.2	838.4	837.4	A	366.2		349.2		4
10	926.5	463.8	909.5	908.5	A	295.2		278.2		3
11	997.5	499.3	980.5	979.5	A	224.2		207.1		2
12	1,149.7	575.3	1,132.6	1,131.6	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-37	sp|P06454|PTMA_HUMAN	SDAAVDTSSEITTK	77.07	Acetyl (Protein N-term)	Heavy	2	733.84648

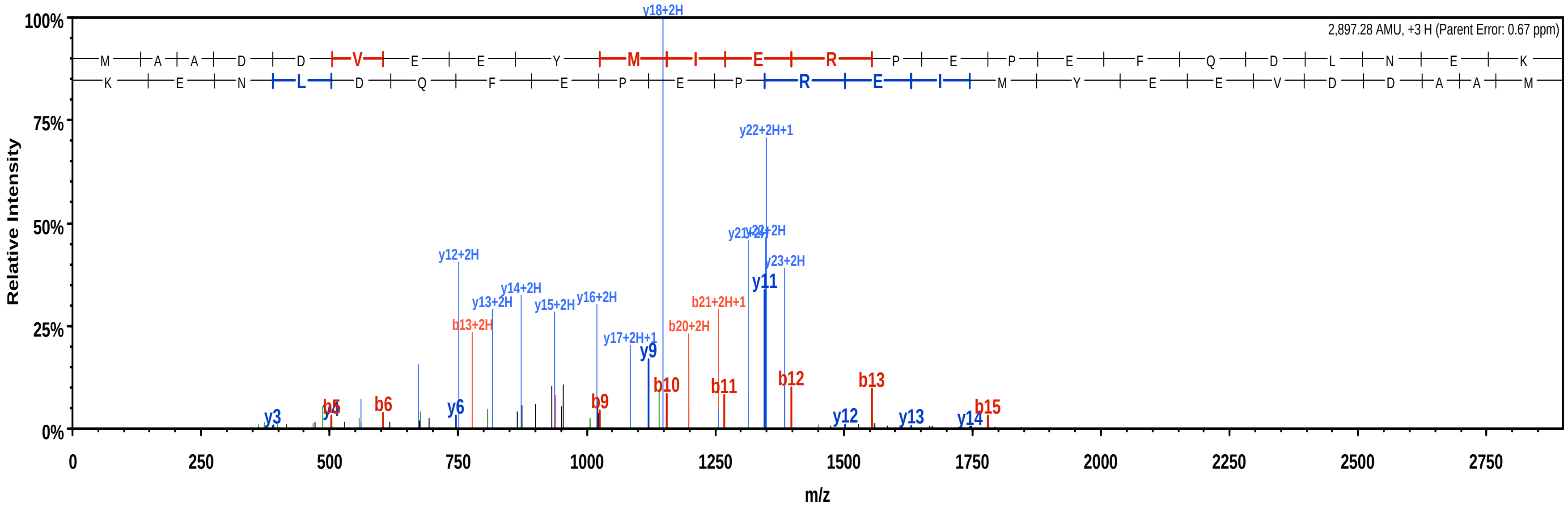


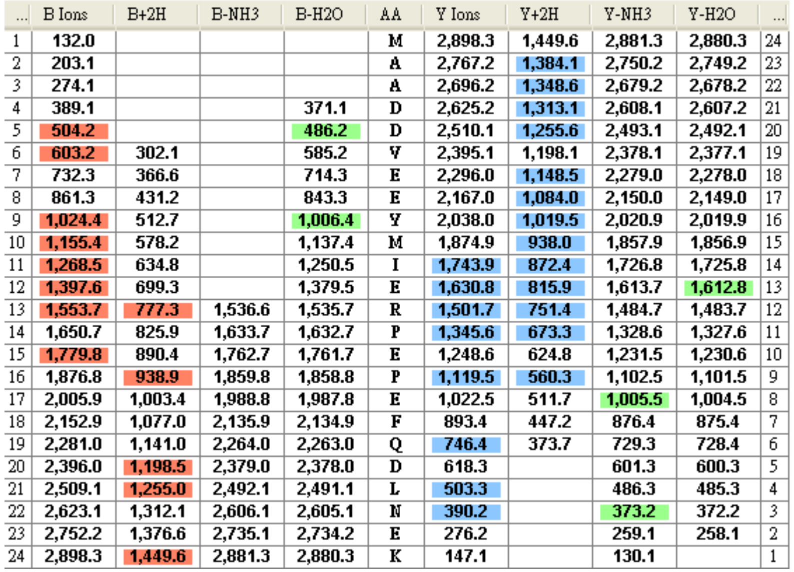


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	S+42	1,472.7	736.9	1,455.7	1,454.7	14
2	245.1			227.1	D	1,343.7	672.3	1,326.6	1,325.7	13
3	316.1			298.1	A	1,228.6	614.8	1,211.6	1,210.6	12
4	387.2			369.1	A	1,157.6	579.3	1,140.6	1,139.6	11
5	486.2			468.2	V	1,086.6	543.8	1,069.5	1,068.6	10
6	601.2	301.1		583.2	D	987.5	494.3	970.5	969.5	9
7	702.3	351.7		684.3	T	872.5	436.7	855.4	854.5	8
8	789.3	395.2		771.3	S	771.4	386.2	754.4	753.4	7
9	876.4	438.7		858.3	S	684.4	342.7	667.4	666.4	6
10	1,005.4	503.2		987.4	E	597.4		580.3	579.3	5
11	1,118.5	559.7		1,100.5	I	468.3		451.3	450.3	4
12	1,219.5	610.3		1,201.5	T	355.2		338.2	337.2	3
13	1,320.6	660.8		1,302.6	T	254.2		237.2	236.2	2
14	1,472.7	736.9	1,455.7	1,454.7	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-38	sp|Q9BUL8|PDC10_HUMAN	MAADDVEEYMIERPEPEFQDLNEK	75.95	Unmodified	Light	3	966.76512

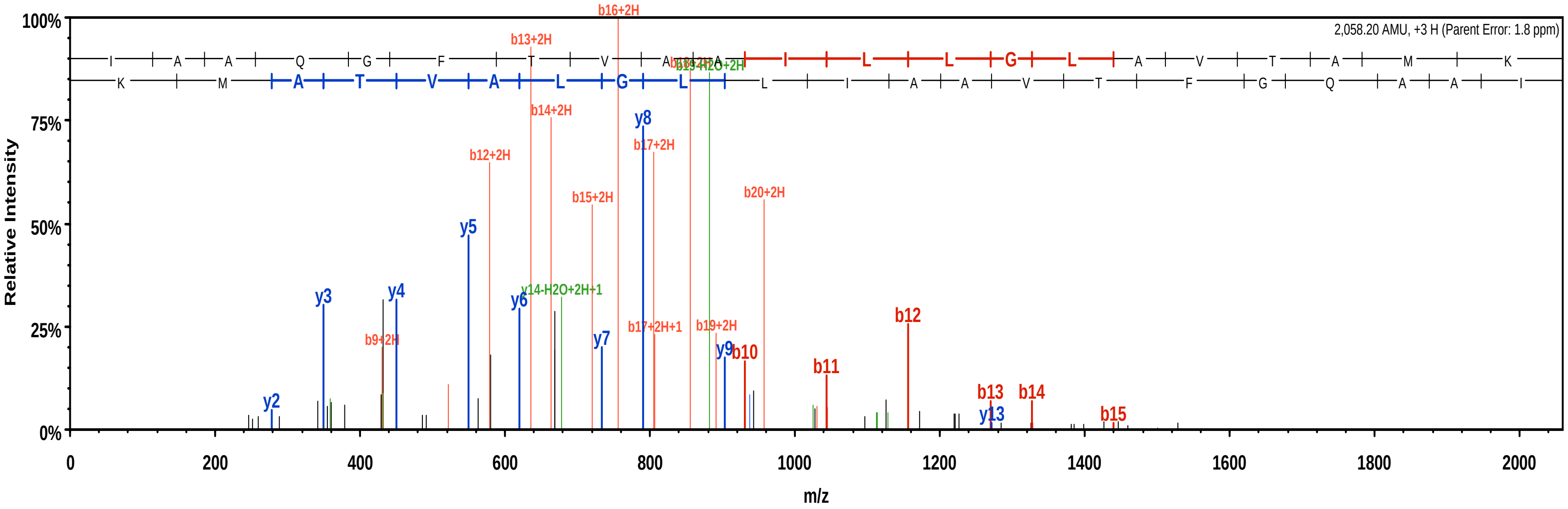


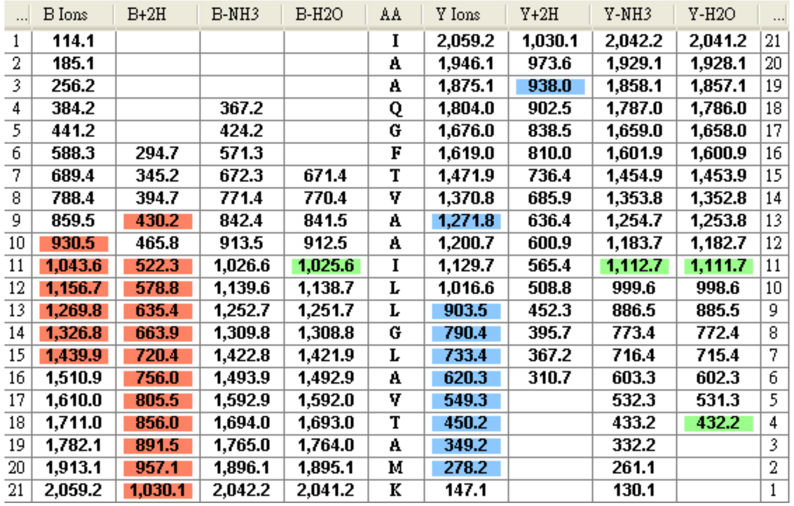


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	132.0				M	2,898.3	1,449.6	2,881.3	2,880.3	24
2	203.1				A	2,767.2	1,384.1	2,750.2	2,749.2	23
3	274.1				A	2,696.2	1,348.6	2,679.2	2,678.2	22
4	389.1			371.1	D	2,625.2	1,313.1	2,608.1	2,607.2	21
5	504.2			486.2	D	2,510.1	1,255.6	2,493.1	2,492.1	20
6	603.2	302.1		585.2	V	2,395.1	1,198.1	2,378.1	2,377.1	19
7	732.3	366.6		714.3	E	2,296.0	1,148.5	2,279.0	2,278.0	18
8	861.3	431.2		843.3	E	2,167.0	1,084.0	2,150.0	2,149.0	17
9	1,024.4	512.7		1,006.4	Y	2,038.0	1,019.5	2,020.9	2,019.9	16
10	1,155.4	578.2		1,137.4	M	1,874.9	938.0	1,857.9	1,856.9	15
11	1,268.5	634.8		1,250.5	I	1,743.9	872.4	1,726.8	1,725.8	14
12	1,397.6	699.3		1,379.5	E	1,630.8	815.9	1,613.7	1,612.8	13
13	1,553.7	777.3	1,536.6	1,535.7	R	1,501.7	751.4	1,484.7	1,483.7	12
14	1,650.7	825.9	1,633.7	1,632.7	P	1,345.6	673.3	1,328.6	1,327.6	11
15	1,779.8	890.4	1,762.7	1,761.7	E	1,248.6	624.8	1,231.5	1,230.6	10
16	1,876.8	938.9	1,859.8	1,858.8	P	1,119.5	560.3	1,102.5	1,101.5	9
17	2,005.9	1,003.4	1,988.8	1,987.8	E	1,022.5	511.7	1,005.5	1,004.5	8
18	2,152.9	1,077.0	2,135.9	2,134.9	F	893.4	447.2	876.4	875.4	7
19	2,281.0	1,141.0	2,264.0	2,263.0	Q	746.4	373.7	729.3	728.4	6
20	2,396.0	1,198.5	2,379.0	2,378.0	D	618.3		601.3	600.3	5
21	2,509.1	1,255.0	2,492.1	2,491.1	L	503.3		486.3	485.3	4
22	2,623.1	1,312.1	2,606.1	2,605.1	N	390.2		373.2	372.2	3
23	2,752.2	1,376.6	2,735.1	2,734.2	E	276.2		259.1	258.1	2
24	2,898.3	1,449.6	2,881.3	2,880.3	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-39	sp|Q9BW72|HIG2A_HUMAN	IAAQGFTVAAILLGLAVTAMK	72.8	Unmodified	Light	3	687.07098

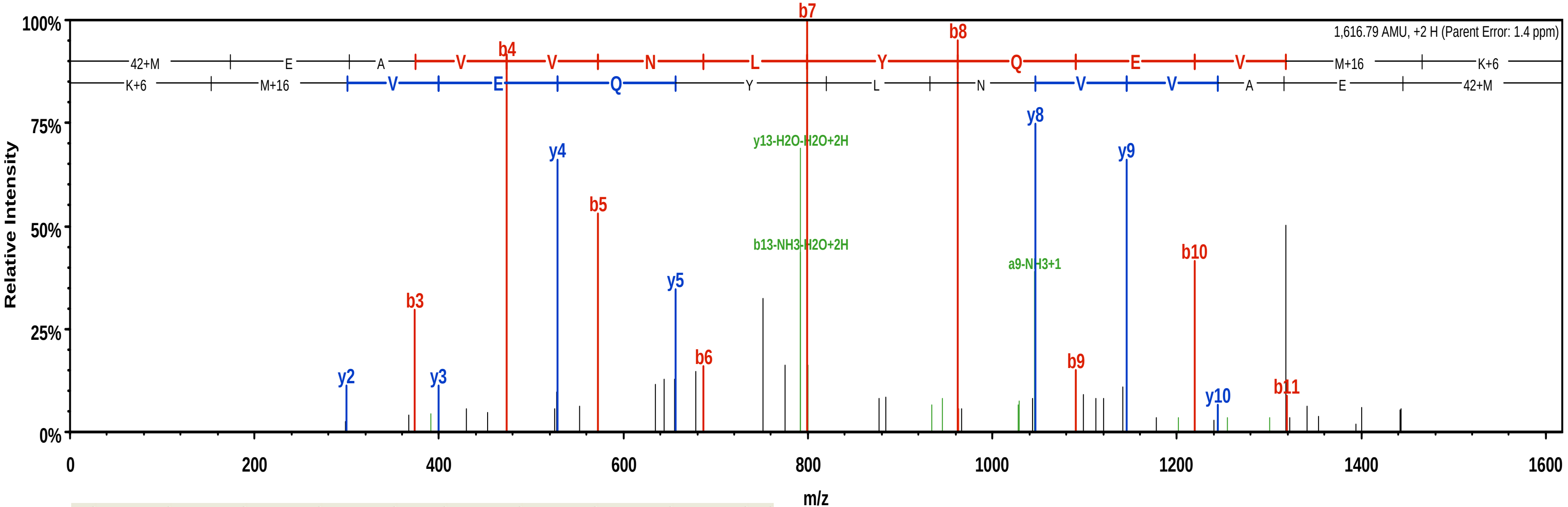


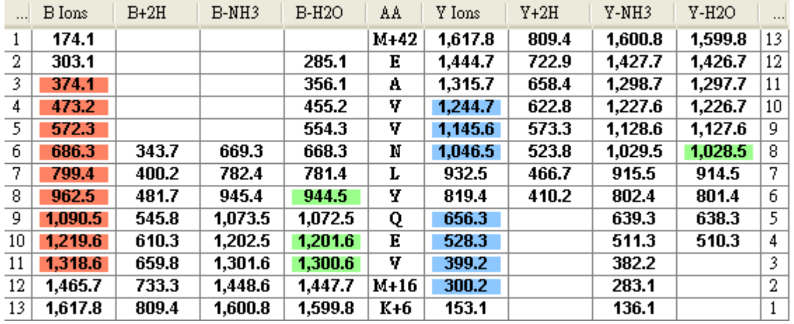


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	2,059.2	1,030.1	2,042.2	2,041.2	21
2	185.1				A	1,946.1	973.6	1,929.1	1,928.1	20
3	256.2				A	1,875.1	938.0	1,858.1	1,857.1	19
4	384.2		367.2		Q	1,804.0	902.5	1,787.0	1,786.0	18
5	441.2		424.2		G	1,676.0	838.5	1,659.0	1,658.0	17
6	588.3	294.7	571.3		F	1,619.0	810.0	1,601.9	1,600.9	16
7	689.4	345.2	672.3	671.4	T	1,471.9	736.4	1,454.9	1,453.9	15
8	788.4	394.7	771.4	770.4	V	1,370.8	685.9	1,353.8	1,352.8	14
9	859.5	430.2	842.4	841.5	A	1,271.8	636.4	1,254.7	1,253.8	13
10	930.5	465.8	913.5	912.5	A	1,200.7	600.9	1,183.7	1,182.7	12
11	1,043.6	522.3	1,026.6	1,025.6	I	1,129.7	565.4	1,112.7	1,111.7	11
12	1,156.7	578.8	1,139.6	1,138.7	L	1,016.6	508.8	999.6	998.6	10
13	1,269.8	635.4	1,252.7	1,251.7	L	903.5	452.3	886.5	885.5	9
14	1,326.8	663.9	1,309.8	1,308.8	G	790.4	395.7	773.4	772.4	8
15	1,439.9	720.4	1,422.8	1,421.9	L	733.4	367.2	716.4	715.4	7
16	1,510.9	756.0	1,493.9	1,492.9	A	620.3	310.7	603.3	602.3	6
17	1,610.0	805.5	1,592.9	1,592.0	V	549.3		532.3	531.3	5
18	1,711.0	856.0	1,694.0	1,693.0	T	450.2		433.2	432.2	4
19	1,782.1	891.5	1,765.0	1,764.0	A	349.2		332.2		3
20	1,913.1	957.1	1,896.1	1,895.1	M	278.2		261.1		2
21	2,059.2	1,030.1	2,042.2	2,041.2	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-40	splQ9BW60lELOV1_HUMAN	MEAVVNLYQEVMK	71.14	Acetyl (Protein N-term),Oxidation (M)	Heavy	2	806.39148

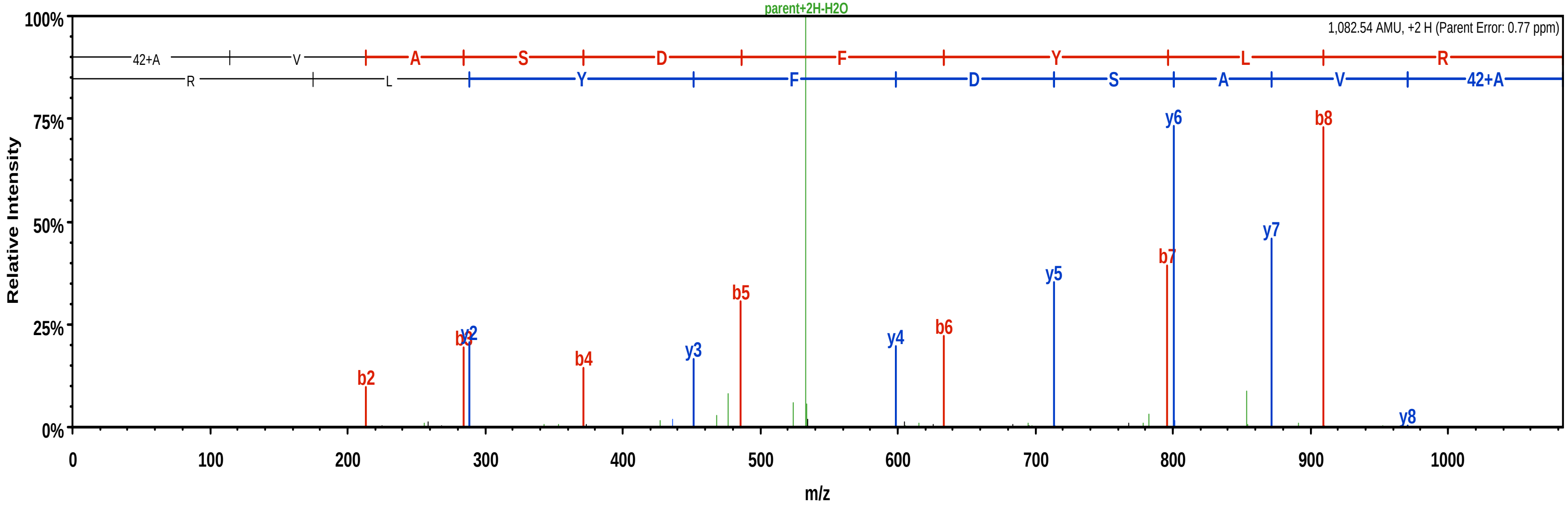


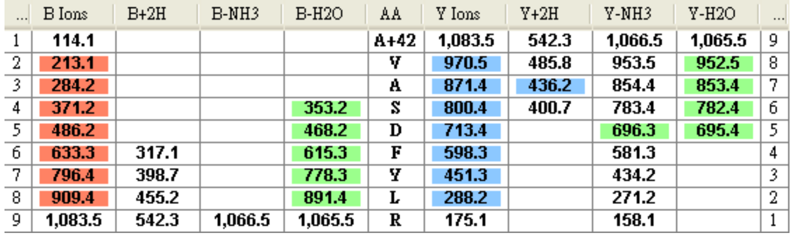


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	174.1				M+42	1,617.8	809.4	1,600.8	1,599.8	13
2	303.1			285.1	E	1,444.7	722.9	1,427.7	1,426.7	12
3	374.1			356.1	A	1,315.7	658.4	1,298.7	1,297.7	11
4	473.2			455.2	V	1,244.7	622.8	1,227.6	1,226.7	10
5	572.3			554.3	V	1,145.6	573.3	1,128.6	1,127.6	9
6	686.3	343.7	669.3	668.3	N	1,046.5	523.8	1,029.5	1,028.5	8
7	799.4	400.2	782.4	781.4	L	932.5	466.7	915.5	914.5	7
8	962.5	481.7	945.4	944.5	Y	819.4	410.2	802.4	801.4	6
9	1,090.5	545.8	1,073.5	1,072.5	Q	656.3		639.3	638.3	5
10	1,219.6	610.3	1,202.5	1,201.6	E	528.3		511.3	510.3	4
11	1,318.6	659.8	1,301.6	1,300.6	V	399.2		382.2		3
12	1,465.7	733.3	1,448.6	1,447.7	M+16	300.2		283.1		2
13	1,617.8	809.4	1,600.8	1,599.8	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-41	sp|Q96A72|MGN2_HUMAN	AVASDFYLR	71.04	Acetyl (Protein N-term)		2	542.27711

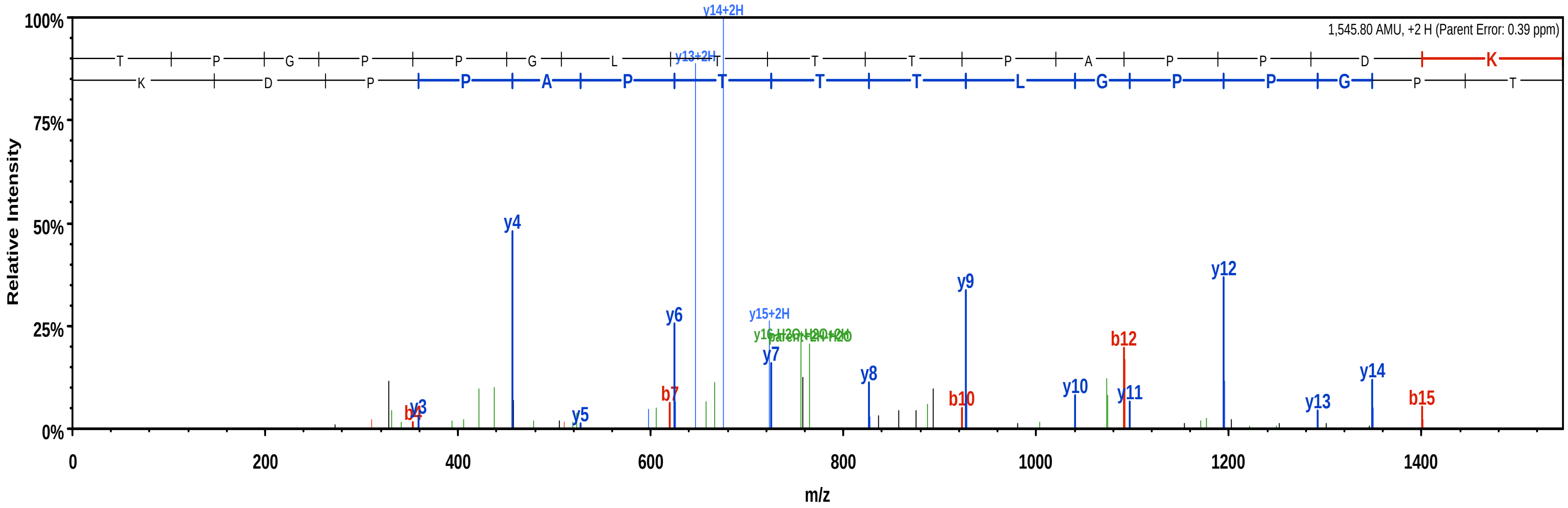


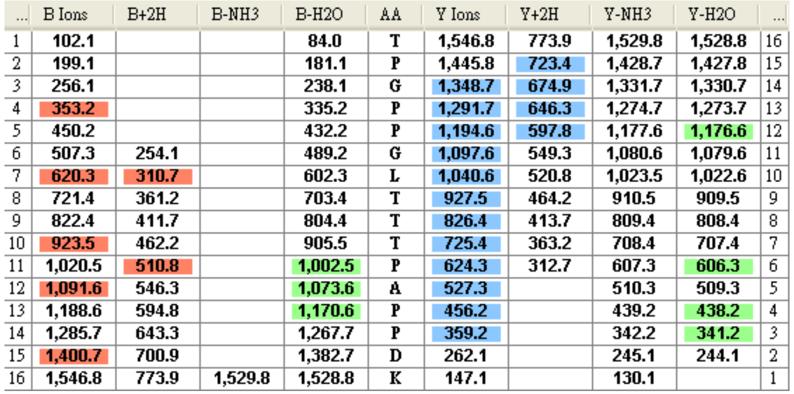


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	1,083.5	542.3	1,066.5	1,065.5	9
2	213.1				V	970.5	485.8	953.5	952.5	8
3	284.2				A	871.4	436.2	854.4	853.4	7
4	371.2			353.2	S	800.4	400.7	783.4	782.4	6
5	486.2			468.2	D	713.4		696.3	695.4	5
6	633.3	317.1		615.3	F	598.3		581.3		4
7	796.4	398.7		778.3	Y	451.3		434.2		3
8	909.4	455.2		891.4	L	288.2		271.2		2
9	1,083.5	542.3	1,066.5	1,065.5	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-42	sp|Q7Z5J4|RAI1_HUMAN	TPGPPGLTTTPAPPDK	70.89	Unmodified	Light	2	773.90921

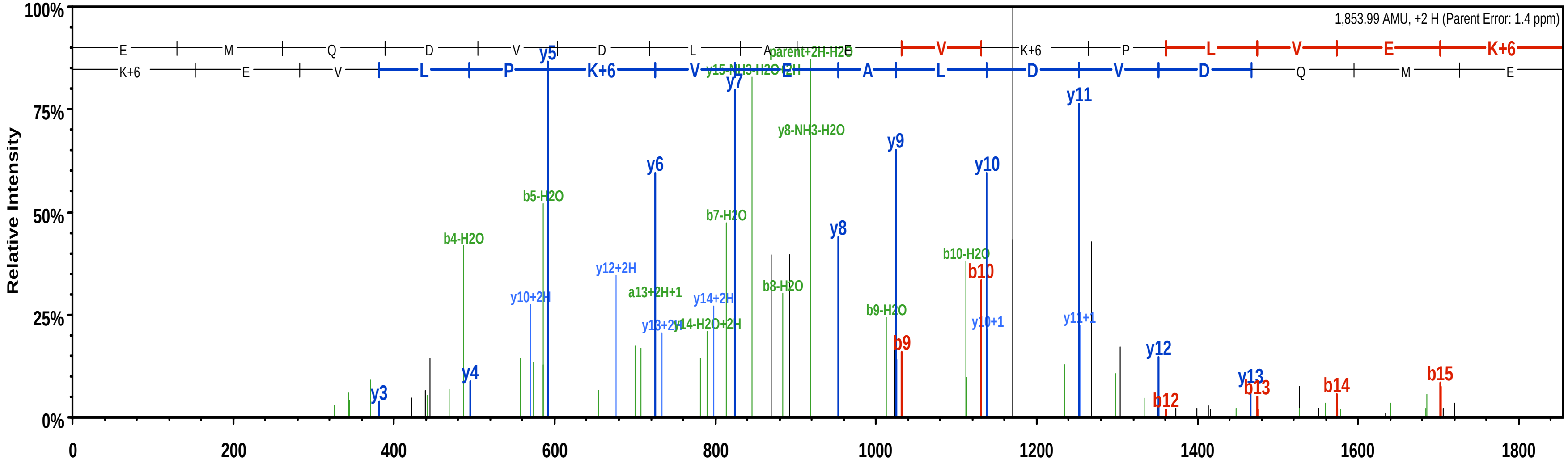


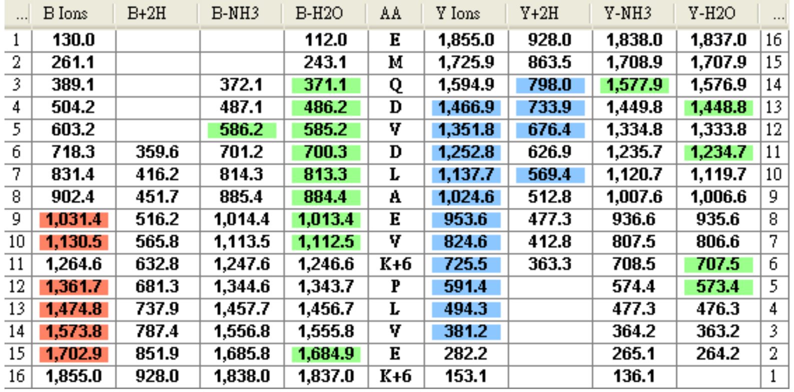


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	102.1			84.0	T	1,546.8	773.9	1,529.8	1,528.8	16
2	199.1			181.1	P	1,445.8	723.4	1,428.7	1,427.8	15
3	256.1			238.1	G	1,348.7	674.9	1,331.7	1,330.7	14
4	353.2			335.2	P	1,291.7	646.3	1,274.7	1,273.7	13
5	450.2			432.2	P	1,194.6	597.8	1,177.6	1,176.6	12
6	507.3	254.1		489.2	G	1,097.6	549.3	1,080.6	1,079.6	11
7	620.3	310.7		602.3	L	1,040.6	520.8	1,023.5	1,022.6	10
8	721.4	361.2		703.4	T	927.5	464.2	910.5	909.5	9
9	822.4	411.7		804.4	T	826.4	413.7	809.4	808.4	8
10	923.5	462.2		905.5	T	725.4	363.2	708.4	707.4	7
11	1,020.5	510.8		1,002.5	P	624.3	312.7	607.3	606.3	6
12	1,091.6	546.3		1,073.6	A	527.3		510.3	509.3	5
13	1,188.6	594.8		1,170.6	P	456.2		439.2	438.2	4
14	1,285.7	643.3		1,267.7	P	359.2		342.2	341.2	3
15	1,400.7	700.9		1,382.7	D	262.1		245.1	244.1	2
16	1,546.8	773.9	1,529.8	1,528.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-43	splQ92597lNDRG1_HUMAN	EMQDVDLAEVKPLVEK	69.48	Unmodified	Heavy	2	921.97951

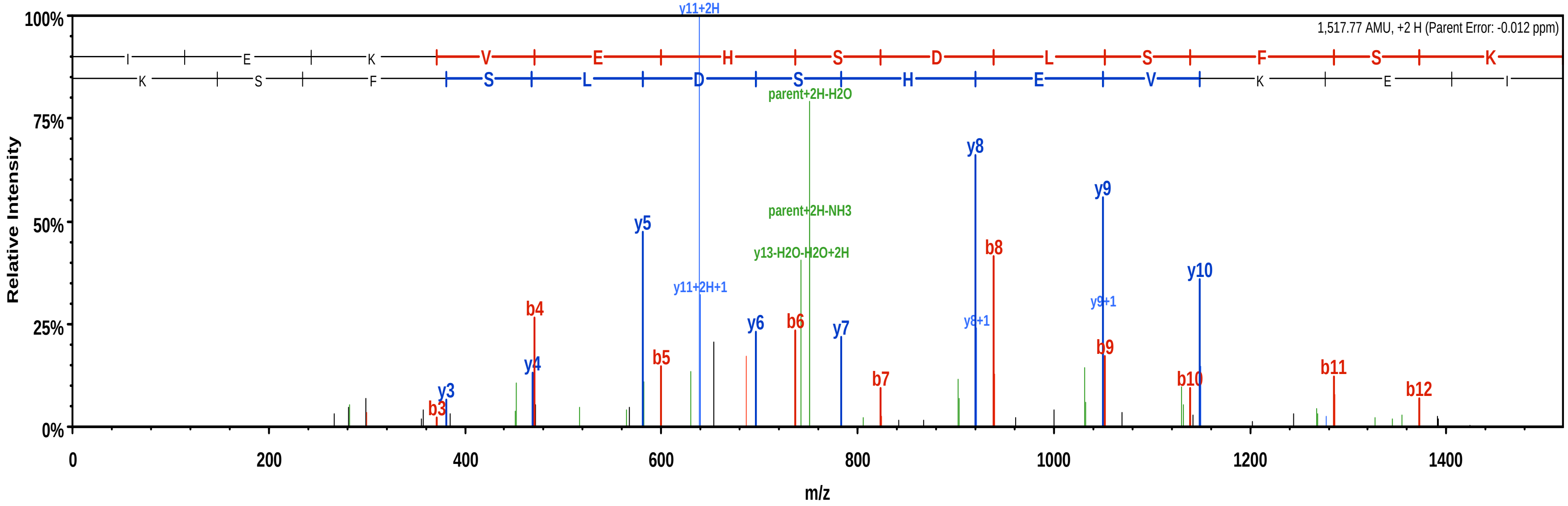


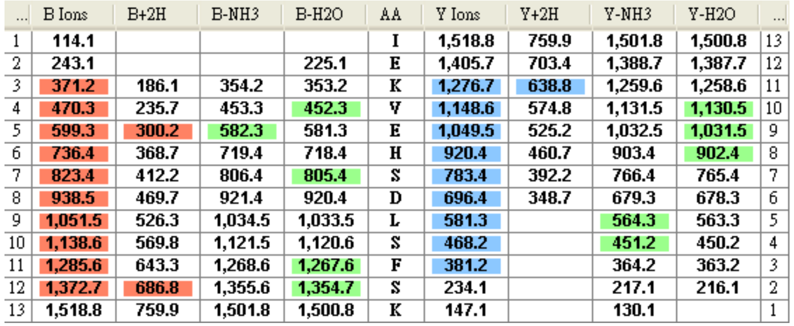


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	1,855.0	928.0	1,838.0	1,837.0	16
2	261.1			243.1	M	1,725.9	863.5	1,708.9	1,707.9	15
3	389.1		372.1	371.1	Q	1,594.9	798.0	1,577.9	1,576.9	14
4	504.2		487.1	486.2	D	1,466.9	733.9	1,449.8	1,448.8	13
5	603.2		586.2	585.2	V	1,351.8	676.4	1,334.8	1,333.8	12
6	718.3	359.6	701.2	700.3	D	1,252.8	626.9	1,235.7	1,234.7	11
7	831.4	416.2	814.3	813.3	L	1,137.7	569.4	1,120.7	1,119.7	10
8	902.4	451.7	885.4	884.4	A	1,024.6	512.8	1,007.6	1,006.6	9
9	1,031.4	516.2	1,014.4	1,013.4	E	953.6	477.3	936.6	935.6	8
10	1,130.5	565.8	1,113.5	1,112.5	V	824.6	412.8	807.5	806.6	7
11	1,264.6	632.8	1,247.6	1,246.6	K+6	725.5	363.3	708.5	707.5	6
12	1,361.7	681.3	1,344.6	1,343.7	P	591.4		574.4	573.4	5
13	1,474.8	737.9	1,457.7	1,456.7	L	494.3		477.3	476.3	4
14	1,573.8	787.4	1,556.8	1,555.8	V	381.2		364.2	363.2	3
15	1,702.9	851.9	1,685.8	1,684.9	E	282.2		265.1	264.2	2
16	1,855.0	928.0	1,838.0	1,837.0	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-44	sp|P61769|B2MG_HUMAN	IEKVEHSDLSFSK	69.32	Unmodified	Light	2	759.89356

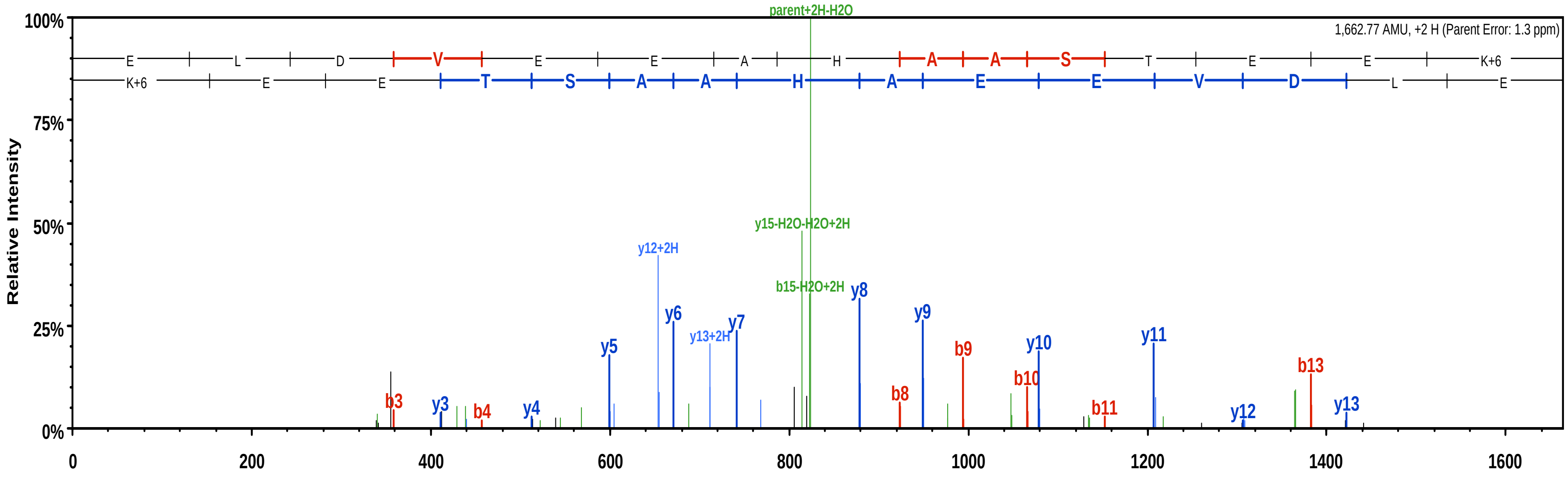


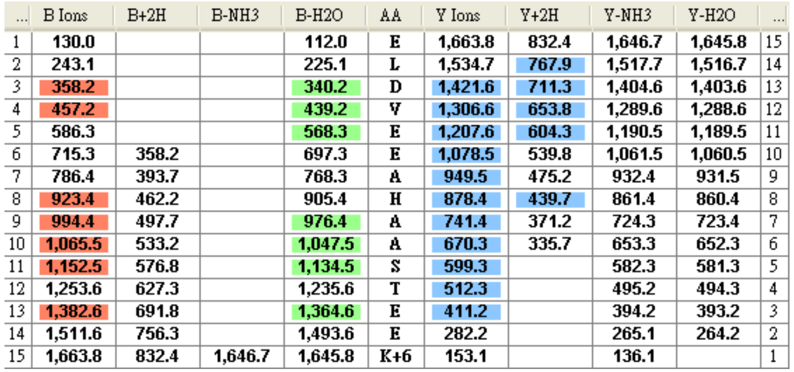


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	1,518.8	759.9	1,501.8	1,500.8	13
2	243.1			225.1	E	1,405.7	703.4	1,388.7	1,387.7	12
3	371.2	186.1	354.2	353.2	K	1,276.7	638.8	1,259.6	1,258.6	11
4	470.3	235.7	453.3	452.3	V	1,148.6	574.8	1,131.5	1,130.5	10
5	599.3	300.2	582.3	581.3	E	1,049.5	525.2	1,032.5	1,031.5	9
6	736.4	368.7	719.4	718.4	H	920.4	460.7	903.4	902.4	8
7	823.4	412.2	806.4	805.4	S	783.4	392.2	766.4	765.4	7
8	938.5	469.7	921.4	920.4	D	696.4	348.7	679.3	678.3	6
9	1,051.5	526.3	1,034.5	1,033.5	L	581.3		564.3	563.3	5
10	1,138.6	569.8	1,121.5	1,120.6	S	468.2		451.2	450.2	4
11	1,285.6	643.3	1,268.6	1,267.6	F	381.2		364.2	363.2	3
12	1,372.7	686.8	1,355.6	1,354.7	S	234.1		217.1	216.1	2
13	1,518.8	759.9	1,501.8	1,500.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-45	sp|Q96C86|DCPS_HUMAN	ELDVEEAHAASTEEK	69.21	Unmodified	Heavy	2	829.38121

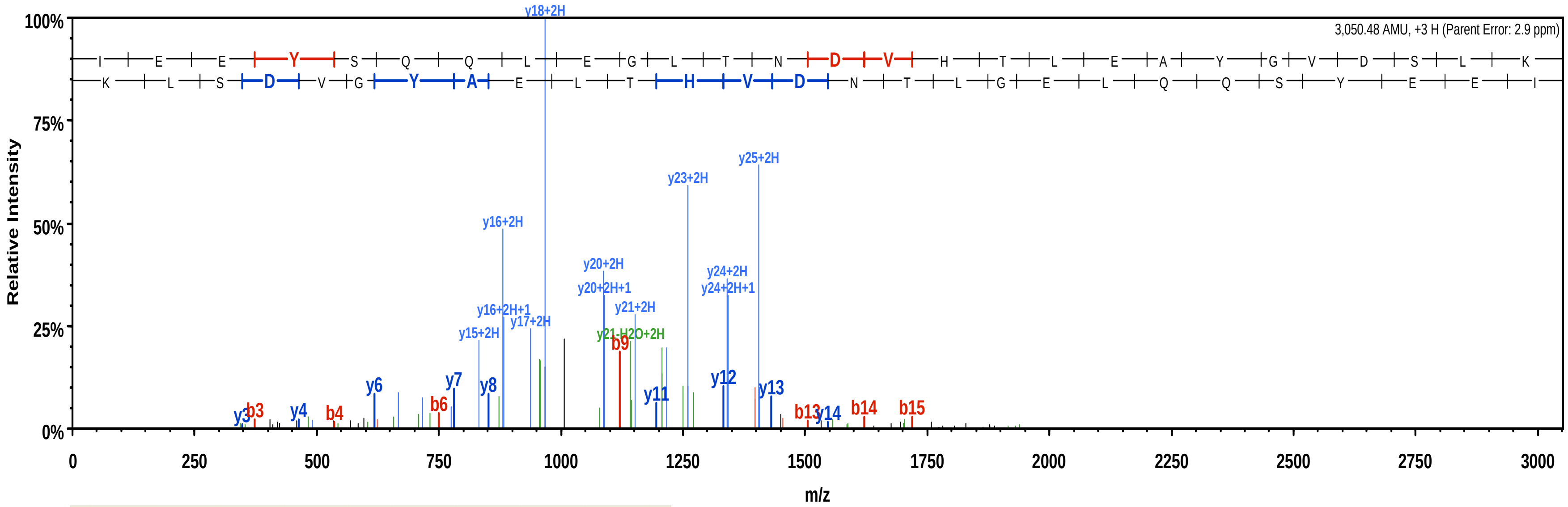


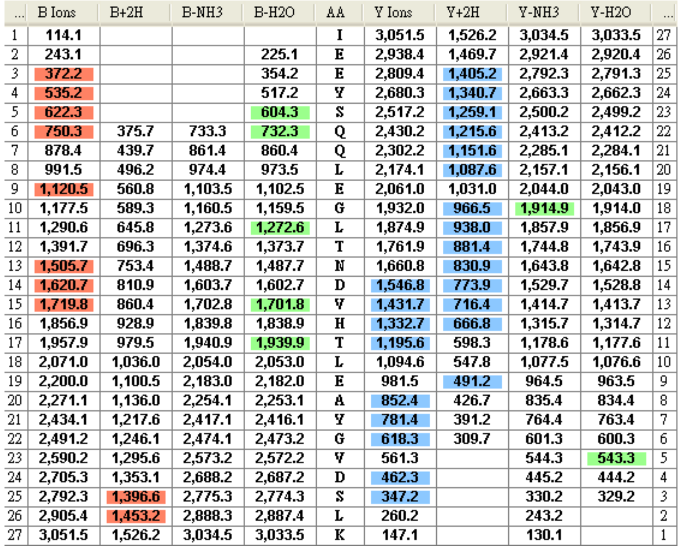


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	1,663.8	832.4	1,646.7	1,645.8	15
2	243.1			225.1	L	1,534.7	767.9	1,517.7	1,516.7	14
3	358.2			340.2	D	1,421.6	711.3	1,404.6	1,403.6	13
4	457.2			439.2	V	1,306.6	653.8	1,289.6	1,288.6	12
5	586.3			568.3	E	1,207.6	604.3	1,190.5	1,189.5	11
6	715.3	358.2		697.3	E	1,078.5	539.8	1,061.5	1,060.5	10
7	786.4	393.7		768.3	A	949.5	475.2	932.4	931.5	9
8	923.4	462.2		905.4	H	878.4	439.7	861.4	860.4	8
9	994.4	497.7		976.4	A	741.4	371.2	724.3	723.4	7
10	1,065.5	533.2		1,047.5	A	670.3	335.7	653.3	652.3	6
11	1,152.5	576.8		1,134.5	S	599.3		582.3	581.3	5
12	1,253.6	627.3		1,235.6	T	512.3		495.2	494.3	4
13	1,382.6	691.8		1,364.6	E	411.2		394.2	393.2	3
14	1,511.6	756.3		1,493.6	E	282.2		265.1	264.2	2
15	1,663.8	832.4	1,646.7	1,645.8	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-46	sp|Q9NZJ4|SACS_HUMAN	IEEYSQQLEGLTNDVHTLEAYGVDSLK	68.97	Unmodified	Light	3	1017.8313

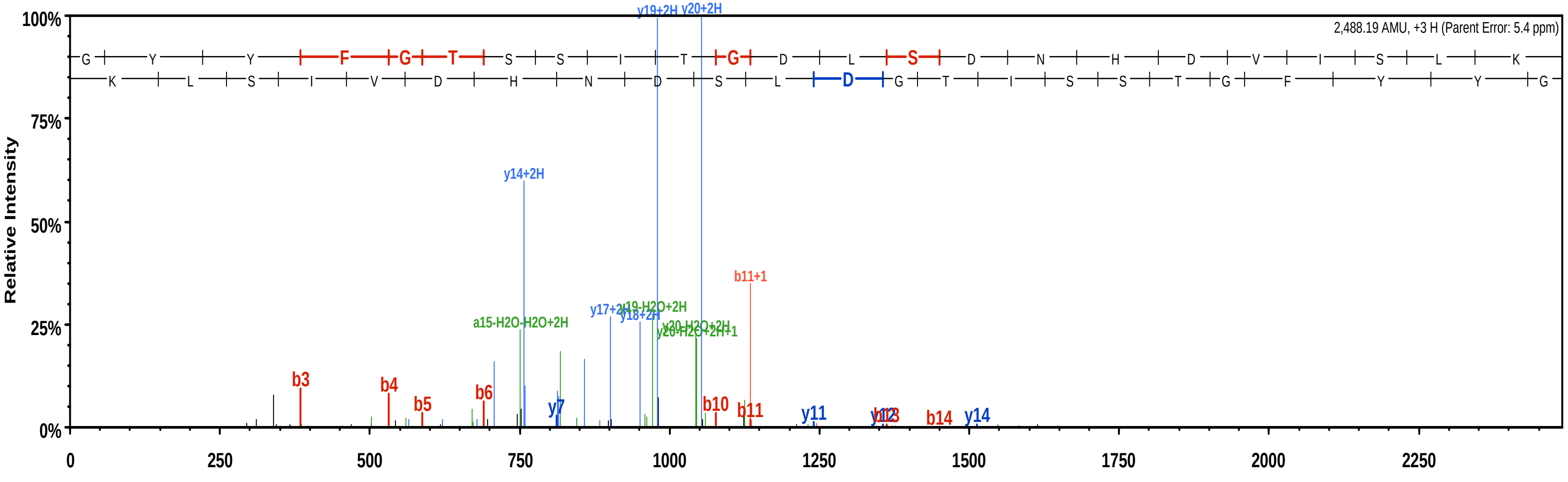


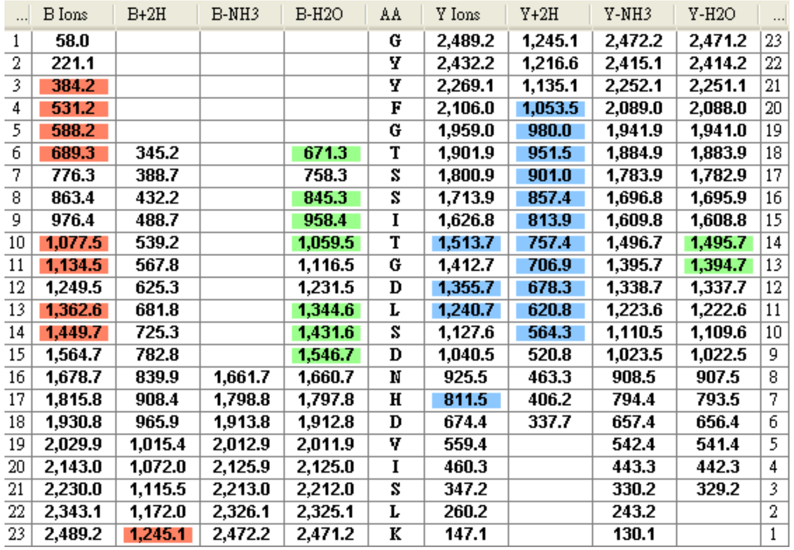


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	3,051.5	1,526.2	3,034.5	3,033.5	27
2	243.1			225.1	E	2,938.4	1,469.7	2,921.4	2,920.4	26
3	372.2			354.2	E	2,809.4	1,405.2	2,792.3	2,791.3	25
4	535.2			517.2	Y	2,680.3	1,340.7	2,663.3	2,662.3	24
5	622.3			604.3	S	2,517.2	1,259.1	2,500.2	2,499.2	23
6	750.3	375.7	733.3	732.3	Q	2,430.2	1,215.6	2,413.2	2,412.2	22
7	878.4	439.7	861.4	860.4	Q	2,302.2	1,151.6	2,285.1	2,284.1	21
8	991.5	496.2	974.4	973.5	L	2,174.1	1,087.6	2,157.1	2,156.1	20
9	1,120.5	560.8	1,103.5	1,102.5	E	2,061.0	1,031.0	2,044.0	2,043.0	19
10	1,177.5	589.3	1,160.5	1,159.5	G	1,932.0	966.5	1,914.9	1,914.0	18
11	1,290.6	645.8	1,273.6	1,272.6	L	1,874.9	938.0	1,857.9	1,856.9	17
12	1,391.7	696.3	1,374.6	1,373.7	T	1,761.9	881.4	1,744.8	1,743.9	16
13	1,505.7	753.4	1,488.7	1,487.7	N	1,660.8	830.9	1,643.8	1,642.8	15
14	1,620.7	810.9	1,603.7	1,602.7	D	1,546.8	773.9	1,529.7	1,528.8	14
15	1,719.8	860.4	1,702.8	1,701.8	V	1,431.7	716.4	1,414.7	1,413.7	13
16	1,856.9	928.9	1,839.8	1,838.9	H	1,332.7	666.8	1,315.7	1,314.7	12
17	1,957.9	979.5	1,940.9	1,939.9	T	1,195.6	598.3	1,178.6	1,177.6	11
18	2,071.0	1,036.0	2,054.0	2,053.0	L	1,094.6	547.8	1,077.5	1,076.6	10
19	2,200.0	1,100.5	2,183.0	2,182.0	E	981.5	491.2	964.5	963.5	9
20	2,271.1	1,136.0	2,254.1	2,253.1	A	852.4	426.7	835.4	834.4	8
21	2,434.1	1,217.6	2,417.1	2,416.1	Y	781.4	391.2	764.4	763.4	7
22	2,491.2	1,246.1	2,474.1	2,473.2	G	618.3	309.7	601.3	600.3	6
23	2,590.2	1,295.6	2,573.2	2,572.2	V	561.3		544.3	543.3	5
24	2,705.3	1,353.1	2,688.2	2,687.2	D	462.3		445.2	444.2	4
25	2,792.3	1,396.6	2,775.3	2,774.3	S	347.2		330.2	329.2	3
26	2,905.4	1,453.2	2,888.3	2,887.4	L	260.2		243.2		2
27	3,051.5	1,526.2	3,034.5	3,033.5	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-47	sp|Q9H0V9|LMA2L_HUMAN	GYYFGTSSITGDLSDNHDVISLK	67.58	Unmodified	Light	3	830.39921

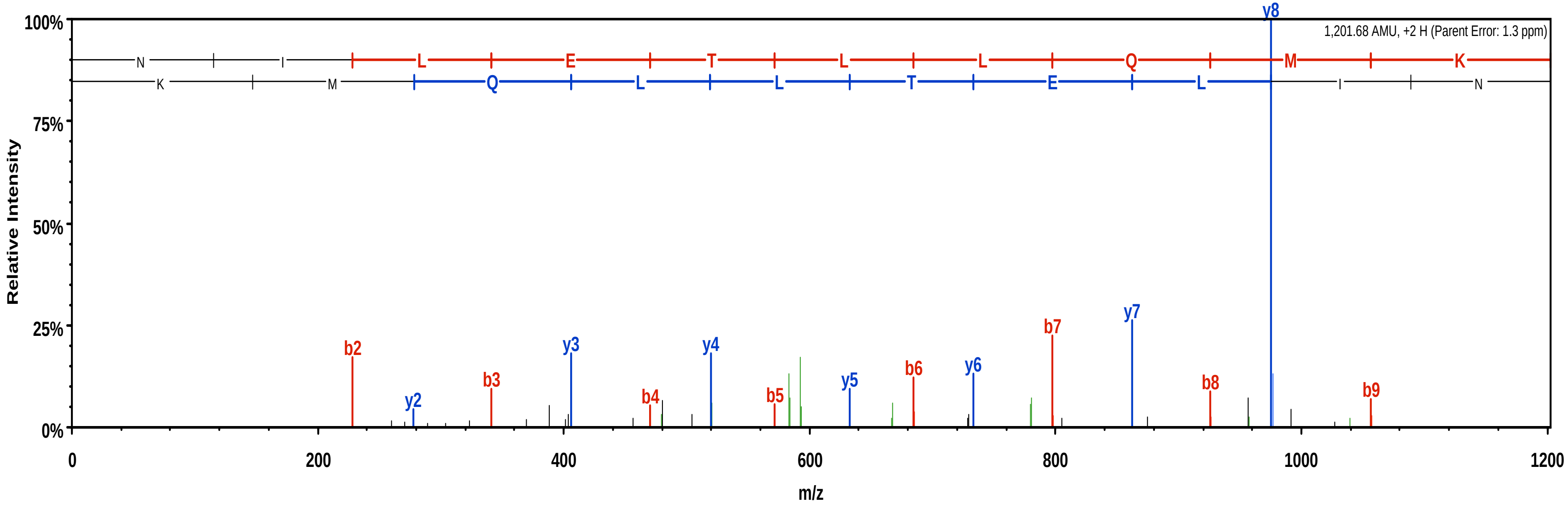


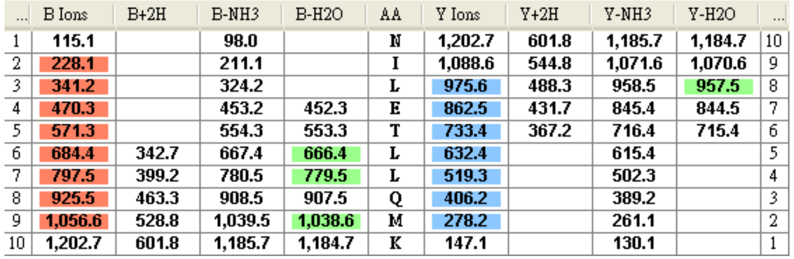


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	2,489.2	1,245.1	2,472.2	2,471.2	23
2	221.1				Y	2,432.2	1,216.6	2,415.1	2,414.2	22
3	384.2				Y	2,269.1	1,135.1	2,252.1	2,251.1	21
4	531.2				F	2,106.0	1,053.5	2,089.0	2,088.0	20
5	588.2				G	1,959.0	980.0	1,941.9	1,941.0	19
6	689.3	345.2		671.3	T	1,901.9	951.5	1,884.9	1,883.9	18
7	776.3	388.7		758.3	S	1,800.9	901.0	1,783.9	1,782.9	17
8	863.4	432.2		845.3	S	1,713.9	857.4	1,696.8	1,695.9	16
9	976.4	488.7		958.4	I	1,626.8	813.9	1,609.8	1,608.8	15
10	1,077.5	539.2		1,059.5	T	1,513.7	757.4	1,496.7	1,495.7	14
11	1,134.5	567.8		1,116.5	G	1,412.7	706.9	1,395.7	1,394.7	13
12	1,249.5	625.3		1,231.5	D	1,355.7	678.3	1,338.7	1,337.7	12
13	1,362.6	681.8		1,344.6	L	1,240.7	620.8	1,223.6	1,222.6	11
14	1,449.7	725.3		1,431.6	S	1,127.6	564.3	1,110.5	1,109.6	10
15	1,564.7	782.8		1,546.7	D	1,040.5	520.8	1,023.5	1,022.5	9
16	1,678.7	839.9	1,661.7	1,660.7	N	925.5	463.3	908.5	907.5	8
17	1,815.8	908.4	1,798.8	1,797.8	H	811.5	406.2	794.4	793.5	7
18	1,930.8	965.9	1,913.8	1,912.8	D	674.4	337.7	657.4	656.4	6
19	2,029.9	1,015.4	2,012.9	2,011.9	V	559.4		542.4	541.4	5
20	2,143.0	1,072.0	2,125.9	2,125.0	I	460.3		443.3	442.3	4
21	2,230.0	1,115.5	2,213.0	2,212.0	S	347.2		330.2	329.2	3
22	2,343.1	1,172.0	2,326.1	2,325.1	L	260.2		243.2		2
23	2,489.2	1,245.1	2,472.2	2,471.2	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-48	sp|P82673|RT35_HUMAN	NILETLLQMK	66.82	Unmodified	Light	2	601.8443

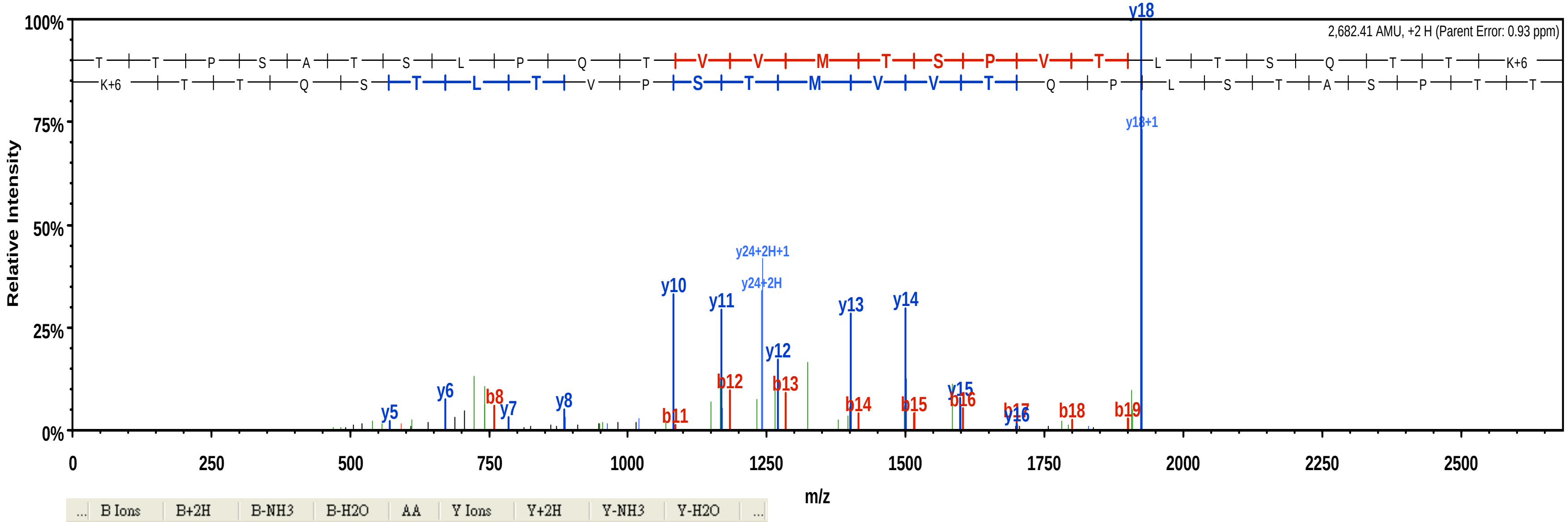


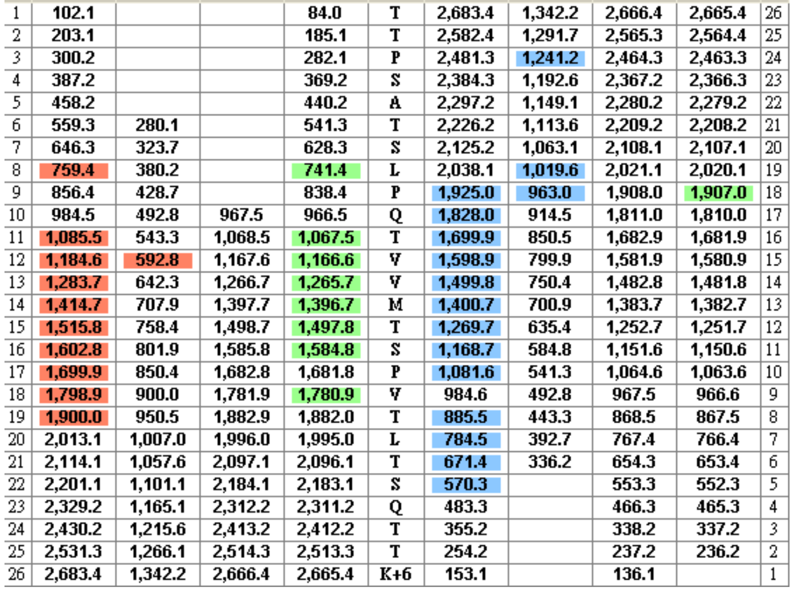


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	115.1		98.0		N	1,202.7	601.8	1,185.7	1,184.7	10
2	228.1		211.1		I	1,088.6	544.8	1,071.6	1,070.6	9
3	341.2		324.2		L	975.6	488.3	958.5	957.5	8
4	470.3		453.2	452.3	E	862.5	431.7	845.4	844.5	7
5	571.3		554.3	553.3	T	733.4	367.2	716.4	715.4	6
6	684.4	342.7	667.4	666.4	L	632.4		615.4		5
7	797.5	399.2	780.5	779.5	L	519.3		502.3		4
8	925.5	463.3	908.5	907.5	Q	406.2		389.2		3
9	1,056.6	528.8	1,039.5	1,038.6	M	278.2		261.1		2
10	1,202.7	601.8	1,185.7	1,184.7	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-49	sp|P18846|ATF1_HUMAN	TTPSATSLPQTVVMTSPVTLTSQTTK	65.43	Unmodified	Heavy	2	1339.2019

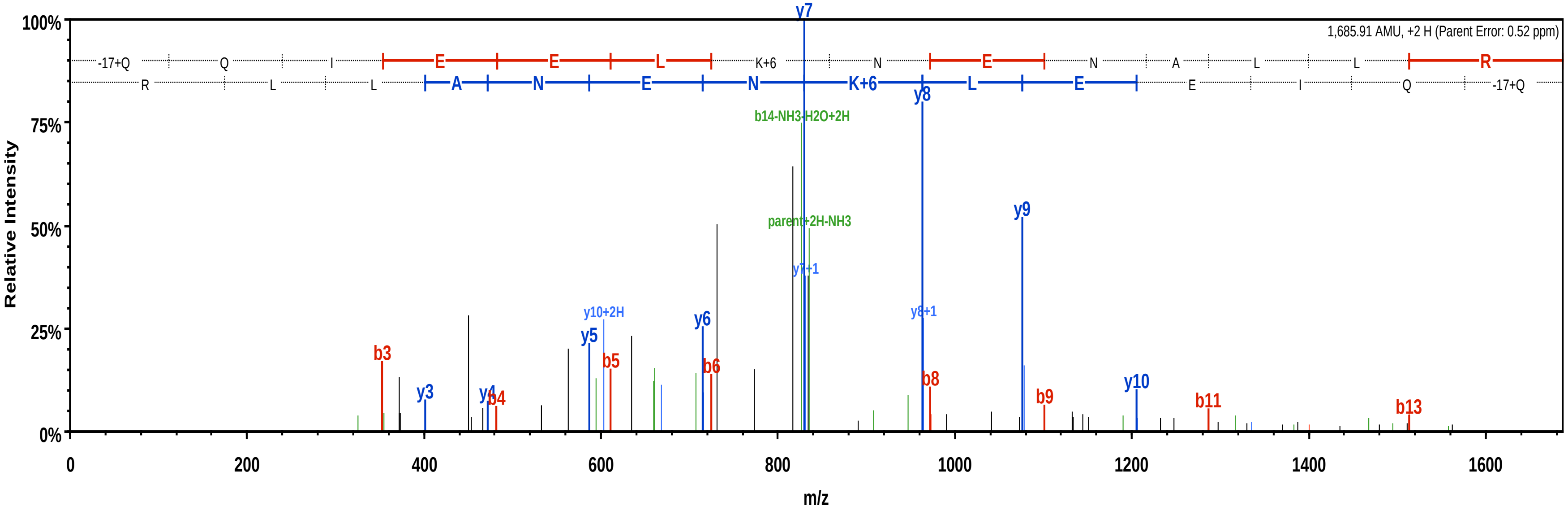


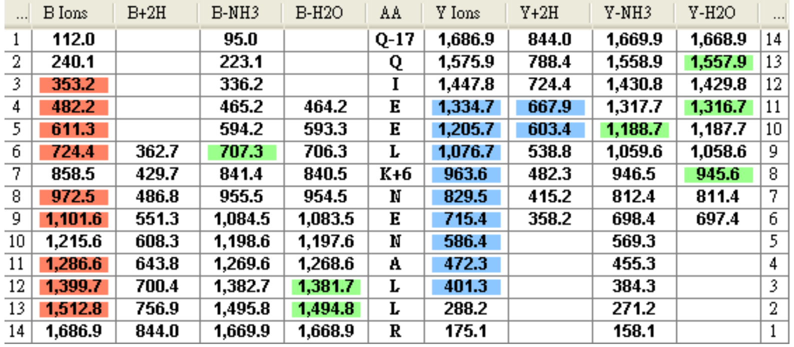


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	102.1			84.0	T	2,683.4	1,342.2	2,666.4	2,665.4	26
2	203.1			185.1	T	2,582.4	1,291.7	2,565.3	2,564.4	25
3	300.2			282.1	P	2,481.3	1,241.2	2,464.3	2,463.3	24
4	387.2			369.2	S	2,384.3	1,192.6	2,367.2	2,366.3	23
5	458.2			440.2	A	2,297.2	1,149.1	2,280.2	2,279.2	22
6	559.3	280.1		541.3	T	2,226.2	1,113.6	2,209.2	2,208.2	21
7	646.3	323.7		628.3	S	2,125.2	1,063.1	2,108.1	2,107.1	20
8	759.4	380.2		741.4	L	2,038.1	1,019.6	2,021.1	2,020.1	19
9	856.4	428.7		838.4	P	1,925.0	963.0	1,908.0	1,907.0	18
10	984.5	492.8	967.5	966.5	Q	1,828.0	914.5	1,811.0	1,810.0	17
11	1,085.5	543.3	1,068.5	1,067.5	T	1,699.9	850.5	1,682.9	1,681.9	16
12	1,184.6	592.8	1,167.6	1,166.6	V	1,598.9	799.9	1,581.9	1,580.9	15
13	1,283.7	642.3	1,266.7	1,265.7	V	1,499.8	750.4	1,482.8	1,481.8	14
14	1,414.7	707.9	1,397.7	1,396.7	M	1,400.7	700.9	1,383.7	1,382.7	13
15	1,515.8	758.4	1,498.7	1,497.8	T	1,269.7	635.4	1,252.7	1,251.7	12
16	1,602.8	801.9	1,585.8	1,584.8	S	1,168.7	584.8	1,151.6	1,150.6	11
17	1,699.9	850.4	1,682.8	1,681.8	P	1,081.6	541.3	1,064.6	1,063.6	10
18	1,798.9	900.0	1,781.9	1,780.9	V	984.6	492.8	967.5	966.6	9
19	1,900.0	950.5	1,882.9	1,882.0	T	885.5	443.3	868.5	867.5	8
20	2,013.1	1,007.0	1,996.0	1,995.0	L	784.5	392.7	767.4	766.4	7
21	2,114.1	1,057.6	2,097.1	2,096.1	T	671.4	336.2	654.3	653.4	6
22	2,201.1	1,101.1	2,184.1	2,183.1	S	570.3		553.3	552.3	5
23	2,329.2	1,165.1	2,312.2	2,311.2	Q	483.3		466.3	465.3	4
24	2,430.2	1,215.6	2,413.2	2,412.2	T	355.2		338.2	337.2	3
25	2,531.3	1,266.1	2,514.3	2,513.3	T	254.2		237.2	236.2	2
26	2,683.4	1,342.2	2,666.4	2,665.4	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-50	sp|Q15853|USF2_HUMAN	QQIEELKNENALLR	40.5	Gln->pyro-Glu (N-term Q)	Heavy	2	840.9494

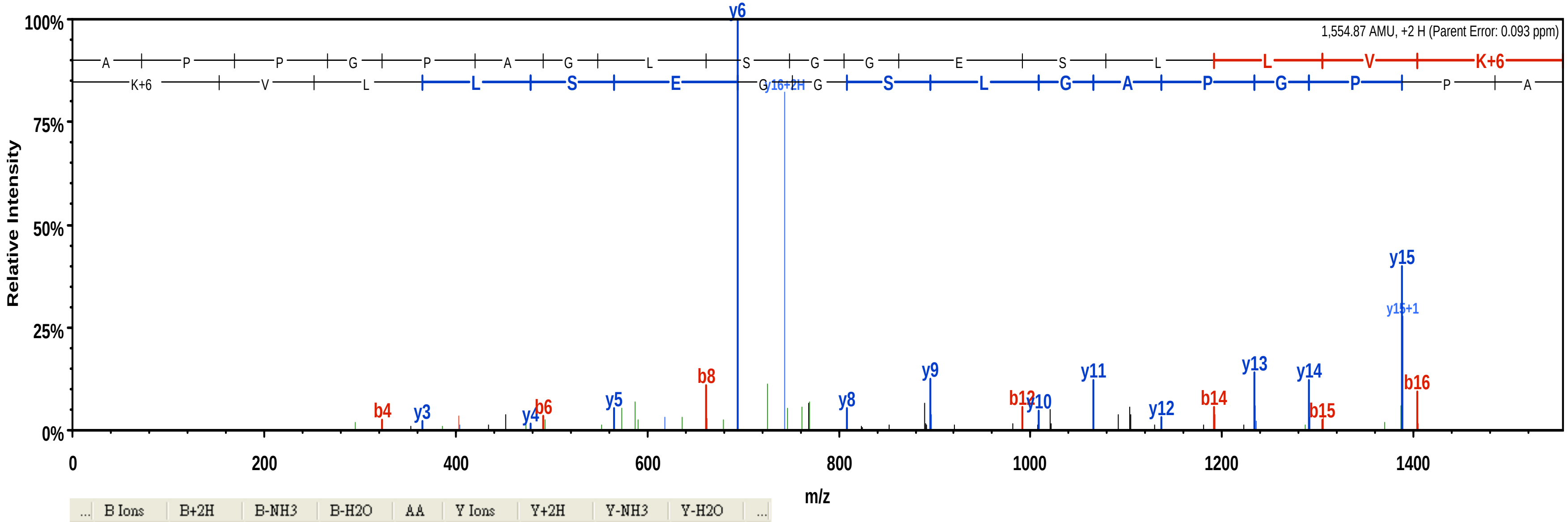


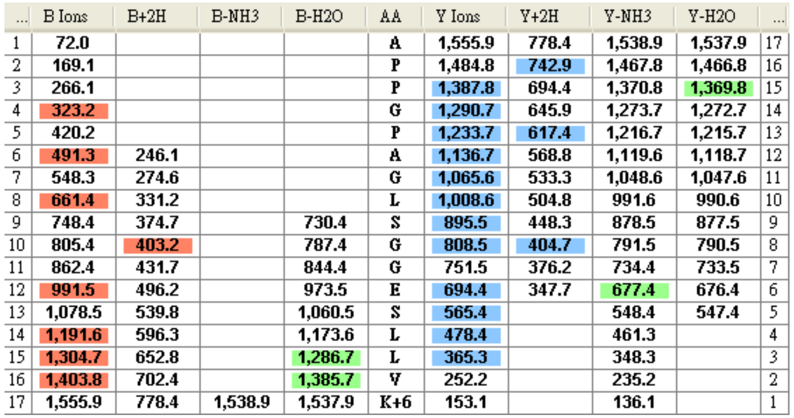


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	1,686.9	844.0	1,669.9	1,668.9	14
2	240.1		223.1		Q	1,575.9	788.4	1,558.9	1,557.9	13
3	353.2		336.2		I	1,447.8	724.4	1,430.8	1,429.8	12
4	482.2		465.2	464.2	E	1,334.7	667.9	1,317.7	1,316.7	11
5	611.3		594.2	593.3	E	1,205.7	603.4	1,188.7	1,187.7	10
6	724.4	362.7	707.3	706.3	L	1,076.7	538.8	1,059.6	1,058.6	9
7	858.5	429.7	841.4	840.5	K+6	963.6	482.3	946.5	945.6	8
8	972.5	486.8	955.5	954.5	N	829.5	415.2	812.4	811.4	7
9	1,101.6	551.3	1,084.5	1,083.5	E	715.4	358.2	698.4	697.4	6
10	1,215.6	608.3	1,198.6	1,197.6	N	586.4		569.3		5
11	1,286.6	643.8	1,269.6	1,268.6	A	472.3		455.3		4
12	1,399.7	700.4	1,382.7	1,381.7	L	401.3		384.3		3
13	1,512.8	756.9	1,495.8	1,494.8	L	288.2		271.2		2
14	1,686.9	844.0	1,669.9	1,668.9	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-51	sp|Q9NRL3|STRN4_HUMAN	APPGPAGLSGGESLLVK	65.02	Unmodified	Heavy	2	775.43286

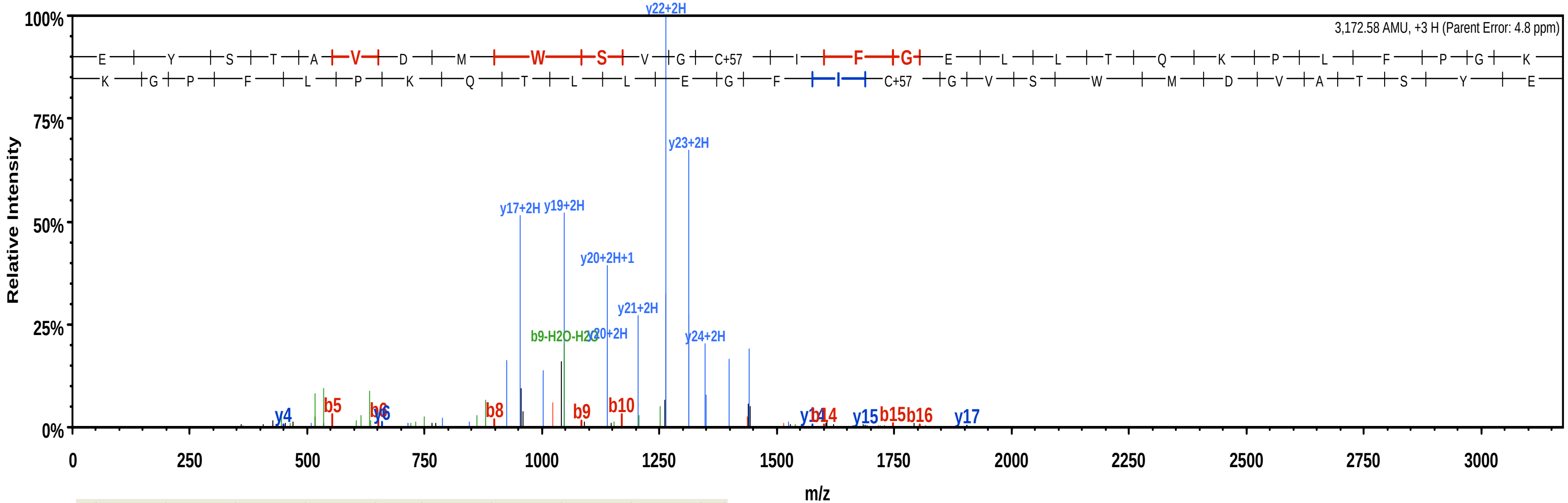


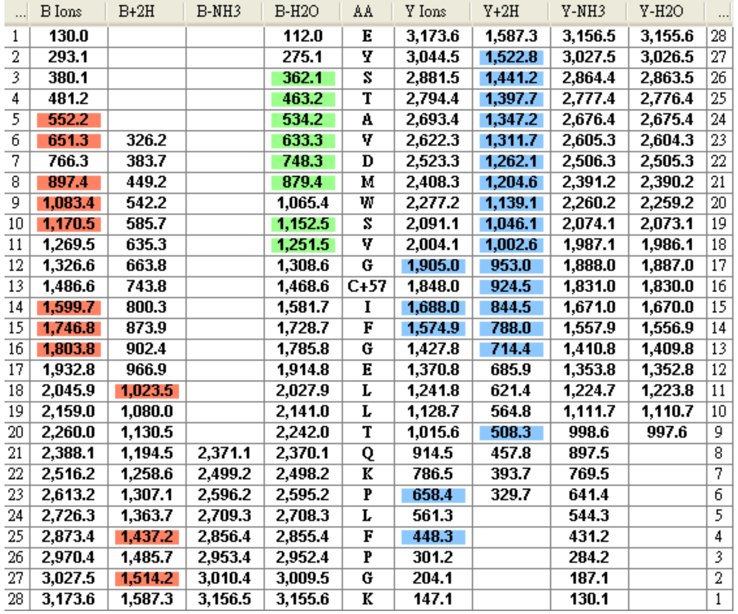


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	1,555.9	778.4	1,538.9	1,537.9	17
2	169.1				P	1,484.8	742.9	1,467.8	1,466.8	16
3	266.1				P	1,387.8	694.4	1,370.8	1,369.8	15
4	323.2				G	1,290.7	645.9	1,273.7	1,272.7	14
5	420.2				P	1,233.7	617.4	1,216.7	1,215.7	13
6	491.3	246.1			A	1,136.7	568.8	1,119.6	1,118.7	12
7	548.3	274.6			G	1,065.6	533.3	1,048.6	1,047.6	11
8	661.4	331.2			L	1,008.6	504.8	991.6	990.6	10
9	748.4	374.7		730.4	S	895.5	448.3	878.5	877.5	9
10	805.4	403.2		787.4	G	808.5	404.7	791.5	790.5	8
11	862.4	431.7		844.4	G	751.5	376.2	734.4	733.5	7
12	991.5	496.2		973.5	E	694.4	347.7	677.4	676.4	6
13	1,078.5	539.8		1,060.5	S	565.4		548.4	547.4	5
14	1,191.6	596.3		1,173.6	L	478.4		461.3		4
15	1,304.7	652.8		1,286.7	L	365.3		348.3		3
16	1,403.8	702.4		1,385.7	V	252.2		235.2		2
17	1,555.9	778.4	1,538.9	1,537.9	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-52	sp|P21127|CD2L1_HUMAN	EYSTAVDMWSVGCIFGELLTQKPLFPGK	64.16	Unmodified	Light	3	1058.5277

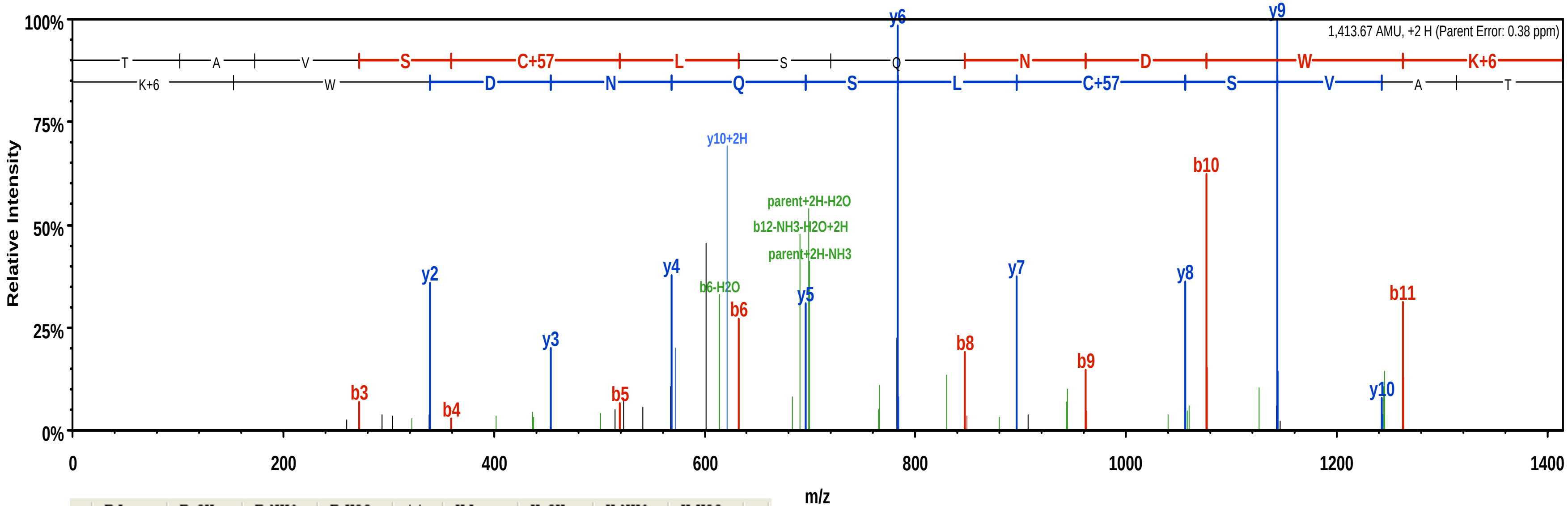


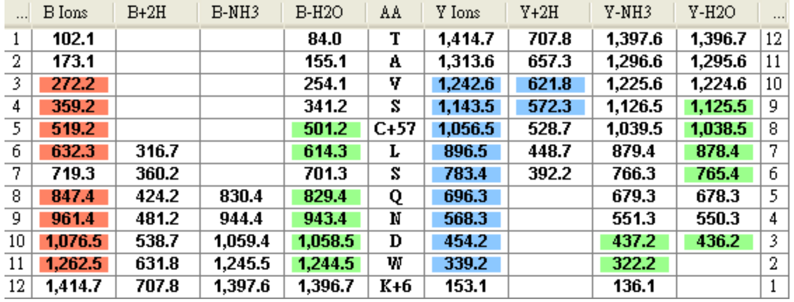


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	3,173.6	1,587.3	3,156.5	3,155.6	28
2	293.1			275.1	Y	3,044.5	1,522.8	3,027.5	3,026.5	27
3	380.1			362.1	S	2,881.5	1,441.2	2,864.4	2,863.5	26
4	481.2			463.2	T	2,794.4	1,397.7	2,777.4	2,776.4	25
5	552.2			534.2	A	2,693.4	1,347.2	2,676.4	2,675.4	24
6	651.3	326.2		633.3	V	2,622.3	1,311.7	2,605.3	2,604.3	23
7	766.3	383.7		748.3	D	2,523.3	1,262.1	2,506.3	2,505.3	22
8	897.4	449.2		879.4	M	2,408.3	1,204.6	2,391.2	2,390.2	21
9	1,083.4	542.2		1,065.4	W	2,277.2	1,139.1	2,260.2	2,259.2	20
10	1,170.5	585.7		1,152.5	S	2,091.1	1,046.1	2,074.1	2,073.1	19
11	1,269.5	635.3		1,251.5	V	2,004.1	1,002.6	1,987.1	1,986.1	18
12	1,326.6	663.8		1,308.6	G	1,905.0	953.0	1,888.0	1,887.0	17
13	1,486.6	743.8		1,468.6	C+57	1,848.0	924.5	1,831.0	1,830.0	16
14	1,599.7	800.3		1,581.7	I	1,688.0	844.5	1,671.0	1,670.0	15
15	1,746.8	873.9		1,728.7	F	1,574.9	788.0	1,557.9	1,556.9	14
16	1,803.8	902.4		1,785.8	G	1,427.8	714.4	1,410.8	1,409.8	13
17	1,932.8	966.9		1,914.8	E	1,370.8	685.9	1,353.8	1,352.8	12
18	2,045.9	1,023.5		2,027.9	L	1,241.8	621.4	1,224.7	1,223.8	11
19	2,159.0	1,080.0		2,141.0	L	1,128.7	564.8	1,111.7	1,110.7	10
20	2,260.0	1,130.5		2,242.0	T	1,015.6	508.3	998.6	997.6	9
21	2,388.1	1,194.5	2,371.1	2,370.1	Q	914.5	457.8	897.5		8
22	2,516.2	1,258.6	2,499.2	2,498.2	K	786.5	393.7	769.5		7
23	2,613.2	1,307.1	2,596.2	2,595.2	P	658.4	329.7	641.4		6
24	2,726.3	1,363.7	2,709.3	2,708.3	L	561.3		544.3		5
25	2,873.4	1,437.2	2,856.4	2,855.4	F	448.3		431.2		4
26	2,970.4	1,485.7	2,953.4	2,952.4	P	301.2		284.2		3
27	3,027.5	1,514.2	3,010.4	3,009.5	G	204.1		187.1		2
28	3,173.6	1,587.3	3,156.5	3,155.6	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-53	sp|Q96GG9|DCNL1_HUMAN	TAVSCLSQNDWK	64.13	Unmodified	Heavy	2	704.82991

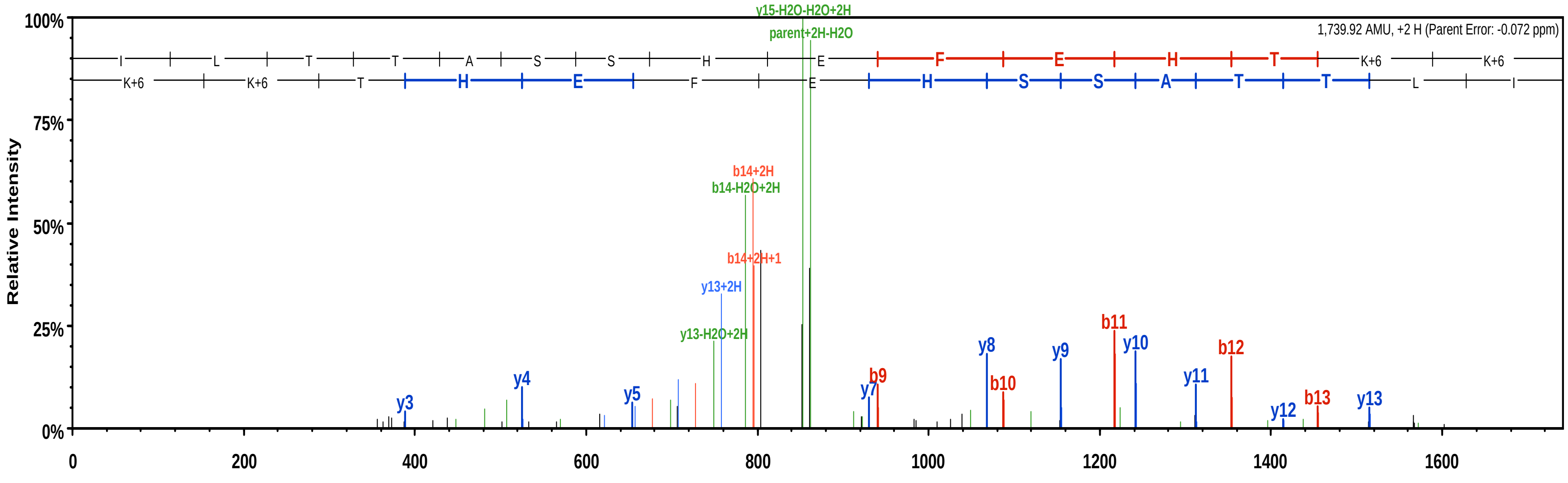


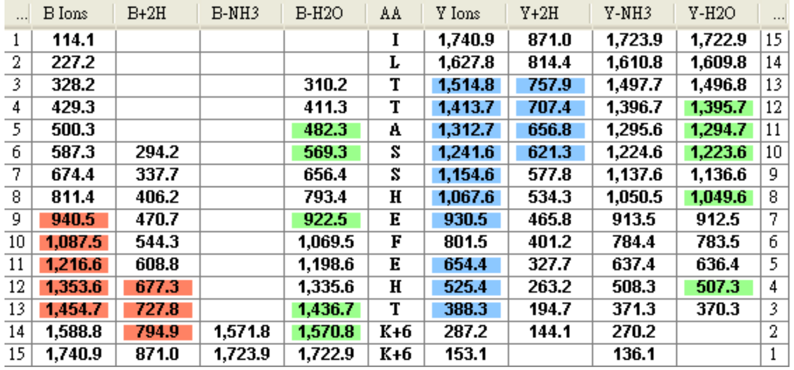


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	102.1			84.0	T	1,414.7	707.8	1,397.6	1,396.7	12
2	173.1			155.1	A	1,313.6	657.3	1,296.6	1,295.6	11
3	272.2			254.1	V	1,242.6	621.8	1,225.6	1,224.6	10
4	359.2			341.2	S	1,143.5	572.3	1,126.5	1,125.5	9
5	519.2			501.2	C+57	1,056.5	528.7	1,039.5	1,038.5	8
6	632.3	316.7		614.3	L	896.5	448.7	879.4	878.4	7
7	719.3	360.2		701.3	S	783.4	392.2	766.3	765.4	6
8	847.4	424.2	830.4	829.4	Q	696.3		679.3	678.3	5
9	961.4	481.2	944.4	943.4	N	568.3		551.3	550.3	4
10	1,076.5	538.7	1,059.4	1,058.5	D	454.2		437.2	436.2	3
11	1,262.5	631.8	1,245.5	1,244.5	W	339.2		322.2		2
12	1,414.7	707.8	1,397.6	1,396.7	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-54	sp|Q16851|UGPA_HUMAN	ILTTASSHEFEHTKK	63.61	Unmodified	Heavy	2	864.9494

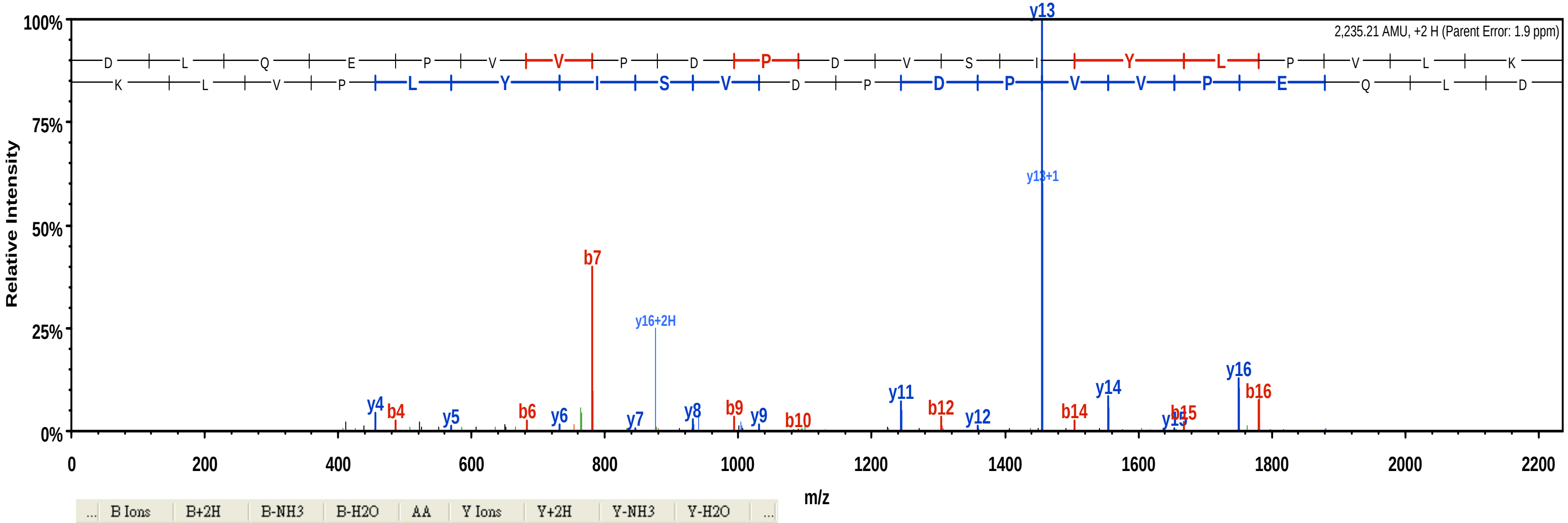


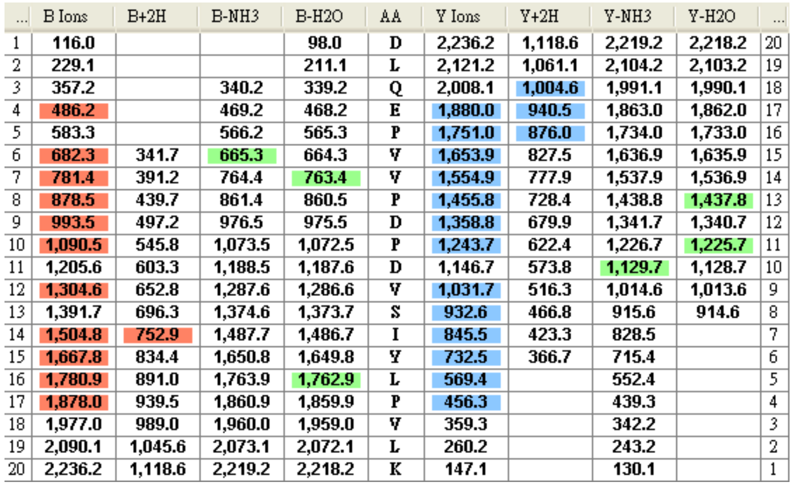


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	1,740.9	871.0	1,723.9	1,722.9	15
2	227.2				L	1,627.8	814.4	1,610.8	1,609.8	14
3	328.2			310.2	T	1,514.8	757.9	1,497.7	1,496.8	13
4	429.3			411.3	T	1,413.7	707.4	1,396.7	1,395.7	12
5	500.3			482.3	A	1,312.7	656.8	1,295.6	1,294.7	11
6	587.3	294.2		569.3	S	1,241.6	621.3	1,224.6	1,223.6	10
7	674.4	337.7		656.4	S	1,154.6	577.8	1,137.6	1,136.6	9
8	811.4	406.2		793.4	H	1,067.6	534.3	1,050.5	1,049.6	8
9	940.5	470.7		922.5	E	930.5	465.8	913.5	912.5	7
10	1,087.5	544.3		1,069.5	F	801.5	401.2	784.4	783.5	6
11	1,216.6	608.8		1,198.6	E	654.4	327.7	637.4	636.4	5
12	1,353.6	677.3		1,335.6	H	525.4	263.2	508.3	507.3	4
13	1,454.7	727.8		1,436.7	T	388.3	194.7	371.3	370.3	3
14	1,588.8	794.9	1,571.8	1,570.8	K+6	287.2	144.1	270.2		2
15	1,740.9	871.0	1,723.9	1,722.9	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-55	sp|O60921|HUS1_HUMAN	DLQEPVVPDPDVSIYLPVLK	63.45	Unmodified	Light	2	1118.6092

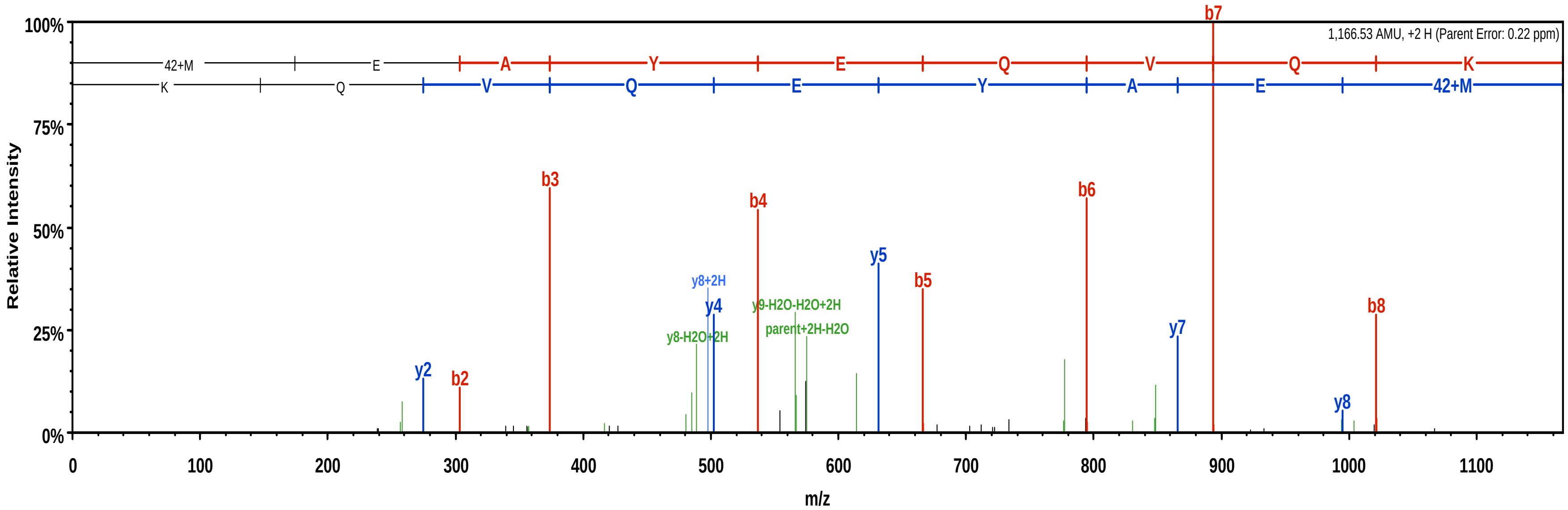


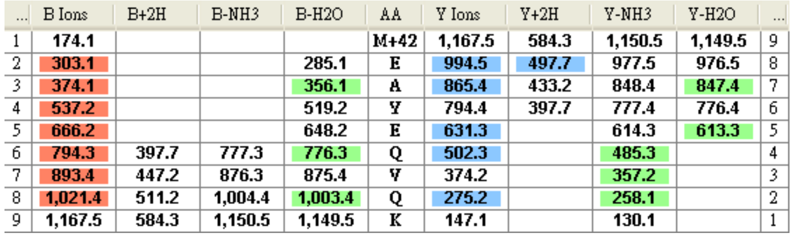


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	2,236.2	1,118.6	2,219.2	2,218.2	20
2	229.1			211.1	L	2,121.2	1,061.1	2,104.2	2,103.2	19
3	357.2		340.2	339.2	Q	2,008.1	1,004.6	1,991.1	1,990.1	18
4	486.2		469.2	468.2	E	1,880.0	940.5	1,863.0	1,862.0	17
5	583.3		566.2	565.3	P	1,751.0	876.0	1,734.0	1,733.0	16
6	682.3	341.7	665.3	664.3	V	1,653.9	827.5	1,636.9	1,635.9	15
7	781.4	391.2	764.4	763.4	V	1,554.9	777.9	1,537.9	1,536.9	14
8	878.5	439.7	861.4	860.5	P	1,455.8	728.4	1,438.8	1,437.8	13
9	993.5	497.2	976.5	975.5	D	1,358.8	679.9	1,341.7	1,340.7	12
10	1,090.5	545.8	1,073.5	1,072.5	P	1,243.7	622.4	1,226.7	1,225.7	11
11	1,205.6	603.3	1,188.5	1,187.6	D	1,146.7	573.8	1,129.7	1,128.7	10
12	1,304.6	652.8	1,287.6	1,286.6	V	1,031.7	516.3	1,014.6	1,013.6	9
13	1,391.7	696.3	1,374.6	1,373.7	S	932.6	466.8	915.6	914.6	8
14	1,504.8	752.9	1,487.7	1,486.7	I	845.5	423.3	828.5		7
15	1,667.8	834.4	1,650.8	1,649.8	Y	732.5	366.7	715.4		6
16	1,780.9	891.0	1,763.9	1,762.9	L	569.4		552.4		5
17	1,878.0	939.5	1,860.9	1,859.9	P	456.3		439.3		4
18	1,977.0	989.0	1,960.0	1,959.0	V	359.3		342.2		3
19	2,090.1	1,045.6	2,073.1	2,072.1	L	260.2		243.2		2
20	2,236.2	1,118.6	2,219.2	2,218.2	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-56	sp|Q9Y421|FA32A_HUMAN	MEAYEQVQK	63.37	Acetyl (Protein N-term)	Light	2	584.27116

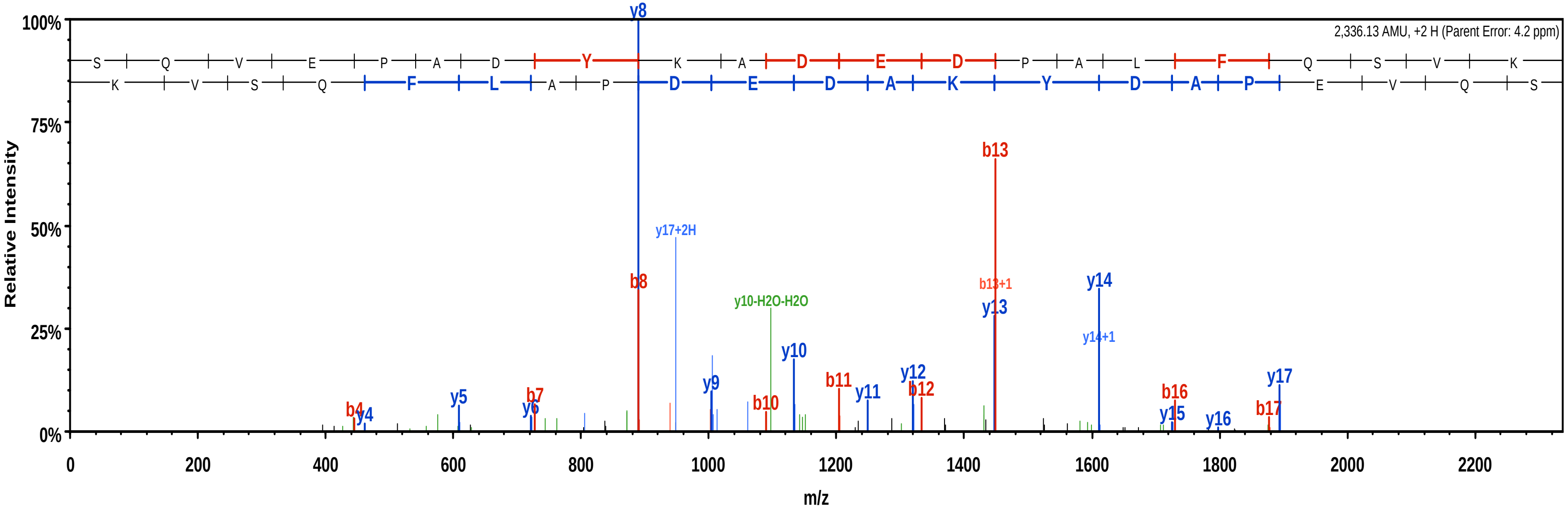


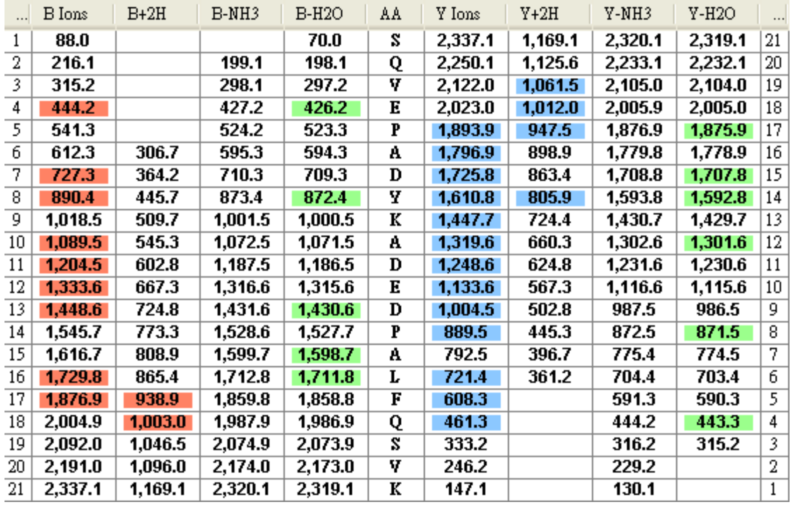


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	174.1				M+42	1,167.5	584.3	1,150.5	1,149.5	9
2	303.1			285.1	E	994.5	497.7	977.5	976.5	8
3	374.1			356.1	A	865.4	433.2	848.4	847.4	7
4	537.2			519.2	Y	794.4	397.7	777.4	776.4	6
5	666.2			648.2	E	631.3		614.3	613.3	5
6	794.3	397.7	777.3	776.3	Q	502.3		485.3		4
7	893.4	447.2	876.3	875.4	V	374.2		357.2		3
8	1,021.4	511.2	1,004.4	1,003.4	Q	275.2		258.1		2
9	1,167.5	584.3	1,150.5	1,149.5	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-57	sp|P48739|PIPNB_HUMAN	SQVEPADYKADEDPALFQSVK	62.78	Unmodified	Light	2	1169.0659

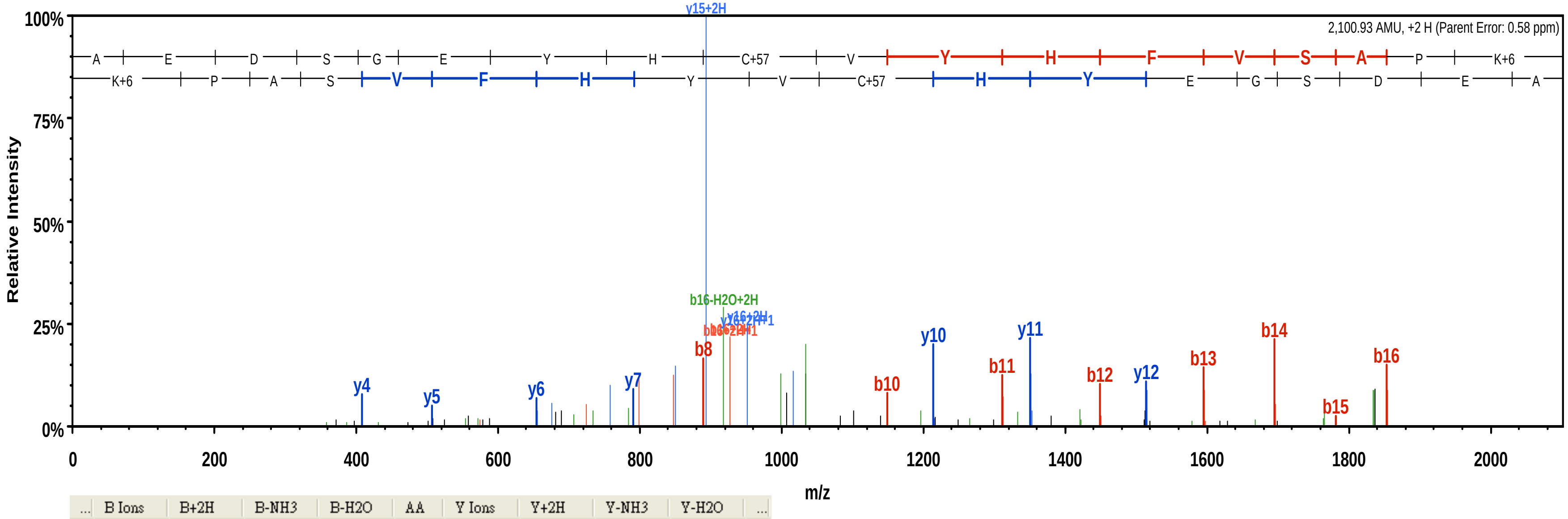


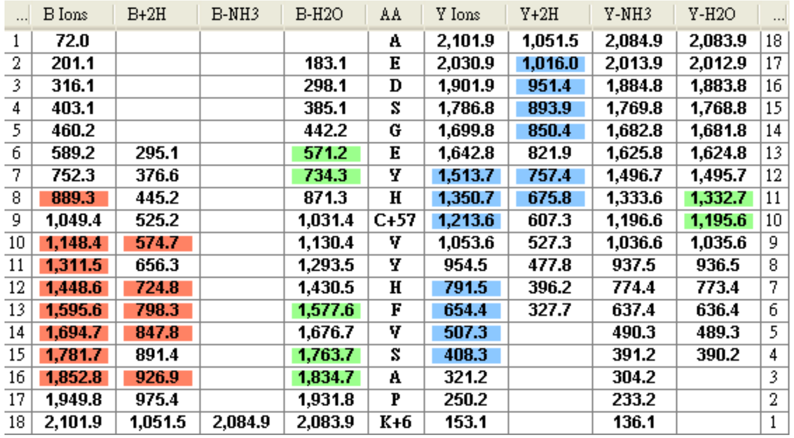


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	2,337.1	1,169.1	2,320.1	2,319.1	21
2	216.1		199.1	198.1	Q	2,250.1	1,125.6	2,233.1	2,232.1	20
3	315.2		298.1	297.2	V	2,122.0	1,061.5	2,105.0	2,104.0	19
4	444.2		427.2	426.2	E	2,023.0	1,012.0	2,005.9	2,005.0	18
5	541.3		524.2	523.3	P	1,893.9	947.5	1,876.9	1,875.9	17
6	612.3	306.7	595.3	594.3	A	1,796.9	898.9	1,779.8	1,778.9	16
7	727.3	364.2	710.3	709.3	D	1,725.8	863.4	1,708.8	1,707.8	15
8	890.4	445.7	873.4	872.4	Y	1,610.8	805.9	1,593.8	1,592.8	14
9	1,018.5	509.7	1,001.5	1,000.5	K	1,447.7	724.4	1,430.7	1,429.7	13
10	1,089.5	545.3	1,072.5	1,071.5	A	1,319.6	660.3	1,302.6	1,301.6	12
11	1,204.5	602.8	1,187.5	1,186.5	D	1,248.6	624.8	1,231.6	1,230.6	11
12	1,333.6	667.3	1,316.6	1,315.6	E	1,133.6	567.3	1,116.6	1,115.6	10
13	1,448.6	724.8	1,431.6	1,430.6	D	1,004.5	502.8	987.5	986.5	9
14	1,545.7	773.3	1,528.6	1,527.7	P	889.5	445.3	872.5	871.5	8
15	1,616.7	808.9	1,599.7	1,598.7	A	792.5	396.7	775.4	774.5	7
16	1,729.8	865.4	1,712.8	1,711.8	L	721.4	361.2	704.4	703.4	6
17	1,876.9	938.9	1,859.8	1,858.8	F	608.3		591.3	590.3	5
18	2,004.9	1,003.0	1,987.9	1,986.9	Q	461.3		444.2	443.3	4
19	2,092.0	1,046.5	2,074.9	2,073.9	S	333.2		316.2	315.2	3
20	2,191.0	1,096.0	2,174.0	2,173.0	V	246.2		229.2		2
21	2,337.1	1,169.1	2,320.1	2,319.1	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-58	sp|Q9Y639|NPTN_HUMAN	AEDSGEYHCVYHFVSAPK	62.25	Unmodified	Heavy	2	1048.4625

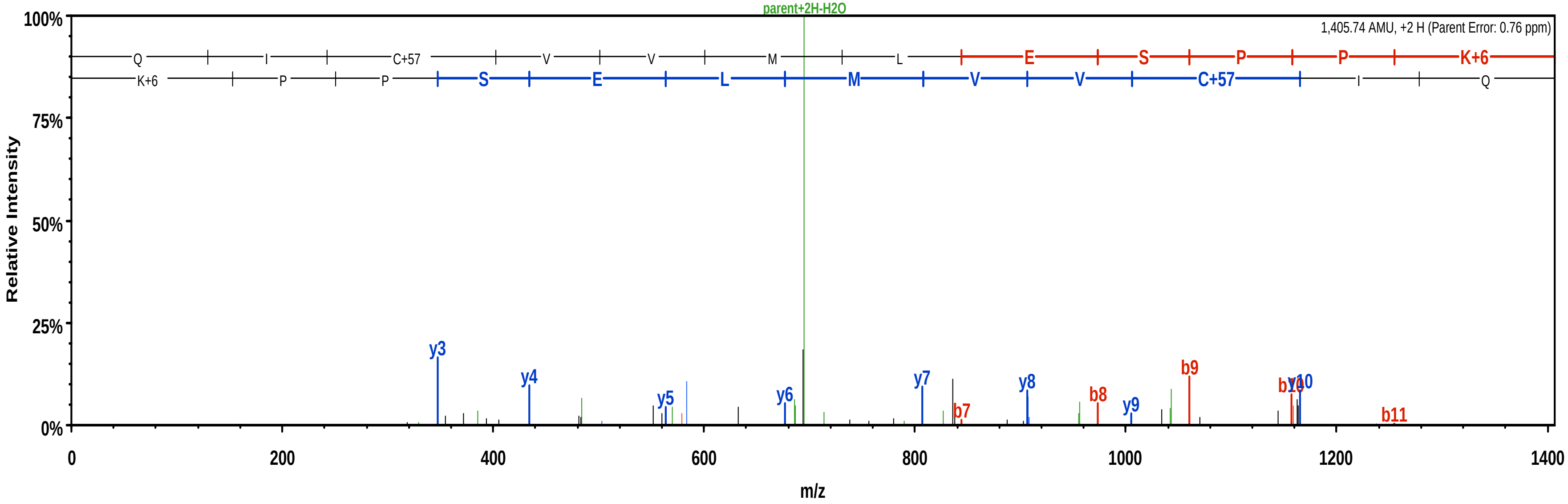


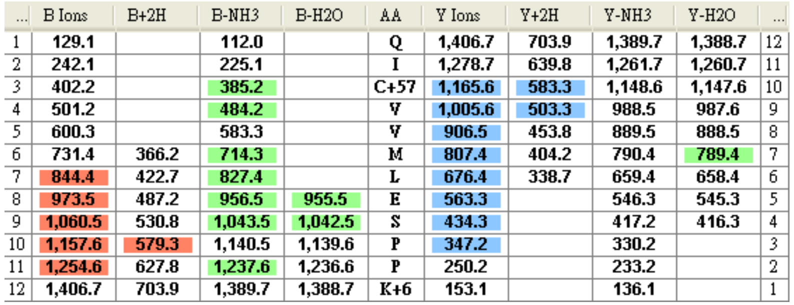


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	2,101.9	1,051.5	2,084.9	2,083.9	18
2	201.1			183.1	E	2,030.9	1,016.0	2,013.9	2,012.9	17
3	316.1			298.1	D	1,901.9	951.4	1,884.8	1,883.8	16
4	403.1			385.1	S	1,786.8	893.9	1,769.8	1,768.8	15
5	460.2			442.2	G	1,699.8	850.4	1,682.8	1,681.8	14
6	589.2	295.1		571.2	E	1,642.8	821.9	1,625.8	1,624.8	13
7	752.3	376.6		734.3	Y	1,513.7	757.4	1,496.7	1,495.7	12
8	889.3	445.2		871.3	H	1,350.7	675.8	1,333.6	1,332.7	11
9	1,049.4	525.2		1,031.4	C+57	1,213.6	607.3	1,196.6	1,195.6	10
10	1,148.4	574.7		1,130.4	V	1,053.6	527.3	1,036.6	1,035.6	9
11	1,311.5	656.3		1,293.5	Y	954.5	477.8	937.5	936.5	8
12	1,448.6	724.8		1,430.5	H	791.5	396.2	774.4	773.4	7
13	1,595.6	798.3		1,577.6	F	654.4	327.7	637.4	636.4	6
14	1,694.7	847.8		1,676.7	V	507.3		490.3	489.3	5
15	1,781.7	891.4		1,763.7	S	408.3		391.2	390.2	4
16	1,852.8	926.9		1,834.7	A	321.2		304.2		3
17	1,949.8	975.4		1,931.8	P	250.2		233.2		2
18	2,101.9	1,051.5	2,084.9	2,083.9	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-59	sp|P57721|PCBP3_HUMAN	QICVVMLESPPK	53.6	Unmodified	Heavy	2	700.86745

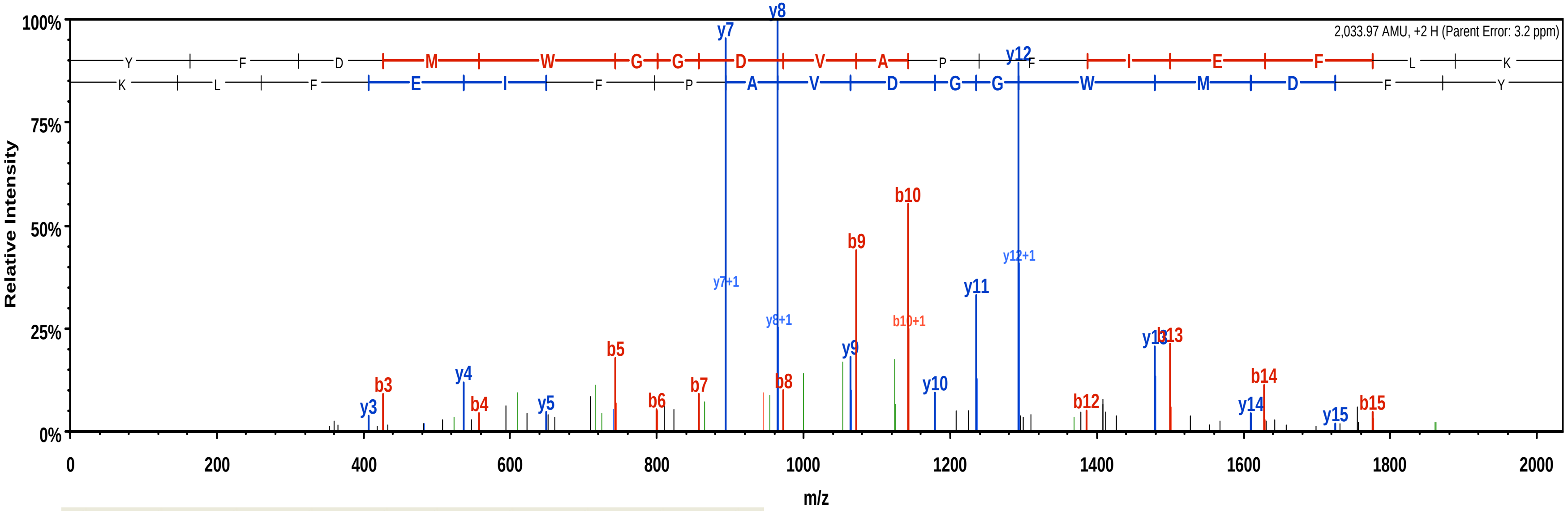


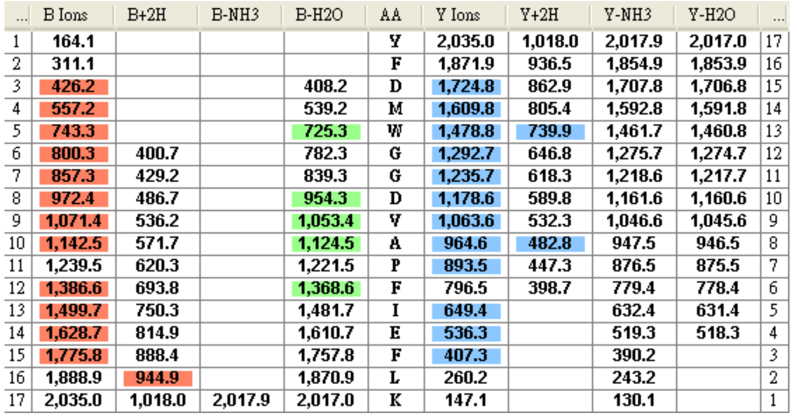


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	129.1		112.0		Q	1,406.7	703.9	1,389.7	1,388.7	12
2	242.1		225.1		I	1,278.7	639.8	1,261.7	1,260.7	11
3	402.2		385.2		C+57	1,165.6	583.3	1,148.6	1,147.6	10
4	501.2		484.2		V	1,005.6	503.3	988.5	987.6	9
5	600.3		583.3		V	906.5	453.8	889.5	888.5	8
6	731.4	366.2	714.3		M	807.4	404.2	790.4	789.4	7
7	844.4	422.7	827.4		L	676.4	338.7	659.4	658.4	6
8	973.5	487.2	956.5	955.5	E	563.3		546.3	545.3	5
9	1,060.5	530.8	1,043.5	1,042.5	S	434.3		417.2	416.3	4
10	1,157.6	579.3	1,140.5	1,139.6	P	347.2		330.2		3
11	1,254.6	627.8	1,237.6	1,236.6	P	250.2		233.2		2
12	1,406.7	703.9	1,389.7	1,388.7	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-60	sp|Q92520|FAM3C_HUMAN	YFDMWGGDVAPFIEFLK	60.18	Unmodified	Light	2	1017.9871

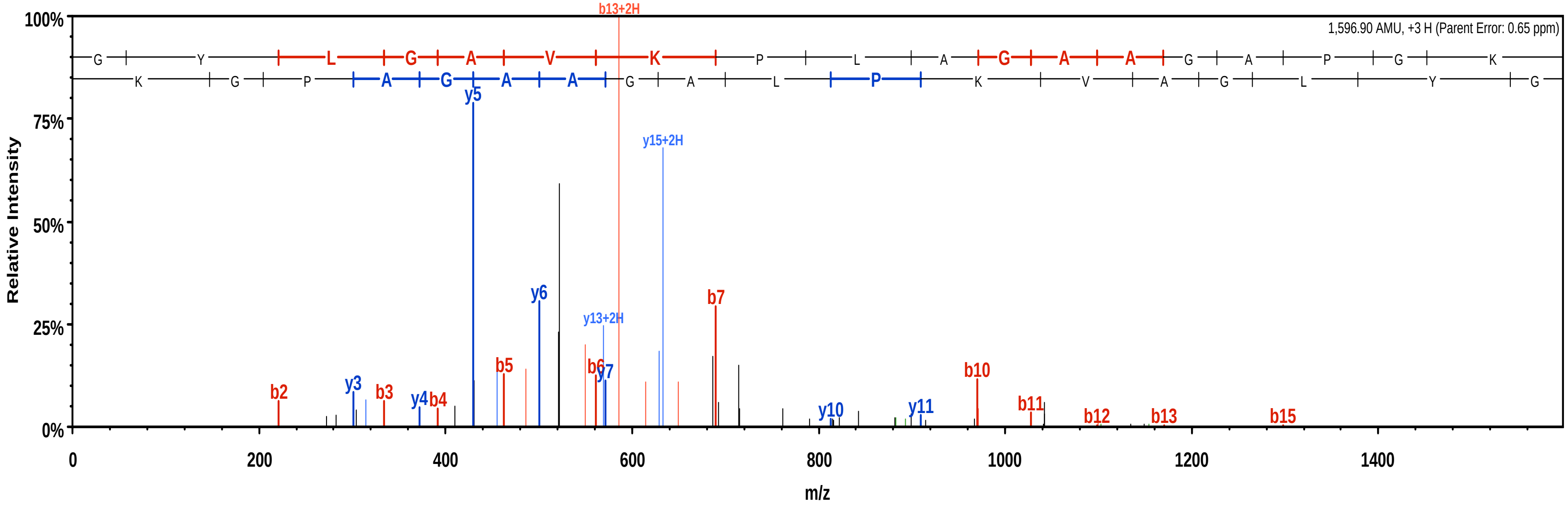


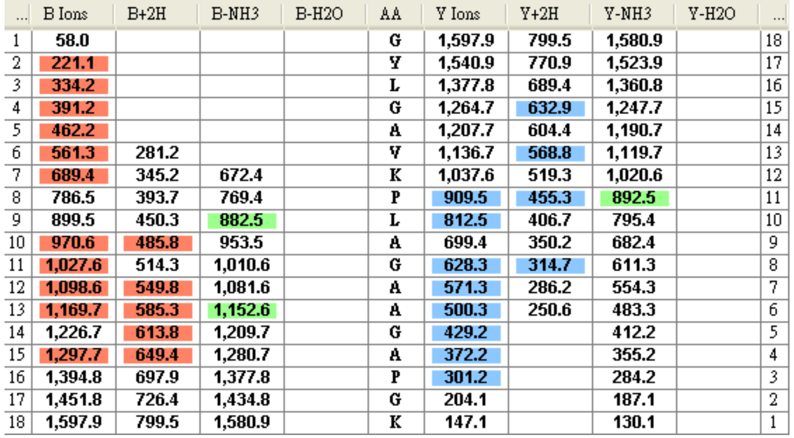


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	164.1				Y	2,035.0	1,018.0	2,017.9	2,017.0	17
2	311.1				F	1,871.9	936.5	1,854.9	1,853.9	16
3	426.2			408.2	D	1,724.8	862.9	1,707.8	1,706.8	15
4	557.2			539.2	M	1,609.8	805.4	1,592.8	1,591.8	14
5	743.3			725.3	W	1,478.8	739.9	1,461.7	1,460.8	13
6	800.3	400.7		782.3	G	1,292.7	646.8	1,275.7	1,274.7	12
7	857.3	429.2		839.3	G	1,235.7	618.3	1,218.6	1,217.7	11
8	972.4	486.7		954.3	D	1,178.6	589.8	1,161.6	1,160.6	10
9	1,071.4	536.2		1,053.4	V	1,063.6	532.3	1,046.6	1,045.6	9
10	1,142.5	571.7		1,124.5	A	964.6	482.8	947.5	946.5	8
11	1,239.5	620.3		1,221.5	P	893.5	447.3	876.5	875.5	7
12	1,386.6	693.8		1,368.6	F	796.5	398.7	779.4	778.4	6
13	1,499.7	750.3		1,481.7	I	649.4		632.4	631.4	5
14	1,628.7	814.9		1,610.7	E	536.3		519.3	518.3	4
15	1,775.8	888.4		1,757.8	F	407.3		390.2		3
16	1,888.9	944.9		1,870.9	L	260.2		243.2		2
17	2,035.0	1,018.0	2,017.9	2,017.0	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-61	sp|O00257|CBX4_HUMAN	GYLGAVKPLAGAAGAPGK	59.36	Unmodified	Light	3	533.30687

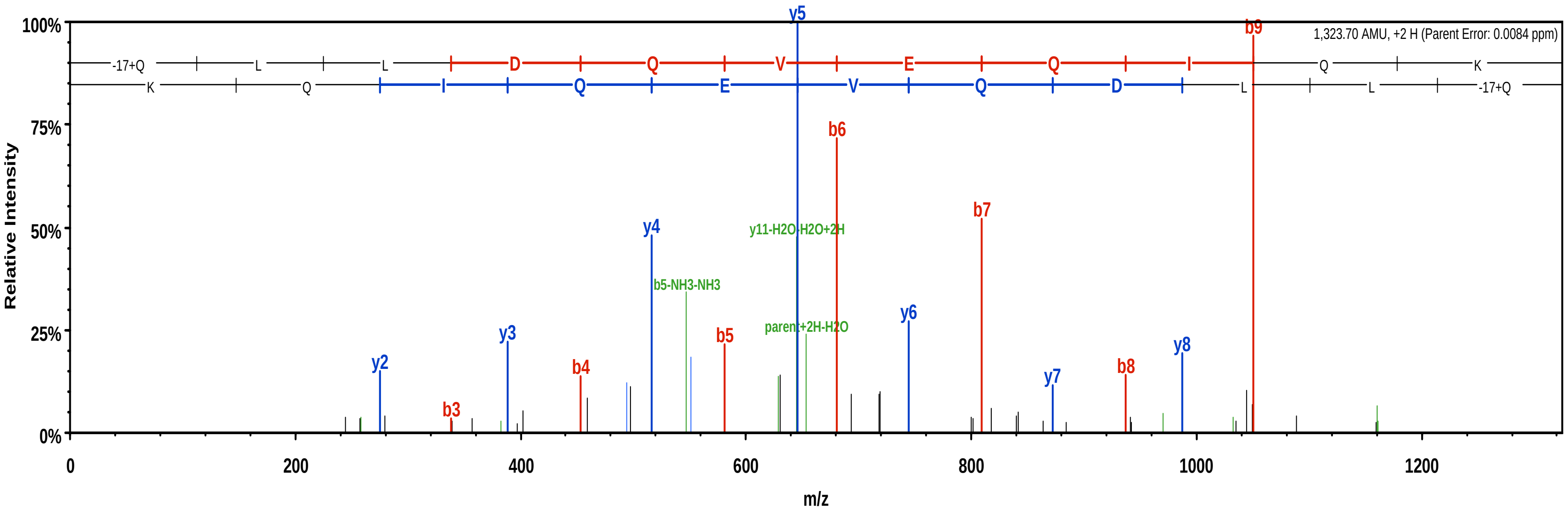


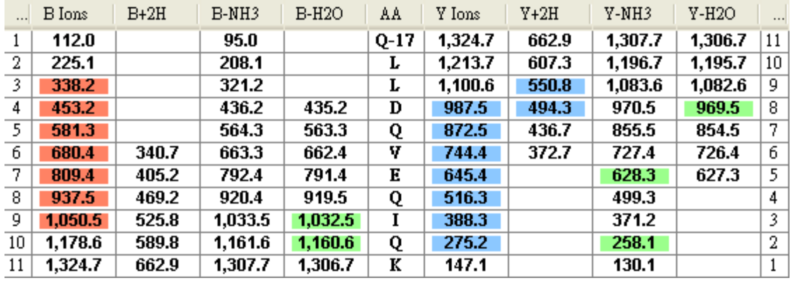


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	1,597.9	799.5	1,580.9		18
2	221.1				Y	1,540.9	770.9	1,523.9		17
3	334.2				L	1,377.8	689.4	1,360.8		16
4	391.2				G	1,264.7	632.9	1,247.7		15
5	462.2				A	1,207.7	604.4	1,190.7		14
6	561.3	281.2			V	1,136.7	568.8	1,119.7		13
7	689.4	345.2	672.4		K	1,037.6	519.3	1,020.6		12
8	786.5	393.7	769.4		P	909.5	455.3	892.5		11
9	899.5	450.3	882.5		L	812.5	406.7	795.4		10
10	970.6	485.8	953.5		A	699.4	350.2	682.4		9
11	1,027.6	514.3	1,010.6		G	628.3	314.7	611.3		8
12	1,098.6	549.8	1,081.6		A	571.3	286.2	554.3		7
13	1,169.7	585.3	1,152.6		A	500.3	250.6	483.3		6
14	1,226.7	613.8	1,209.7		G	429.2		412.2		5
15	1,297.7	649.4	1,280.7		A	372.2		355.2		4
16	1,394.8	697.9	1,377.8		P	301.2		284.2		3
17	1,451.8	726.4	1,434.8		G	204.1		187.1		2
18	1,597.9	799.5	1,580.9		K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-62	sp|Q7Z7H5|TMED4_HUMAN	QLLDQVEQIQK	59.26	Gln->pyro-Glu (N-term Q)	Light	2	662.85899

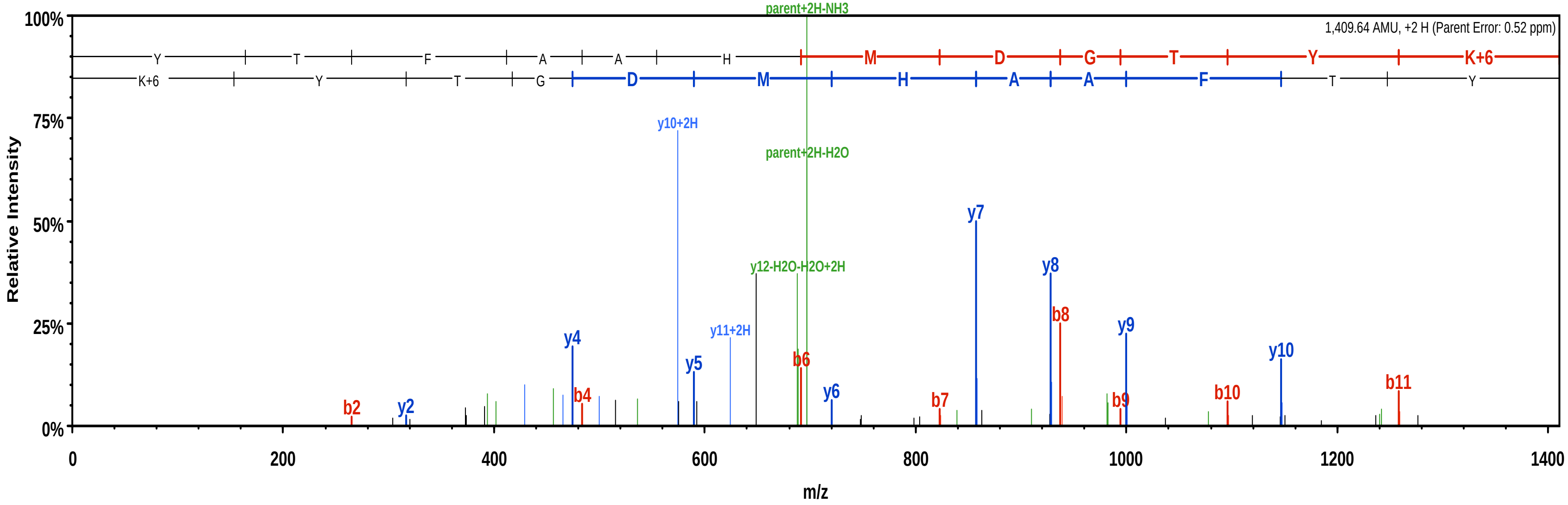


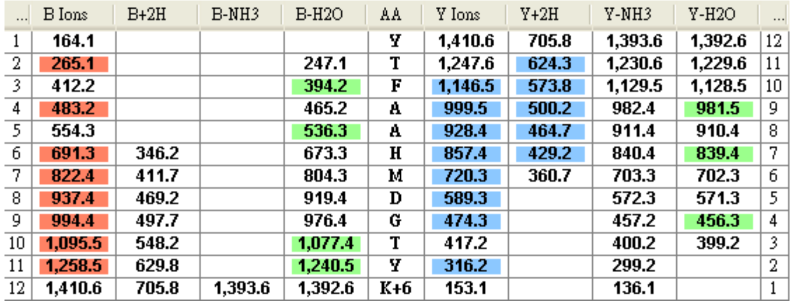


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	1,324.7	662.9	1,307.7	1,306.7	11
2	225.1		208.1		L	1,213.7	607.3	1,196.7	1,195.7	10
3	338.2		321.2		L	1,100.6	550.8	1,083.6	1,082.6	9
4	453.2		436.2	435.2	D	987.5	494.3	970.5	969.5	8
5	581.3		564.3	563.3	Q	872.5	436.7	855.5	854.5	7
6	680.4	340.7	663.3	662.4	V	744.4	372.7	727.4	726.4	6
7	809.4	405.2	792.4	791.4	E	645.4		628.3	627.3	5
8	937.5	469.2	920.4	919.5	Q	516.3		499.3		4
9	1,050.5	525.8	1,033.5	1,032.5	I	388.3		371.2		3
10	1,178.6	589.8	1,161.6	1,160.6	Q	275.2		258.1		2
11	1,324.7	662.9	1,307.7	1,306.7	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-63	sp|Q15363|TMED2_HUMAN	YTFAAHMDGTYK	58.82	Unmodified	Heavy	2	702.81627

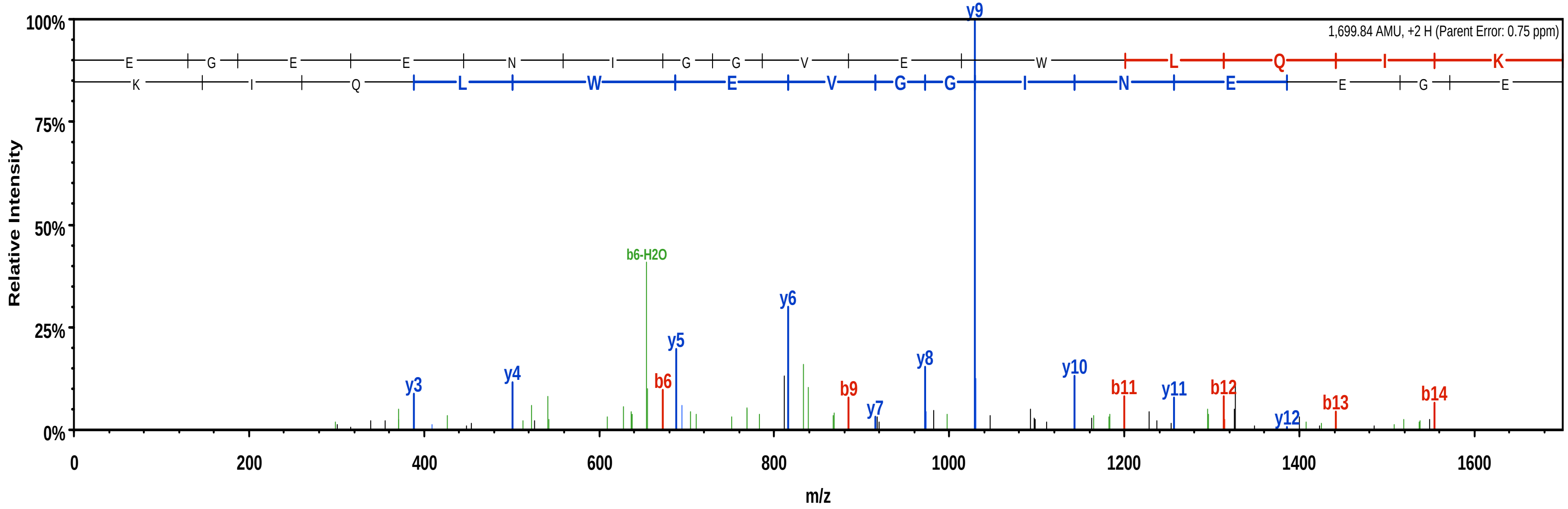


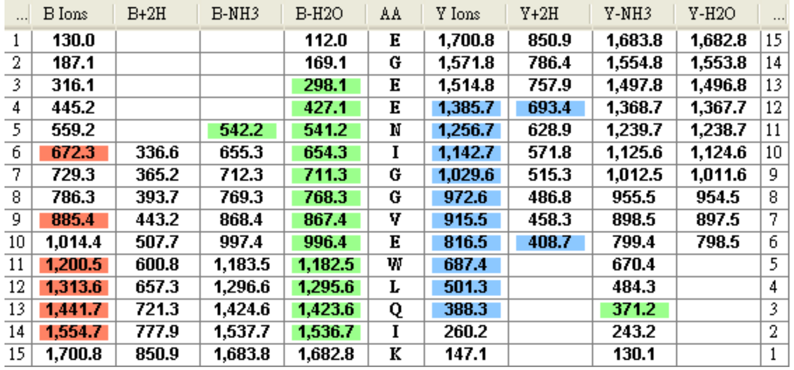


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	164.1				Y	1,410.6	705.8	1,393.6	1,392.6	12
2	265.1			247.1	T	1,247.6	624.3	1,230.6	1,229.6	11
3	412.2			394.2	F	1,146.5	573.8	1,129.5	1,128.5	10
4	483.2			465.2	A	999.5	500.2	982.4	981.5	9
5	554.3			536.3	A	928.4	464.7	911.4	910.4	8
6	691.3	346.2		673.3	H	857.4	429.2	840.4	839.4	7
7	822.4	411.7		804.3	M	720.3	360.7	703.3	702.3	6
8	937.4	469.2		919.4	D	589.3		572.3	571.3	5
9	994.4	497.7		976.4	G	474.3		457.2	456.3	4
10	1,095.5	548.2		1,077.4	T	417.2		400.2	399.2	3
11	1,258.5	629.8		1,240.5	Y	316.2		299.2		2
12	1,410.6	705.8	1,393.6	1,392.6	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-64	sp|Q969F1|TF3C6_HUMAN	EGEENIGGVEWLQIK	58.06	Unmodified	Light	2	850.92813

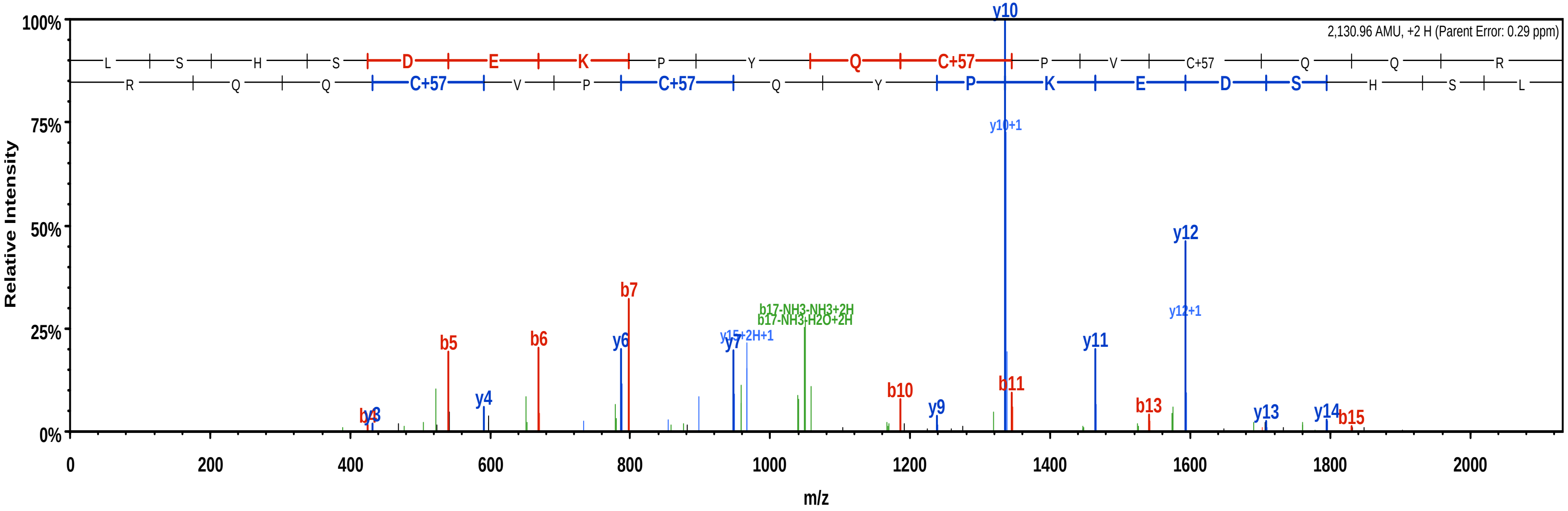


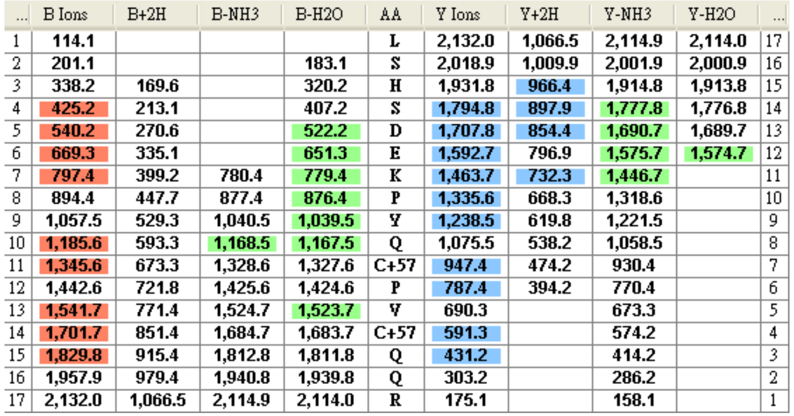


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	1,700.8	850.9	1,683.8	1,682.8	15
2	187.1			169.1	G	1,571.8	786.4	1,554.8	1,553.8	14
3	316.1			298.1	E	1,514.8	757.9	1,497.8	1,496.8	13
4	445.2			427.1	E	1,385.7	693.4	1,368.7	1,367.7	12
5	559.2		542.2	541.2	N	1,256.7	628.9	1,239.7	1,238.7	11
6	672.3	336.6	655.3	654.3	I	1,142.7	571.8	1,125.6	1,124.6	10
7	729.3	365.2	712.3	711.3	G	1,029.6	515.3	1,012.5	1,011.6	9
8	786.3	393.7	769.3	768.3	G	972.6	486.8	955.5	954.5	8
9	885.4	443.2	868.4	867.4	V	915.5	458.3	898.5	897.5	7
10	1,014.4	507.7	997.4	996.4	E	816.5	408.7	799.4	798.5	6
11	1,200.5	600.8	1,183.5	1,182.5	W	687.4		670.4		5
12	1,313.6	657.3	1,296.6	1,295.6	L	501.3		484.3		4
13	1,441.7	721.3	1,424.6	1,423.6	Q	388.3		371.2		3
14	1,554.7	777.9	1,537.7	1,536.7	I	260.2		243.2		2
15	1,700.8	850.9	1,683.8	1,682.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-65	sp|P56270|MAZ_HUMAN	LSHSDEKPYQCPVCQQR	58	Unmodified	Light	2	1066.486

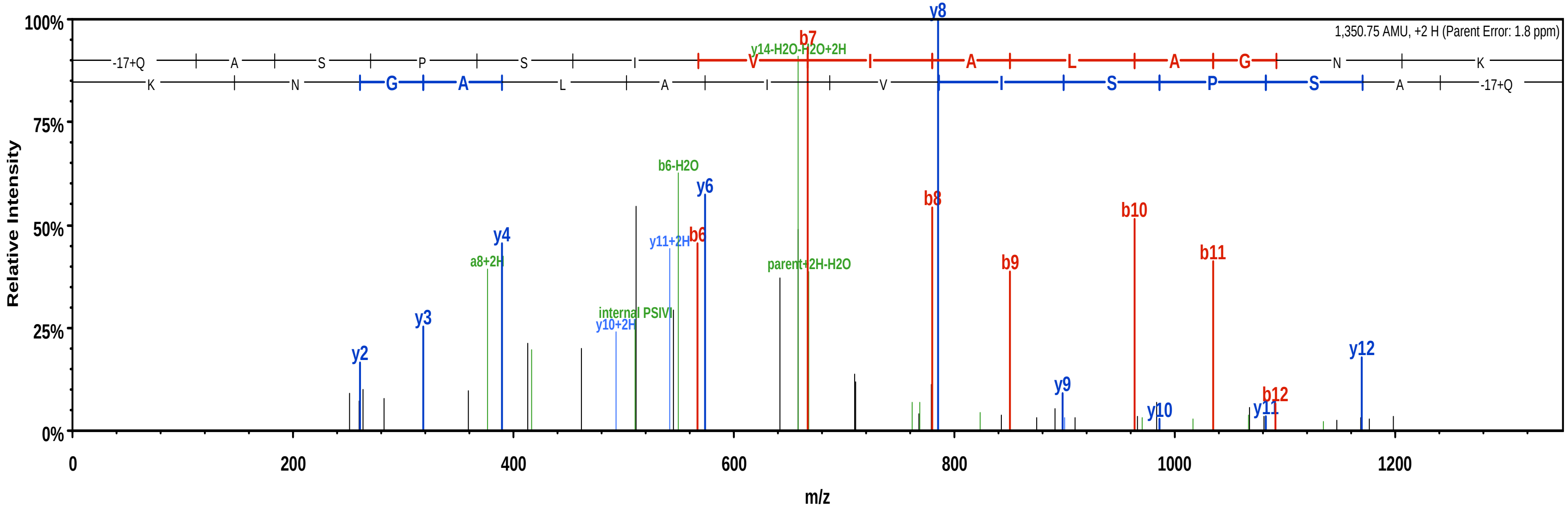


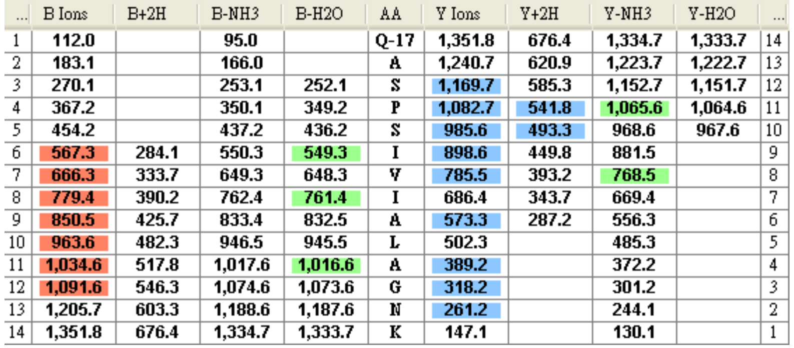


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	2,132.0	1,066.5	2,114.9	2,114.0	17
2	201.1			183.1	S	2,018.9	1,009.9	2,001.9	2,000.9	16
3	338.2	169.6		320.2	H	1,931.8	966.4	1,914.8	1,913.8	15
4	425.2	213.1		407.2	S	1,794.8	897.9	1,777.8	1,776.8	14
5	540.2	270.6		522.2	D	1,707.8	854.4	1,690.7	1,689.7	13
6	669.3	335.1		651.3	E	1,592.7	796.9	1,575.7	1,574.7	12
7	797.4	399.2	780.4	779.4	K	1,463.7	732.3	1,446.7		11
8	894.4	447.7	877.4	876.4	P	1,335.6	668.3	1,318.6		10
9	1,057.5	529.3	1,040.5	1,039.5	Y	1,238.5	619.8	1,221.5		9
10	1,185.6	593.3	1,168.5	1,167.5	Q	1,075.5	538.2	1,058.5		8
11	1,345.6	673.3	1,328.6	1,327.6	C+57	947.4	474.2	930.4		7
12	1,442.6	721.8	1,425.6	1,424.6	P	787.4	394.2	770.4		6
13	1,541.7	771.4	1,524.7	1,523.7	V	690.3		673.3		5
14	1,701.7	851.4	1,684.7	1,683.7	C+57	591.3		574.2		4
15	1,829.8	915.4	1,812.8	1,811.8	Q	431.2		414.2		3
16	1,957.9	979.4	1,940.8	1,939.8	Q	303.2		286.2		2
17	2,132.0	1,066.5	2,114.9	2,114.0	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-66	sp|P61020|RAB5B_HUMAN	QASPSIVIALAGNK	57.67	Gln->pyro-Glu (N-term Q)	Light	2	676.38263

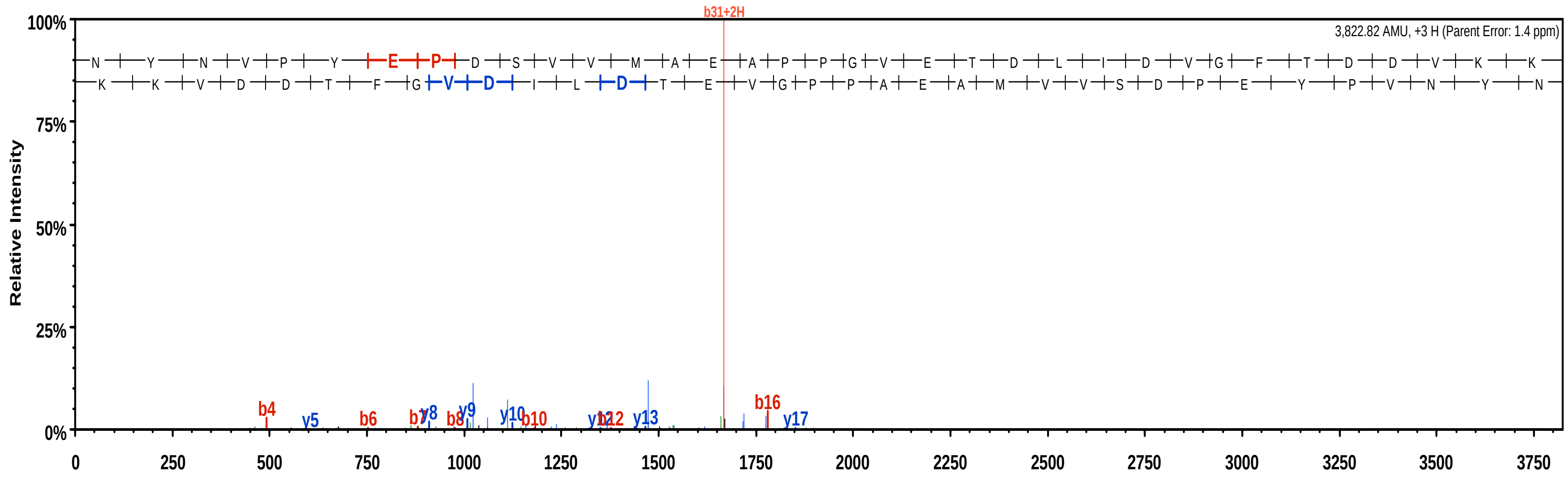


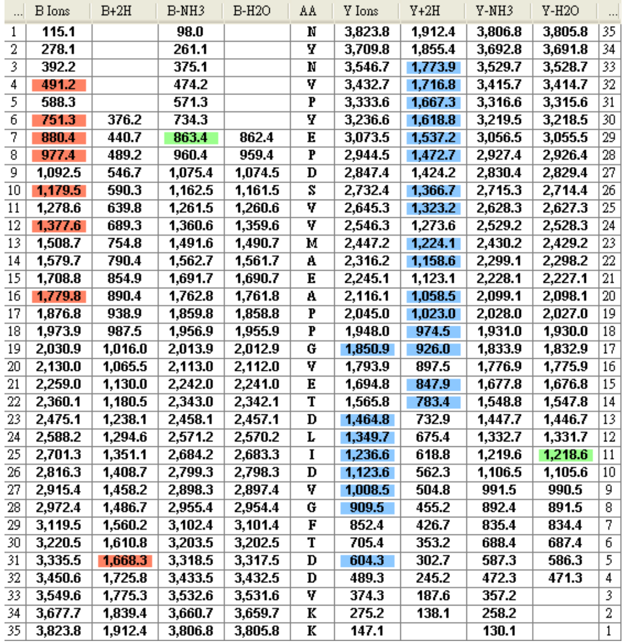


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	1,351.8	676.4	1,334.7	1,333.7	14
2	183.1		166.0		A	1,240.7	620.9	1,223.7	1,222.7	13
3	270.1		253.1	252.1	S	1,169.7	585.3	1,152.7	1,151.7	12
4	367.2		350.1	349.2	P	1,082.7	541.8	1,065.6	1,064.6	11
5	454.2		437.2	436.2	S	985.6	493.3	968.6	967.6	10
6	567.3	284.1	550.3	549.3	I	898.6	449.8	881.5		9
7	666.3	333.7	649.3	648.3	V	785.5	393.2	768.5		8
8	779.4	390.2	762.4	761.4	I	686.4	343.7	669.4		7
9	850.5	425.7	833.4	832.5	A	573.3	287.2	556.3		6
10	963.6	482.3	946.5	945.5	L	502.3		485.3		5
11	1,034.6	517.8	1,017.6	1,016.6	A	389.2		372.2		4
12	1,091.6	546.3	1,074.6	1,073.6	G	318.2		301.2		3
13	1,205.7	603.3	1,188.6	1,187.6	N	261.2		244.1		2
14	1,351.8	676.4	1,334.7	1,333.7	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-67	sp|P53990|K0174_HUMAN	NYNVPYEPDSVVMAEAPPGVETDLIDVGFTDDVKK	57.13	Unmodified	Light	3	1275.2801

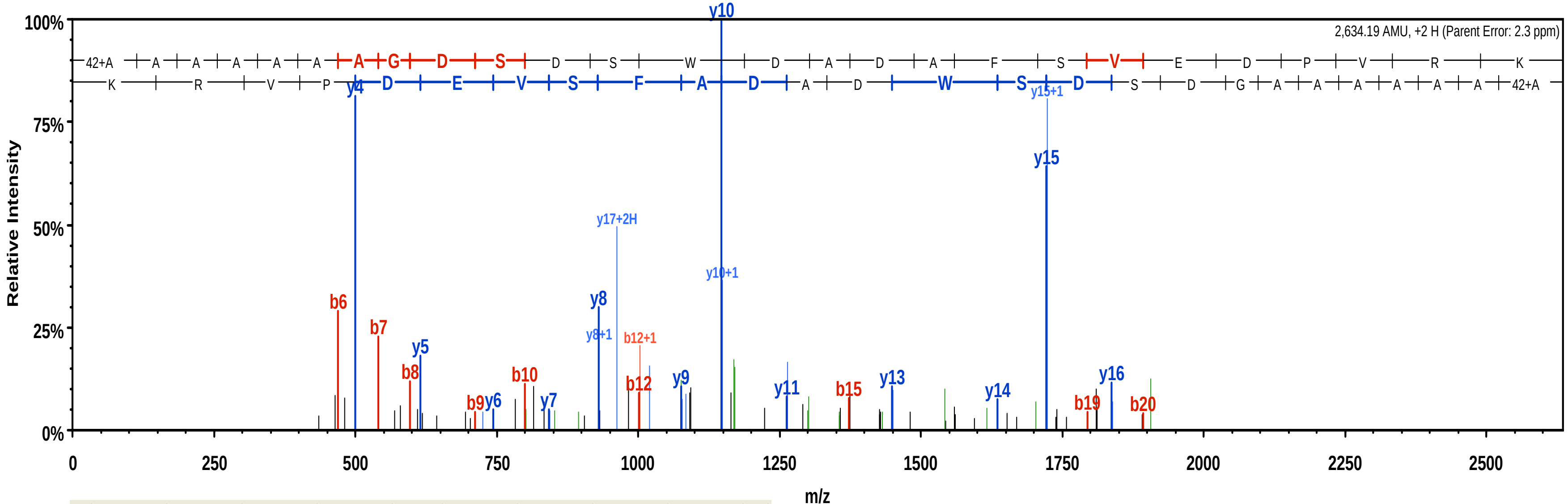


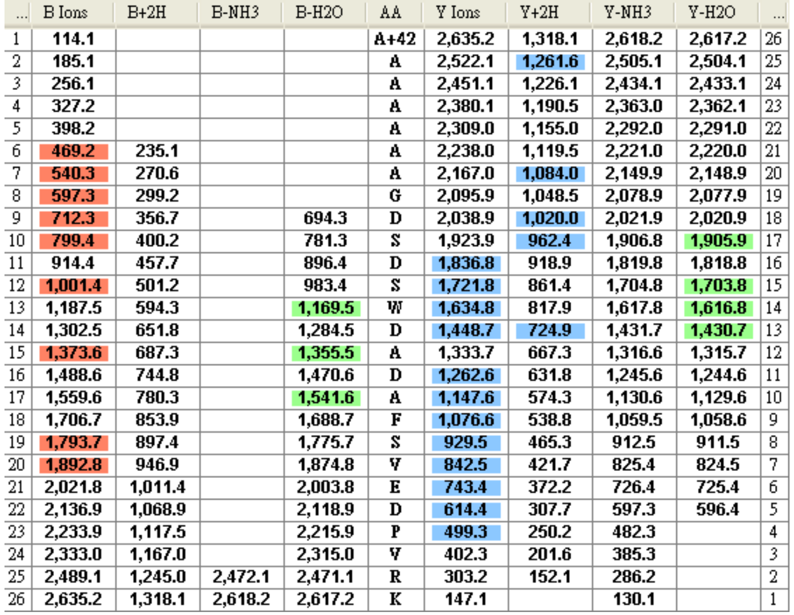


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	115.1		98.0		N	3,823.8	1,912.4	3,806.8	3,805.8	35
2	278.1		261.1		Y	3,709.8	1,855.4	3,692.8	3,691.8	34
3	392.2		375.1		N	3,546.7	1,773.9	3,529.7	3,528.7	33
4	491.2		474.2		V	3,432.7	1,716.8	3,415.7	3,414.7	32
5	588.3		571.3		P	3,333.6	1,667.3	3,316.6	3,315.6	31
6	751.3	376.2	734.3		Y	3,236.6	1,618.8	3,219.5	3,218.5	30
7	880.4	440.7	863.4	862.4	E	3,073.5	1,537.2	3,056.5	3,055.5	29
8	977.4	489.2	960.4	959.4	P	2,944.5	1,472.7	2,927.4	2,926.4	28
9	1,092.5	546.7	1,075.4	1,074.5	D	2,847.4	1,424.2	2,830.4	2,829.4	27
10	1,179.5	590.3	1,162.5	1,161.5	S	2,732.4	1,366.7	2,715.3	2,714.4	26
11	1,278.6	639.8	1,261.5	1,260.6	V	2,645.3	1,323.2	2,628.3	2,627.3	25
12	1,377.6	689.3	1,360.6	1,359.6	V	2,546.3	1,273.6	2,529.2	2,528.3	24
13	1,508.7	754.8	1,491.6	1,490.7	M	2,447.2	1,224.1	2,430.2	2,429.2	23
14	1,579.7	790.4	1,562.7	1,561.7	A	2,316.2	1,158.6	2,299.1	2,298.2	22
15	1,708.8	854.9	1,691.7	1,690.7	E	2,245.1	1,123.1	2,228.1	2,227.1	21
16	1,779.8	890.4	1,762.8	1,761.8	A	2,116.1	1,058.5	2,099.1	2,098.1	20
17	1,876.8	938.9	1,859.8	1,858.8	P	2,045.0	1,023.0	2,028.0	2,027.0	19
18	1,973.9	987.5	1,956.9	1,955.9	P	1,948.0	974.5	1,931.0	1,930.0	18
19	2,030.9	1,016.0	2,013.9	2,012.9	G	1,850.9	926.0	1,833.9	1,832.9	17
20	2,130.0	1,065.5	2,113.0	2,112.0	V	1,793.9	897.5	1,776.9	1,775.9	16
21	2,259.0	1,130.0	2,242.0	2,241.0	E	1,694.8	847.9	1,677.8	1,676.8	15
22	2,360.1	1,180.5	2,343.0	2,342.1	T	1,565.8	783.4	1,548.8	1,547.8	14
23	2,475.1	1,238.1	2,458.1	2,457.1	D	1,464.8	732.9	1,447.7	1,446.7	13
24	2,588.2	1,294.6	2,571.2	2,570.2	L	1,349.7	675.4	1,332.7	1,331.7	12
25	2,701.3	1,351.1	2,684.2	2,683.3	I	1,236.6	618.8	1,219.6	1,218.6	11
26	2,816.3	1,408.7	2,799.3	2,798.3	D	1,123.6	562.3	1,106.5	1,105.6	10
27	2,915.4	1,458.2	2,898.3	2,897.4	V	1,008.5	504.8	991.5	990.5	9
28	2,972.4	1,486.7	2,955.4	2,954.4	G	909.5	455.2	892.4	891.5	8
29	3,119.5	1,560.2	3,102.4	3,101.4	F	852.4	426.7	835.4	834.4	7
30	3,220.5	1,610.8	3,203.5	3,202.5	T	705.4	353.2	688.4	687.4	6
31	3,335.5	1,668.3	3,318.5	3,317.5	D	604.3	302.7	587.3	586.3	5
32	3,450.6	1,725.8	3,433.5	3,432.5	D	489.3	245.2	472.3	471.3	4
33	3,549.6	1,775.3	3,532.6	3,531.6	V	374.3	187.6	357.2		3
34	3,677.7	1,839.4	3,660.7	3,659.7	K	275.2	138.1	258.2		2
35	3,823.8	1,912.4	3,806.8	3,805.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-68	sp|O75822|EIF3J_HUMAN	AAAAAAAGDSDSWDADAFSVEDPVRK	56.92	Acetyl (Protein N-term)	Light	2	1318.099

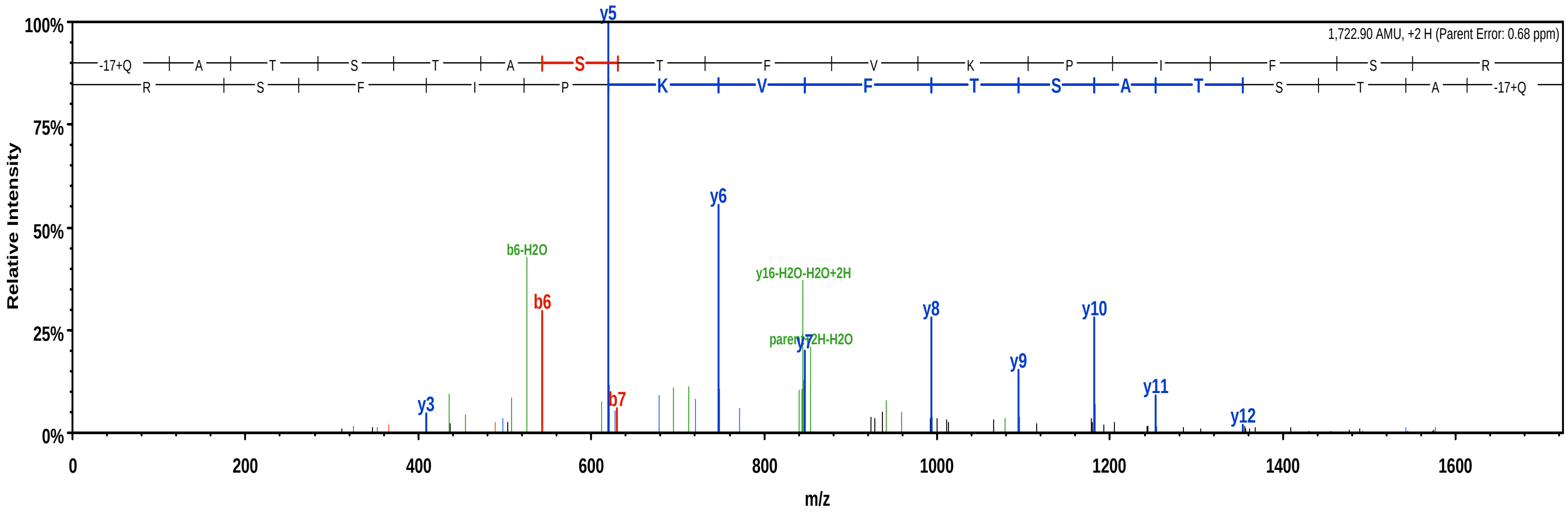


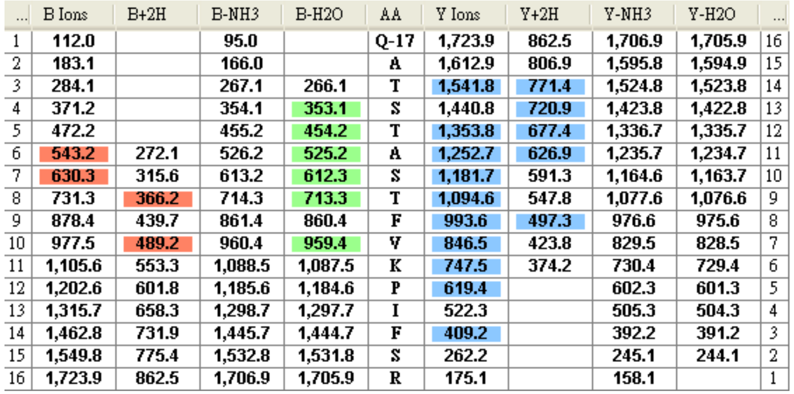


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	2,635.2	1,318.1	2,618.2	2,617.2	26
2	185.1				A	2,522.1	1,261.6	2,505.1	2,504.1	25
3	256.1				A	2,451.1	1,226.1	2,434.1	2,433.1	24
4	327.2				A	2,380.1	1,190.5	2,363.0	2,362.1	23
5	398.2				A	2,309.0	1,155.0	2,292.0	2,291.0	22
6	469.2	235.1			A	2,238.0	1,119.5	2,221.0	2,220.0	21
7	540.3	270.6			A	2,167.0	1,084.0	2,149.9	2,148.9	20
8	597.3	299.2			G	2,095.9	1,048.5	2,078.9	2,077.9	19
9	712.3	356.7		694.3	D	2,038.9	1,020.0	2,021.9	2,020.9	18
10	799.4	400.2		781.3	S	1,923.9	962.4	1,906.8	1,905.9	17
11	914.4	457.7		896.4	D	1,836.8	918.9	1,819.8	1,818.8	16
12	1,001.4	501.2		983.4	S	1,721.8	861.4	1,704.8	1,703.8	15
13	1,187.5	594.3		1,169.5	W	1,634.8	817.9	1,617.8	1,616.8	14
14	1,302.5	651.8		1,284.5	D	1,448.7	724.9	1,431.7	1,430.7	13
15	1,373.6	687.3		1,355.5	A	1,333.7	667.3	1,316.6	1,315.7	12
16	1,488.6	744.8		1,470.6	D	1,262.6	631.8	1,245.6	1,244.6	11
17	1,559.6	780.3		1,541.6	A	1,147.6	574.3	1,130.6	1,129.6	10
18	1,706.7	853.9		1,688.7	F	1,076.6	538.8	1,059.5	1,058.6	9
19	1,793.7	897.4		1,775.7	S	929.5	465.3	912.5	911.5	8
20	1,892.8	946.9		1,874.8	V	842.5	421.7	825.4	824.5	7
21	2,021.8	1,011.4		2,003.8	E	743.4	372.2	726.4	725.4	6
22	2,136.9	1,068.9		2,118.9	D	614.4	307.7	597.3	596.4	5
23	2,233.9	1,117.5		2,215.9	P	499.3	250.2	482.3		4
24	2,333.0	1,167.0		2,315.0	V	402.3	201.6	385.3		3
25	2,489.1	1,245.0	2,472.1	2,471.1	R	303.2	152.1	286.2		2
26	2,635.2	1,318.1	2,618.2	2,617.2	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-69	sp|P56556|NDUA6_HUMAN	QATSTASTFVKPIFSR	56.84	Gln->pyro-Glu (N-term Q)	Light	2	862.45432

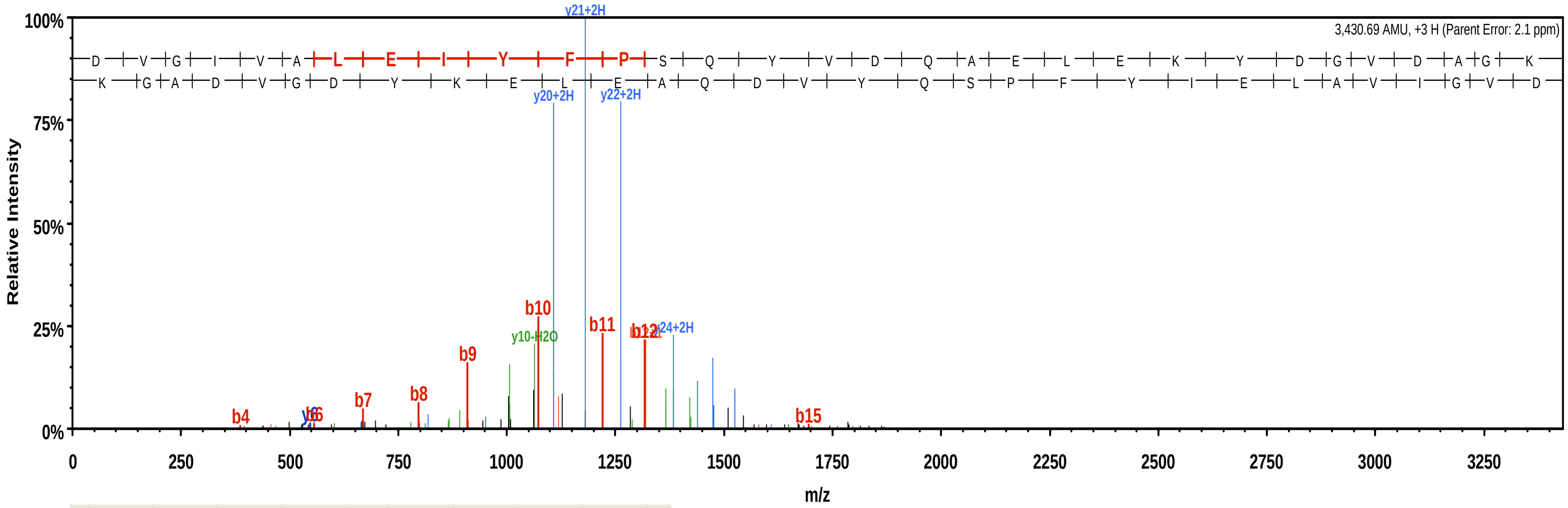


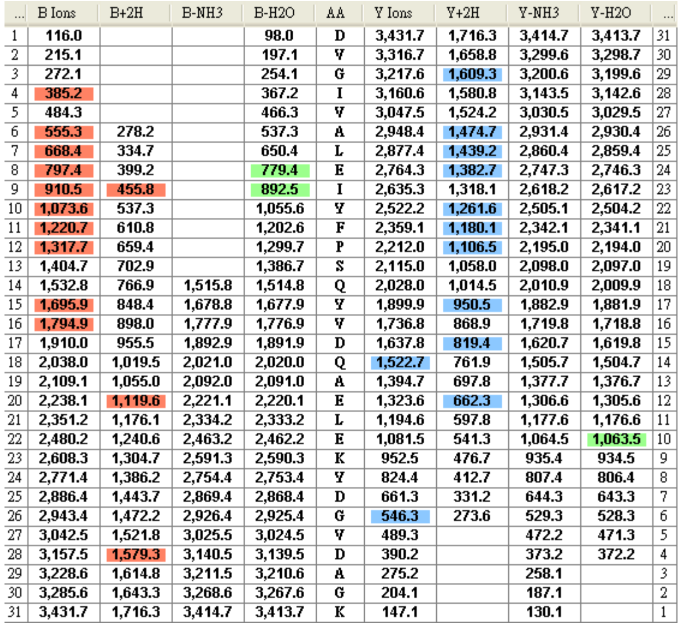


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	1,723.9	862.5	1,706.9	1,705.9	16
2	183.1		166.0		A	1,612.9	806.9	1,595.8	1,594.9	15
3	284.1		267.1	266.1	T	1,541.8	771.4	1,524.8	1,523.8	14
4	371.2		354.1	353.1	S	1,440.8	720.9	1,423.8	1,422.8	13
5	472.2		455.2	454.2	T	1,353.8	677.4	1,336.7	1,335.7	12
6	543.2	272.1	526.2	525.2	A	1,252.7	626.9	1,235.7	1,234.7	11
7	630.3	315.6	613.2	612.3	S	1,181.7	591.3	1,164.6	1,163.7	10
8	731.3	366.2	714.3	713.3	T	1,094.6	547.8	1,077.6	1,076.6	9
9	878.4	439.7	861.4	860.4	F	993.6	497.3	976.6	975.6	8
10	977.5	489.2	960.4	959.4	V	846.5	423.8	829.5	828.5	7
11	1,105.6	553.3	1,088.5	1,087.5	K	747.5	374.2	730.4	729.4	6
12	1,202.6	601.8	1,185.6	1,184.6	P	619.4		602.3	601.3	5
13	1,315.7	658.3	1,298.7	1,297.7	I	522.3		505.3	504.3	4
14	1,462.8	731.9	1,445.7	1,444.7	F	409.2		392.2	391.2	3
15	1,549.8	775.4	1,532.8	1,531.8	S	262.2		245.1	244.1	2
16	1,723.9	862.5	1,706.9	1,705.9	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-70	sp|Q01581|HMCS1_HUMAN	DVGIVALEIYFPSQYVDQAELEKYDGVDAGK	56.18	Unmodified	Light	3	1144.568

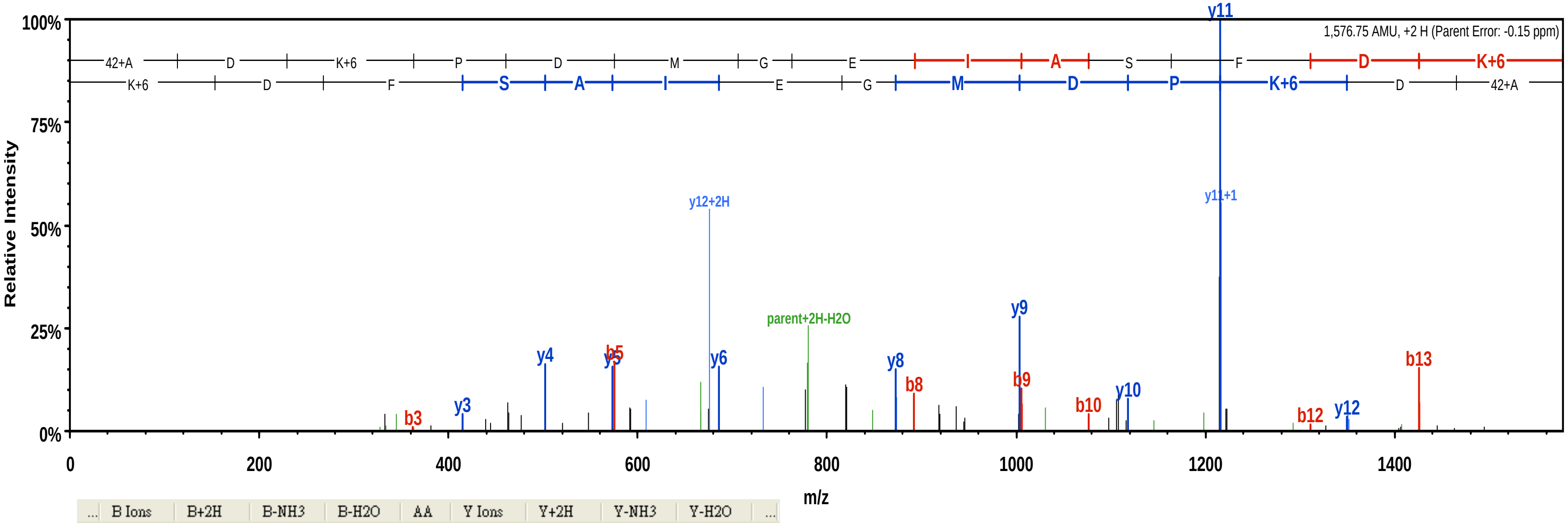


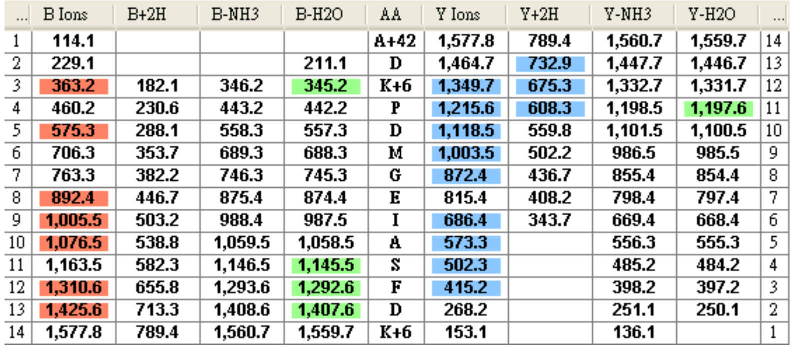


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	3,431.7	1,716.3	3,414.7	3,413.7	31
2	215.1			197.1	V	3,316.7	1,658.8	3,299.6	3,298.7	30
3	272.1			254.1	G	3,217.6	1,609.3	3,200.6	3,199.6	29
4	385.2			367.2	I	3,160.6	1,580.8	3,143.5	3,142.6	28
5	484.3			466.3	V	3,047.5	1,524.2	3,030.5	3,029.5	27
6	555.3	278.2		537.3	A	2,948.4	1,474.7	2,931.4	2,930.4	26
7	668.4	334.7		650.4	L	2,877.4	1,439.2	2,860.4	2,859.4	25
8	797.4	399.2		779.4	E	2,764.3	1,382.7	2,747.3	2,746.3	24
9	910.5	455.8		892.5	I	2,635.3	1,318.1	2,618.2	2,617.2	23
10	1,073.6	537.3		1,055.6	Y	2,522.2	1,261.6	2,505.1	2,504.2	22
11	1,220.7	610.8		1,202.6	F	2,359.1	1,180.1	2,342.1	2,341.1	21
12	1,317.7	659.4		1,299.7	P	2,212.0	1,106.5	2,195.0	2,194.0	20
13	1,404.7	702.9		1,386.7	S	2,115.0	1,058.0	2,098.0	2,097.0	19
14	1,532.8	766.9	1,515.8	1,514.8	Q	2,028.0	1,014.5	2,010.9	2,009.9	18
15	1,695.9	848.4	1,678.8	1,677.9	Y	1,899.9	950.5	1,882.9	1,881.9	17
16	1,794.9	898.0	1,777.9	1,776.9	V	1,736.8	868.9	1,719.8	1,718.8	16
17	1,910.0	955.5	1,892.9	1,891.9	D	1,637.8	819.4	1,620.7	1,619.8	15
18	2,038.0	1,019.5	2,021.0	2,020.0	Q	1,522.7	761.9	1,505.7	1,504.7	14
19	2,109.1	1,055.0	2,092.0	2,091.0	A	1,394.7	697.8	1,377.7	1,376.7	13
20	2,238.1	1,119.6	2,221.1	2,220.1	E	1,323.6	662.3	1,306.6	1,305.6	12
21	2,351.2	1,176.1	2,334.2	2,333.2	L	1,194.6	597.8	1,177.6	1,176.6	11
22	2,480.2	1,240.6	2,463.2	2,462.2	E	1,081.5	541.3	1,064.5	1,063.5	10
23	2,608.3	1,304.7	2,591.3	2,590.3	K	952.5	476.7	935.4	934.5	9
24	2,771.4	1,386.2	2,754.4	2,753.4	Y	824.4	412.7	807.4	806.4	8
25	2,886.4	1,443.7	2,869.4	2,868.4	D	661.3	331.2	644.3	643.3	7
26	2,943.4	1,472.2	2,926.4	2,925.4	G	546.3	273.6	529.3	528.3	6
27	3,042.5	1,521.8	3,025.5	3,024.5	V	489.3		472.2	471.3	5
28	3,157.5	1,579.3	3,140.5	3,139.5	D	390.2		373.2	372.2	4
29	3,228.6	1,614.8	3,211.5	3,210.6	A	275.2		258.1		3
30	3,285.6	1,643.3	3,268.6	3,267.6	G	204.1		187.1		2
31	3,431.7	1,716.3	3,414.7	3,413.7	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-71	splP63313lTYB10_HUMAN	ADKPDMGEIASFDK	55.89	Acetyl (Protein N-term)	Heavy	2	783.36124

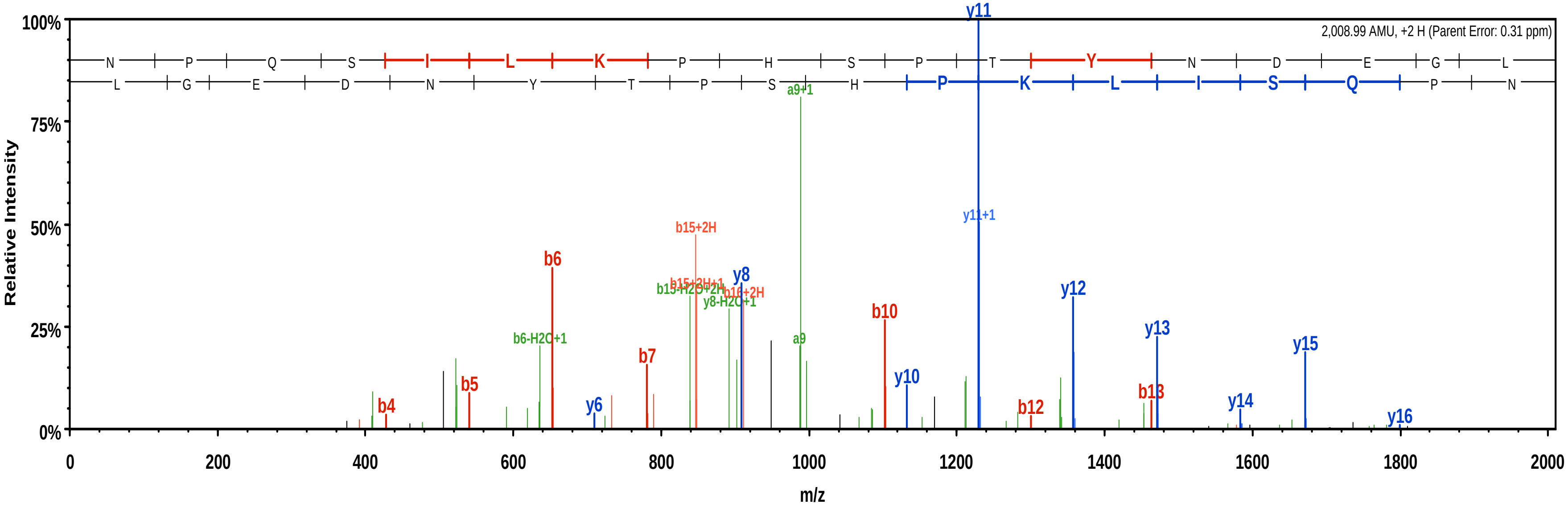


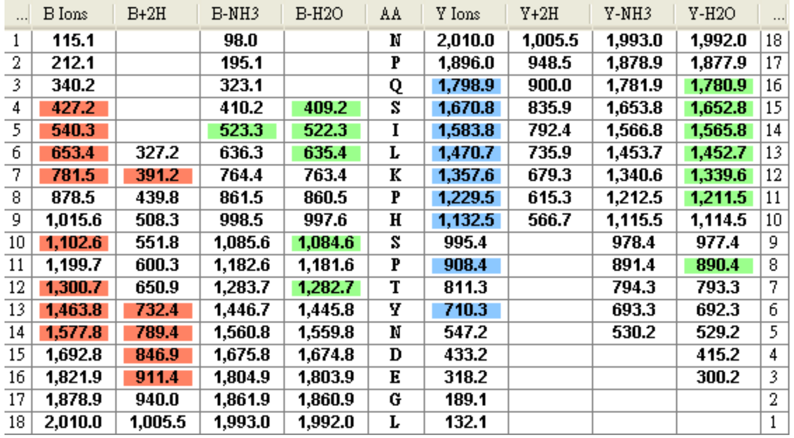


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	1,577.8	789.4	1,560.7	1,559.7	14
2	229.1			211.1	D	1,464.7	732.9	1,447.7	1,446.7	13
3	363.2	182.1	346.2	345.2	K+6	1,349.7	675.3	1,332.7	1,331.7	12
4	460.2	230.6	443.2	442.2	P	1,215.6	608.3	1,198.5	1,197.6	11
5	575.3	288.1	558.3	557.3	D	1,118.5	559.8	1,101.5	1,100.5	10
6	706.3	353.7	689.3	688.3	M	1,003.5	502.2	986.5	985.5	9
7	763.3	382.2	746.3	745.3	G	872.4	436.7	855.4	854.4	8
8	892.4	446.7	875.4	874.4	E	815.4	408.2	798.4	797.4	7
9	1,005.5	503.2	988.4	987.5	I	686.4	343.7	669.4	668.4	6
10	1,076.5	538.8	1,059.5	1,058.5	A	573.3		556.3	555.3	5
11	1,163.5	582.3	1,146.5	1,145.5	S	502.3		485.2	484.2	4
12	1,310.6	655.8	1,293.6	1,292.6	F	415.2		398.2	397.2	3
13	1,425.6	713.3	1,408.6	1,407.6	D	268.2		251.1	250.1	2
14	1,577.8	789.4	1,560.7	1,559.7	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-72	sp|Q9NVA1|UQCC_HUMAN	NPQSILKPHSPTYNDEGL	55.83	Unmodified	Light	2	1005.5

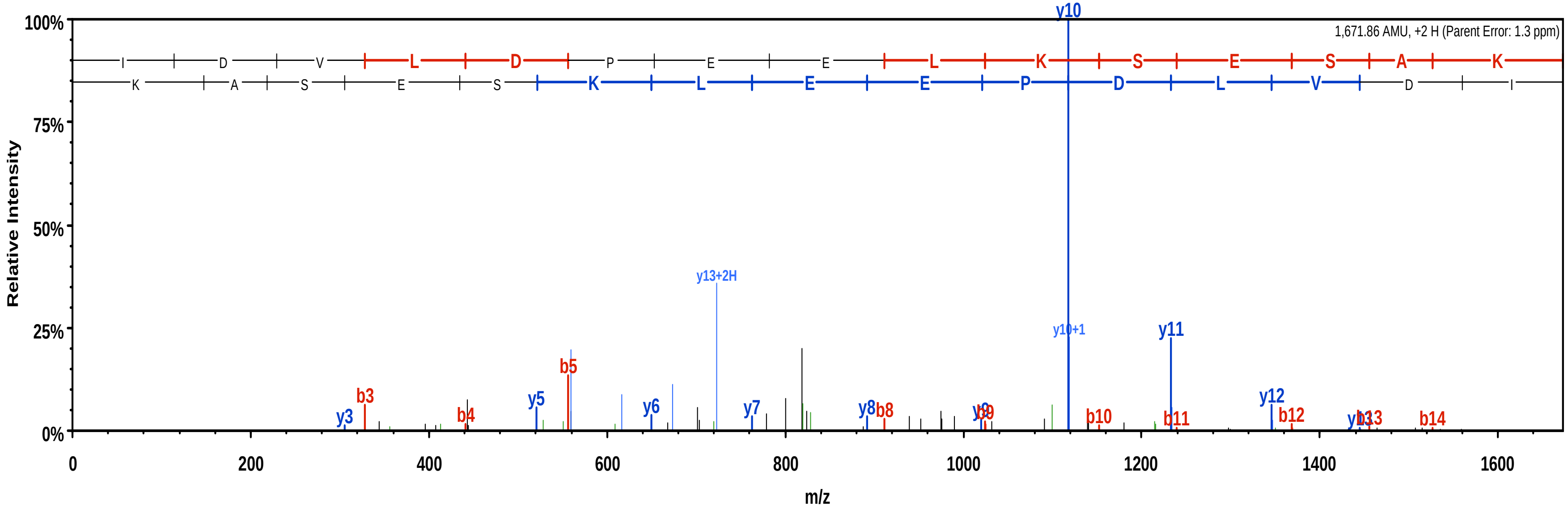


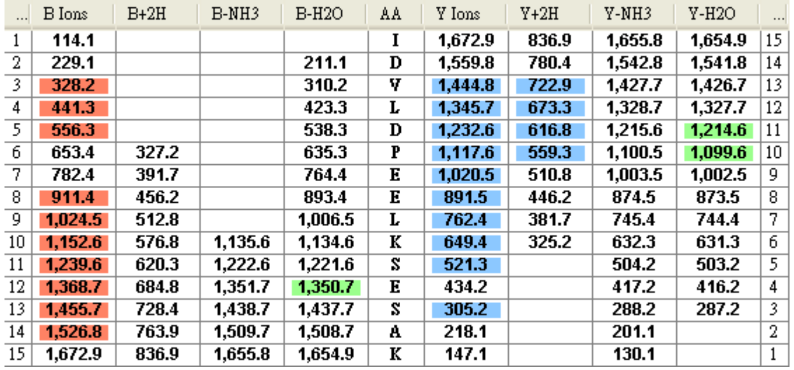


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	115.1		98.0		N	2,010.0	1,005.5	1,993.0	1,992.0	18
2	212.1		195.1		P	1,896.0	948.5	1,878.9	1,877.9	17
3	340.2		323.1		Q	1,798.9	900.0	1,781.9	1,780.9	16
4	427.2		410.2	409.2	S	1,670.8	835.9	1,653.8	1,652.8	15
5	540.3		523.3	522.3	I	1,583.8	792.4	1,566.8	1,565.8	14
6	653.4	327.2	636.3	635.4	L	1,470.7	735.9	1,453.7	1,452.7	13
7	781.5	391.2	764.4	763.4	K	1,357.6	679.3	1,340.6	1,339.6	12
8	878.5	439.8	861.5	860.5	P	1,229.5	615.3	1,212.5	1,211.5	11
9	1,015.6	508.3	998.5	997.6	H	1,132.5	566.7	1,115.5	1,114.5	10
10	1,102.6	551.8	1,085.6	1,084.6	S	995.4		978.4	977.4	9
11	1,199.7	600.3	1,182.6	1,181.6	P	908.4		891.4	890.4	8
12	1,300.7	650.9	1,283.7	1,282.7	T	811.3		794.3	793.3	7
13	1,463.8	732.4	1,446.7	1,445.8	Y	710.3		693.3	692.3	6
14	1,577.8	789.4	1,560.8	1,559.8	N	547.2		530.2	529.2	5
15	1,692.8	846.9	1,675.8	1,674.8	D	433.2			415.2	4
16	1,821.9	911.4	1,804.9	1,803.9	E	318.2			300.2	3
17	1,878.9	940.0	1,861.9	1,860.9	G	189.1				2
18	2,010.0	1,005.5	1,993.0	1,992.0	L	132.1				1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-73	sp|Q9BVG4|CX026_HUMAN	IDVLDPEELKSESAK	55.57	Unmodified	Light	2	836.93562

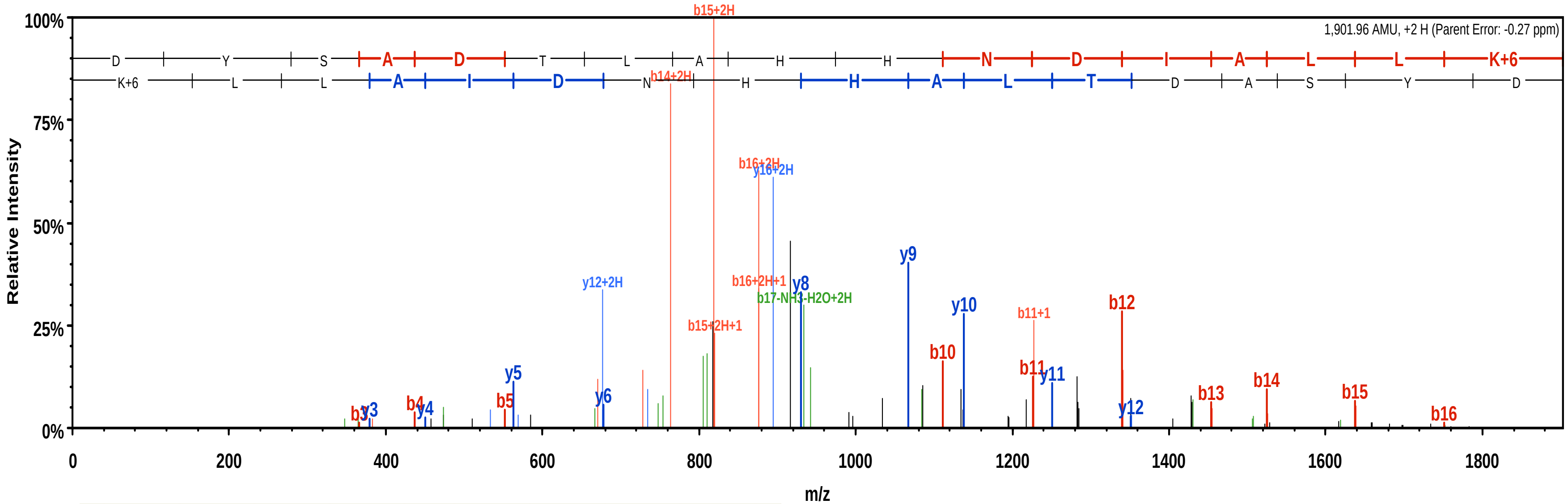


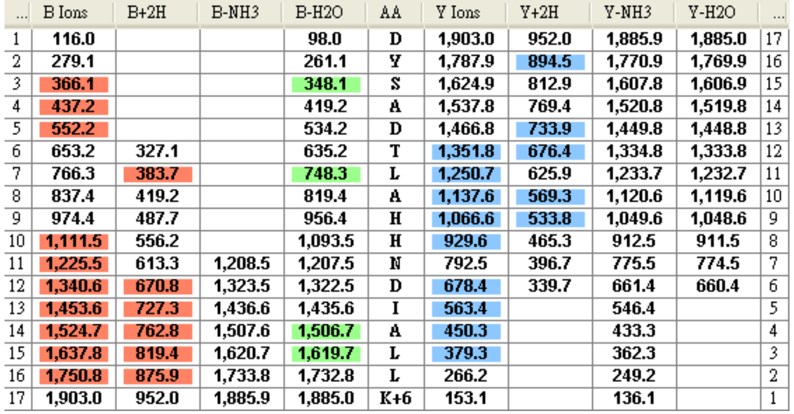


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	1,672.9	836.9	1,655.8	1,654.9	15
2	229.1			211.1	D	1,559.8	780.4	1,542.8	1,541.8	14
3	328.2			310.2	V	1,444.8	722.9	1,427.7	1,426.7	13
4	441.3			423.3	L	1,345.7	673.3	1,328.7	1,327.7	12
5	556.3			538.3	D	1,232.6	616.8	1,215.6	1,214.6	11
6	653.4	327.2		635.3	P	1,117.6	559.3	1,100.5	1,099.6	10
7	782.4	391.7		764.4	E	1,020.5	510.8	1,003.5	1,002.5	9
8	911.4	456.2		893.4	E	891.5	446.2	874.5	873.5	8
9	1,024.5	512.8		1,006.5	L	762.4	381.7	745.4	744.4	7
10	1,152.6	576.8	1,135.6	1,134.6	K	649.4	325.2	632.3	631.3	6
11	1,239.6	620.3	1,222.6	1,221.6	S	521.3		504.2	503.2	5
12	1,368.7	684.8	1,351.7	1,350.7	E	434.2		417.2	416.2	4
13	1,455.7	728.4	1,438.7	1,437.7	S	305.2		288.2	287.2	3
14	1,526.8	763.9	1,509.7	1,508.7	A	218.1		201.1		2
15	1,672.9	836.9	1,655.8	1,654.9	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-74	splP00749lUROK_HUMAN	DYSADTLAHHNDIALLK	54.07	Unmodified	Heavy	2	948.97615

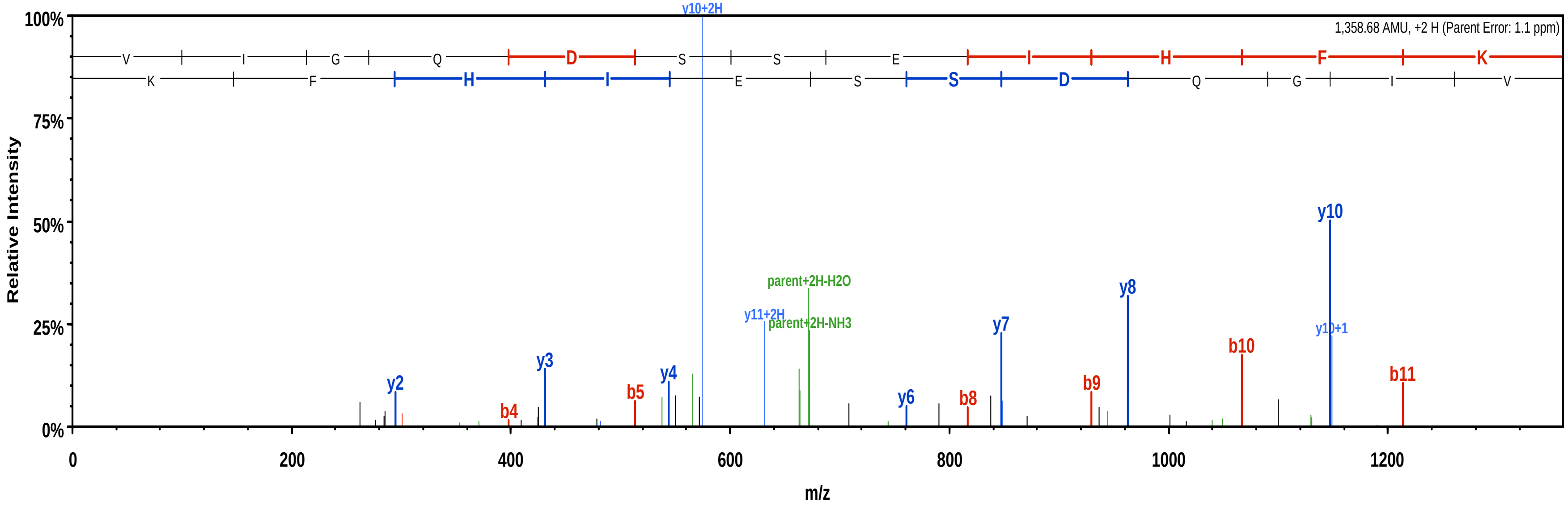


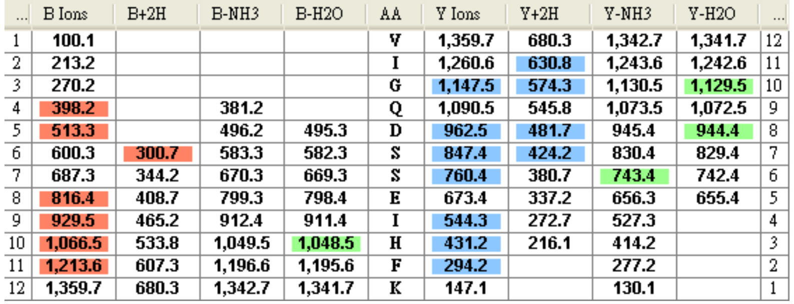


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	1,903.0	952.0	1,885.9	1,885.0	17
2	279.1			261.1	Y	1,787.9	894.5	1,770.9	1,769.9	16
3	366.1			348.1	S	1,624.9	812.9	1,607.8	1,606.9	15
4	437.2			419.2	A	1,537.8	769.4	1,520.8	1,519.8	14
5	552.2			534.2	D	1,466.8	733.9	1,449.8	1,448.8	13
6	653.2	327.1		635.2	T	1,351.8	676.4	1,334.8	1,333.8	12
7	766.3	383.7		748.3	L	1,250.7	625.9	1,233.7	1,232.7	11
8	837.4	419.2		819.4	A	1,137.6	569.3	1,120.6	1,119.6	10
9	974.4	487.7		956.4	H	1,066.6	533.8	1,049.6	1,048.6	9
10	1,111.5	556.2		1,093.5	H	929.6	465.3	912.5	911.5	8
11	1,225.5	613.3	1,208.5	1,207.5	N	792.5	396.7	775.5	774.5	7
12	1,340.6	670.8	1,323.5	1,322.5	D	678.4	339.7	661.4	660.4	6
13	1,453.6	727.3	1,436.6	1,435.6	I	563.4		546.4		5
14	1,524.7	762.8	1,507.6	1,506.7	A	450.3		433.3		4
15	1,637.8	819.4	1,620.7	1,619.7	L	379.3		362.3		3
16	1,750.8	875.9	1,733.8	1,732.8	L	266.2		249.2		2
17	1,903.0	952.0	1,885.9	1,885.0	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-75	sp|P63165|SUMO1_HUMAN	VIGQDSSEIHFK	54.03	Unmodified	Light	2	680.34879

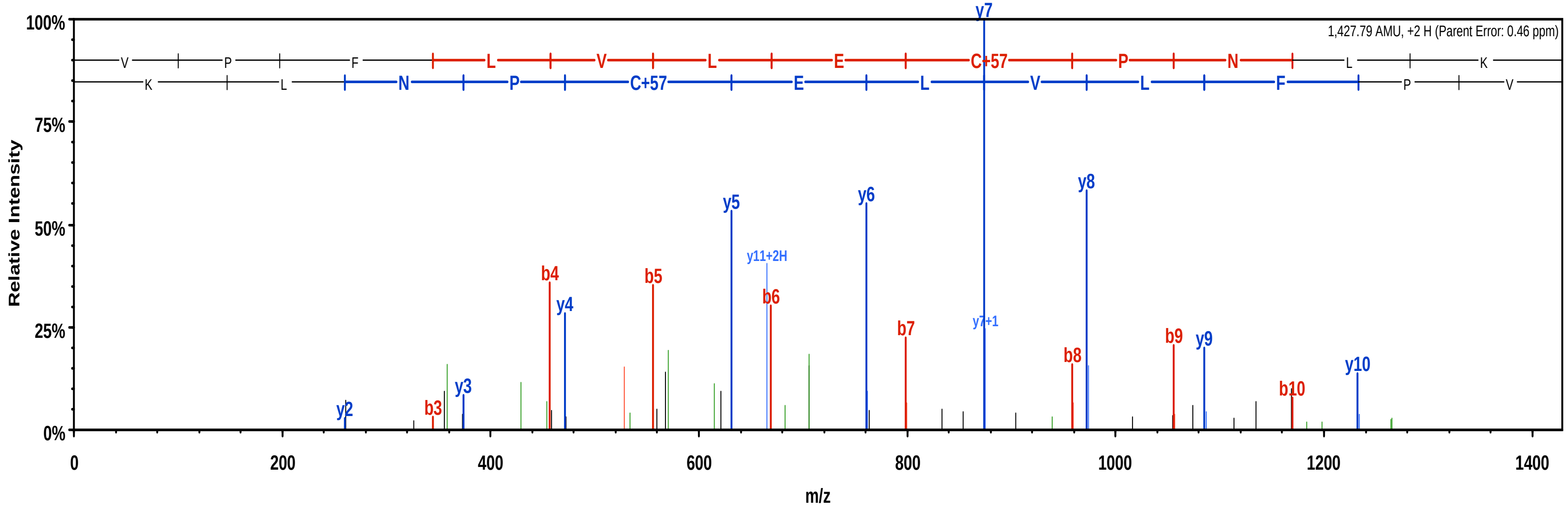


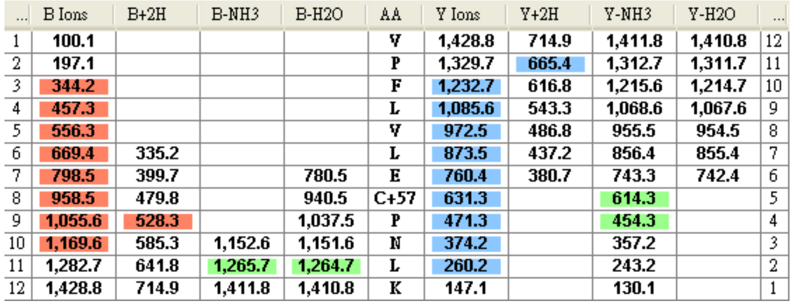


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	1,359.7	680.3	1,342.7	1,341.7	12
2	213.2				I	1,260.6	630.8	1,243.6	1,242.6	11
3	270.2				G	1,147.5	574.3	1,130.5	1,129.5	10
4	398.2		381.2		Q	1,090.5	545.8	1,073.5	1,072.5	9
5	513.3		496.2	495.3	D	962.5	481.7	945.4	944.4	8
6	600.3	300.7	583.3	582.3	S	847.4	424.2	830.4	829.4	7
7	687.3	344.2	670.3	669.3	S	760.4	380.7	743.4	742.4	6
8	816.4	408.7	799.3	798.4	E	673.4	337.2	656.3	655.4	5
9	929.5	465.2	912.4	911.4	I	544.3	272.7	527.3		4
10	1,066.5	533.8	1,049.5	1,048.5	H	431.2	216.1	414.2		3
11	1,213.6	607.3	1,196.6	1,195.6	F	294.2		277.2		2
12	1,359.7	680.3	1,342.7	1,341.7	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-76	sp|Q9NRP0|U527_HUMAN	VPFLVLECPNLK	53.58	Unmodified	Light	2	714.8996

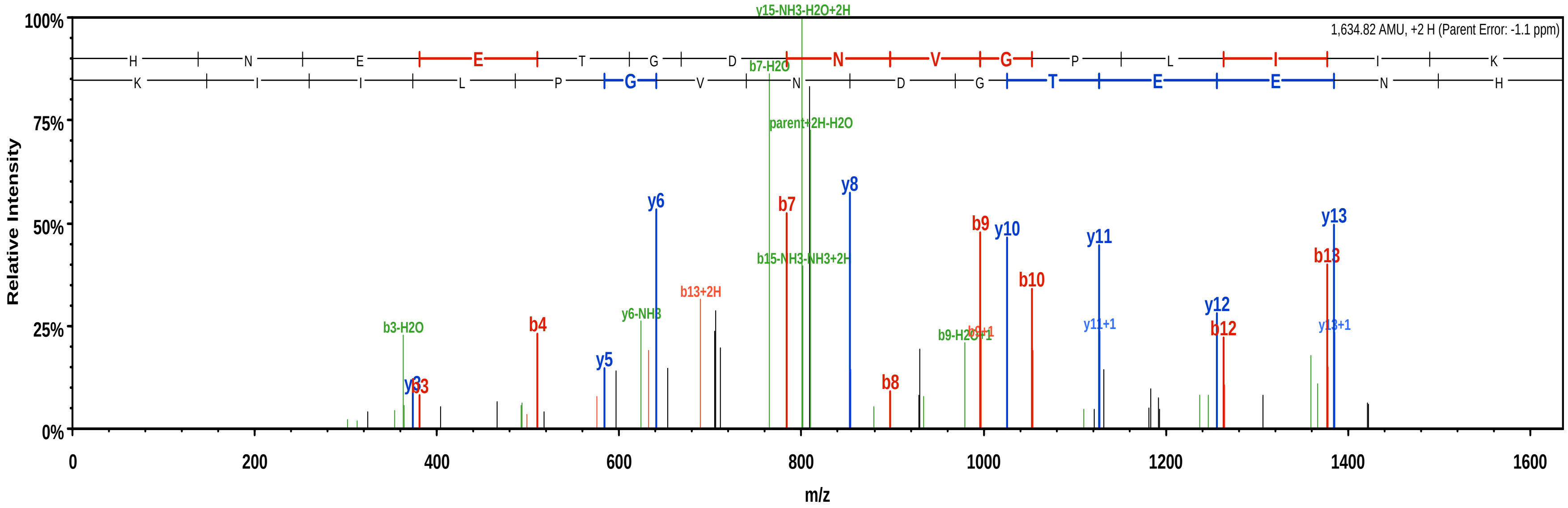


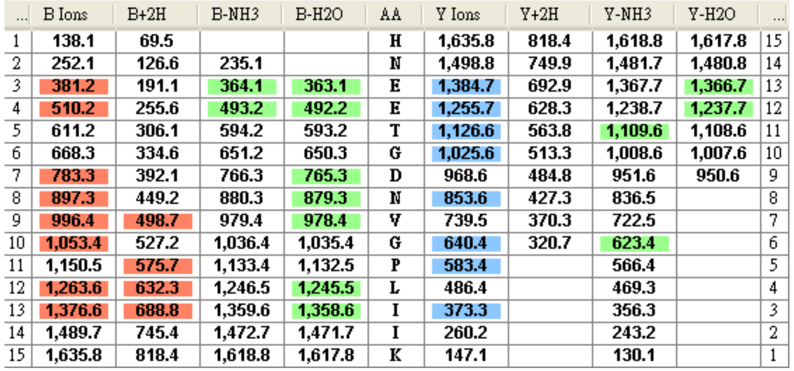


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	1,428.8	714.9	1,411.8	1,410.8	12
2	197.1				P	1,329.7	665.4	1,312.7	1,311.7	11
3	344.2				F	1,232.7	616.8	1,215.6	1,214.7	10
4	457.3				L	1,085.6	543.3	1,068.6	1,067.6	9
5	556.3				V	972.5	486.8	955.5	954.5	8
6	669.4	335.2			L	873.5	437.2	856.4	855.4	7
7	798.5	399.7		780.5	E	760.4	380.7	743.3	742.4	6
8	958.5	479.8		940.5	C+57	631.3		614.3		5
9	1,055.6	528.3		1,037.5	P	471.3		454.3		4
10	1,169.6	585.3	1,152.6	1,151.6	N	374.2		357.2		3
11	1,282.7	641.8	1,265.7	1,264.7	L	260.2		243.2		2
12	1,428.8	714.9	1,411.8	1,410.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-77	sp|Q9NZ45|CISD1_HUMAN	HNEETGDNVGPLIIK	53.38	Unmodified	Light	2	818.42048

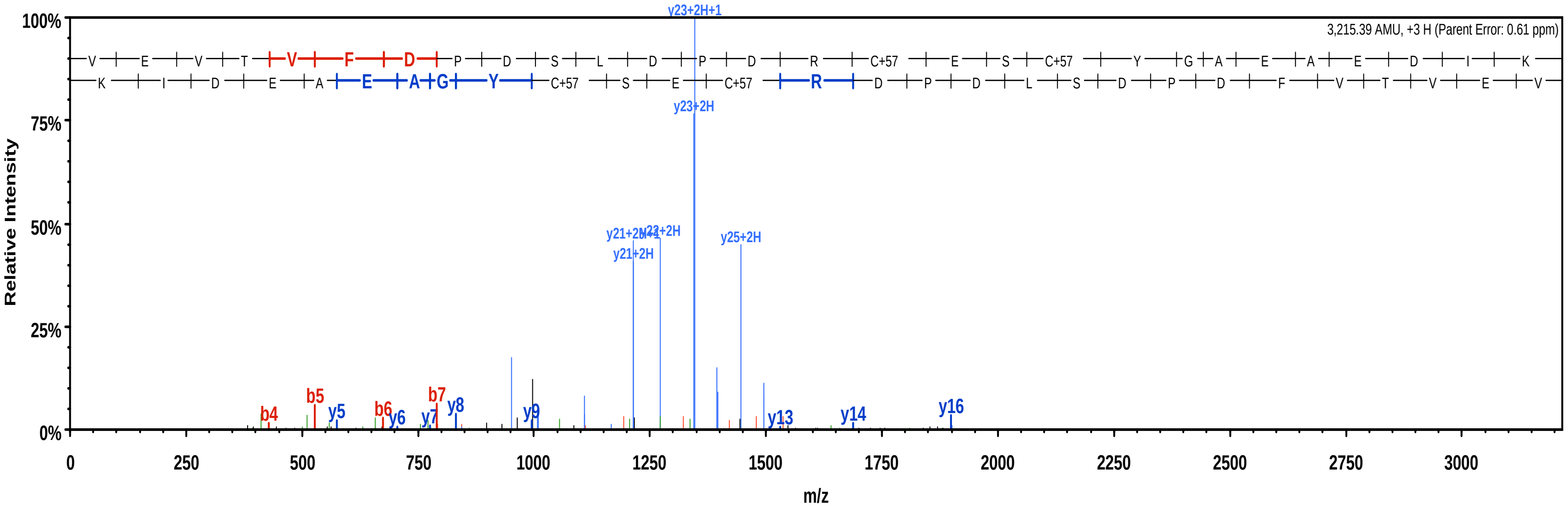


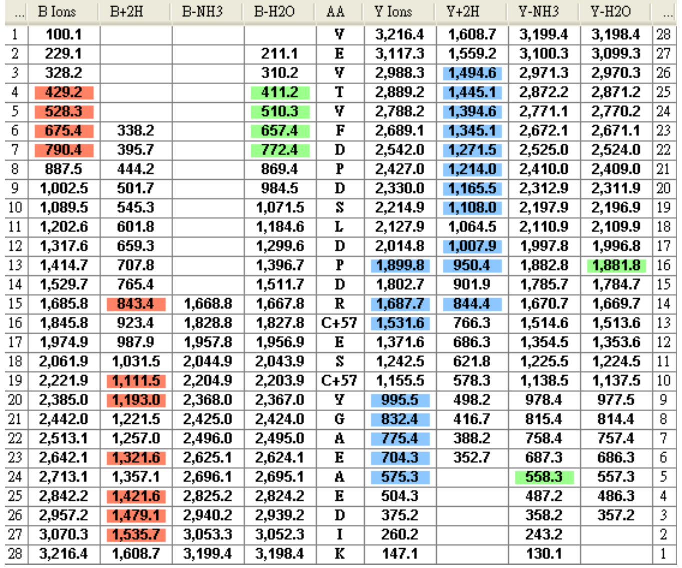


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	138.1	69.5			H	1,635.8	818.4	1,618.8	1,617.8	15
2	252.1	126.6	235.1		N	1,498.8	749.9	1,481.7	1,480.8	14
3	381.2	191.1	364.1	363.1	E	1,384.7	692.9	1,367.7	1,366.7	13
4	510.2	255.6	493.2	492.2	E	1,255.7	628.3	1,238.7	1,237.7	12
5	611.2	306.1	594.2	593.2	T	1,126.6	563.8	1,109.6	1,108.6	11
6	668.3	334.6	651.2	650.3	G	1,025.6	513.3	1,008.6	1,007.6	10
7	783.3	392.1	766.3	765.3	D	968.6	484.8	951.6	950.6	9
8	897.3	449.2	880.3	879.3	N	853.6	427.3	836.5		8
9	996.4	498.7	979.4	978.4	V	739.5	370.3	722.5		7
10	1,053.4	527.2	1,036.4	1,035.4	G	640.4	320.7	623.4		6
11	1,150.5	575.7	1,133.4	1,132.5	P	583.4		566.4		5
12	1,263.6	632.3	1,246.5	1,245.5	L	486.4		469.3		4
13	1,376.6	688.8	1,359.6	1,358.6	I	373.3		356.3		3
14	1,489.7	745.4	1,472.7	1,471.7	I	260.2		243.2		2
15	1,635.8	818.4	1,618.8	1,617.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-78	sp|Q9Y282|ERGI3_HUMAN	VEVTVFDPDSLDPDRCESCYGAEAEDIK	53.1	Unmodified	Light	3	1072.8043

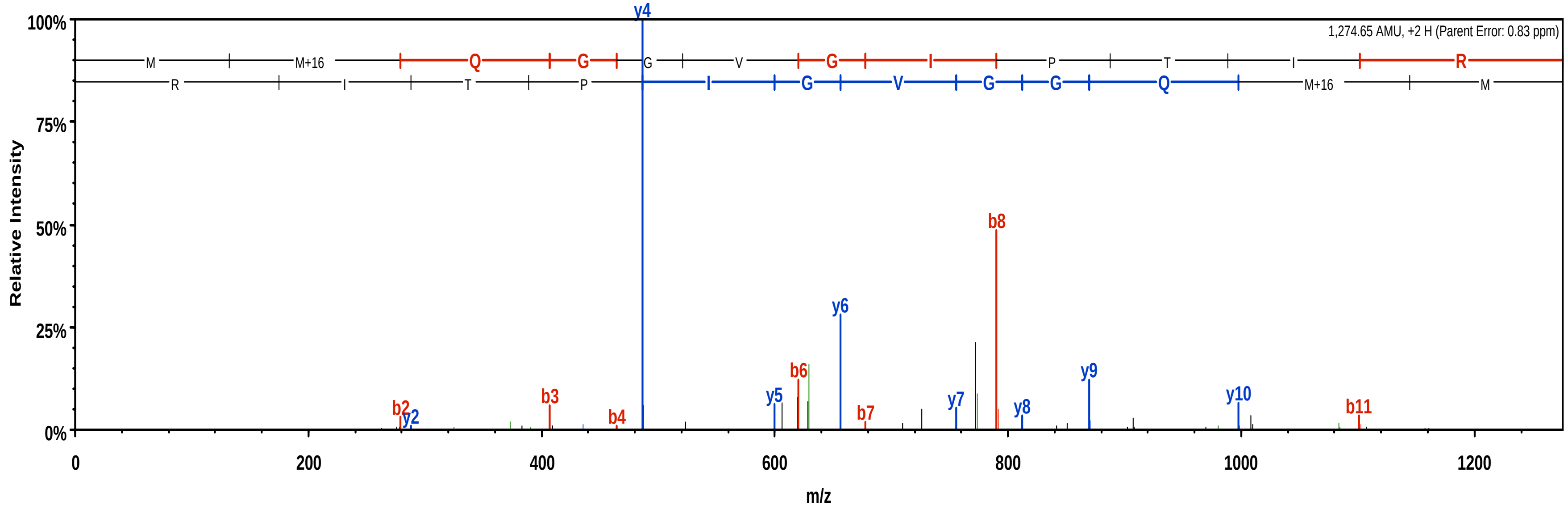


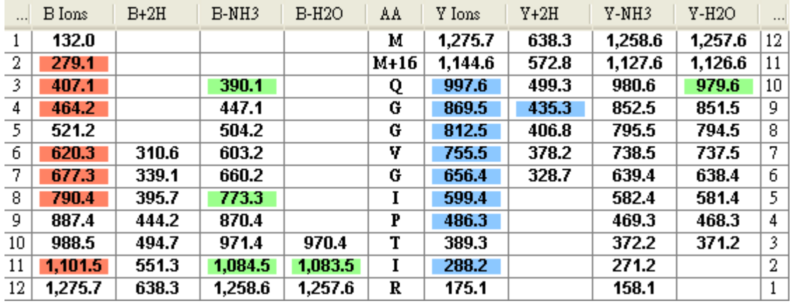


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.1				V	3,216.4	1,608.7	3,199.4	3,198.4	28
2	229.1			211.1	E	3,117.3	1,559.2	3,100.3	3,099.3	27
3	328.2			310.2	V	2,988.3	1,494.6	2,971.3	2,970.3	26
4	429.2			411.2	T	2,889.2	1,445.1	2,872.2	2,871.2	25
5	528.3			510.3	V	2,788.2	1,394.6	2,771.1	2,770.2	24
6	675.4	338.2		657.4	F	2,689.1	1,345.1	2,672.1	2,671.1	23
7	790.4	395.7		772.4	D	2,542.0	1,271.5	2,525.0	2,524.0	22
8	887.5	444.2		869.4	P	2,427.0	1,214.0	2,410.0	2,409.0	21
9	1,002.5	501.7		984.5	D	2,330.0	1,165.5	2,312.9	2,311.9	20
10	1,089.5	545.3		1,071.5	S	2,214.9	1,108.0	2,197.9	2,196.9	19
11	1,202.6	601.8		1,184.6	L	2,127.9	1,064.5	2,110.9	2,109.9	18
12	1,317.6	659.3		1,299.6	D	2,014.8	1,007.9	1,997.8	1,996.8	17
13	1,414.7	707.8		1,396.7	P	1,899.8	950.4	1,882.8	1,881.8	16
14	1,529.7	765.4		1,511.7	D	1,802.7	901.9	1,785.7	1,784.7	15
15	1,685.8	843.4	1,668.8	1,667.8	R	1,687.7	844.4	1,670.7	1,669.7	14
16	1,845.8	923.4	1,828.8	1,827.8	C+57	1,531.6	766.3	1,514.6	1,513.6	13
17	1,974.9	987.9	1,957.8	1,956.9	E	1,371.6	686.3	1,354.5	1,353.6	12
18	2,061.9	1,031.5	2,044.9	2,043.9	S	1,242.5	621.8	1,225.5	1,224.5	11
19	2,221.9	1,111.5	2,204.9	2,203.9	C+57	1,155.5	578.3	1,138.5	1,137.5	10
20	2,385.0	1,193.0	2,368.0	2,367.0	Y	995.5	498.2	978.4	977.5	9
21	2,442.0	1,221.5	2,425.0	2,424.0	G	832.4	416.7	815.4	814.4	8
22	2,513.1	1,257.0	2,496.0	2,495.0	A	775.4	388.2	758.4	757.4	7
23	2,642.1	1,321.6	2,625.1	2,624.1	E	704.3	352.7	687.3	686.3	6
24	2,713.1	1,357.1	2,696.1	2,695.1	A	575.3		558.3	557.3	5
25	2,842.2	1,421.6	2,825.2	2,824.2	E	504.3		487.2	486.3	4
26	2,957.2	1,479.1	2,940.2	2,939.2	D	375.2		358.2	357.2	3
27	3,070.3	1,535.7	3,053.3	3,052.3	I	260.2		243.2		2
28	3,216.4	1,608.7	3,199.4	3,198.4	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-79	sp|P48730|KC1D_HUMAN	MMQGGVGIPTIR	53.08	Oxidation (M)		2	638.33103

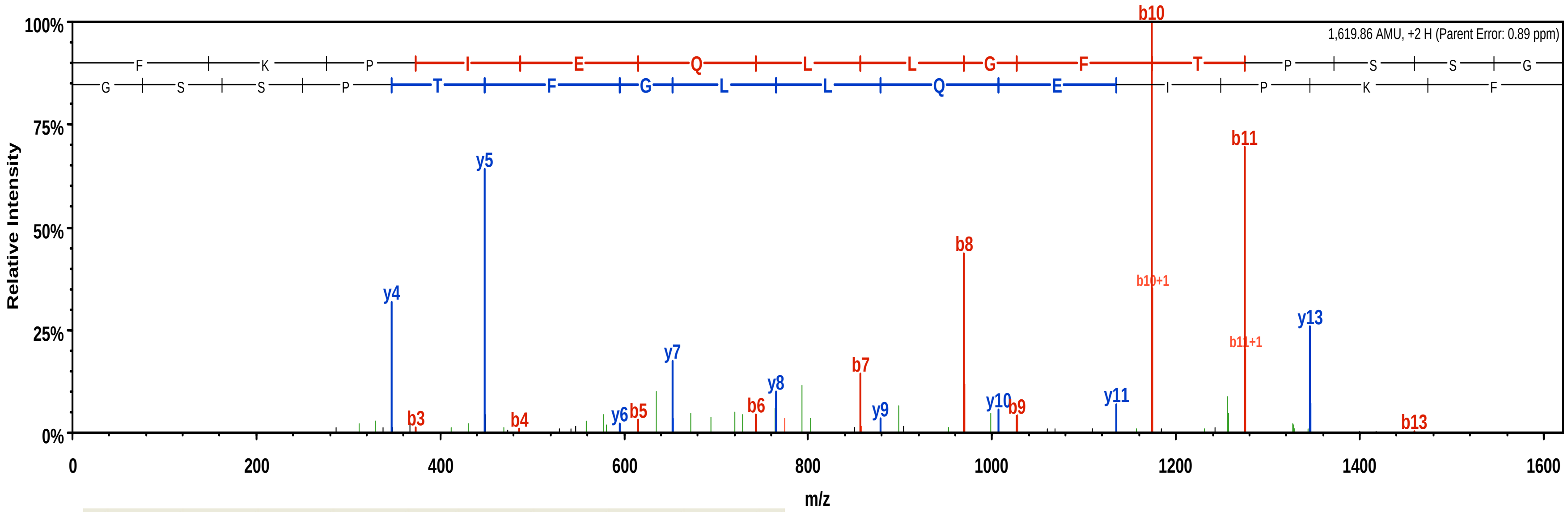


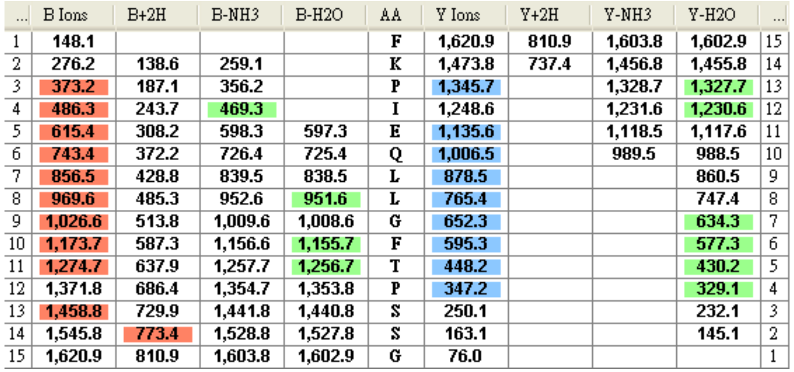


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	132.0				M	1,275.7	638.3	1,258.6	1,257.6	12
2	279.1				M+16	1,144.6	572.8	1,127.6	1,126.6	11
3	407.1		390.1		Q	997.6	499.3	980.6	979.6	10
4	464.2		447.1		G	869.5	435.3	852.5	851.5	9
5	521.2		504.2		G	812.5	406.8	795.5	794.5	8
6	620.3	310.6	603.2		V	755.5	378.2	738.5	737.5	7
7	677.3	339.1	660.2		G	656.4	328.7	639.4	638.4	6
8	790.4	395.7	773.3		I	599.4		582.4	581.4	5
9	887.4	444.2	870.4		P	486.3		469.3	468.3	4
10	988.5	494.7	971.4	970.4	T	389.3		372.2	371.2	3
11	1,101.5	551.3	1,084.5	1,083.5	I	288.2		271.2		2
12	1,275.7	638.3	1,258.6	1,257.6	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-80	splQ96DE5lCJ104_HUMAN	FKPIEQLLGFTPSSG	53.01	Unmodified	Light	2	810.93523

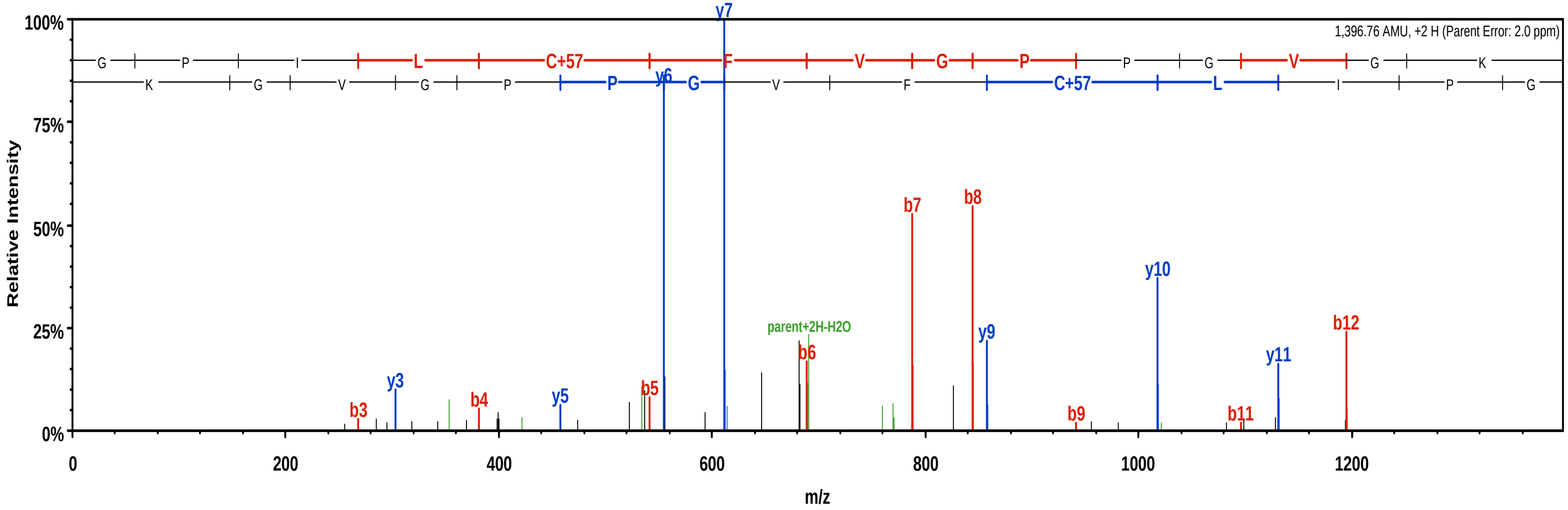


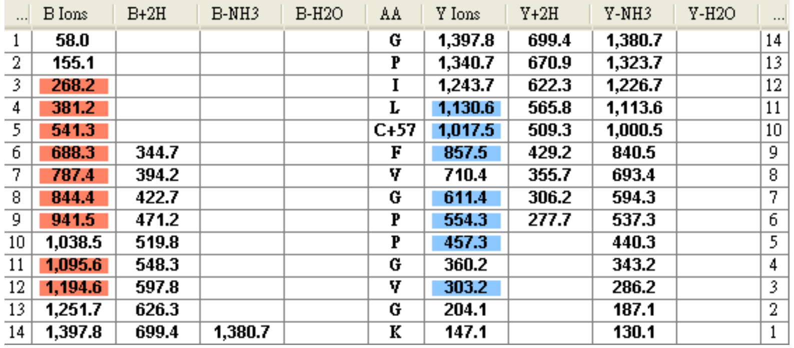


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.1				F	1,620.9	810.9	1,603.8	1,602.9	15
2	276.2	138.6	259.1		K	1,473.8	737.4	1,456.8	1,455.8	14
3	373.2	187.1	356.2		P	1,345.7		1,328.7	1,327.7	13
4	486.3	243.7	469.3		I	1,248.6		1,231.6	1,230.6	12
5	615.4	308.2	598.3	597.3	E	1,135.6		1,118.5	1,117.6	11
6	743.4	372.2	726.4	725.4	Q	1,006.5		989.5	988.5	10
7	856.5	428.8	839.5	838.5	L	878.5			860.5	9
8	969.6	485.3	952.6	951.6	L	765.4			747.4	8
9	1,026.6	513.8	1,009.6	1,008.6	G	652.3			634.3	7
10	1,173.7	587.3	1,156.6	1,155.7	F	595.3			577.3	6
11	1,274.7	637.9	1,257.7	1,256.7	T	448.2			430.2	5
12	1,371.8	686.4	1,354.7	1,353.8	P	347.2			329.1	4
13	1,458.8	729.9	1,441.8	1,440.8	S	250.1			232.1	3
14	1,545.8	773.4	1,528.8	1,527.8	S	163.1			145.1	2
15	1,620.9	810.9	1,603.8	1,602.9	G	76.0				1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-81	sp|Q86WA8|LONP2_HUMAN	GPILCFVGPPGVGK	52.9	Unmodified	Light	2	699.38412

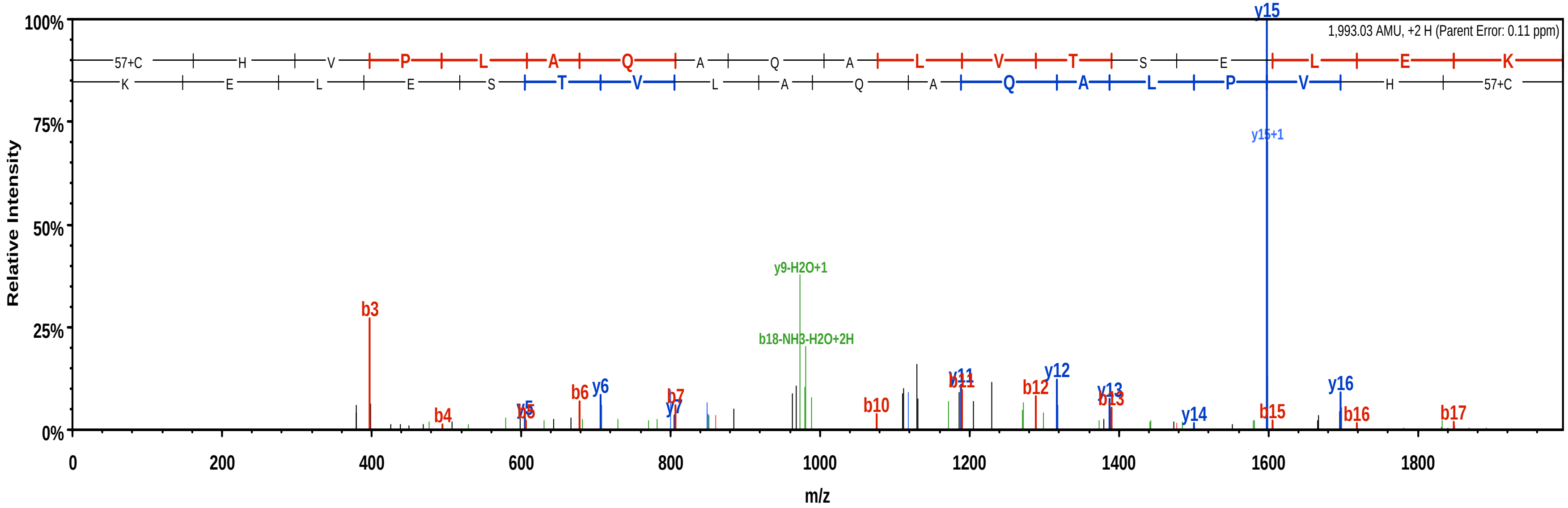


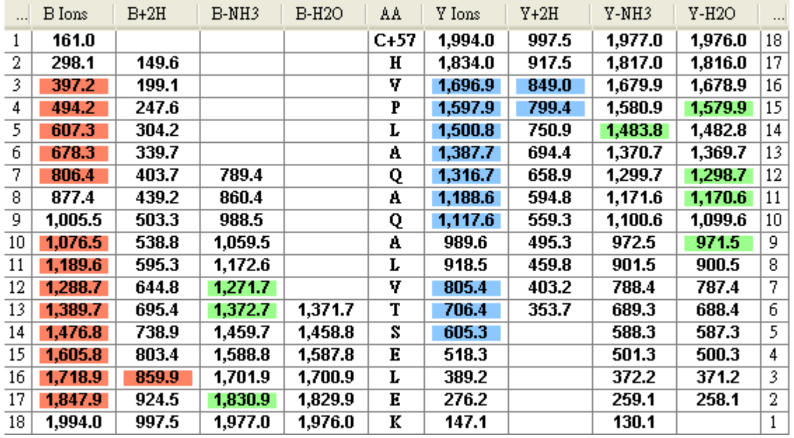


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	1,397.8	699.4	1,380.7		14
2	155.1				P	1,340.7	670.9	1,323.7		13
3	268.2				I	1,243.7	622.3	1,226.7		12
4	381.2				L	1,130.6	565.8	1,113.6		11
5	541.3				C+57	1,017.5	509.3	1,000.5		10
6	688.3	344.7			F	857.5	429.2	840.5		9
7	787.4	394.2			V	710.4	355.7	693.4		8
8	844.4	422.7			G	611.4	306.2	594.3		7
9	941.5	471.2			P	554.3	277.7	537.3		6
10	1,038.5	519.8			P	457.3		440.3		5
11	1,095.6	548.3			G	360.2		343.2		4
12	1,194.6	597.8			V	303.2		286.2		3
13	1,251.7	626.3			G	204.1		187.1		2
14	1,397.8	699.4	1,380.7		K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-82	sp|Q96C01|F136A_HUMAN	CHVPLAQAQALVTSELEK	52.5	Unmodified	Light	2	997.5224

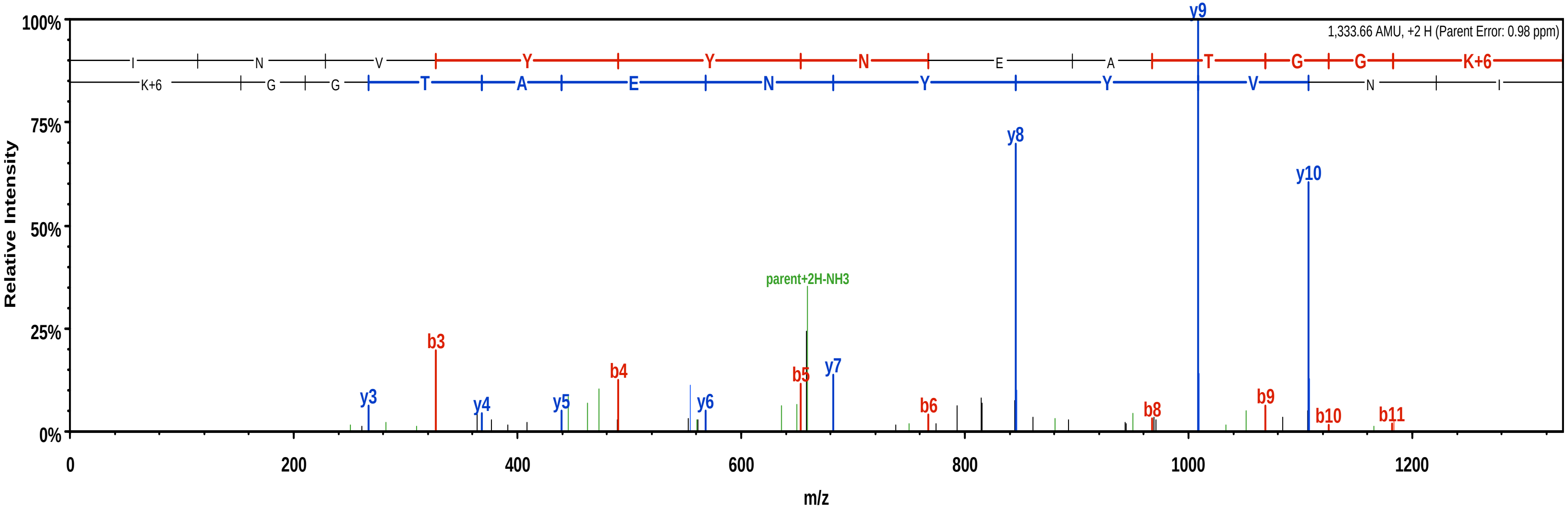


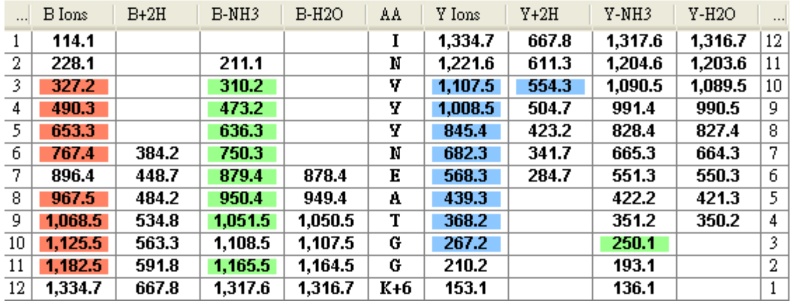


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	161.0				C+57	1,994.0	997.5	1,977.0	1,976.0	18
2	298.1	149.6			H	1,834.0	917.5	1,817.0	1,816.0	17
3	397.2	199.1			V	1,696.9	849.0	1,679.9	1,678.9	16
4	494.2	247.6			P	1,597.9	799.4	1,580.9	1,579.9	15
5	607.3	304.2			L	1,500.8	750.9	1,483.8	1,482.8	14
6	678.3	339.7			A	1,387.7	694.4	1,370.7	1,369.7	13
7	806.4	403.7	789.4		Q	1,316.7	658.9	1,299.7	1,298.7	12
8	877.4	439.2	860.4		A	1,188.6	594.8	1,171.6	1,170.6	11
9	1,005.5	503.3	988.5		Q	1,117.6	559.3	1,100.6	1,099.6	10
10	1,076.5	538.8	1,059.5		A	989.6	495.3	972.5	971.5	9
11	1,189.6	595.3	1,172.6		L	918.5	459.8	901.5	900.5	8
12	1,288.7	644.8	1,271.7		V	805.4	403.2	788.4	787.4	7
13	1,389.7	695.4	1,372.7	1,371.7	T	706.4	353.7	689.3	688.4	6
14	1,476.8	738.9	1,459.7	1,458.8	S	605.3		588.3	587.3	5
15	1,605.8	803.4	1,588.8	1,587.8	E	518.3		501.3	500.3	4
16	1,718.9	859.9	1,701.9	1,700.9	L	389.2		372.2	371.2	3
17	1,847.9	924.5	1,830.9	1,829.9	E	276.2		259.1	258.1	2
18	1,994.0	997.5	1,977.0	1,976.0	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-83	sp|P68371|TBB2C_HUMAN	INVYYNEATGGK	52.3	Unmodified	Heavy	2	664.82769

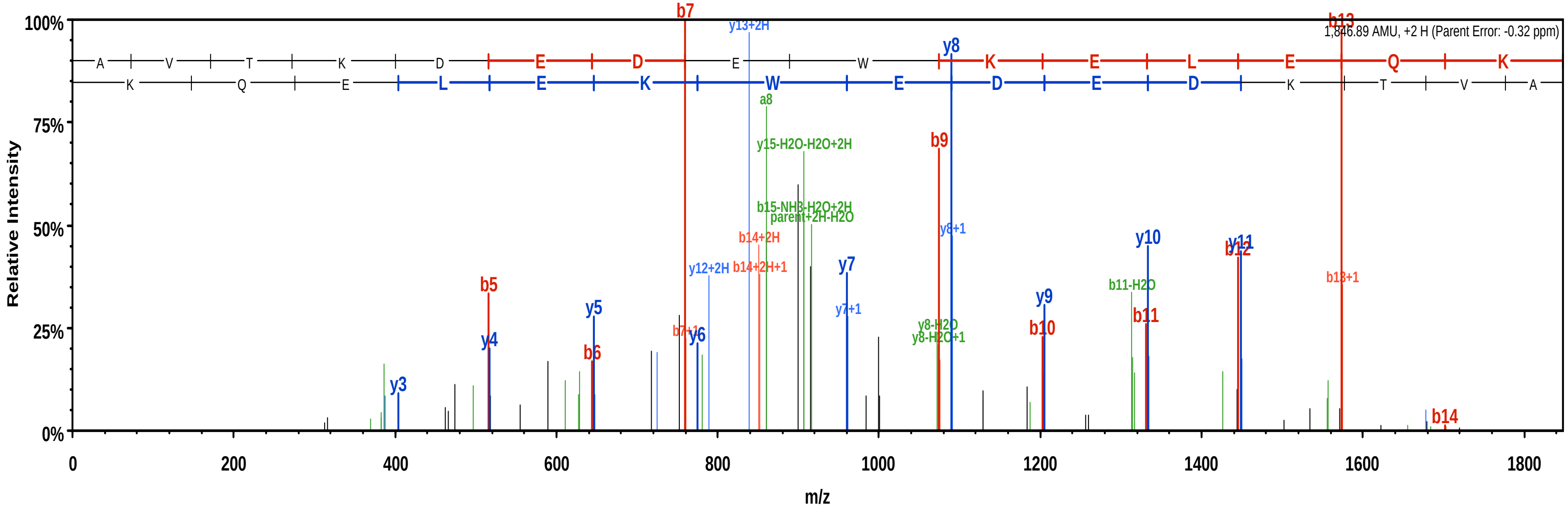


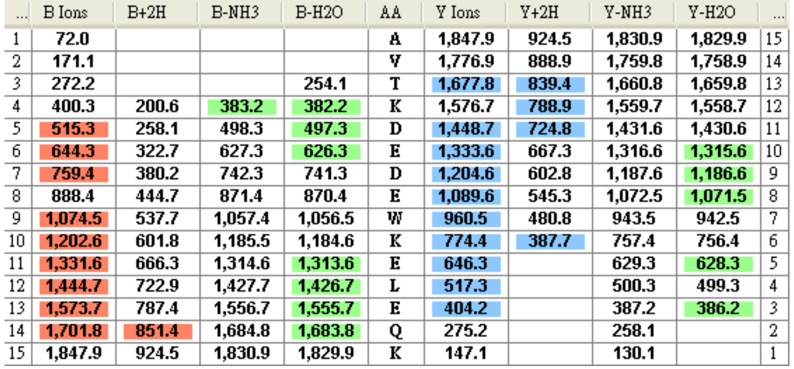


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	1,334.7	667.8	1,317.6	1,316.7	12
2	228.1		211.1		N	1,221.6	611.3	1,204.6	1,203.6	11
3	327.2		310.2		V	1,107.5	554.3	1,090.5	1,089.5	10
4	490.3		473.2		Y	1,008.5	504.7	991.4	990.5	9
5	653.3		636.3		Y	845.4	423.2	828.4	827.4	8
6	767.4	384.2	750.3		N	682.3	341.7	665.3	664.3	7
7	896.4	448.7	879.4	878.4	E	568.3	284.7	551.3	550.3	6
8	967.5	484.2	950.4	949.4	A	439.3		422.2	421.3	5
9	1,068.5	534.8	1,051.5	1,050.5	T	368.2		351.2	350.2	4
10	1,125.5	563.3	1,108.5	1,107.5	G	267.2		250.1		3
11	1,182.5	591.8	1,165.5	1,164.5	G	210.2		193.1		2
12	1,334.7	667.8	1,317.6	1,316.7	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-84	sp|Q9UKY7|CDV3_HUMAN	AVTKDEDEWKELEQK	52.19	Unmodified	Light	2	924.45471

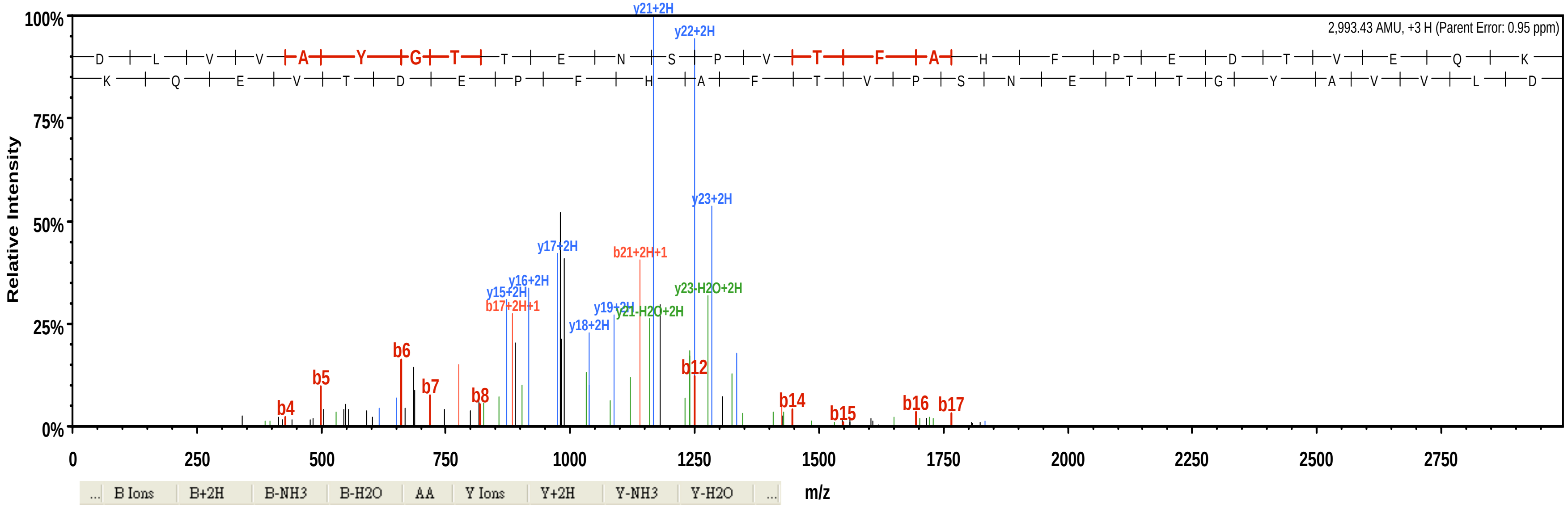


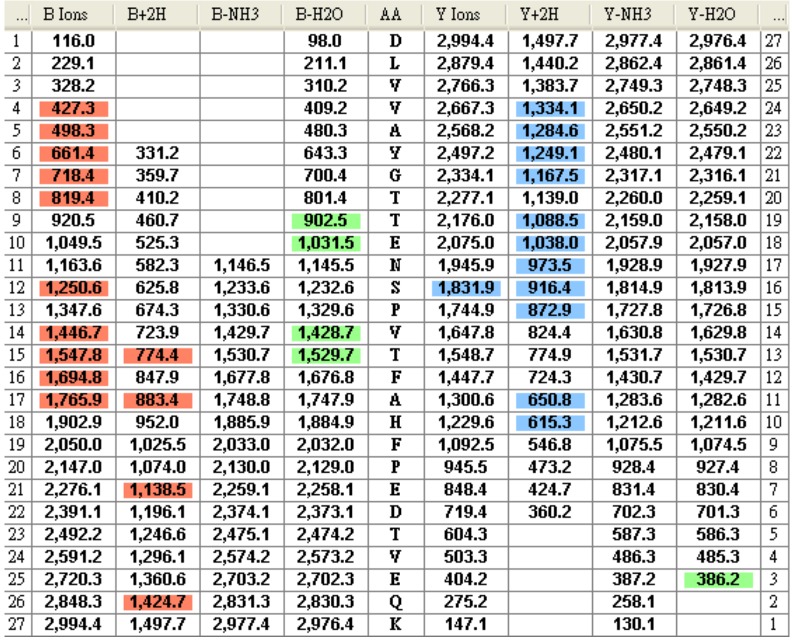


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	1,847.9	924.5	1,830.9	1,829.9	15
2	171.1				V	1,776.9	888.9	1,759.8	1,758.9	14
3	272.2			254.1	T	1,677.8	839.4	1,660.8	1,659.8	13
4	400.3	200.6	383.2	382.2	K	1,576.7	788.9	1,559.7	1,558.7	12
5	515.3	258.1	498.3	497.3	D	1,448.7	724.8	1,431.6	1,430.6	11
6	644.3	322.7	627.3	626.3	E	1,333.6	667.3	1,316.6	1,315.6	10
7	759.4	380.2	742.3	741.3	D	1,204.6	602.8	1,187.6	1,186.6	9
8	888.4	444.7	871.4	870.4	E	1,089.6	545.3	1,072.5	1,071.5	8
9	1,074.5	537.7	1,057.4	1,056.5	W	960.5	480.8	943.5	942.5	7
10	1,202.6	601.8	1,185.5	1,184.6	K	774.4	387.7	757.4	756.4	6
11	1,331.6	666.3	1,314.6	1,313.6	E	646.3		629.3	628.3	5
12	1,444.7	722.9	1,427.7	1,426.7	L	517.3		500.3	499.3	4
13	1,573.7	787.4	1,556.7	1,555.7	E	404.2		387.2	386.2	3
14	1,701.8	851.4	1,684.8	1,683.8	Q	275.2		258.1		2
15	1,847.9	924.5	1,830.9	1,829.9	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-85	sp|Q96CM8|ACSF2_HUMAN	DLVVAYGTTENSPVTFAHFPEDTVEQK	51.41	Unmodified	Light	3	998.81709

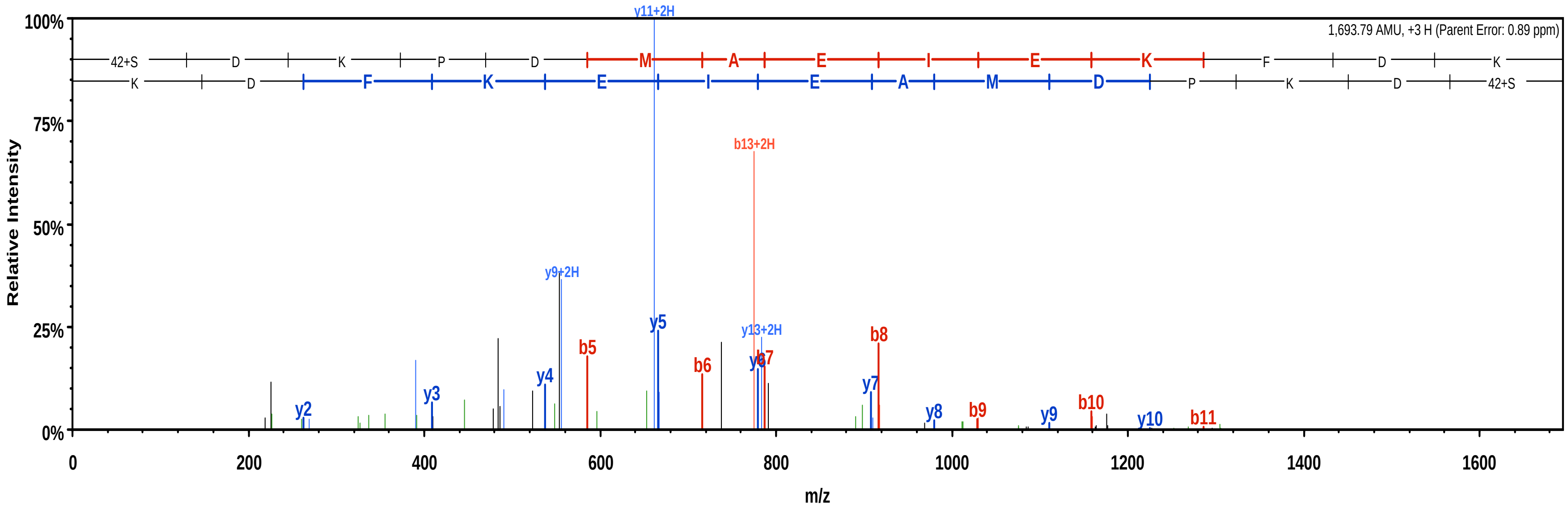


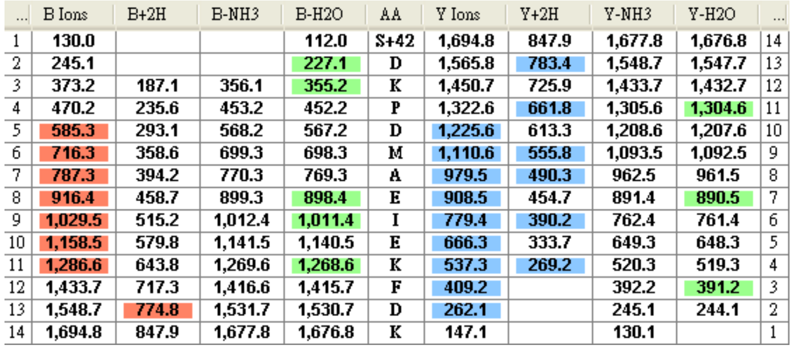


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	2,994.4	1,497.7	2,977.4	2,976.4	27
2	229.1			211.1	L	2,879.4	1,440.2	2,862.4	2,861.4	26
3	328.2			310.2	V	2,766.3	1,383.7	2,749.3	2,748.3	25
4	427.3			409.2	V	2,667.3	1,334.1	2,650.2	2,649.2	24
5	498.3			480.3	A	2,568.2	1,284.6	2,551.2	2,550.2	23
6	661.4	331.2		643.3	Y	2,497.2	1,249.1	2,480.1	2,479.1	22
7	718.4	359.7		700.4	G	2,334.1	1,167.5	2,317.1	2,316.1	21
8	819.4	410.2		801.4	T	2,277.1	1,139.0	2,260.0	2,259.1	20
9	920.5	460.7		902.5	T	2,176.0	1,088.5	2,159.0	2,158.0	19
10	1,049.5	525.3		1,031.5	E	2,075.0	1,038.0	2,057.9	2,057.0	18
11	1,163.6	582.3	1,146.5	1,145.5	N	1,945.9	973.5	1,928.9	1,927.9	17
12	1,250.6	625.8	1,233.6	1,232.6	S	1,831.9	916.4	1,814.9	1,813.9	16
13	1,347.6	674.3	1,330.6	1,329.6	P	1,744.9	872.9	1,727.8	1,726.8	15
14	1,446.7	723.9	1,429.7	1,428.7	V	1,647.8	824.4	1,630.8	1,629.8	14
15	1,547.8	774.4	1,530.7	1,529.7	T	1,548.7	774.9	1,531.7	1,530.7	13
16	1,694.8	847.9	1,677.8	1,676.8	F	1,447.7	724.3	1,430.7	1,429.7	12
17	1,765.9	883.4	1,748.8	1,747.9	A	1,300.6	650.8	1,283.6	1,282.6	11
18	1,902.9	952.0	1,885.9	1,884.9	H	1,229.6	615.3	1,212.6	1,211.6	10
19	2,050.0	1,025.5	2,033.0	2,032.0	F	1,092.5	546.8	1,075.5	1,074.5	9
20	2,147.0	1,074.0	2,130.0	2,129.0	P	945.5	473.2	928.4	927.4	8
21	2,276.1	1,138.5	2,259.1	2,258.1	E	848.4	424.7	831.4	830.4	7
22	2,391.1	1,196.1	2,374.1	2,373.1	D	719.4	360.2	702.3	701.3	6
23	2,492.2	1,246.6	2,475.1	2,474.2	T	604.3		587.3	586.3	5
24	2,591.2	1,296.1	2,574.2	2,573.2	V	503.3		486.3	485.3	4
25	2,720.3	1,360.6	2,703.2	2,702.3	E	404.2		387.2	386.2	3
26	2,848.3	1,424.7	2,831.3	2,830.3	Q	275.2		258.1		2
27	2,994.4	1,497.7	2,977.4	2,976.4	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-86	sp|A8MW06|TMSL3_HUMAN	SDKPDMAEIEKFDK	51.06	Acetyl (Protein N-term)	Light	3	565.60291

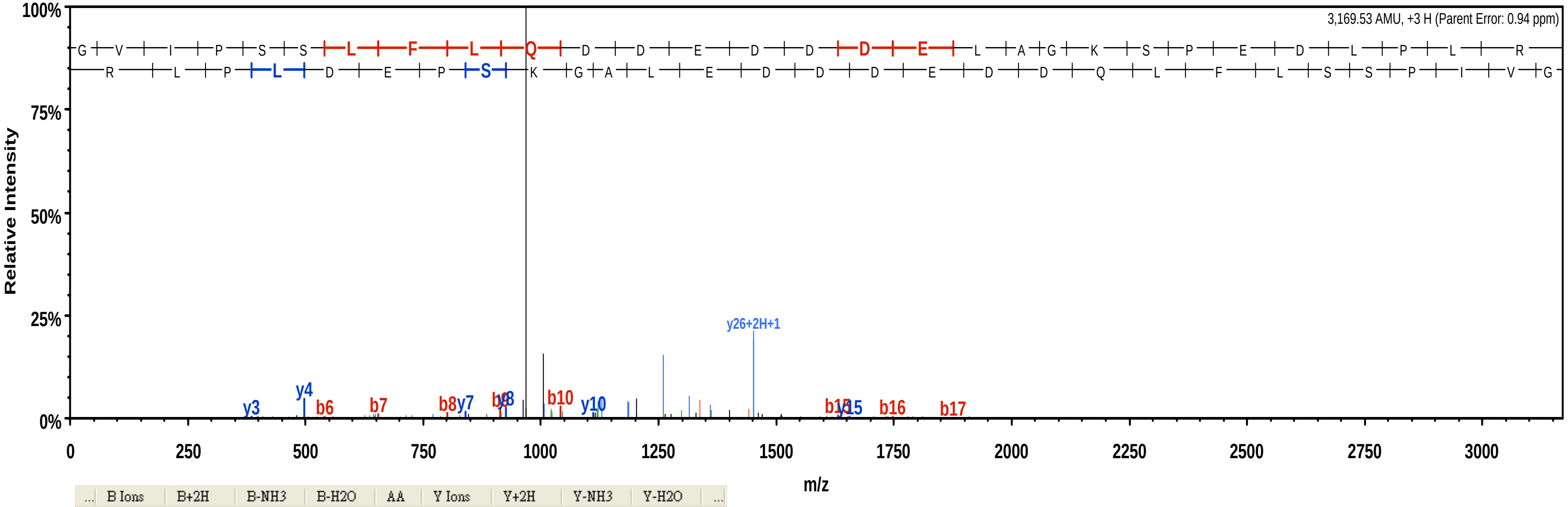


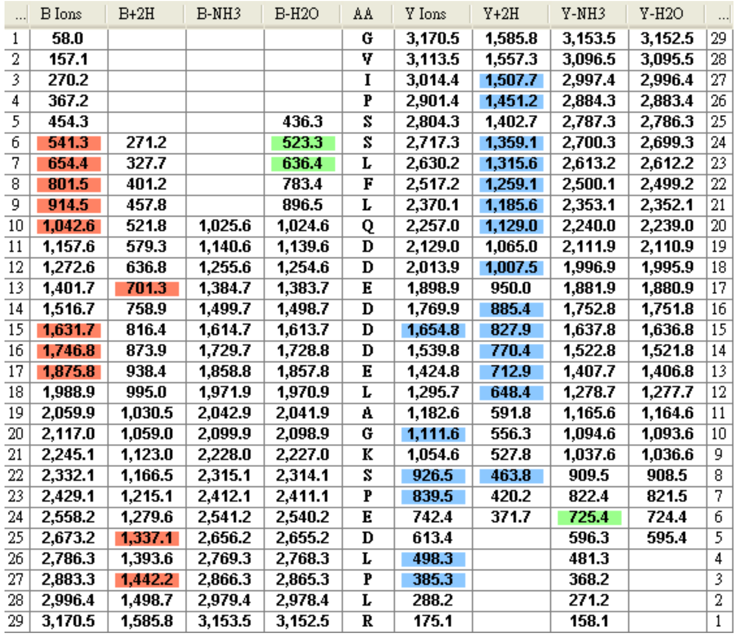


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	S+42	1,694.8	847.9	1,677.8	1,676.8	14
2	245.1			227.1	D	1,565.8	783.4	1,548.7	1,547.7	13
3	373.2	187.1	356.1	355.2	K	1,450.7	725.9	1,433.7	1,432.7	12
4	470.2	235.6	453.2	452.2	P	1,322.6	661.8	1,305.6	1,304.6	11
5	585.3	293.1	568.2	567.2	D	1,225.6	613.3	1,208.6	1,207.6	10
6	716.3	358.6	699.3	698.3	M	1,110.6	555.8	1,093.5	1,092.5	9
7	787.3	394.2	770.3	769.3	A	979.5	490.3	962.5	961.5	8
8	916.4	458.7	899.3	898.4	E	908.5	454.7	891.4	890.5	7
9	1,029.5	515.2	1,012.4	1,011.4	I	779.4	390.2	762.4	761.4	6
10	1,158.5	579.8	1,141.5	1,140.5	E	666.3	333.7	649.3	648.3	5
11	1,286.6	643.8	1,269.6	1,268.6	K	537.3	269.2	520.3	519.3	4
12	1,433.7	717.3	1,416.6	1,415.7	F	409.2		392.2	391.2	3
13	1,548.7	774.8	1,531.7	1,530.7	D	262.1		245.1	244.1	2
14	1,694.8	847.9	1,677.8	1,676.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-87	sp|O76024|WFS1_HUMAN	GVIPSSLFLQDDEDDDELAGKSPEDLPLR	50.5	Unmodified	Light	3	1057.5174

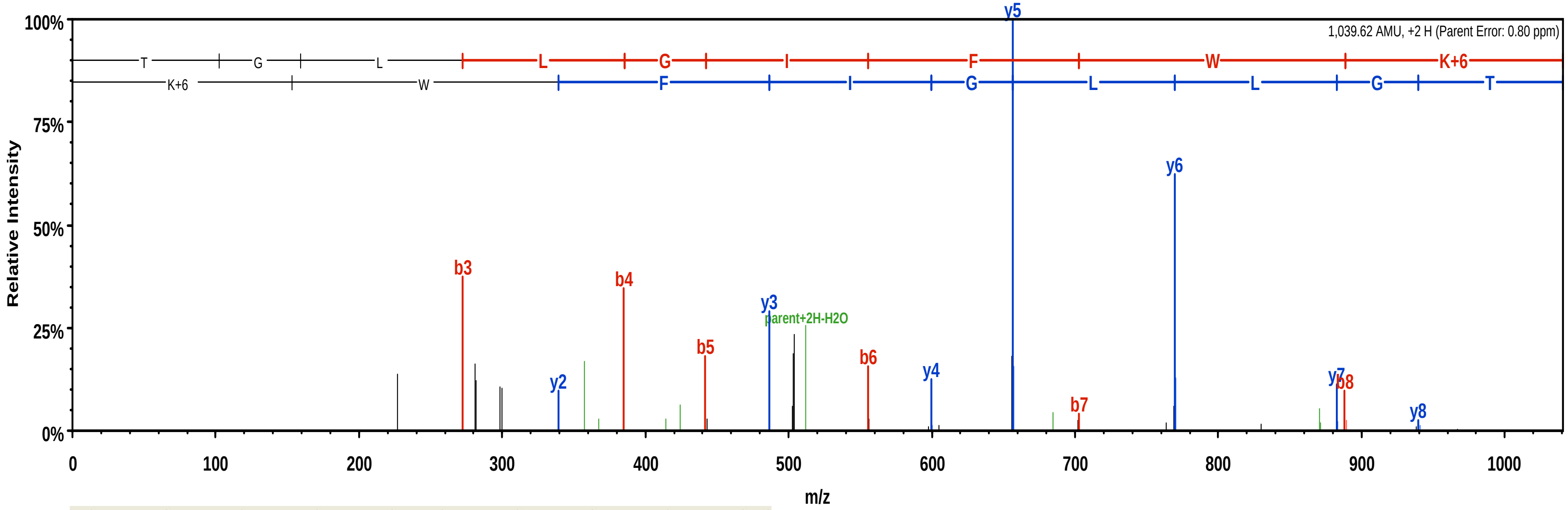


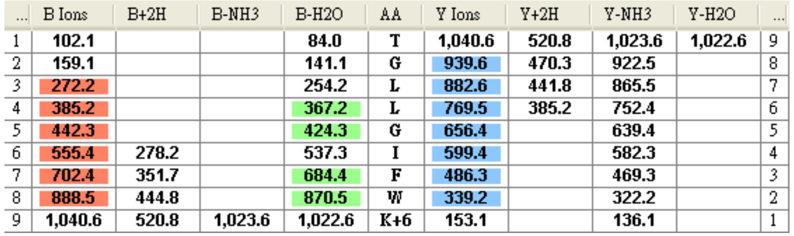


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	3,170.5	1,585.8	3,153.5	3,152.5	29
2	157.1				V	3,113.5	1,557.3	3,096.5	3,095.5	28
3	270.2				I	3,014.4	1,507.7	2,997.4	2,996.4	27
4	367.2				P	2,901.4	1,451.2	2,884.3	2,883.4	26
5	454.3			436.3	S	2,804.3	1,402.7	2,787.3	2,786.3	25
6	541.3	271.2		523.3	S	2,717.3	1,359.1	2,700.3	2,699.3	24
7	654.4	327.7		636.4	L	2,630.2	1,315.6	2,613.2	2,612.2	23
8	801.5	401.2		783.4	F	2,517.2	1,259.1	2,500.1	2,499.2	22
9	914.5	457.8		896.5	L	2,370.1	1,185.6	2,353.1	2,352.1	21
10	1,042.6	521.8	1,025.6	1,024.6	Q	2,257.0	1,129.0	2,240.0	2,239.0	20
11	1,157.6	579.3	1,140.6	1,139.6	D	2,129.0	1,065.0	2,111.9	2,110.9	19
12	1,272.6	636.8	1,255.6	1,254.6	D	2,013.9	1,007.5	1,996.9	1,995.9	18
13	1,401.7	701.3	1,384.7	1,383.7	E	1,898.9	950.0	1,881.9	1,880.9	17
14	1,516.7	758.9	1,499.7	1,498.7	D	1,769.9	885.4	1,752.8	1,751.8	16
15	1,631.7	816.4	1,614.7	1,613.7	D	1,654.8	827.9	1,637.8	1,636.8	15
16	1,746.8	873.9	1,729.7	1,728.8	D	1,539.8	770.4	1,522.8	1,521.8	14
17	1,875.8	938.4	1,858.8	1,857.8	E	1,424.8	712.9	1,407.7	1,406.8	13
18	1,988.9	995.0	1,971.9	1,970.9	L	1,295.7	648.4	1,278.7	1,277.7	12
19	2,059.9	1,030.5	2,042.9	2,041.9	A	1,182.6	591.8	1,165.6	1,164.6	11
20	2,117.0	1,059.0	2,099.9	2,098.9	G	1,111.6	556.3	1,094.6	1,093.6	10
21	2,245.1	1,123.0	2,228.0	2,227.0	K	1,054.6	527.8	1,037.6	1,036.6	9
22	2,332.1	1,166.5	2,315.1	2,314.1	S	926.5	463.8	909.5	908.5	8
23	2,429.1	1,215.1	2,412.1	2,411.1	P	839.5	420.2	822.4	821.5	7
24	2,558.2	1,279.6	2,541.2	2,540.2	E	742.4	371.7	725.4	724.4	6
25	2,673.2	1,337.1	2,656.2	2,655.2	D	613.4		596.3	595.4	5
26	2,786.3	1,393.6	2,769.3	2,768.3	L	498.3		481.3		4
27	2,883.3	1,442.2	2,866.3	2,865.3	P	385.3		368.2		3
28	2,996.4	1,498.7	2,979.4	2,978.4	L	288.2		271.2		2
29	3,170.5	1,585.8	3,153.5	3,152.5	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-88	sp|Q8TBQ9|T167A_HUMAN	TGLLGIFWK	50.16	Unmodified	Heavy	2	517.8053

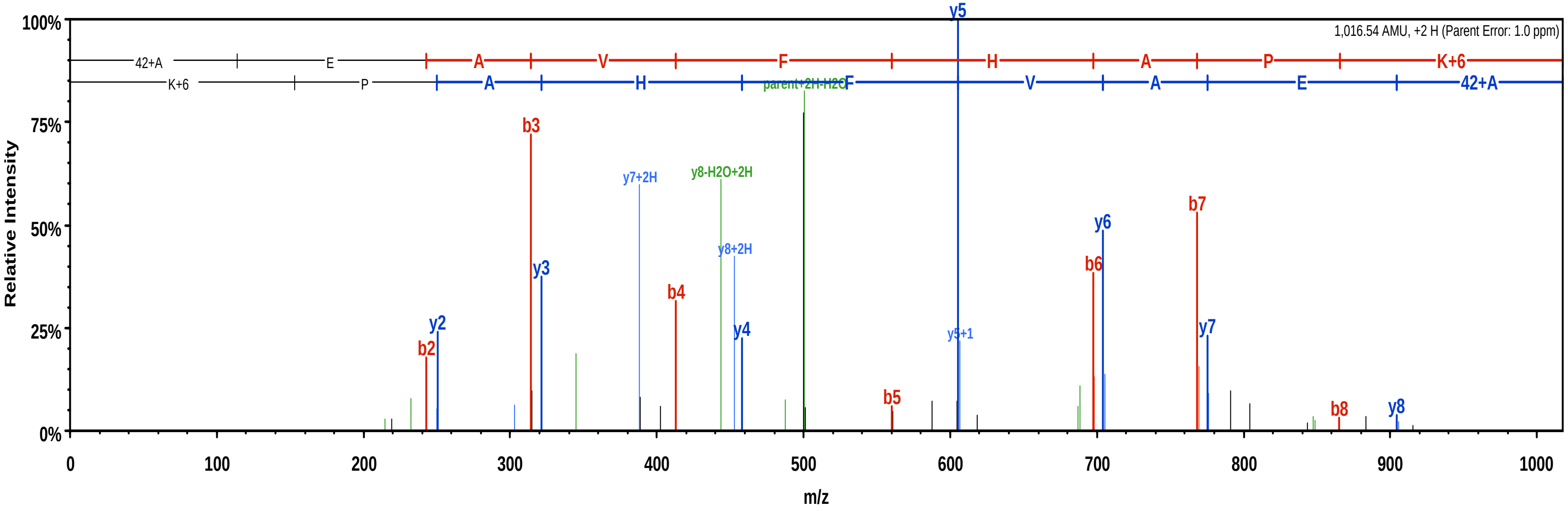


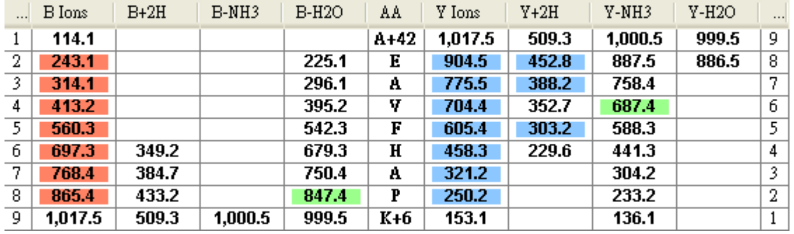


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	102.1			84.0	T	1,040.6	520.8	1,023.6	1,022.6	9
2	159.1			141.1	G	939.6	470.3	922.5		8
3	272.2			254.2	L	882.6	441.8	865.5		7
4	385.2			367.2	L	769.5	385.2	752.4		6
5	442.3			424.3	G	656.4		639.4		5
6	555.4	278.2		537.3	I	599.4		582.3		4
7	702.4	351.7		684.4	F	486.3		469.3		3
8	888.5	444.8		870.5	W	339.2		322.2		2
9	1,040.6	520.8	1,023.6	1,022.6	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-89	sp|Q8NCE0|SEN2_HUMAN	AEAVFHAPK	48.01	Acetyl (Protein N-term)	Heavy	2	506.26654

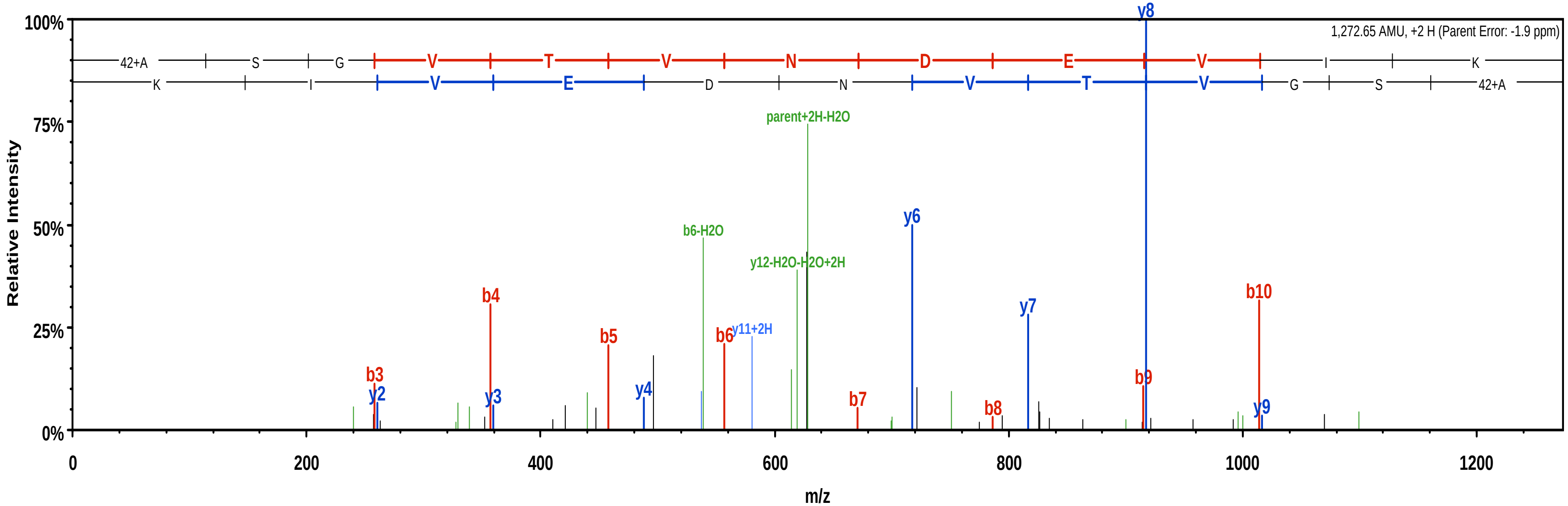


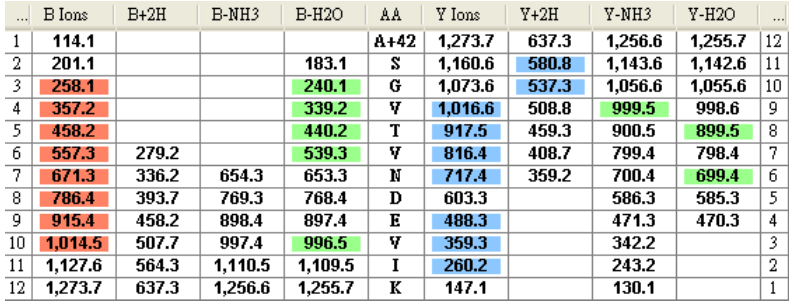


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	1,017.5	509.3	1,000.5	999.5	9
2	243.1			225.1	E	904.5	452.8	887.5	886.5	8
3	314.1			296.1	A	775.5	388.2	758.4		7
4	413.2			395.2	V	704.4	352.7	687.4		6
5	560.3			542.3	F	605.4	303.2	588.3		5
6	697.3	349.2		679.3	H	458.3	229.6	441.3		4
7	768.4	384.7		750.4	A	321.2		304.2		3
8	865.4	433.2		847.4	P	250.2		233.2		2
9	1,017.5	509.3	1,000.5	999.5	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-90	sp|Q9Y281|COF2_HUMAN	ASGVTVNDEVIK	47.76	Acetyl (Protein N-term)	Light	2	637.33535

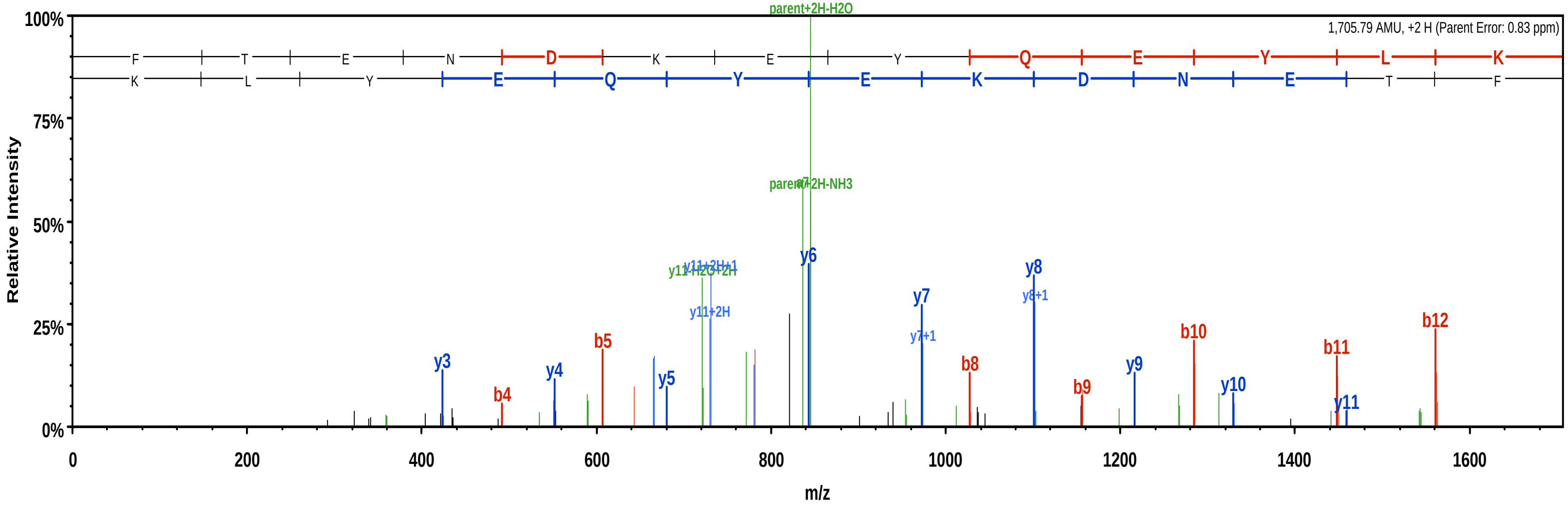


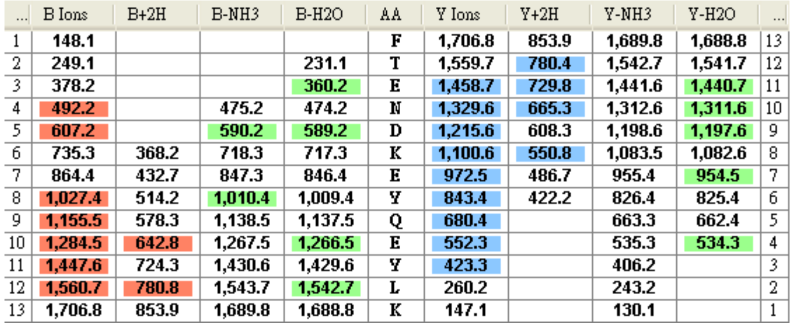


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	1,273.7	637.3	1,256.6	1,255.7	12
2	201.1			183.1	S	1,160.6	580.8	1,143.6	1,142.6	11
3	258.1			240.1	G	1,073.6	537.3	1,056.6	1,055.6	10
4	357.2			339.2	V	1,016.6	508.8	999.5	998.6	9
5	458.2			440.2	T	917.5	459.3	900.5	899.5	8
6	557.3	279.2		539.3	V	816.4	408.7	799.4	798.4	7
7	671.3	336.2	654.3	653.3	N	717.4	359.2	700.4	699.4	6
8	786.4	393.7	769.3	768.4	D	603.3		586.3	585.3	5
9	915.4	458.2	898.4	897.4	E	488.3		471.3	470.3	4
10	1,014.5	507.7	997.4	996.5	V	359.3		342.2		3
11	1,127.6	564.3	1,110.5	1,109.5	I	260.2		243.2		2
12	1,273.7	637.3	1,256.6	1,255.7	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-91	sp|Q9BTL3|F103A_HUMAN	FTENDKEYQEYLK	47.4	Unmodified	Light	2	853.89904

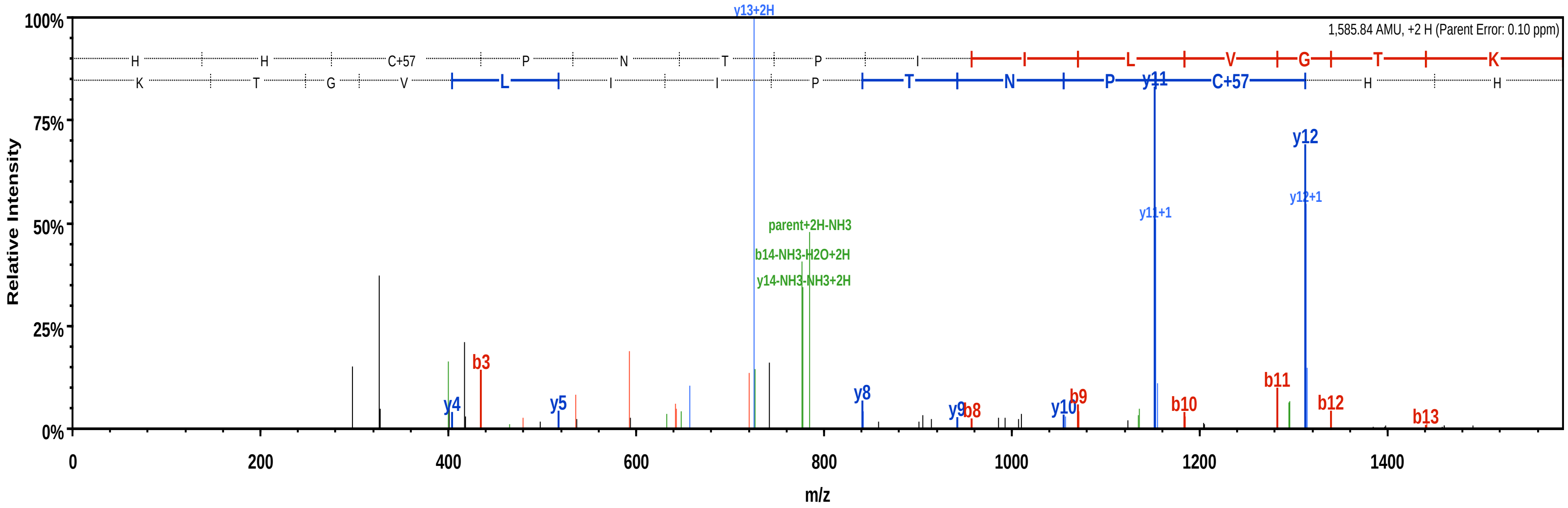


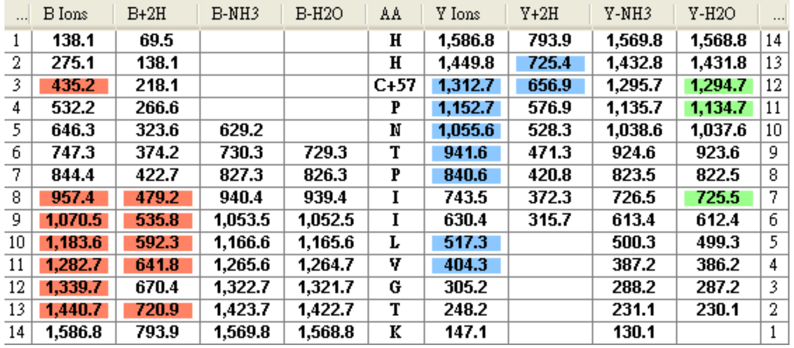


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.1				F	1,706.8	853.9	1,689.8	1,688.8	13
2	249.1			231.1	T	1,559.7	780.4	1,542.7	1,541.7	12
3	378.2			360.2	E	1,458.7	729.8	1,441.6	1,440.7	11
4	492.2		475.2	474.2	N	1,329.6	665.3	1,312.6	1,311.6	10
5	607.2		590.2	589.2	D	1,215.6	608.3	1,198.6	1,197.6	9
6	735.3	368.2	718.3	717.3	K	1,100.6	550.8	1,083.5	1,082.6	8
7	864.4	432.7	847.3	846.4	E	972.5	486.7	955.4	954.5	7
8	1,027.4	514.2	1,010.4	1,009.4	Y	843.4	422.2	826.4	825.4	6
9	1,155.5	578.3	1,138.5	1,137.5	Q	680.4		663.3	662.4	5
10	1,284.5	642.8	1,267.5	1,266.5	E	552.3		535.3	534.3	4
11	1,447.6	724.3	1,430.6	1,429.6	Y	423.3		406.2		3
12	1,560.7	780.8	1,543.7	1,542.7	L	260.2		243.2		2
13	1,706.8	853.9	1,689.8	1,688.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-92	sp|P63000|RAC1_HUMAN	HHCPNTPIILVGTK	37.04	Unmodified	Light	2	793.9274

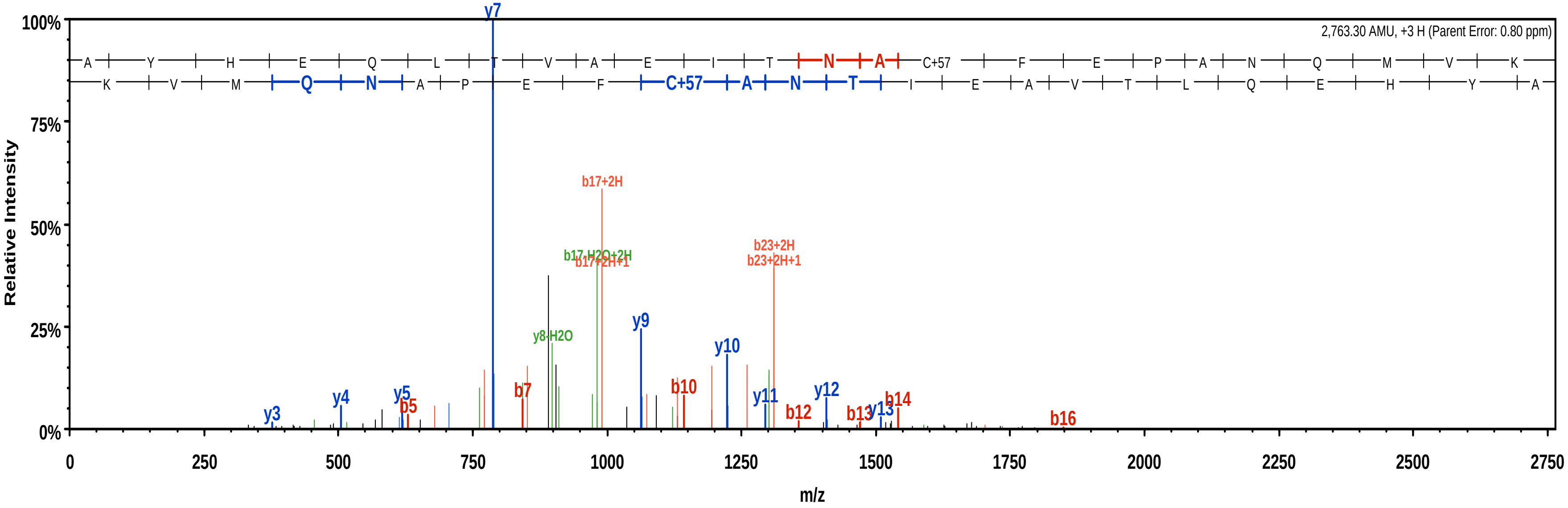


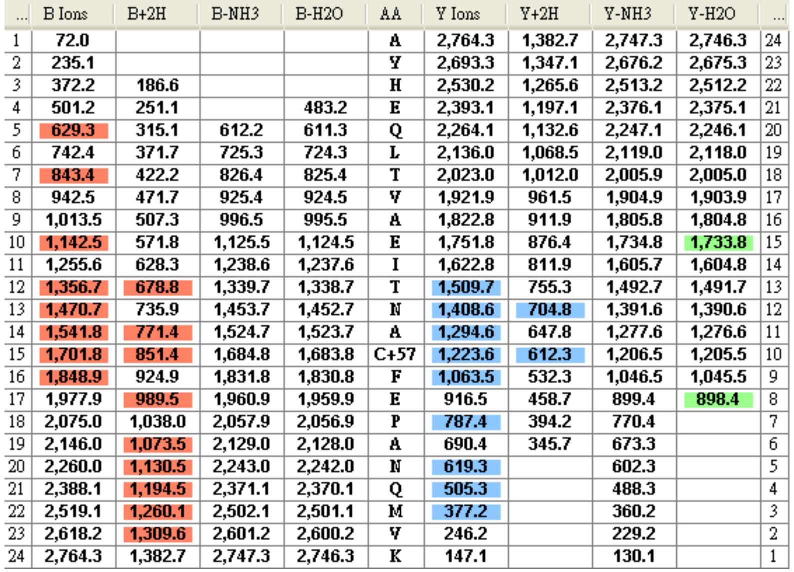


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	138.1	69.5			H	1,586.8	793.9	1,569.8	1,568.8	14
2	275.1	138.1			H	1,449.8	725.4	1,432.8	1,431.8	13
3	435.2	218.1			C+57	1,312.7	656.9	1,295.7	1,294.7	12
4	532.2	266.6			P	1,152.7	576.9	1,135.7	1,134.7	11
5	646.3	323.6	629.2		N	1,055.6	528.3	1,038.6	1,037.6	10
6	747.3	374.2	730.3	729.3	T	941.6	471.3	924.6	923.6	9
7	844.4	422.7	827.3	826.3	P	840.6	420.8	823.5	822.5	8
8	957.4	479.2	940.4	939.4	I	743.5	372.3	726.5	725.5	7
9	1,070.5	535.8	1,053.5	1,052.5	I	630.4	315.7	613.4	612.4	6
10	1,183.6	592.3	1,166.6	1,165.6	L	517.3		500.3	499.3	5
11	1,282.7	641.8	1,265.6	1,264.7	V	404.3		387.2	386.2	4
12	1,339.7	670.4	1,322.7	1,321.7	G	305.2		288.2	287.2	3
13	1,440.7	720.9	1,423.7	1,422.7	T	248.2		231.1	230.1	2
14	1,586.8	793.9	1,569.8	1,568.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-93	sp|Q9BQE3|TBA1C_HUMAN	AYHEQLTVAEITNACFEPANQMVK	47.09	Unmodified	Light	3	922.10715

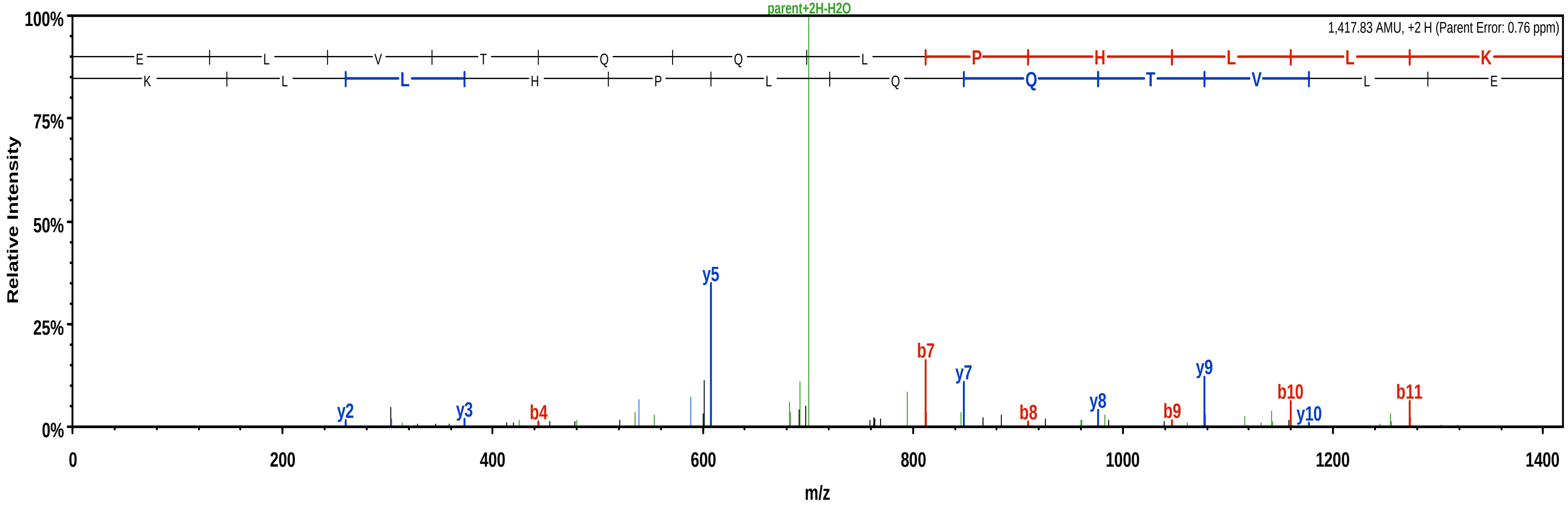


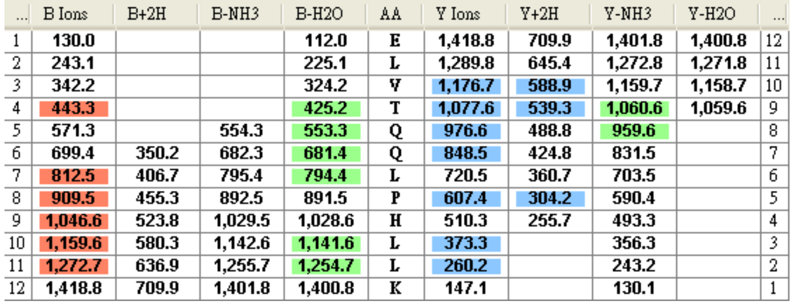


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	2,764.3	1,382.7	2,747.3	2,746.3	24
2	235.1				Y	2,693.3	1,347.1	2,676.2	2,675.3	23
3	372.2	186.6			H	2,530.2	1,265.6	2,513.2	2,512.2	22
4	501.2	251.1		483.2	E	2,393.1	1,197.1	2,376.1	2,375.1	21
5	629.3	315.1	612.2	611.3	Q	2,264.1	1,132.6	2,247.1	2,246.1	20
6	742.4	371.7	725.3	724.3	L	2,136.0	1,068.5	2,119.0	2,118.0	19
7	843.4	422.2	826.4	825.4	T	2,023.0	1,012.0	2,005.9	2,005.0	18
8	942.5	471.7	925.4	924.5	V	1,921.9	961.5	1,904.9	1,903.9	17
9	1,013.5	507.3	996.5	995.5	A	1,822.8	911.9	1,805.8	1,804.8	16
10	1,142.5	571.8	1,125.5	1,124.5	E	1,751.8	876.4	1,734.8	1,733.8	15
11	1,255.6	628.3	1,238.6	1,237.6	I	1,622.8	811.9	1,605.7	1,604.8	14
12	1,356.7	678.8	1,339.7	1,338.7	T	1,509.7	755.3	1,492.7	1,491.7	13
13	1,470.7	735.9	1,453.7	1,452.7	N	1,408.6	704.8	1,391.6	1,390.6	12
14	1,541.8	771.4	1,524.7	1,523.7	A	1,294.6	647.8	1,277.6	1,276.6	11
15	1,701.8	851.4	1,684.8	1,683.8	C+57	1,223.6	612.3	1,206.5	1,205.5	10
16	1,848.9	924.9	1,831.8	1,830.8	F	1,063.5	532.3	1,046.5	1,045.5	9
17	1,977.9	989.5	1,960.9	1,959.9	E	916.5	458.7	899.4	898.4	8
18	2,075.0	1,038.0	2,057.9	2,056.9	P	787.4	394.2	770.4		7
19	2,146.0	1,073.5	2,129.0	2,128.0	A	690.4	345.7	673.3		6
20	2,260.0	1,130.5	2,243.0	2,242.0	N	619.3		602.3		5
21	2,388.1	1,194.5	2,371.1	2,370.1	Q	505.3		488.3		4
22	2,519.1	1,260.1	2,502.1	2,501.1	M	377.2		360.2		3
23	2,618.2	1,309.6	2,601.2	2,600.2	V	246.2		229.2		2
24	2,764.3	1,382.7	2,747.3	2,746.3	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-94	sp|Q99584|S10AD_HUMAN	ELVTQQLPHLLK	46.64	Unmodified	Light	2	709.92193

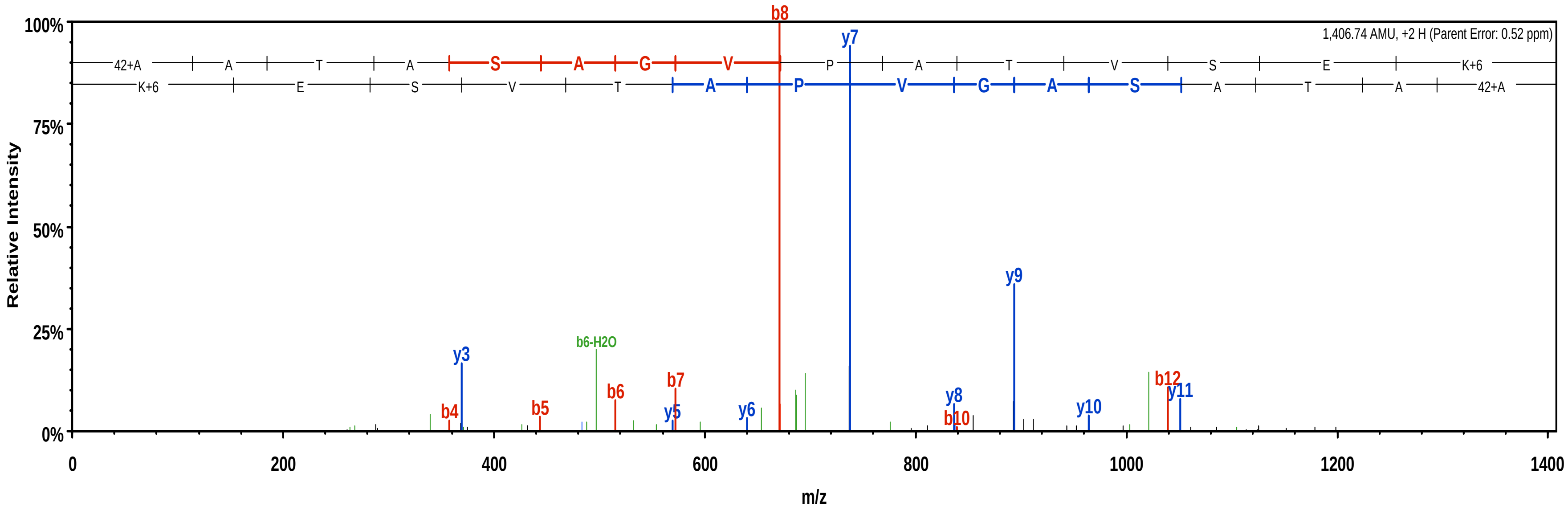


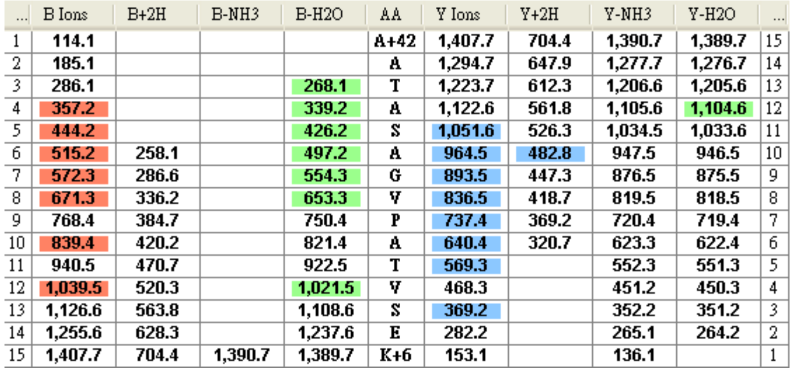


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	1,418.8	709.9	1,401.8	1,400.8	12
2	243.1			225.1	L	1,289.8	645.4	1,272.8	1,271.8	11
3	342.2			324.2	V	1,176.7	588.9	1,159.7	1,158.7	10
4	443.3			425.2	T	1,077.6	539.3	1,060.6	1,059.6	9
5	571.3		554.3	553.3	Q	976.6	488.8	959.6		8
6	699.4	350.2	682.3	681.4	Q	848.5	424.8	831.5		7
7	812.5	406.7	795.4	794.4	L	720.5	360.7	703.5		6
8	909.5	455.3	892.5	891.5	P	607.4	304.2	590.4		5
9	1,046.6	523.8	1,029.5	1,028.6	H	510.3	255.7	493.3		4
10	1,159.6	580.3	1,142.6	1,141.6	L	373.3		356.3		3
11	1,272.7	636.9	1,255.7	1,254.7	L	260.2		243.2		2
12	1,418.8	709.9	1,401.8	1,400.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-95	sp|O60518|RNBP6_HUMAN	AATASAGVPATVSEK	46.4	Acetyl (Protein N-term)	Heavy	2	701.36464

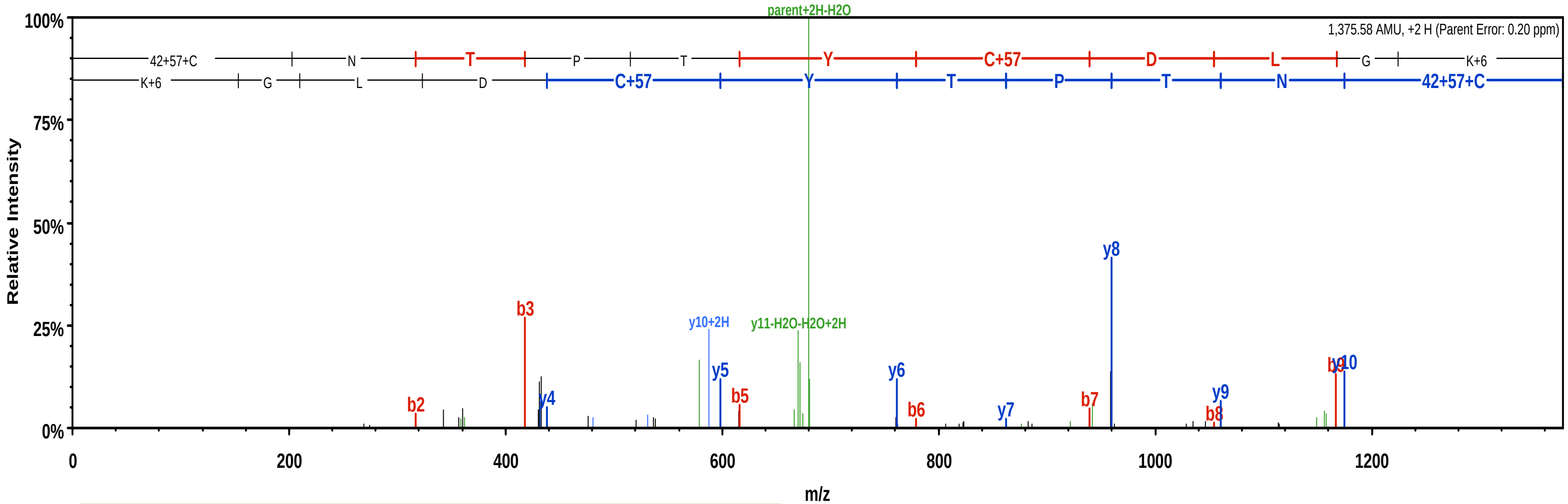


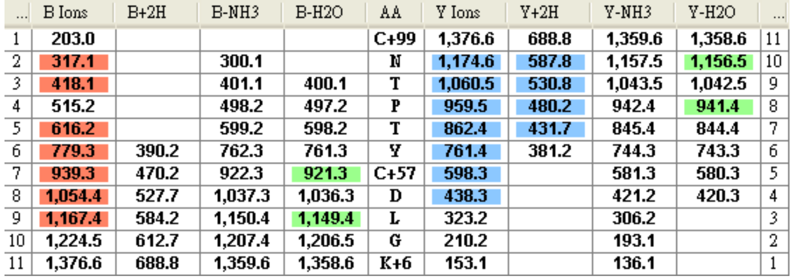


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	1,407.7	704.4	1,390.7	1,389.7	15
2	185.1				A	1,294.7	647.9	1,277.7	1,276.7	14
3	286.1			268.1	T	1,223.7	612.3	1,206.6	1,205.6	13
4	357.2			339.2	A	1,122.6	561.8	1,105.6	1,104.6	12
5	444.2			426.2	S	1,051.6	526.3	1,034.5	1,033.6	11
6	515.2	258.1		497.2	A	964.5	482.8	947.5	946.5	10
7	572.3	286.6		554.3	G	893.5	447.3	876.5	875.5	9
8	671.3	336.2		653.3	V	836.5	418.7	819.5	818.5	8
9	768.4	384.7		750.4	P	737.4	369.2	720.4	719.4	7
10	839.4	420.2		821.4	A	640.4	320.7	623.3	622.4	6
11	940.5	470.7		922.5	T	569.3		552.3	551.3	5
12	1,039.5	520.3		1,021.5	V	468.3		451.2	450.3	4
13	1,126.6	563.8		1,108.6	S	369.2		352.2	351.2	3
14	1,255.6	628.3		1,237.6	E	282.2		265.1	264.2	2
15	1,407.7	704.4	1,390.7	1,389.7	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-96	sp|Q9Y277|VDAC3_HUMAN	CNTPTYCDLGK	45.65	Acetyl (Protein N-term)	Heavy	2	685.78939

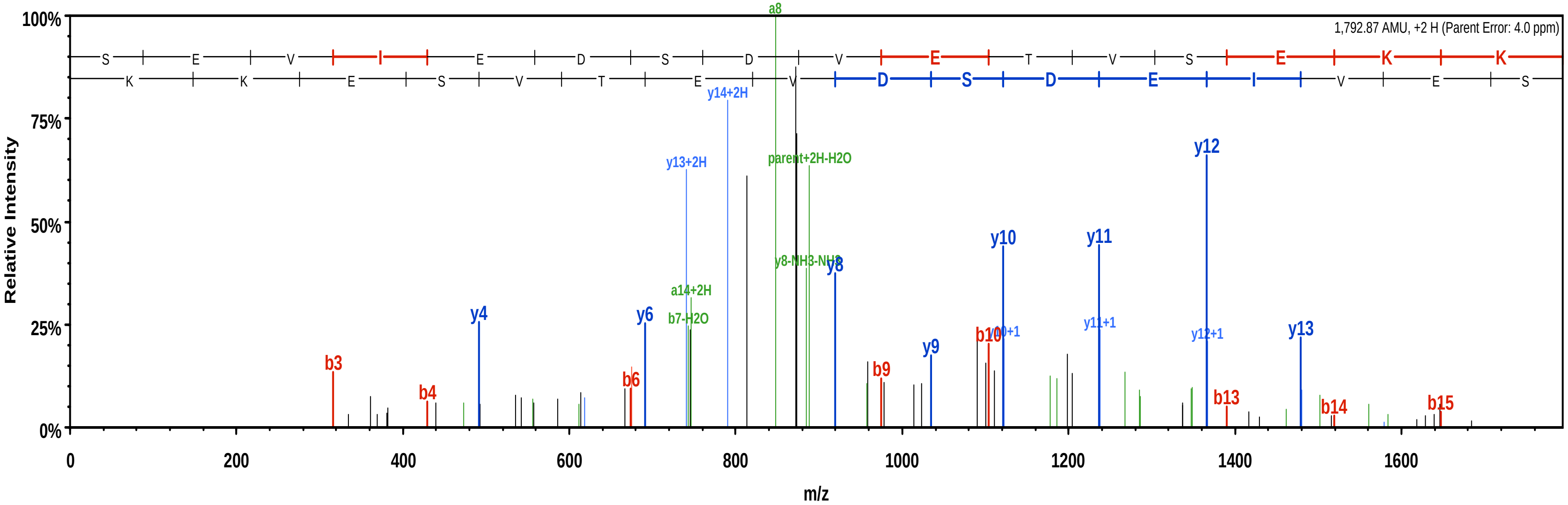


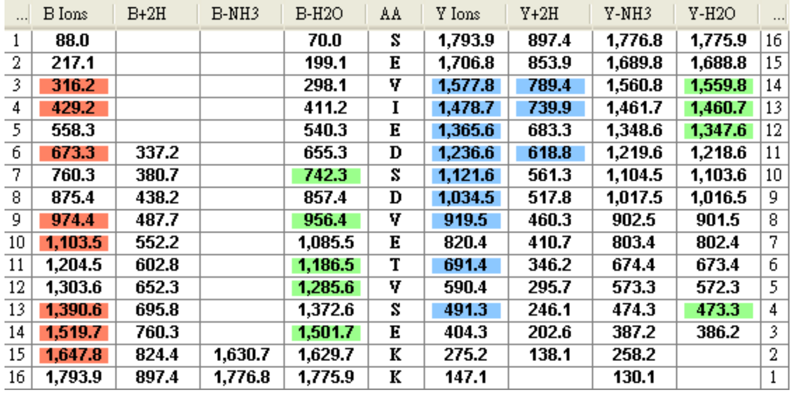


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	203.0				C+99	1,376.6	688.8	1,359.6	1,358.6	11
2	317.1		300.1		N	1,174.6	587.8	1,157.5	1,156.5	10
3	418.1		401.1	400.1	T	1,060.5	530.8	1,043.5	1,042.5	9
4	515.2		498.2	497.2	P	959.5	480.2	942.4	941.4	8
5	616.2		599.2	598.2	T	862.4	431.7	845.4	844.4	7
6	779.3	390.2	762.3	761.3	Y	761.4	381.2	744.3	743.3	6
7	939.3	470.2	922.3	921.3	C+57	598.3		581.3	580.3	5
8	1,054.4	527.7	1,037.3	1,036.3	D	438.3		421.2	420.3	4
9	1,167.4	584.2	1,150.4	1,149.4	L	323.2		306.2		3
10	1,224.5	612.7	1,207.4	1,206.5	G	210.2		193.1		2
11	1,376.6	688.8	1,359.6	1,358.6	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-97	sp|Q56NI9|ESCO2_HUMAN	SEVIEDSDVETVSEKK	44.81	Unmodified	Light	2	897.43619

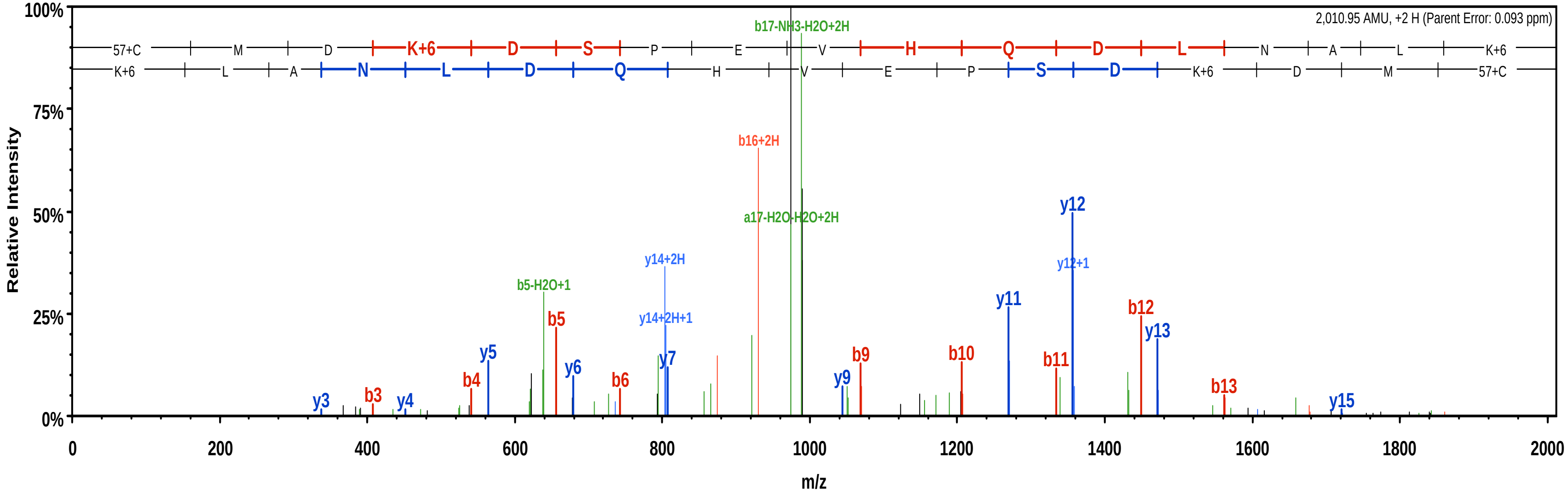


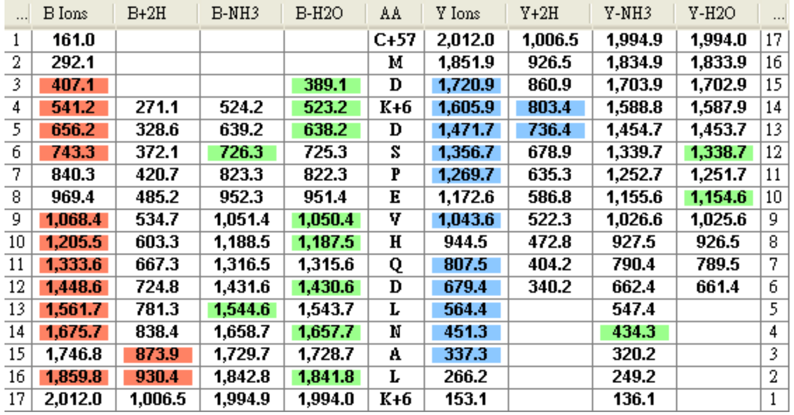


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	1,793.9	897.4	1,776.8	1,775.9	16
2	217.1			199.1	E	1,706.8	853.9	1,689.8	1,688.8	15
3	316.2			298.1	V	1,577.8	789.4	1,560.8	1,559.8	14
4	429.2			411.2	I	1,478.7	739.9	1,461.7	1,460.7	13
5	558.3			540.3	E	1,365.6	683.3	1,348.6	1,347.6	12
6	673.3	337.2		655.3	D	1,236.6	618.8	1,219.6	1,218.6	11
7	760.3	380.7		742.3	S	1,121.6	561.3	1,104.5	1,103.6	10
8	875.4	438.2		857.4	D	1,034.5	517.8	1,017.5	1,016.5	9
9	974.4	487.7		956.4	V	919.5	460.3	902.5	901.5	8
10	1,103.5	552.2		1,085.5	E	820.4	410.7	803.4	802.4	7
11	1,204.5	602.8		1,186.5	T	691.4	346.2	674.4	673.4	6
12	1,303.6	652.3		1,285.6	V	590.4	295.7	573.3	572.3	5
13	1,390.6	695.8		1,372.6	S	491.3	246.1	474.3	473.3	4
14	1,519.7	760.3		1,501.7	E	404.3	202.6	387.2	386.2	3
15	1,647.8	824.4	1,630.7	1,629.7	K	275.2	138.1	258.2		2
16	1,793.9	897.4	1,776.8	1,775.9	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-98	sp|Q9NWA0|MED9_HUMAN	CMDKDSPEVHQDLNALK	44.77	Unmodified	Heavy	2	1000.4642

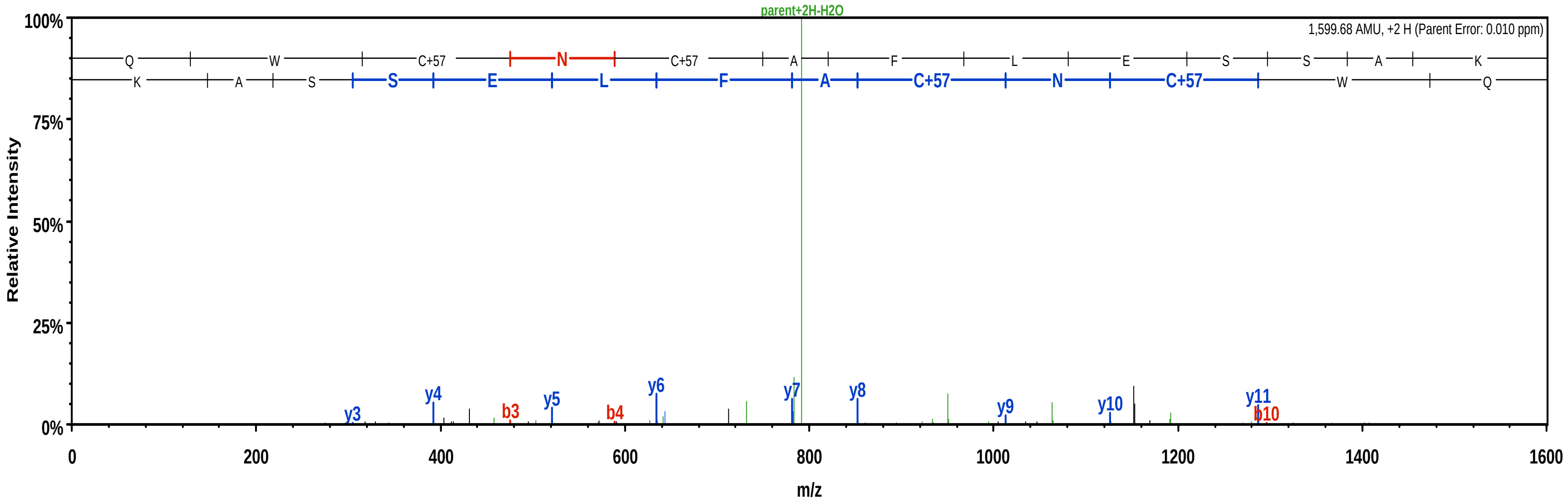


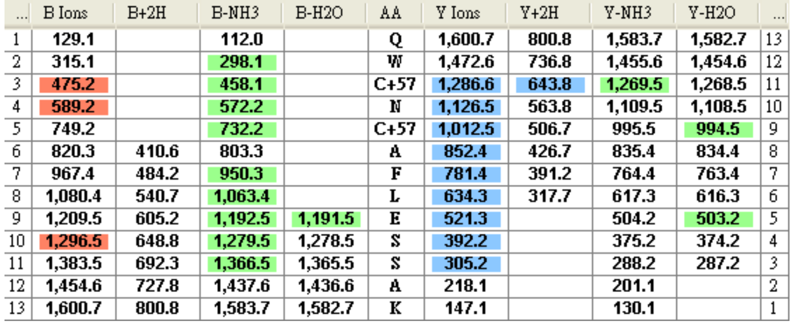


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	161.0				C+57	2,012.0	1,006.5	1,994.9	1,994.0	17
2	292.1				M	1,851.9	926.5	1,834.9	1,833.9	16
3	407.1			389.1	D	1,720.9	860.9	1,703.9	1,702.9	15
4	541.2	271.1	524.2	523.2	K+6	1,605.9	803.4	1,588.8	1,587.9	14
5	656.2	328.6	639.2	638.2	D	1,471.7	736.4	1,454.7	1,453.7	13
6	743.3	372.1	726.3	725.3	S	1,356.7	678.9	1,339.7	1,338.7	12
7	840.3	420.7	823.3	822.3	P	1,269.7	635.3	1,252.7	1,251.7	11
8	969.4	485.2	952.3	951.4	E	1,172.6	586.8	1,155.6	1,154.6	10
9	1,068.4	534.7	1,051.4	1,050.4	V	1,043.6	522.3	1,026.6	1,025.6	9
10	1,205.5	603.3	1,188.5	1,187.5	H	944.5	472.8	927.5	926.5	8
11	1,333.6	667.3	1,316.5	1,315.6	Q	807.5	404.2	790.4	789.5	7
12	1,448.6	724.8	1,431.6	1,430.6	D	679.4	340.2	662.4	661.4	6
13	1,561.7	781.3	1,544.6	1,543.7	L	564.4		547.4		5
14	1,675.7	838.4	1,658.7	1,657.7	N	451.3		434.3		4
15	1,746.8	873.9	1,729.7	1,728.7	A	337.3		320.2		3
16	1,859.8	930.4	1,842.8	1,841.8	L	266.2		249.2		2
17	2,012.0	1,006.5	1,994.9	1,994.0	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-99	sp|P62834|RAP1A_HUMAN	QWCNCAFLESSAK	44.6	Unmodified	Light	2	800.84777

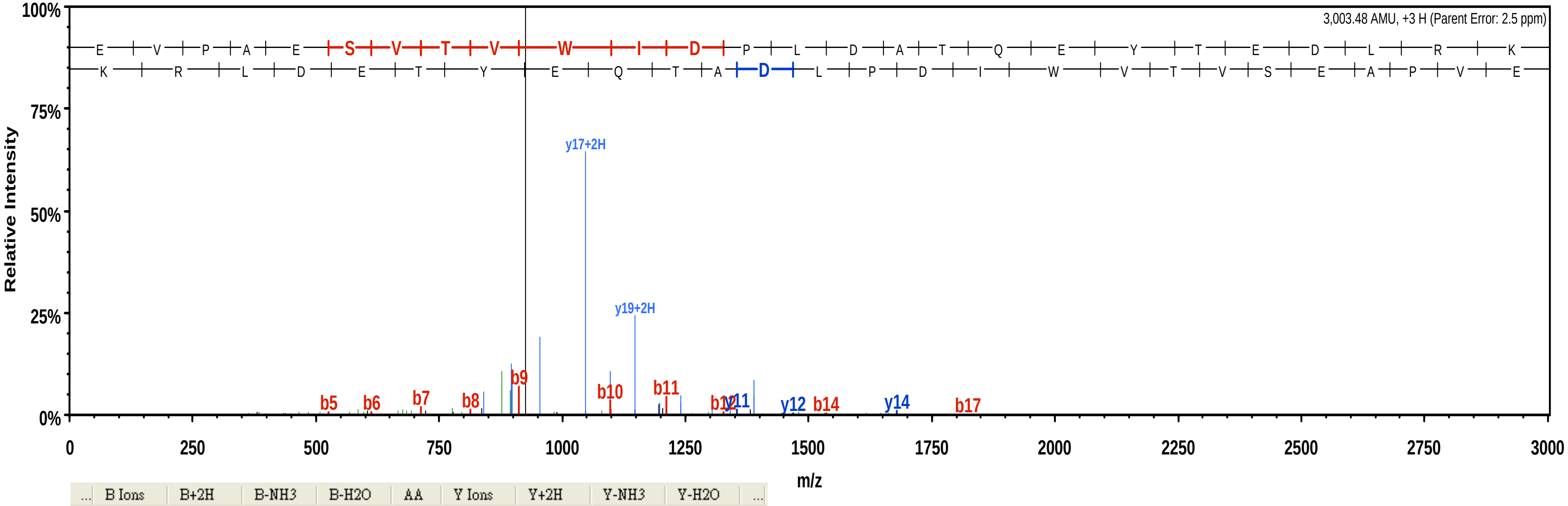


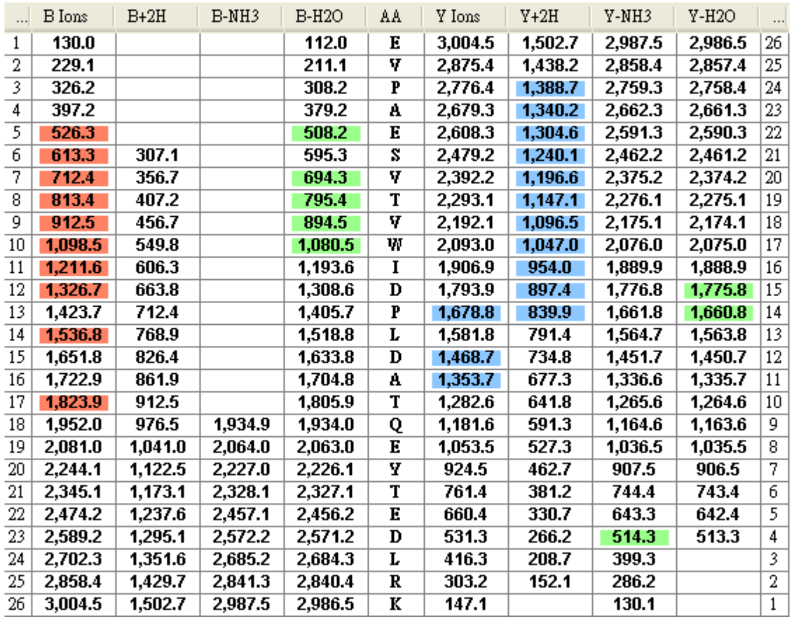


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	129.1		112.0		Q	1,600.7	800.8	1,583.7	1,582.7	13
2	315.1		298.1		W	1,472.6	736.8	1,455.6	1,454.6	12
3	475.2		458.1		C+57	1,286.6	643.8	1,269.5	1,268.5	11
4	589.2		572.2		N	1,126.5	563.8	1,109.5	1,108.5	10
5	749.2		732.2		C+57	1,012.5	506.7	995.5	994.5	9
6	820.3	410.6	803.3		A	852.4	426.7	835.4	834.4	8
7	967.4	484.2	950.3		F	781.4	391.2	764.4	763.4	7
8	1,080.4	540.7	1,063.4		L	634.3	317.7	617.3	616.3	6
9	1,209.5	605.2	1,192.5	1,191.5	E	521.3		504.2	503.2	5
10	1,296.5	648.8	1,279.5	1,278.5	S	392.2		375.2	374.2	4
11	1,383.5	692.3	1,366.5	1,365.5	S	305.2		288.2	287.2	3
12	1,454.6	727.8	1,437.6	1,436.6	A	218.1		201.1		2
13	1,600.7	800.8	1,583.7	1,582.7	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-100	sp|Q9NX62|IMPA3_HUMAN	EVPAESVTVWIDPLDATQEYTEDLRK	44.26	Unmodified	Light	3	1002.1644

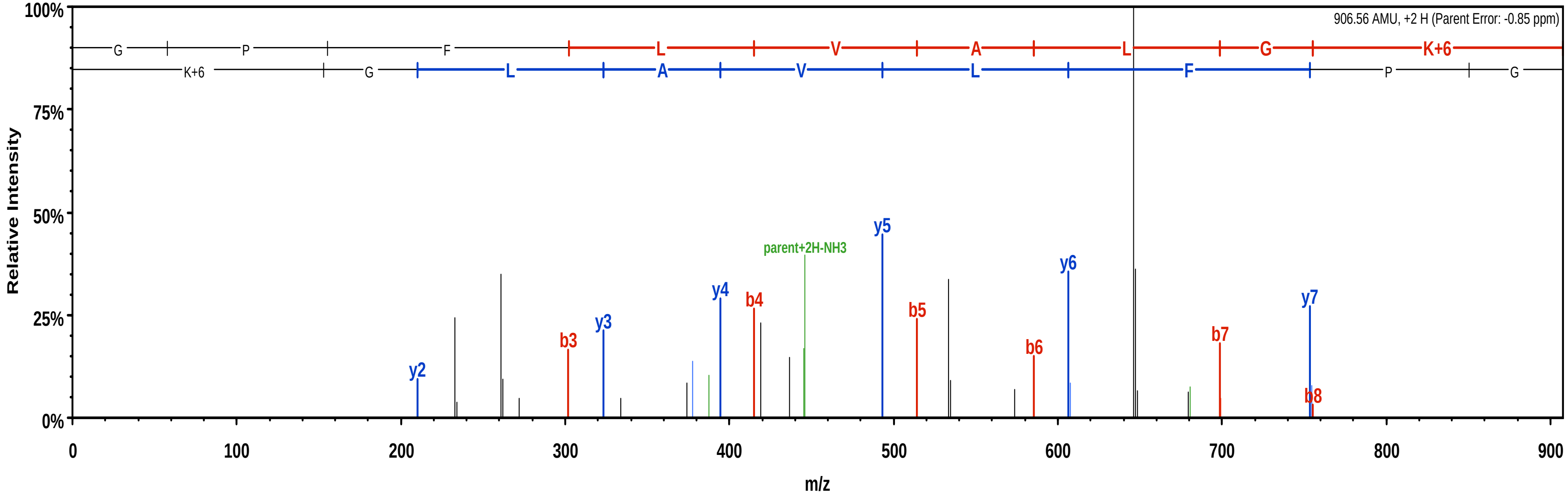


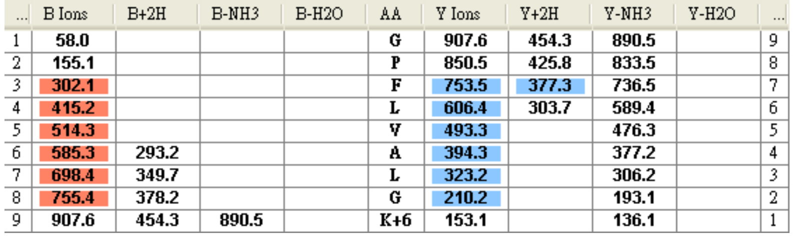


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	E	3,004.5	1,502.7	2,987.5	2,986.5	26
2	229.1			211.1	V	2,875.4	1,438.2	2,858.4	2,857.4	25
3	326.2			308.2	P	2,776.4	1,388.7	2,759.3	2,758.4	24
4	397.2			379.2	A	2,679.3	1,340.2	2,662.3	2,661.3	23
5	526.3			508.2	E	2,608.3	1,304.6	2,591.3	2,590.3	22
6	613.3	307.1		595.3	S	2,479.2	1,240.1	2,462.2	2,461.2	21
7	712.4	356.7		694.3	V	2,392.2	1,196.6	2,375.2	2,374.2	20
8	813.4	407.2		795.4	T	2,293.1	1,147.1	2,276.1	2,275.1	19
9	912.5	456.7		894.5	V	2,192.1	1,096.5	2,175.1	2,174.1	18
10	1,098.5	549.8		1,080.5	W	2,093.0	1,047.0	2,076.0	2,075.0	17
11	1,211.6	606.3		1,193.6	I	1,906.9	954.0	1,889.9	1,888.9	16
12	1,326.7	663.8		1,308.6	D	1,793.9	897.4	1,776.8	1,775.8	15
13	1,423.7	712.4		1,405.7	P	1,678.8	839.9	1,661.8	1,660.8	14
14	1,536.8	768.9		1,518.8	L	1,581.8	791.4	1,564.7	1,563.8	13
15	1,651.8	826.4		1,633.8	D	1,468.7	734.8	1,451.7	1,450.7	12
16	1,722.9	861.9		1,704.8	A	1,353.7	677.3	1,336.6	1,335.7	11
17	1,823.9	912.5		1,805.9	T	1,282.6	641.8	1,265.6	1,264.6	10
18	1,952.0	976.5	1,934.9	1,934.0	Q	1,181.6	591.3	1,164.6	1,163.6	9
19	2,081.0	1,041.0	2,064.0	2,063.0	E	1,053.5	527.3	1,036.5	1,035.5	8
20	2,244.1	1,122.5	2,227.0	2,226.1	Y	924.5	462.7	907.5	906.5	7
21	2,345.1	1,173.1	2,328.1	2,327.1	T	761.4	381.2	744.4	743.4	6
22	2,474.2	1,237.6	2,457.1	2,456.2	E	660.4	330.7	643.3	642.4	5
23	2,589.2	1,295.1	2,572.2	2,571.2	D	531.3	266.2	514.3	513.3	4
24	2,702.3	1,351.6	2,685.2	2,684.3	L	416.3	208.7	399.3		3
25	2,858.4	1,429.7	2,841.3	2,840.4	R	303.2	152.1	286.2		2
26	3,004.5	1,502.7	2,987.5	2,986.5	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-101	sp|Q96HC4|PDLI5_HUMAN	GPFLVALGK	43.67	Unmodified	Heavy	2	451.27892

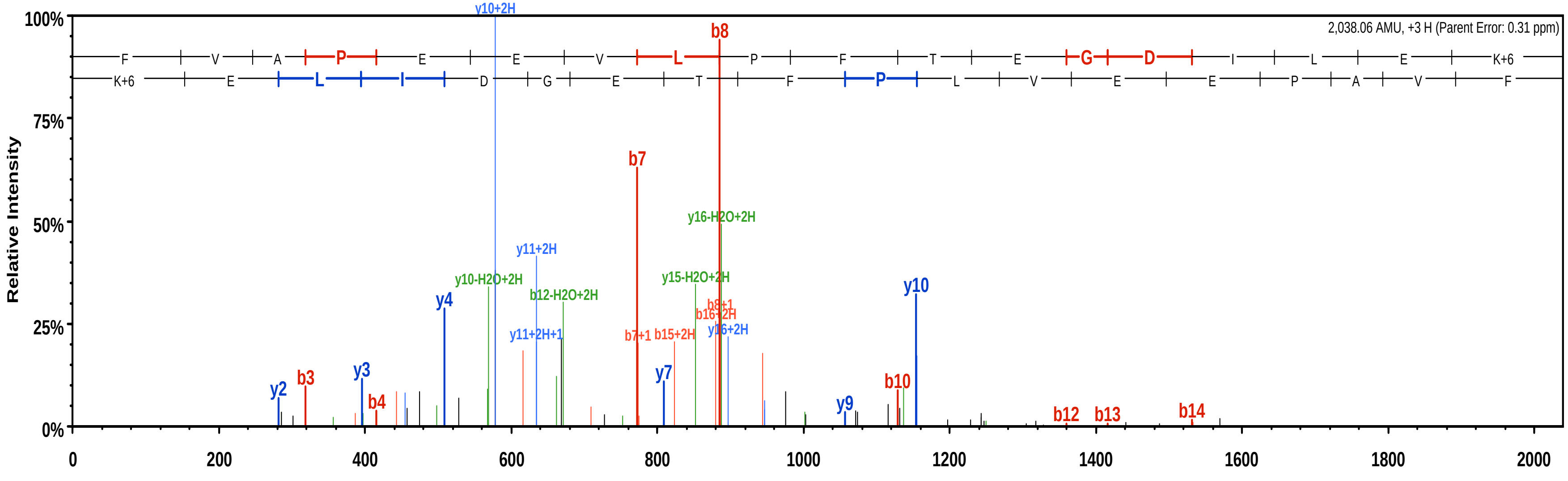


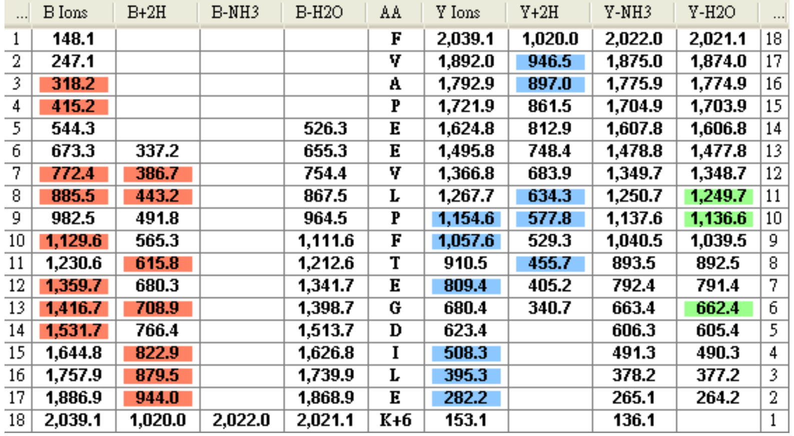


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	58.0				G	907.6	454.3	890.5		9
2	155.1				P	850.5	425.8	833.5		8
3	302.1				F	753.5	377.3	736.5		7
4	415.2				L	606.4	303.7	589.4		6
5	514.3				V	493.3		476.3		5
6	585.3	293.2			A	394.3		377.2		4
7	698.4	349.7			L	323.2		306.2		3
8	755.4	378.2			G	210.2		193.1		2
9	907.6	454.3	890.5		K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-102	sp|P49770|EI2BB_HUMAN	FVAPEEVLPFTEGDILEK	42.18	Unmodified	Heavy	3	678.3541

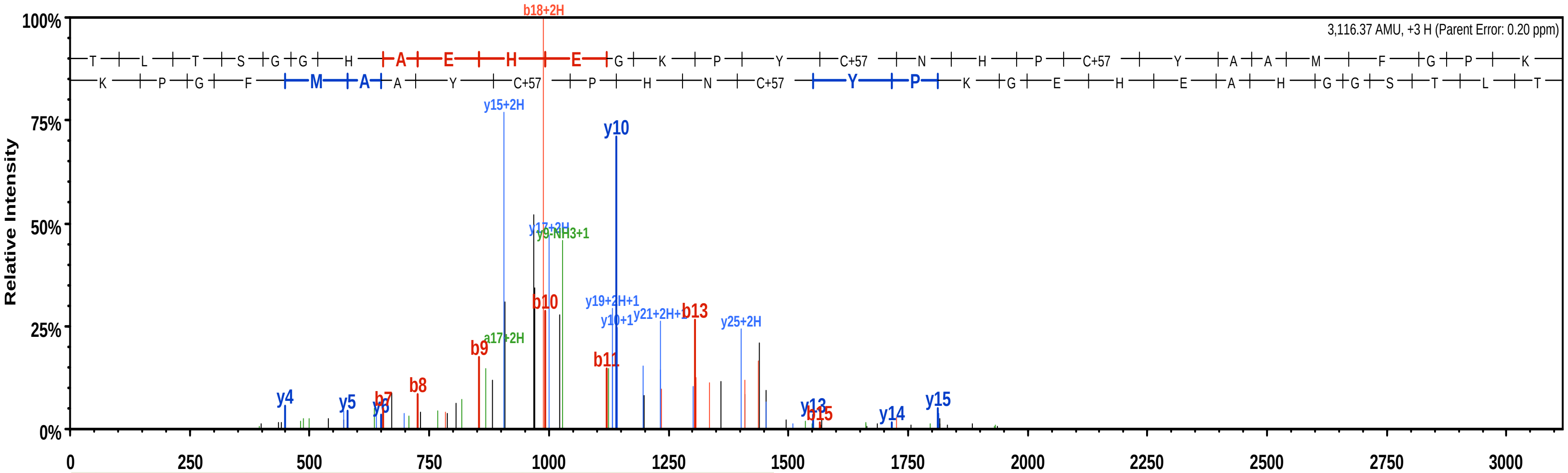


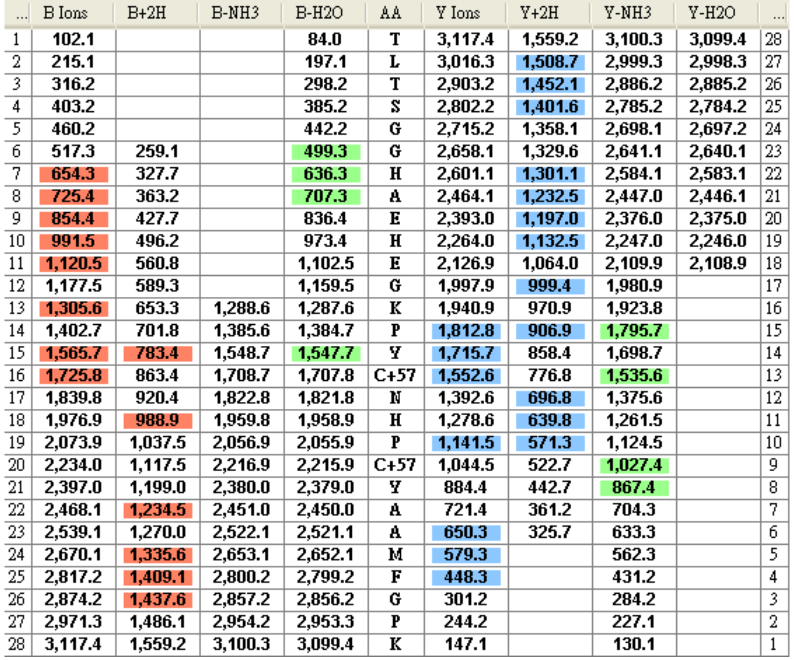


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.1				F	2,039.1	1,020.0	2,022.0	2,021.1	18
2	247.1				V	1,892.0	946.5	1,875.0	1,874.0	17
3	318.2				A	1,792.9	897.0	1,775.9	1,774.9	16
4	415.2				P	1,721.9	861.5	1,704.9	1,703.9	15
5	544.3			526.3	E	1,624.8	812.9	1,607.8	1,606.8	14
6	673.3	337.2		655.3	E	1,495.8	748.4	1,478.8	1,477.8	13
7	772.4	386.7		754.4	V	1,366.8	683.9	1,349.7	1,348.7	12
8	885.5	443.2		867.5	L	1,267.7	634.3	1,250.7	1,249.7	11
9	982.5	491.8		964.5	P	1,154.6	577.8	1,137.6	1,136.6	10
10	1,129.6	565.3		1,111.6	F	1,057.6	529.3	1,040.5	1,039.5	9
11	1,230.6	615.8		1,212.6	T	910.5	455.7	893.5	892.5	8
12	1,359.7	680.3		1,341.7	E	809.4	405.2	792.4	791.4	7
13	1,416.7	708.9		1,398.7	G	680.4	340.7	663.4	662.4	6
14	1,531.7	766.4		1,513.7	D	623.4		606.3	605.4	5
15	1,644.8	822.9		1,626.8	I	508.3		491.3	490.3	4
16	1,757.9	879.5		1,739.9	L	395.3		378.2	377.2	3
17	1,886.9	944.0		1,868.9	E	282.2		265.1	264.2	2
18	2,039.1	1,020.0	2,022.0	2,021.1	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-103	sp|P50238|CRIP1_HUMAN	TLTSGGHAEHEGKPYCNHPCYAAMFGPK	41.9	Unmodified	Light	3	1039.797

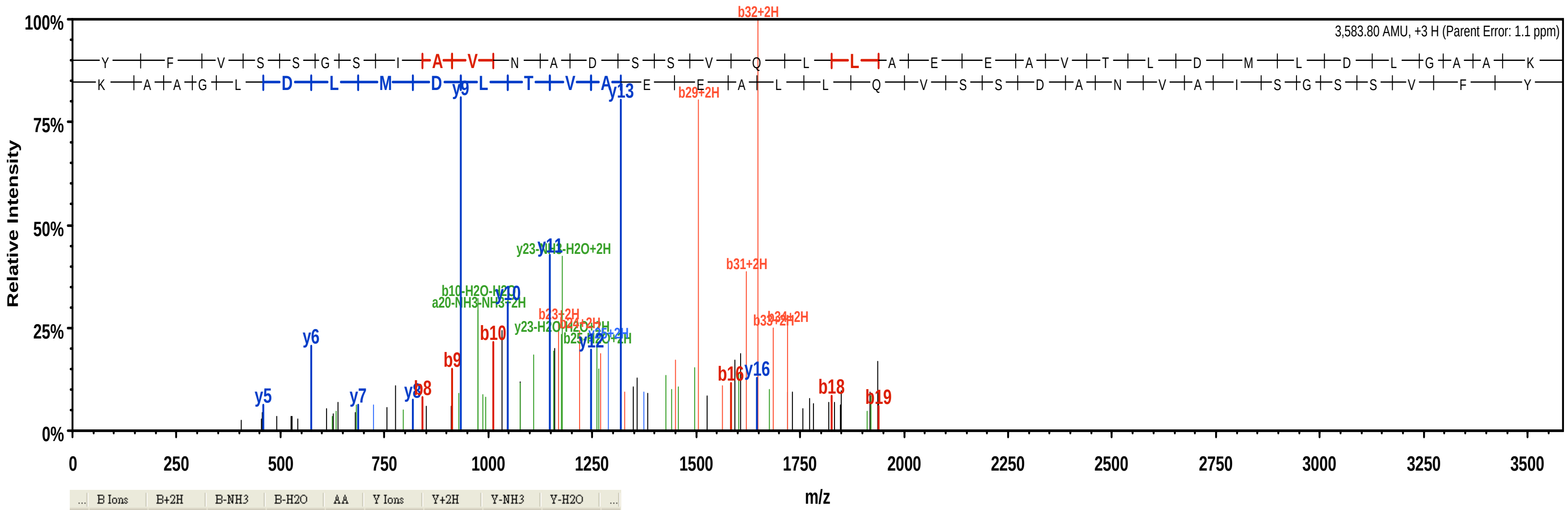


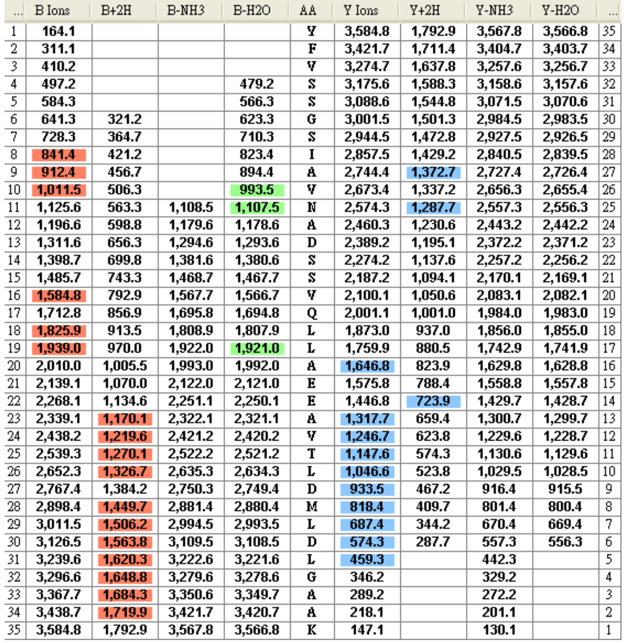


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	102.1			84.0	T	3,117.4	1,559.2	3,100.3	3,099.4	28
2	215.1			197.1	L	3,016.3	1,508.7	2,999.3	2,998.3	27
3	316.2			298.2	T	2,903.2	1,452.1	2,886.2	2,885.2	26
4	403.2			385.2	S	2,802.2	1,401.6	2,785.2	2,784.2	25
5	460.2			442.2	G	2,715.2	1,358.1	2,698.1	2,697.2	24
6	517.3	259.1		499.3	G	2,658.1	1,329.6	2,641.1	2,640.1	23
7	654.3	327.7		636.3	H	2,601.1	1,301.1	2,584.1	2,583.1	22
8	725.4	363.2		707.3	A	2,464.1	1,232.5	2,447.0	2,446.1	21
9	854.4	427.7		836.4	E	2,393.0	1,197.0	2,376.0	2,375.0	20
10	991.5	496.2		973.4	H	2,264.0	1,132.5	2,247.0	2,246.0	19
11	1,120.5	560.8		1,102.5	E	2,126.9	1,064.0	2,109.9	2,108.9	18
12	1,177.5	589.3		1,159.5	G	1,997.9	999.4	1,980.9		17
13	1,305.6	653.3	1,288.6	1,287.6	K	1,940.9	970.9	1,923.8		16
14	1,402.7	701.8	1,385.6	1,384.7	P	1,812.8	906.9	1,795.7		15
15	1,565.7	783.4	1,548.7	1,547.7	Y	1,715.7	858.4	1,698.7		14
16	1,725.8	863.4	1,708.7	1,707.8	C+57	1,552.6	776.8	1,535.6		13
17	1,839.8	920.4	1,822.8	1,821.8	N	1,392.6	696.8	1,375.6		12
18	1,976.9	988.9	1,959.8	1,958.9	H	1,278.6	639.8	1,261.5		11
19	2,073.9	1,037.5	2,056.9	2,055.9	P	1,141.5	571.3	1,124.5		10
20	2,234.0	1,117.5	2,216.9	2,215.9	C+57	1,044.5	522.7	1,027.4		9
21	2,397.0	1,199.0	2,380.0	2,379.0	Y	884.4	442.7	867.4		8
22	2,468.1	1,234.5	2,451.0	2,450.0	A	721.4	361.2	704.3		7
23	2,539.1	1,270.0	2,522.1	2,521.1	A	650.3	325.7	633.3		6
24	2,670.1	1,335.6	2,653.1	2,652.1	M	579.3		562.3		5
25	2,817.2	1,409.1	2,800.2	2,799.2	F	448.3		431.2		4
26	2,874.2	1,437.6	2,857.2	2,856.2	G	301.2		284.2		3
27	2,971.3	1,486.1	2,954.2	2,953.3	P	244.2		227.1		2
28	3,117.4	1,559.2	3,100.3	3,099.4	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-104	sp|P30049|ATPD_HUMAN	YFVSSGSIAVNADSSVQLLAEEAVTLDMLDLGAAK	41.39	Unmodified	Light	3	1195.6062

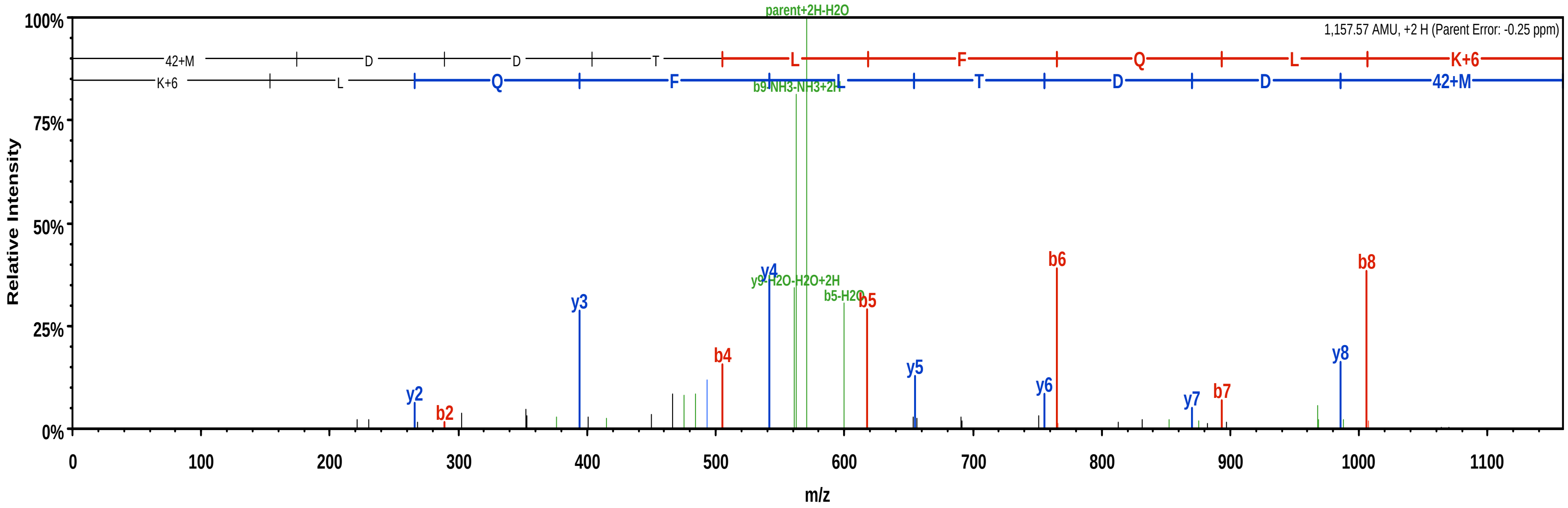


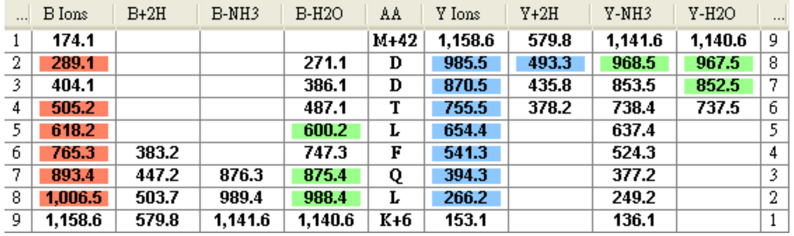


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	164.1				Y	3,584.8	1,792.9	3,567.8	3,566.8	35
2	311.1				F	3,421.7	1,711.4	3,404.7	3,403.7	34
3	410.2				V	3,274.7	1,637.8	3,257.6	3,256.7	33
4	497.2			479.2	S	3,175.6	1,588.3	3,158.6	3,157.6	32
5	584.3			566.3	S	3,088.6	1,544.8	3,071.5	3,070.6	31
6	641.3	321.2		623.3	G	3,001.5	1,501.3	2,984.5	2,983.5	30
7	728.3	364.7		710.3	S	2,944.5	1,472.8	2,927.5	2,926.5	29
8	841.4	421.2		823.4	I	2,857.5	1,429.2	2,840.5	2,839.5	28
9	912.4	456.7		894.4	A	2,744.4	1,372.7	2,727.4	2,726.4	27
10	1,011.5	506.3		993.5	V	2,673.4	1,337.2	2,656.3	2,655.4	26
11	1,125.6	563.3	1,108.5	1,107.5	N	2,574.3	1,287.7	2,557.3	2,556.3	25
12	1,196.6	598.8	1,179.6	1,178.6	A	2,460.3	1,230.6	2,443.2	2,442.2	24
13	1,311.6	656.3	1,294.6	1,293.6	D	2,389.2	1,195.1	2,372.2	2,371.2	23
14	1,398.7	699.8	1,381.6	1,380.6	S	2,274.2	1,137.6	2,257.2	2,256.2	22
15	1,485.7	743.3	1,468.7	1,467.7	S	2,187.2	1,094.1	2,170.1	2,169.1	21
16	1,584.8	792.9	1,567.7	1,566.7	V	2,100.1	1,050.6	2,083.1	2,082.1	20
17	1,712.8	856.9	1,695.8	1,694.8	Q	2,001.1	1,001.0	1,984.0	1,983.0	19
18	1,825.9	913.5	1,808.9	1,807.9	L	1,873.0	937.0	1,856.0	1,855.0	18
19	1,939.0	970.0	1,922.0	1,921.0	L	1,759.9	880.5	1,742.9	1,741.9	17
20	2,010.0	1,005.5	1,993.0	1,992.0	A	1,646.8	823.9	1,629.8	1,628.8	16
21	2,139.1	1,070.0	2,122.0	2,121.0	E	1,575.8	788.4	1,558.8	1,557.8	15
22	2,268.1	1,134.6	2,251.1	2,250.1	E	1,446.8	723.9	1,429.7	1,428.7	14
23	2,339.1	1,170.1	2,322.1	2,321.1	A	1,317.7	659.4	1,300.7	1,299.7	13
24	2,438.2	1,219.6	2,421.2	2,420.2	V	1,246.7	623.8	1,229.6	1,228.7	12
25	2,539.3	1,270.1	2,522.2	2,521.2	T	1,147.6	574.3	1,130.6	1,129.6	11
26	2,652.3	1,326.7	2,635.3	2,634.3	L	1,046.6	523.8	1,029.5	1,028.5	10
27	2,767.4	1,384.2	2,750.3	2,749.4	D	933.5	467.2	916.4	915.5	9
28	2,898.4	1,449.7	2,881.4	2,880.4	M	818.4	409.7	801.4	800.4	8
29	3,011.5	1,506.2	2,994.5	2,993.5	L	687.4	344.2	670.4	669.4	7
30	3,126.5	1,563.8	3,109.5	3,108.5	D	574.3	287.7	557.3	556.3	6
31	3,239.6	1,620.3	3,222.6	3,221.6	L	459.3		442.3		5
32	3,296.6	1,648.8	3,279.6	3,278.6	G	346.2		329.2		4
33	3,367.7	1,684.3	3,350.6	3,349.7	A	289.2		272.2		3
34	3,438.7	1,719.9	3,421.7	3,420.7	A	218.1		201.1		2
35	3,584.8	1,792.9	3,567.8	3,566.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-105	sp|Q9HD42|CHM1A_HUMAN	MDDTLFQLK	40.97	Acetyl (Protein N-term)	Heavy	2	576.78391

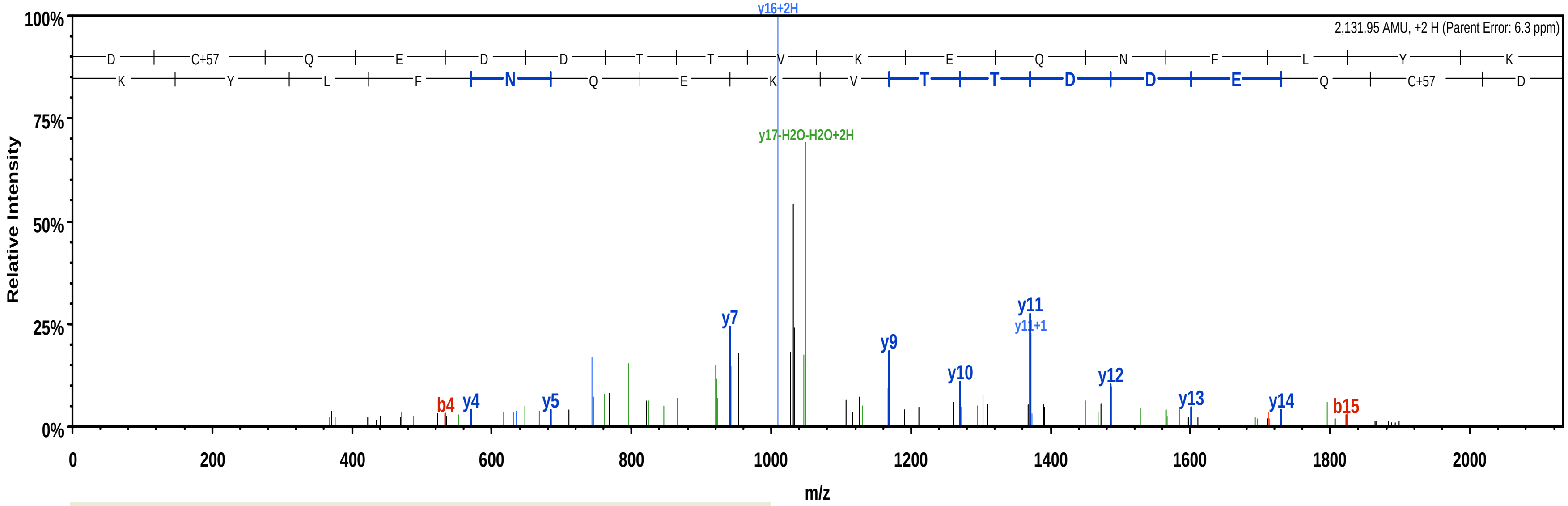


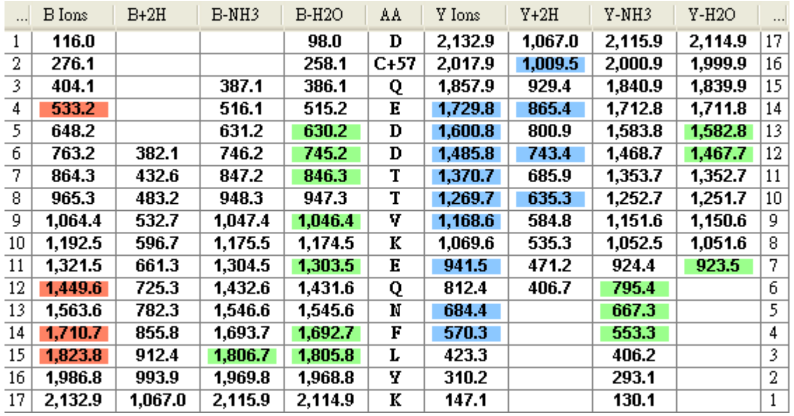


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	174.1				M+42	1,158.6	579.8	1,141.6	1,140.6	9
2	289.1			271.1	D	985.5	493.3	968.5	967.5	8
3	404.1			386.1	D	870.5	435.8	853.5	852.5	7
4	505.2			487.1	T	755.5	378.2	738.4	737.5	6
5	618.2			600.2	L	654.4		637.4		5
6	765.3	383.2		747.3	F	541.3		524.3		4
7	893.4	447.2	876.3	875.4	Q	394.3		377.2		3
8	1,006.5	503.7	989.4	988.4	L	266.2		249.2		2
9	1,158.6	579.8	1,141.6	1,140.6	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-106	sp|Q9UBU7|DBF4A_HUMAN	DCQEDDTTVKEQNFLYK	40.53	Unmodified	Light	2	1066.9757

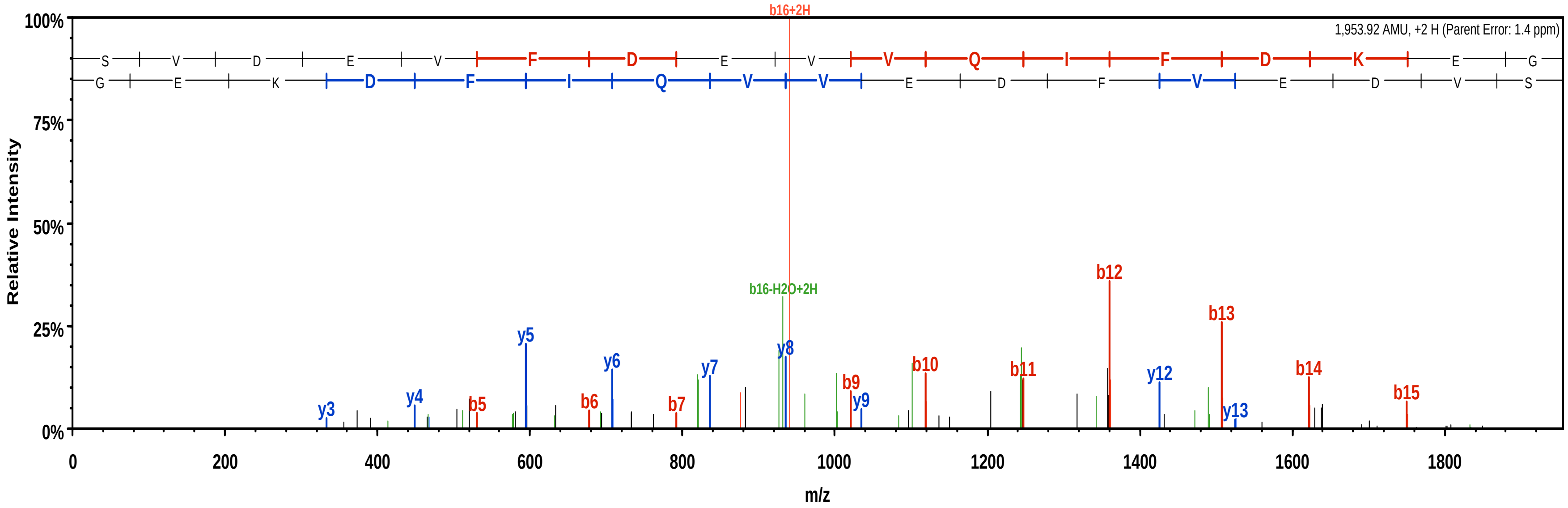


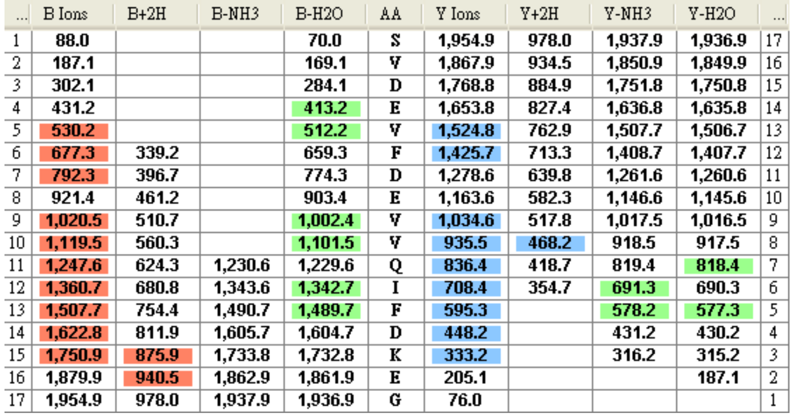


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	116.0			98.0	D	2,132.9	1,067.0	2,115.9	2,114.9	17
2	276.1			258.1	C+57	2,017.9	1,009.5	2,000.9	1,999.9	16
3	404.1		387.1	386.1	Q	1,857.9	929.4	1,840.9	1,839.9	15
4	533.2		516.1	515.2	E	1,729.8	865.4	1,712.8	1,711.8	14
5	648.2		631.2	630.2	D	1,600.8	800.9	1,583.8	1,582.8	13
6	763.2	382.1	746.2	745.2	D	1,485.8	743.4	1,468.7	1,467.7	12
7	864.3	432.6	847.2	846.3	T	1,370.7	685.9	1,353.7	1,352.7	11
8	965.3	483.2	948.3	947.3	T	1,269.7	635.3	1,252.7	1,251.7	10
9	1,064.4	532.7	1,047.4	1,046.4	V	1,168.6	584.8	1,151.6	1,150.6	9
10	1,192.5	596.7	1,175.5	1,174.5	K	1,069.6	535.3	1,052.5	1,051.6	8
11	1,321.5	661.3	1,304.5	1,303.5	E	941.5	471.2	924.4	923.5	7
12	1,449.6	725.3	1,432.6	1,431.6	Q	812.4	406.7	795.4		6
13	1,563.6	782.3	1,546.6	1,545.6	N	684.4		667.3		5
14	1,710.7	855.8	1,693.7	1,692.7	F	570.3		553.3		4
15	1,823.8	912.4	1,806.7	1,805.8	L	423.3		406.2		3
16	1,986.8	993.9	1,969.8	1,968.8	Y	310.2		293.1		2
17	2,132.9	1,067.0	2,115.9	2,114.9	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-107	sp|P30085|KCY_HUMAN	SVDEVFDEVVQIFDKEG	40.05	Unmodified	Light	2	977.96765

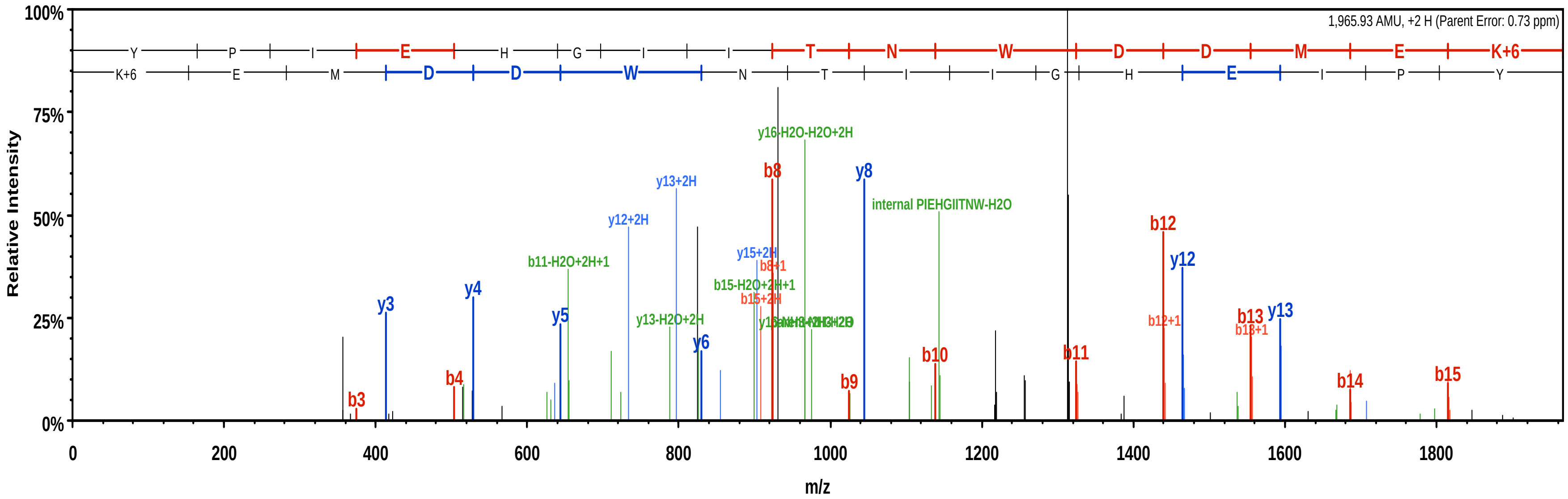


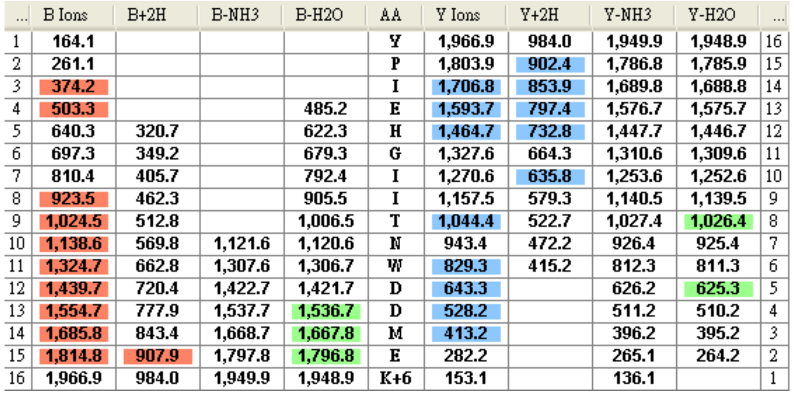


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	1,954.9	978.0	1,937.9	1,936.9	17
2	187.1			169.1	V	1,867.9	934.5	1,850.9	1,849.9	16
3	302.1			284.1	D	1,768.8	884.9	1,751.8	1,750.8	15
4	431.2			413.2	E	1,653.8	827.4	1,636.8	1,635.8	14
5	530.2			512.2	V	1,524.8	762.9	1,507.7	1,506.7	13
6	677.3	339.2		659.3	F	1,425.7	713.3	1,408.7	1,407.7	12
7	792.3	396.7		774.3	D	1,278.6	639.8	1,261.6	1,260.6	11
8	921.4	461.2		903.4	E	1,163.6	582.3	1,146.6	1,145.6	10
9	1,020.5	510.7		1,002.4	V	1,034.6	517.8	1,017.5	1,016.5	9
10	1,119.5	560.3		1,101.5	V	935.5	468.2	918.5	917.5	8
11	1,247.6	624.3	1,230.6	1,229.6	Q	836.4	418.7	819.4	818.4	7
12	1,360.7	680.8	1,343.6	1,342.7	I	708.4	354.7	691.3	690.3	6
13	1,507.7	754.4	1,490.7	1,489.7	F	595.3		578.2	577.3	5
14	1,622.8	811.9	1,605.7	1,604.7	D	448.2		431.2	430.2	4
15	1,750.9	875.9	1,733.8	1,732.8	K	333.2		316.2	315.2	3
16	1,879.9	940.5	1,862.9	1,861.9	E	205.1			187.1	2
17	1,954.9	978.0	1,937.9	1,936.9	G	76.0				1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-108	sp|P68032|ACTC_HUMAN	YPIEHGIITNWDDMEK	38.71	Unmodified	Heavy	2	980.95911

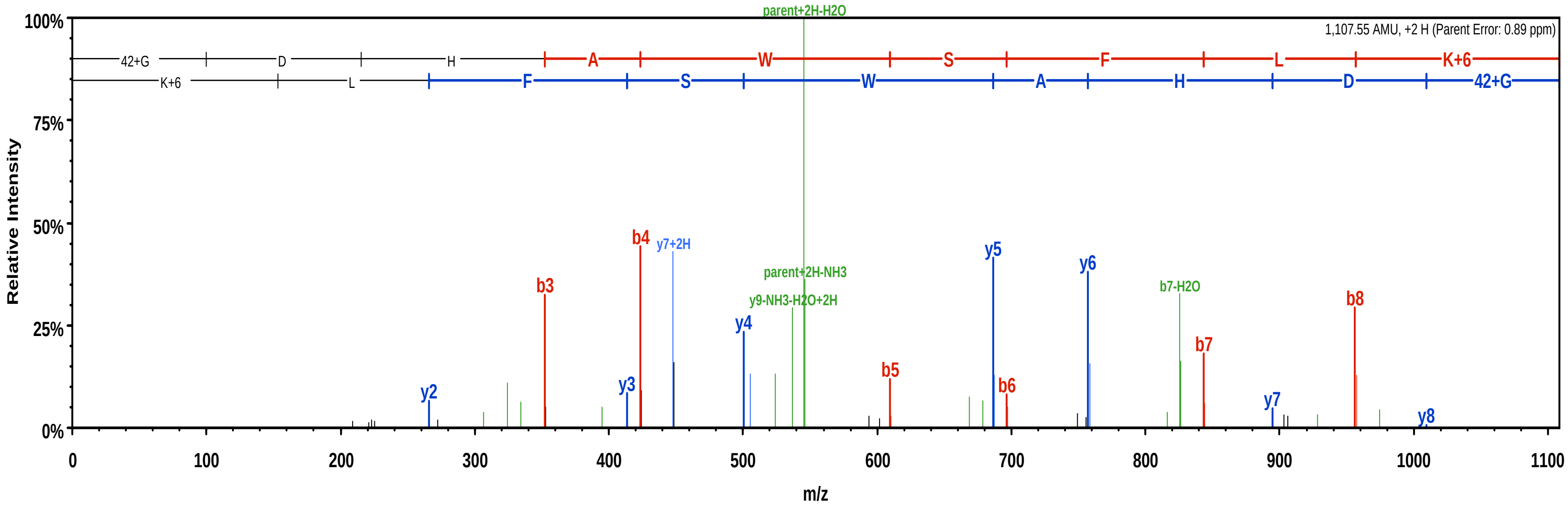


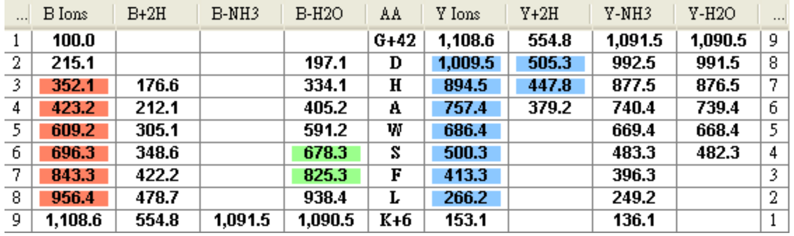


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	164.1				Y	1,966.9	984.0	1,949.9	1,948.9	16
2	261.1				P	1,803.9	902.4	1,786.8	1,785.9	15
3	374.2				I	1,706.8	853.9	1,689.8	1,688.8	14
4	503.3			485.2	E	1,593.7	797.4	1,576.7	1,575.7	13
5	640.3	320.7		622.3	H	1,464.7	732.8	1,447.7	1,446.7	12
6	697.3	349.2		679.3	G	1,327.6	664.3	1,310.6	1,309.6	11
7	810.4	405.7		792.4	I	1,270.6	635.8	1,253.6	1,252.6	10
8	923.5	462.3		905.5	I	1,157.5	579.3	1,140.5	1,139.5	9
9	1,024.5	512.8		1,006.5	T	1,044.4	522.7	1,027.4	1,026.4	8
10	1,138.6	569.8	1,121.6	1,120.6	N	943.4	472.2	926.4	925.4	7
11	1,324.7	662.8	1,307.6	1,306.7	W	829.3	415.2	812.3	811.3	6
12	1,439.7	720.4	1,422.7	1,421.7	D	643.3		626.2	625.3	5
13	1,554.7	777.9	1,537.7	1,536.7	D	528.2		511.2	510.2	4
14	1,685.8	843.4	1,668.7	1,667.8	M	413.2		396.2	395.2	3
15	1,814.8	907.9	1,797.8	1,796.8	E	282.2		265.1	264.2	2
16	1,966.9	984.0	1,949.9	1,948.9	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-109	sp|P12235|ADT1_HUMAN	GDHAWSFLK	37.23	Acetyl (Protein N-term)	Heavy	2	551.76945

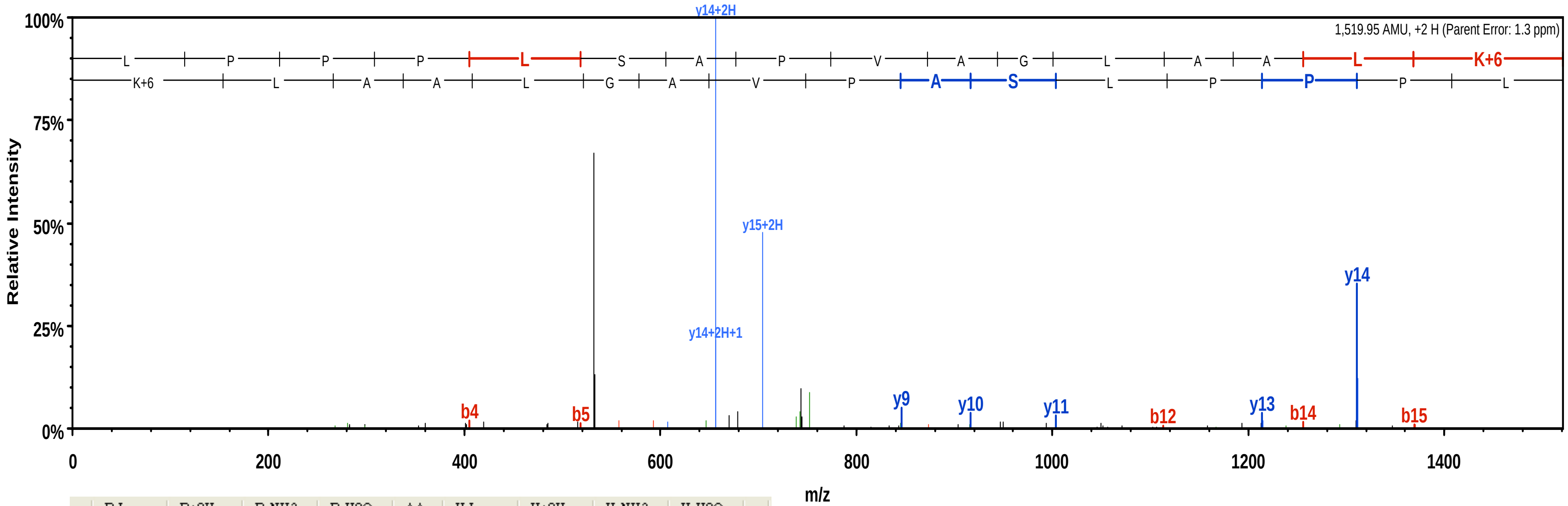


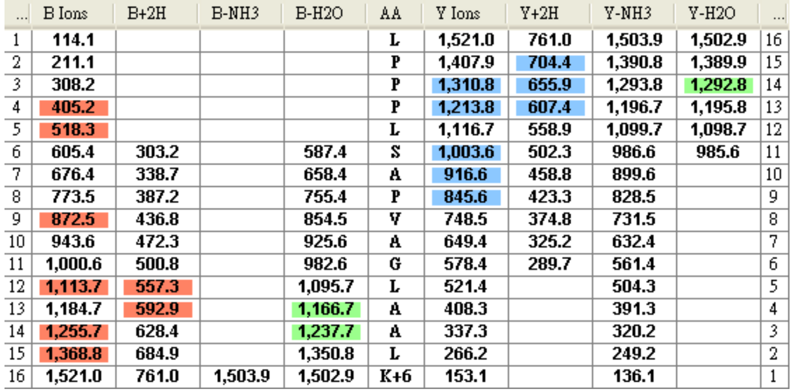


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	100.0				G+42	1,108.6	554.8	1,091.5	1,090.5	9
2	215.1			197.1	D	1,009.5	505.3	992.5	991.5	8
3	352.1	176.6		334.1	H	894.5	447.8	877.5	876.5	7
4	423.2	212.1		405.2	A	757.4	379.2	740.4	739.4	6
5	609.2	305.1		591.2	W	686.4		669.4	668.4	5
6	696.3	348.6		678.3	S	500.3		483.3	482.3	4
7	843.3	422.2		825.3	F	413.3		396.3		3
8	956.4	478.7		938.4	L	266.2		249.2		2
9	1,108.6	554.8	1,091.5	1,090.5	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-110	splQ14781lCBX2_HUMAN	LPPPLSAPVAGLAALK	36.68	Unmodified	Heavy	2	757.96888

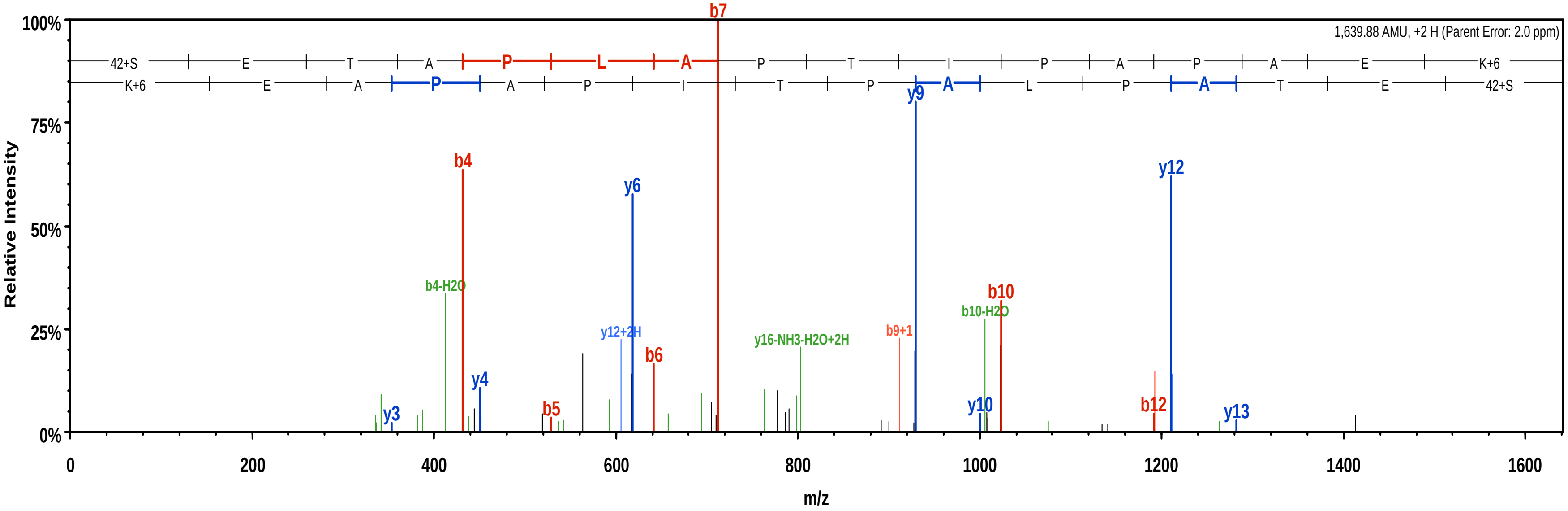


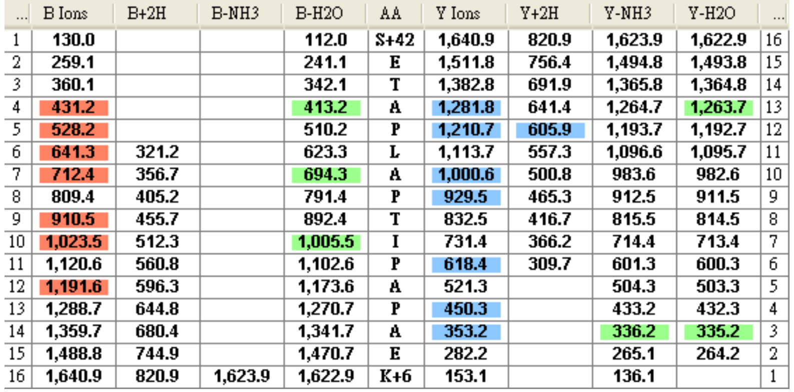


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	1,521.0	761.0	1,503.9	1,502.9	16
2	211.1				P	1,407.9	704.4	1,390.8	1,389.9	15
3	308.2				P	1,310.8	655.9	1,293.8	1,292.8	14
4	405.2				P	1,213.8	607.4	1,196.7	1,195.8	13
5	518.3				L	1,116.7	558.9	1,099.7	1,098.7	12
6	605.4	303.2		587.4	S	1,003.6	502.3	986.6	985.6	11
7	676.4	338.7		658.4	A	916.6	458.8	899.6		10
8	773.5	387.2		755.4	P	845.6	423.3	828.5		9
9	872.5	436.8		854.5	V	748.5	374.8	731.5		8
10	943.6	472.3		925.6	A	649.4	325.2	632.4		7
11	1,000.6	500.8		982.6	G	578.4	289.7	561.4		6
12	1,113.7	557.3		1,095.7	L	521.4		504.3		5
13	1,184.7	592.9		1,166.7	A	408.3		391.3		4
14	1,255.7	628.4		1,237.7	A	337.3		320.2		3
15	1,368.8	684.9		1,350.8	L	266.2		249.2		2
16	1,521.0	761.0	1,503.9	1,502.9	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-111	sp|P16402|H13_HUMAN	SETAPLAPTIPAPAEK	36.53	Acetyl (Protein N-term)	Heavy	2	817.93543

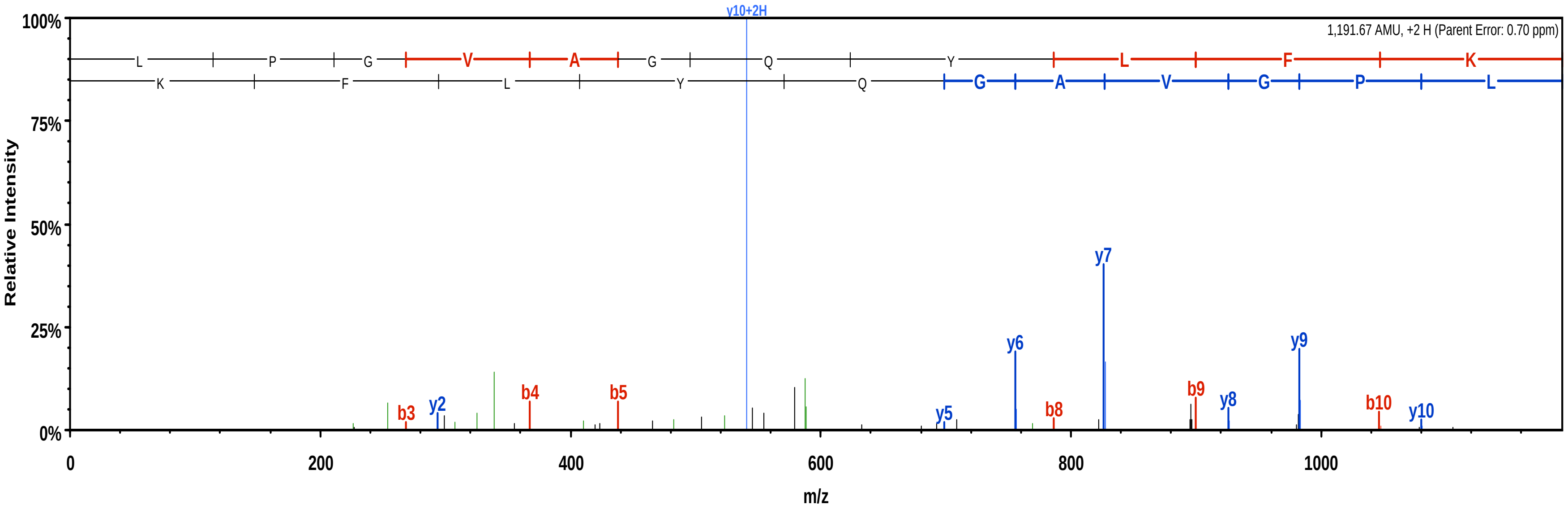


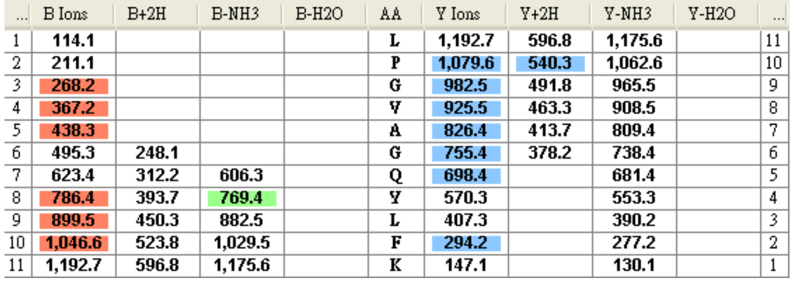


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	S+42	1,640.9	820.9	1,623.9	1,622.9	16
2	259.1			241.1	E	1,511.8	756.4	1,494.8	1,493.8	15
3	360.1			342.1	T	1,382.8	691.9	1,365.8	1,364.8	14
4	431.2			413.2	A	1,281.8	641.4	1,264.7	1,263.7	13
5	528.2			510.2	P	1,210.7	605.9	1,193.7	1,192.7	12
6	641.3	321.2		623.3	L	1,113.7	557.3	1,096.6	1,095.7	11
7	712.4	356.7		694.3	A	1,000.6	500.8	983.6	982.6	10
8	809.4	405.2		791.4	P	929.5	465.3	912.5	911.5	9
9	910.5	455.7		892.4	T	832.5	416.7	815.5	814.5	8
10	1,023.5	512.3		1,005.5	I	731.4	366.2	714.4	713.4	7
11	1,120.6	560.8		1,102.6	P	618.4	309.7	601.3	600.3	6
12	1,191.6	596.3		1,173.6	A	521.3		504.3	503.3	5
13	1,288.7	644.8		1,270.7	P	450.3		433.2	432.3	4
14	1,359.7	680.4		1,341.7	A	353.2		336.2	335.2	3
15	1,488.8	744.9		1,470.7	E	282.2		265.1	264.2	2
16	1,640.9	820.9	1,623.9	1,622.9	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-112	sp|Q86W50|MET10_HUMAN	LPGVAGQYLFK	36.3	Unmodified	Light	2	596.83987

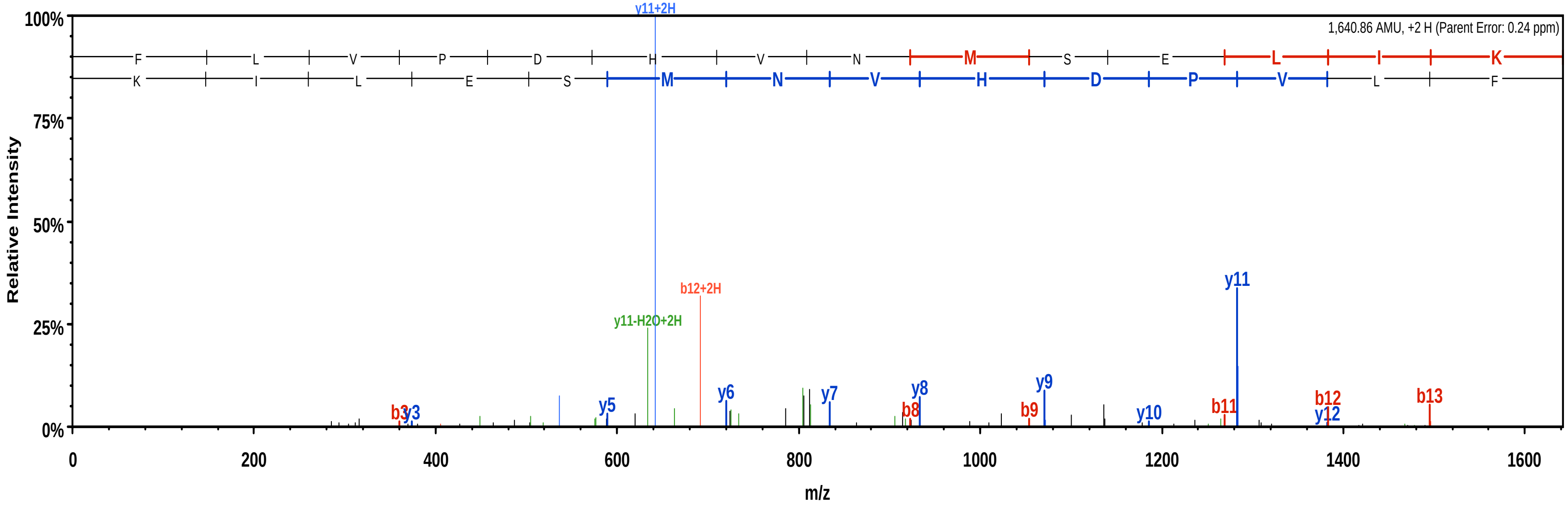


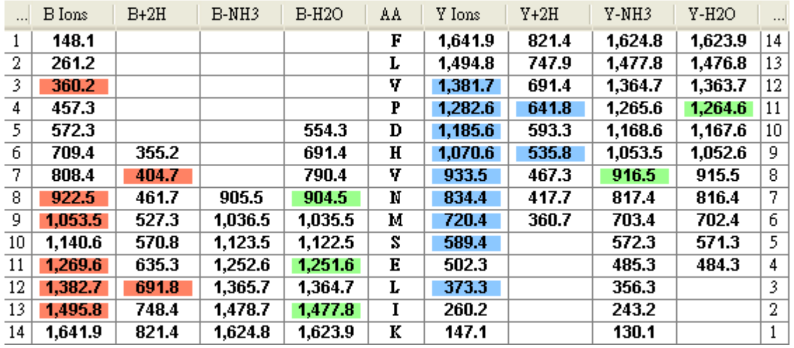


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	1,192.7	596.8	1,175.6		11
2	211.1				P	1,079.6	540.3	1,062.6		10
3	268.2				G	982.5	491.8	965.5		9
4	367.2				V	925.5	463.3	908.5		8
5	438.3				A	826.4	413.7	809.4		7
6	495.3	248.1			G	755.4	378.2	738.4		6
7	623.4	312.2	606.3		Q	698.4		681.4		5
8	786.4	393.7	769.4		Y	570.3		553.3		4
9	899.5	450.3	882.5		L	407.3		390.2		3
10	1,046.6	523.8	1,029.5		F	294.2		277.2		2
11	1,192.7	596.8	1,175.6		K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-113	sp|A6NCE7|MP3B2_HUMAN	FLVPDHVNMSELIK	34.47	Unmodified	Light	2	821.43708

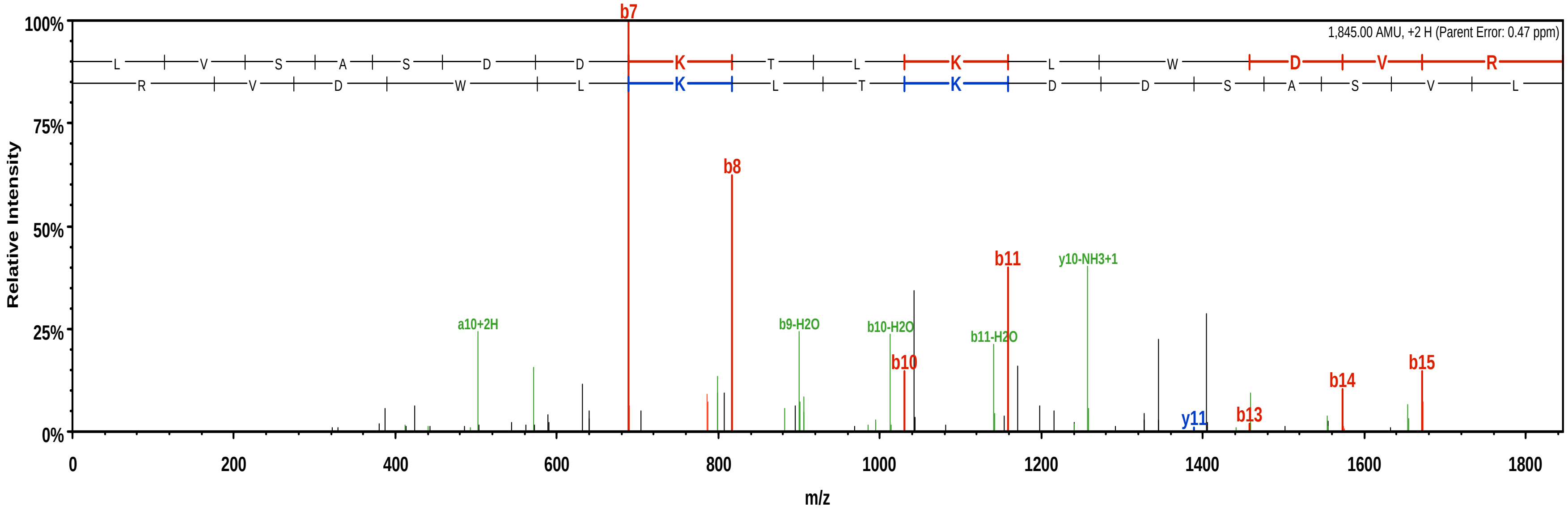


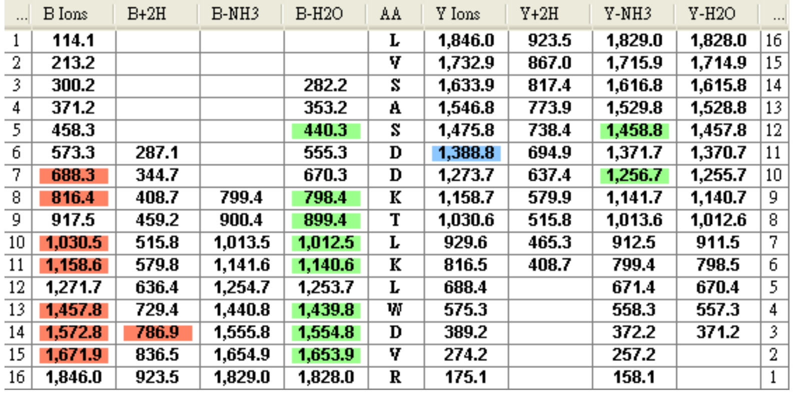


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.1				F	1,641.9	821.4	1,624.8	1,623.9	14
2	261.2				L	1,494.8	747.9	1,477.8	1,476.8	13
3	360.2				V	1,381.7	691.4	1,364.7	1,363.7	12
4	457.3				P	1,282.6	641.8	1,265.6	1,264.6	11
5	572.3			554.3	D	1,185.6	593.3	1,168.6	1,167.6	10
6	709.4	355.2		691.4	H	1,070.6	535.8	1,053.5	1,052.6	9
7	808.4	404.7		790.4	V	933.5	467.3	916.5	915.5	8
8	922.5	461.7	905.5	904.5	N	834.4	417.7	817.4	816.4	7
9	1,053.5	527.3	1,036.5	1,035.5	M	720.4	360.7	703.4	702.4	6
10	1,140.6	570.8	1,123.5	1,122.5	S	589.4		572.3	571.3	5
11	1,269.6	635.3	1,252.6	1,251.6	E	502.3		485.3	484.3	4
12	1,382.7	691.8	1,365.7	1,364.7	L	373.3		356.3		3
13	1,495.8	748.4	1,478.7	1,477.8	I	260.2		243.2		2
14	1,641.9	821.4	1,624.8	1,623.9	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-114	sp|Q86VZ2|WDR5B_HUMAN	LVSASDDKTLKLWDVR	33.99	Unmodified	Light	2	923.50708

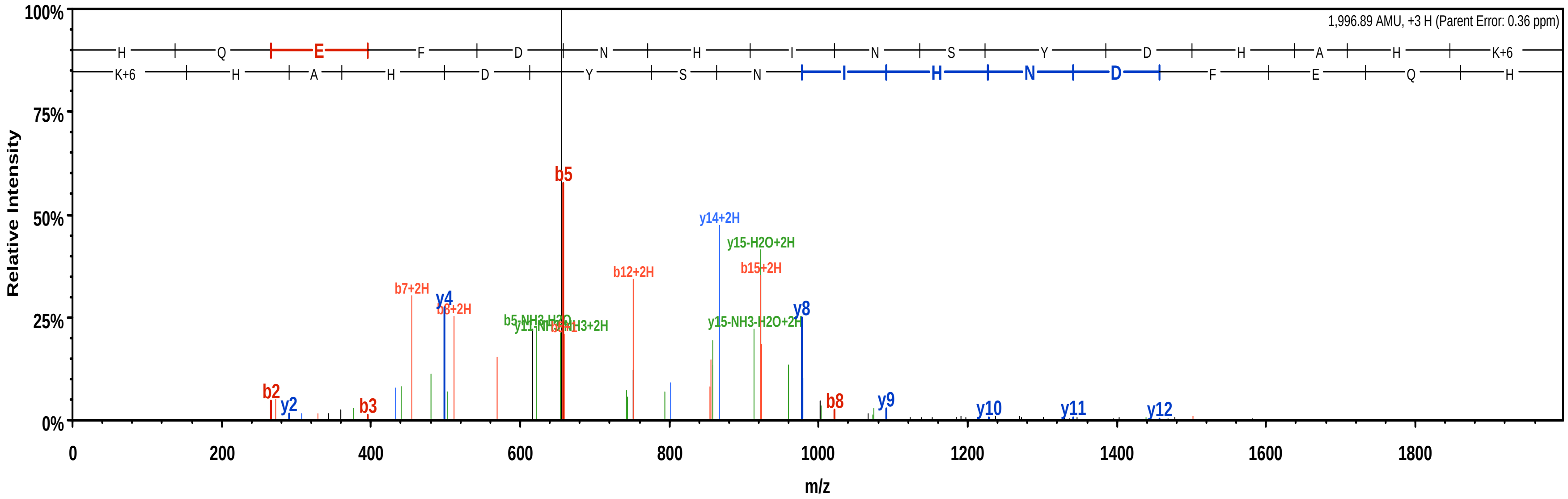


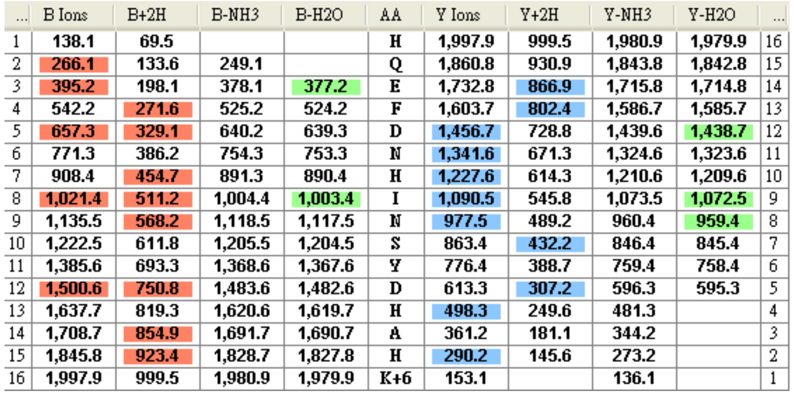


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	1,846.0	923.5	1,829.0	1,828.0	16
2	213.2				V	1,732.9	867.0	1,715.9	1,714.9	15
3	300.2			282.2	S	1,633.9	817.4	1,616.8	1,615.8	14
4	371.2			353.2	A	1,546.8	773.9	1,529.8	1,528.8	13
5	458.3			440.3	S	1,475.8	738.4	1,458.8	1,457.8	12
6	573.3	287.1		555.3	D	1,388.8	694.9	1,371.7	1,370.7	11
7	688.3	344.7		670.3	D	1,273.7	637.4	1,256.7	1,255.7	10
8	816.4	408.7	799.4	798.4	K	1,158.7	579.9	1,141.7	1,140.7	9
9	917.5	459.2	900.4	899.4	T	1,030.6	515.8	1,013.6	1,012.6	8
10	1,030.5	515.8	1,013.5	1,012.5	L	929.6	465.3	912.5	911.5	7
11	1,158.6	579.8	1,141.6	1,140.6	K	816.5	408.7	799.4	798.5	6
12	1,271.7	636.4	1,254.7	1,253.7	L	688.4		671.4	670.4	5
13	1,457.8	729.4	1,440.8	1,439.8	W	575.3		558.3	557.3	4
14	1,572.8	786.9	1,555.8	1,554.8	D	389.2		372.2	371.2	3
15	1,671.9	836.5	1,654.9	1,653.9	V	274.2		257.2		2
16	1,846.0	923.5	1,829.0	1,828.0	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-115	sp|A4D1E1|Z804B_HUMAN	HQEFDNHINSYDHAHK	33.53	Unmodified	Heavy	3	664.62962

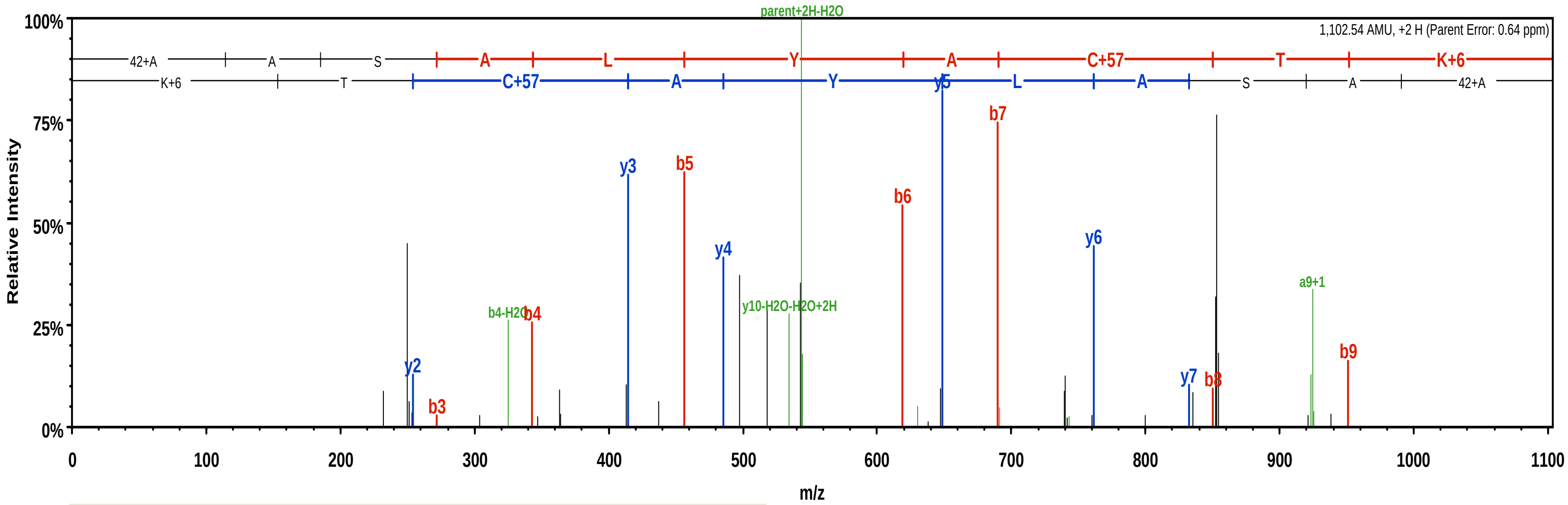


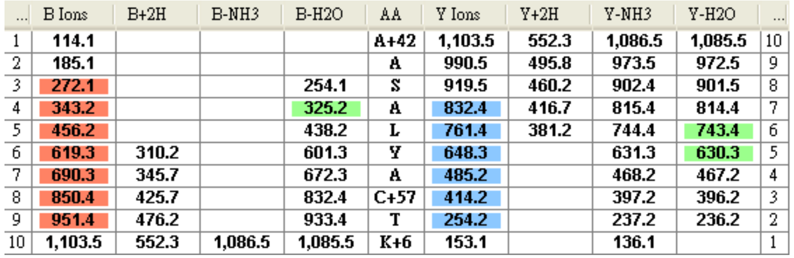


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	138.1	69.5			H	1,997.9	999.5	1,980.9	1,979.9	16
2	266.1	133.6	249.1		Q	1,860.8	930.9	1,843.8	1,842.8	15
3	395.2	198.1	378.1	377.2	E	1,732.8	866.9	1,715.8	1,714.8	14
4	542.2	271.6	525.2	524.2	F	1,603.7	802.4	1,586.7	1,585.7	13
5	657.3	329.1	640.2	639.3	D	1,456.7	728.8	1,439.6	1,438.7	12
6	771.3	386.2	754.3	753.3	N	1,341.6	671.3	1,324.6	1,323.6	11
7	908.4	454.7	891.3	890.4	H	1,227.6	614.3	1,210.6	1,209.6	10
8	1,021.4	511.2	1,004.4	1,003.4	I	1,090.5	545.8	1,073.5	1,072.5	9
9	1,135.5	568.2	1,118.5	1,117.5	N	977.5	489.2	960.4	959.4	8
10	1,222.5	611.8	1,205.5	1,204.5	S	863.4	432.2	846.4	845.4	7
11	1,385.6	693.3	1,368.6	1,367.6	Y	776.4	388.7	759.4	758.4	6
12	1,500.6	750.8	1,483.6	1,482.6	D	613.3	307.2	596.3	595.3	5
13	1,637.7	819.3	1,620.6	1,619.7	H	498.3	249.6	481.3		4
14	1,708.7	854.9	1,691.7	1,690.7	A	361.2	181.1	344.2		3
15	1,845.8	923.4	1,828.7	1,827.8	H	290.2	145.6	273.2		2
16	1,997.9	999.5	1,980.9	1,979.9	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-116	sp|Q5HYJ3|FA76B_HUMAN	AASALYACTK	33.12	Acetyl (Protein N-term)	Heavy	2	549.26842

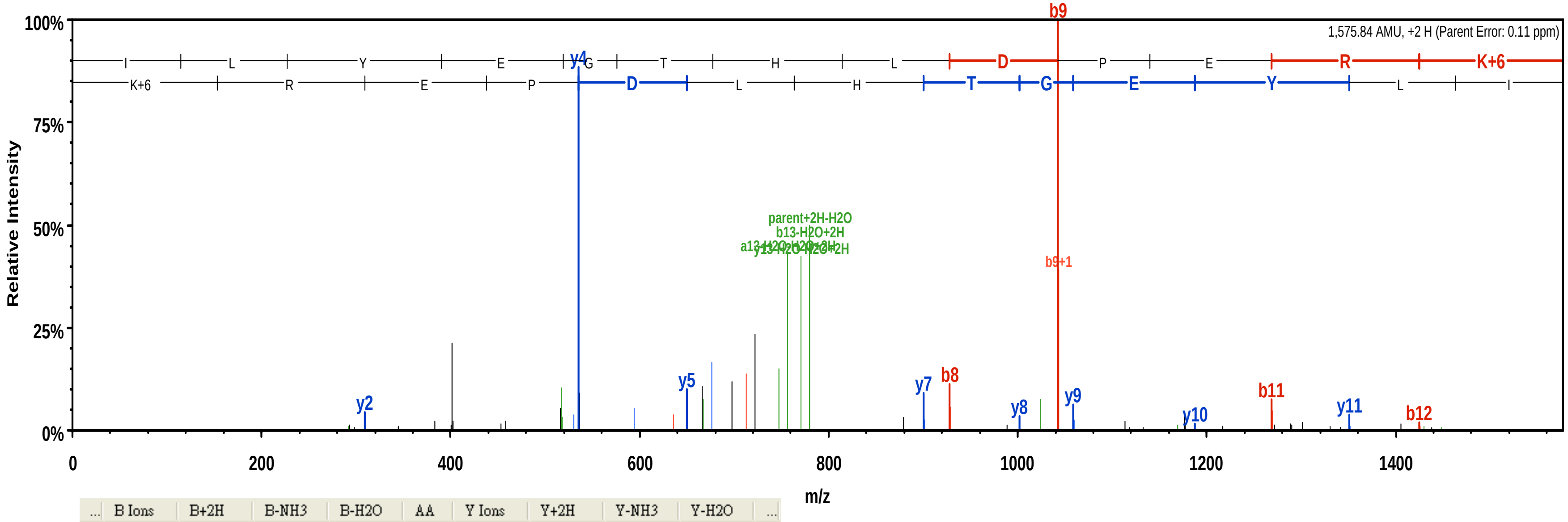


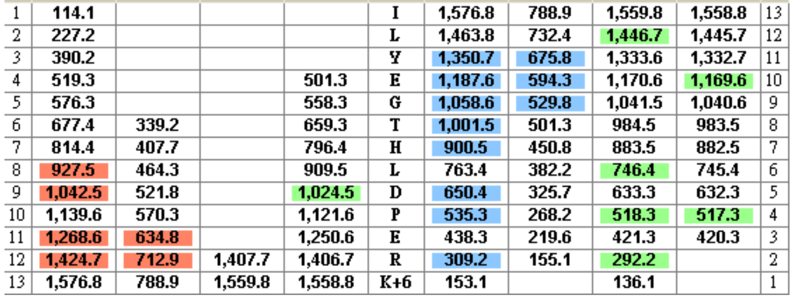


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	1,103.5	552.3	1,086.5	1,085.5	10
2	185.1				A	990.5	495.8	973.5	972.5	9
3	272.1			254.1	S	919.5	460.2	902.4	901.5	8
4	343.2			325.2	A	832.4	416.7	815.4	814.4	7
5	456.2			438.2	L	761.4	381.2	744.4	743.4	6
6	619.3	310.2		601.3	Y	648.3		631.3	630.3	5
7	690.3	345.7		672.3	A	485.2		468.2	467.2	4
8	850.4	425.7		832.4	C+57	414.2		397.2	396.2	3
9	951.4	476.2		933.4	T	254.2		237.2	236.2	2
10	1,103.5	552.3	1,086.5	1,085.5	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-117	sp|Q5RI15|FA36A_HUMAN	ILYEGTHLDPERK	32.87	Unmodified	Heavy	2	785.91483

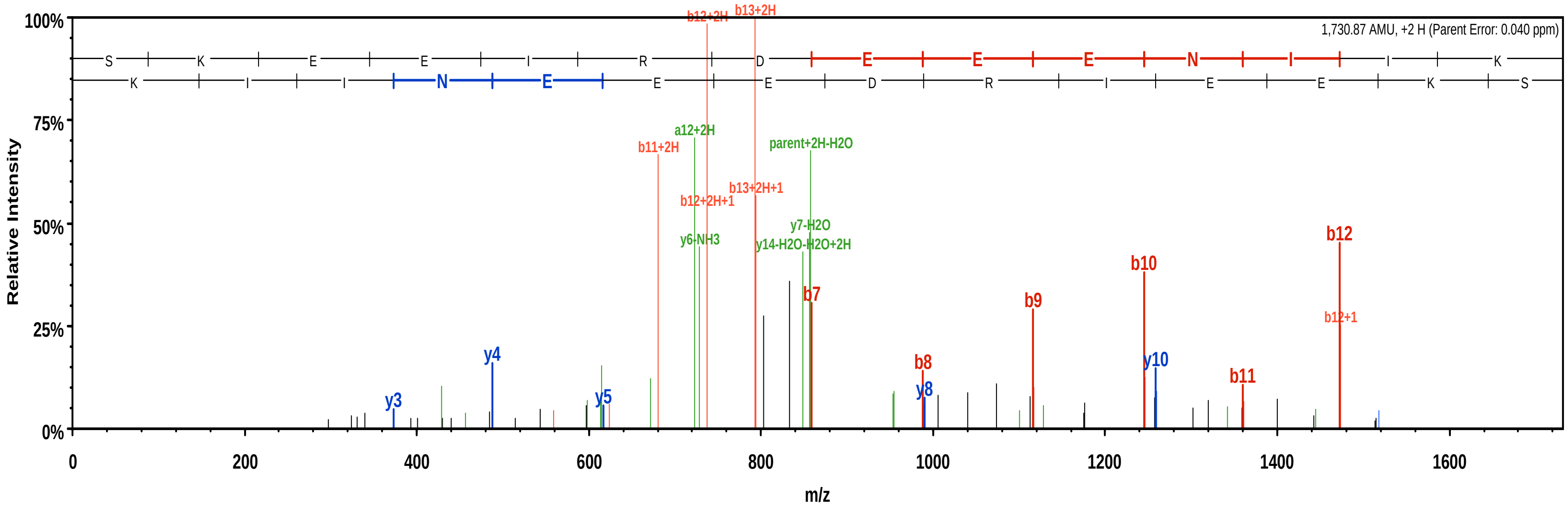


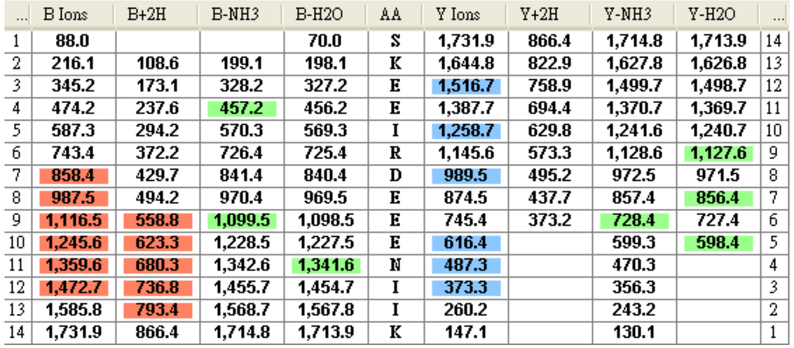


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	1,576.8	788.9	1,559.8	1,558.8	13
2	227.2				L	1,463.8	732.4	1,446.7	1,445.7	12
3	390.2				Y	1,350.7	675.8	1,333.6	1,332.7	11
4	519.3			501.3	E	1,187.6	594.3	1,170.6	1,169.6	10
5	576.3			558.3	G	1,058.6	529.8	1,041.5	1,040.6	9
6	677.4	339.2		659.3	T	1,001.5	501.3	984.5	983.5	8
7	814.4	407.7		796.4	H	900.5	450.8	883.5	882.5	7
8	927.5	464.3		909.5	L	763.4	382.2	746.4	745.4	6
9	1,042.5	521.8		1,024.5	D	650.4	325.7	633.3	632.3	5
10	1,139.6	570.3		1,121.6	P	535.3	268.2	518.3	517.3	4
11	1,268.6	634.8		1,250.6	E	438.3	219.6	421.3	420.3	3
12	1,424.7	712.9	1,407.7	1,406.7	R	309.2	155.1	292.2		2
13	1,576.8	788.9	1,559.8	1,558.8	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-118	sp|Q9H1X3|DJC25_HUMAN	SKEEIRDEEENIIK	31.92	Unmodified	Light	2	866.44161

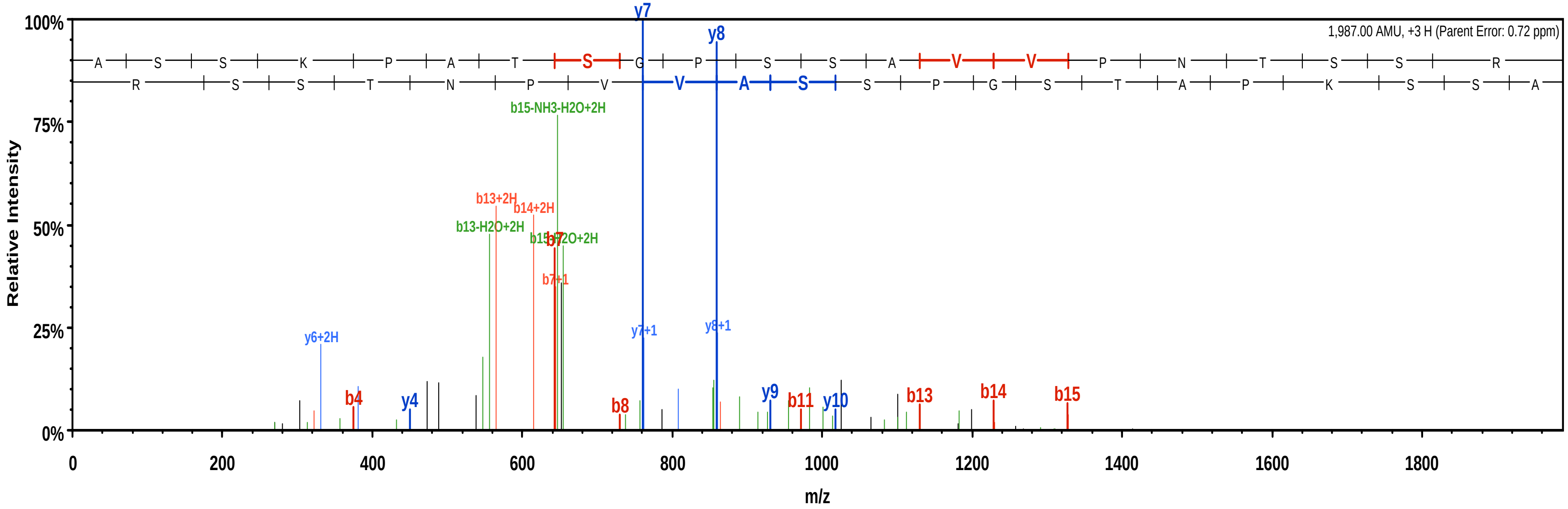


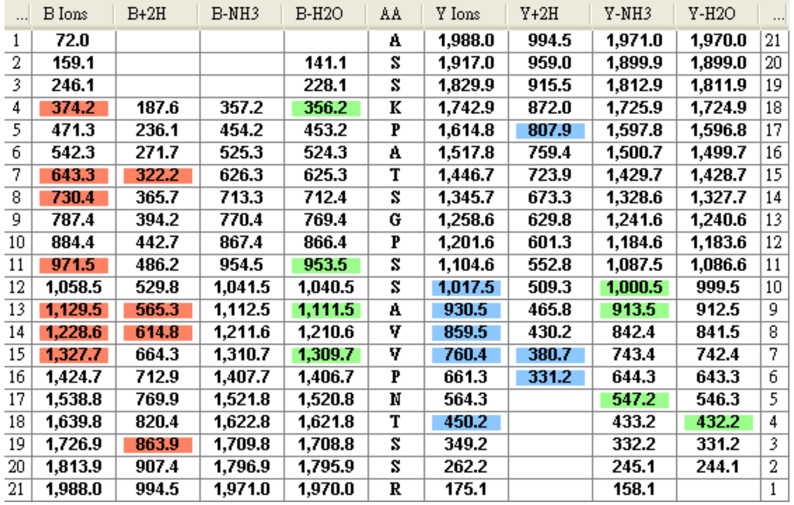


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	88.0			70.0	S	1,731.9	866.4	1,714.8	1,713.9	14
2	216.1	108.6	199.1	198.1	K	1,644.8	822.9	1,627.8	1,626.8	13
3	345.2	173.1	328.2	327.2	E	1,516.7	758.9	1,499.7	1,498.7	12
4	474.2	237.6	457.2	456.2	E	1,387.7	694.4	1,370.7	1,369.7	11
5	587.3	294.2	570.3	569.3	I	1,258.7	629.8	1,241.6	1,240.7	10
6	743.4	372.2	726.4	725.4	R	1,145.6	573.3	1,128.6	1,127.6	9
7	858.4	429.7	841.4	840.4	D	989.5	495.2	972.5	971.5	8
8	987.5	494.2	970.4	969.5	E	874.5	437.7	857.4	856.4	7
9	1,116.5	558.8	1,099.5	1,098.5	E	745.4	373.2	728.4	727.4	6
10	1,245.6	623.3	1,228.5	1,227.5	E	616.4		599.3	598.4	5
11	1,359.6	680.3	1,342.6	1,341.6	N	487.3		470.3		4
12	1,472.7	736.8	1,455.7	1,454.7	I	373.3		356.3		3
13	1,585.8	793.4	1,568.7	1,567.8	I	260.2		243.2		2
14	1,731.9	866.4	1,714.8	1,713.9	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-119	sp|O43314|VIP2_HUMAN	ASSKPATSGPSSAVVPNTSSR	31.91	Unmodified	Light	3	663.33963

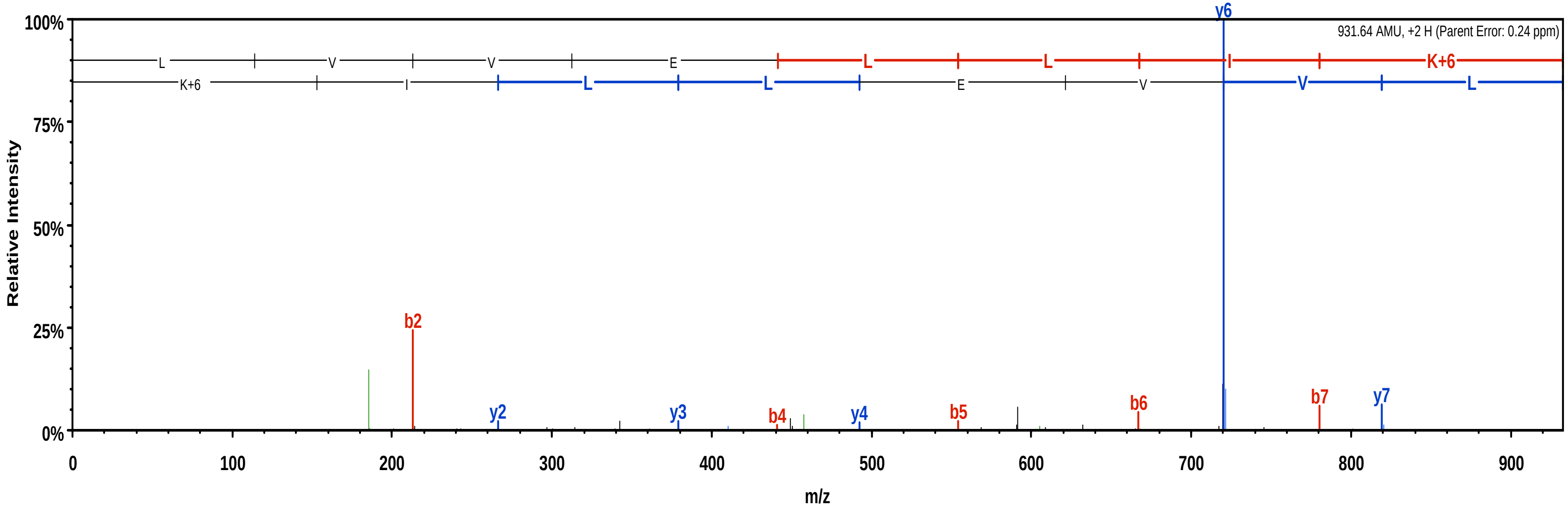


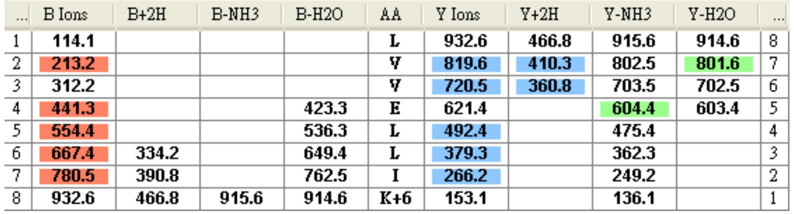


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	72.0				A	1,988.0	994.5	1,971.0	1,970.0	21
2	159.1			141.1	S	1,917.0	959.0	1,899.9	1,899.0	20
3	246.1			228.1	S	1,829.9	915.5	1,812.9	1,811.9	19
4	374.2	187.6	357.2	356.2	K	1,742.9	872.0	1,725.9	1,724.9	18
5	471.3	236.1	454.2	453.2	P	1,614.8	807.9	1,597.8	1,596.8	17
6	542.3	271.7	525.3	524.3	A	1,517.8	759.4	1,500.7	1,499.7	16
7	643.3	322.2	626.3	625.3	T	1,446.7	723.9	1,429.7	1,428.7	15
8	730.4	365.7	713.3	712.4	S	1,345.7	673.3	1,328.6	1,327.7	14
9	787.4	394.2	770.4	769.4	G	1,258.6	629.8	1,241.6	1,240.6	13
10	884.4	442.7	867.4	866.4	P	1,201.6	601.3	1,184.6	1,183.6	12
11	971.5	486.2	954.5	953.5	S	1,104.6	552.8	1,087.5	1,086.6	11
12	1,058.5	529.8	1,041.5	1,040.5	S	1,017.5	509.3	1,000.5	999.5	10
13	1,129.5	565.3	1,112.5	1,111.5	A	930.5	465.8	913.5	912.5	9
14	1,228.6	614.8	1,211.6	1,210.6	V	859.5	430.2	842.4	841.5	8
15	1,327.7	664.3	1,310.7	1,309.7	V	760.4	380.7	743.4	742.4	7
16	1,424.7	712.9	1,407.7	1,406.7	P	661.3	331.2	644.3	643.3	6
17	1,538.8	769.9	1,521.8	1,520.8	N	564.3		547.2	546.3	5
18	1,639.8	820.4	1,622.8	1,621.8	T	450.2		433.2	432.2	4
19	1,726.9	863.9	1,709.8	1,708.8	S	349.2		332.2	331.2	3
20	1,813.9	907.4	1,796.9	1,795.9	S	262.2		245.1	244.1	2
21	1,988.0	994.5	1,971.0	1,970.0	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-120	sp|P15882|CHIN_HUMAN	LVVELLIK	31.91	Unmodified	Heavy	2	463.81788

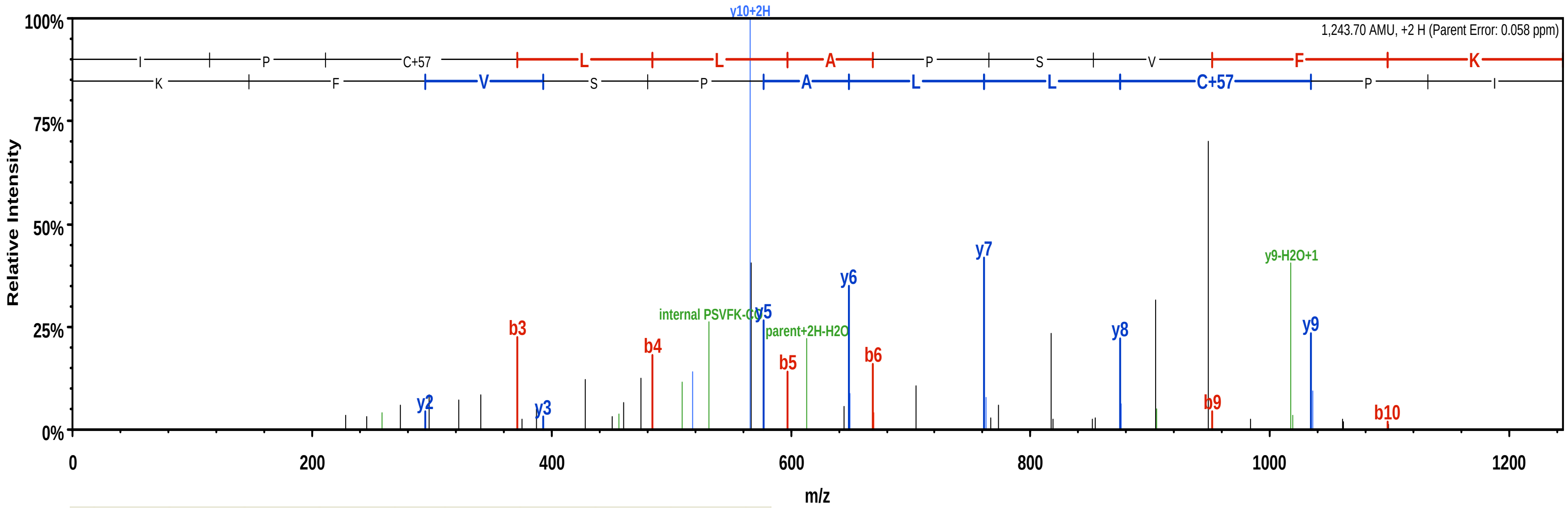


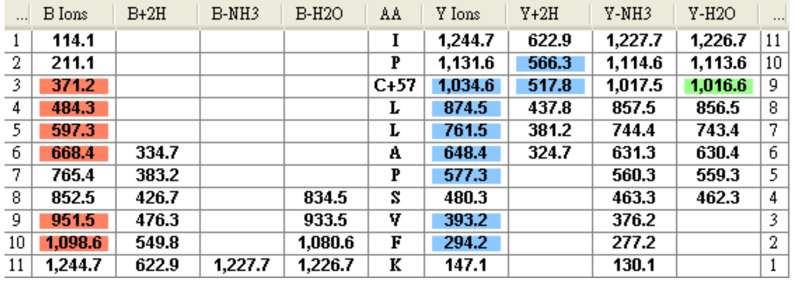


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	932.6	466.8	915.6	914.6	8
2	213.2				V	819.6	410.3	802.5	801.6	7
3	312.2				V	720.5	360.8	703.5	702.5	6
4	441.3			423.3	E	621.4		604.4	603.4	5
5	554.4			536.3	L	492.4		475.4		4
6	667.4	334.2		649.4	L	379.3		362.3		3
7	780.5	390.8		762.5	I	266.2		249.2		2
8	932.6	466.8	915.6	914.6	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-121	sp|Q8N9N5|BANP_HUMAN	IPCLLAPSVFK	31.54	Unmodified	Light	2	622.85721

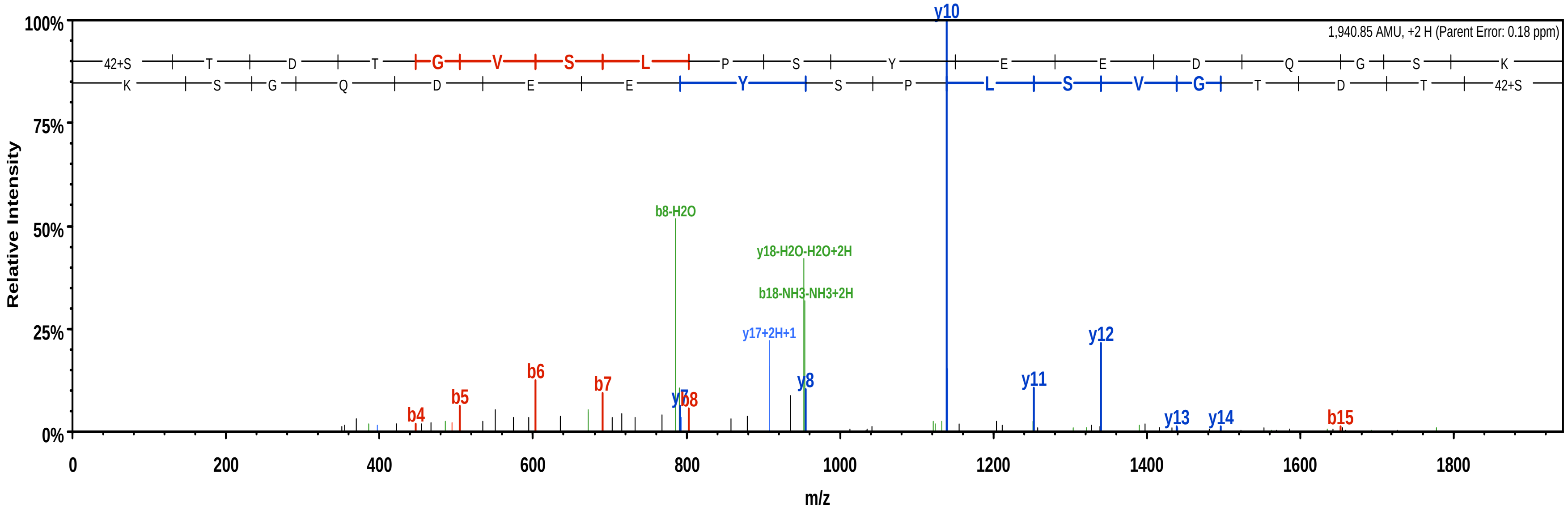


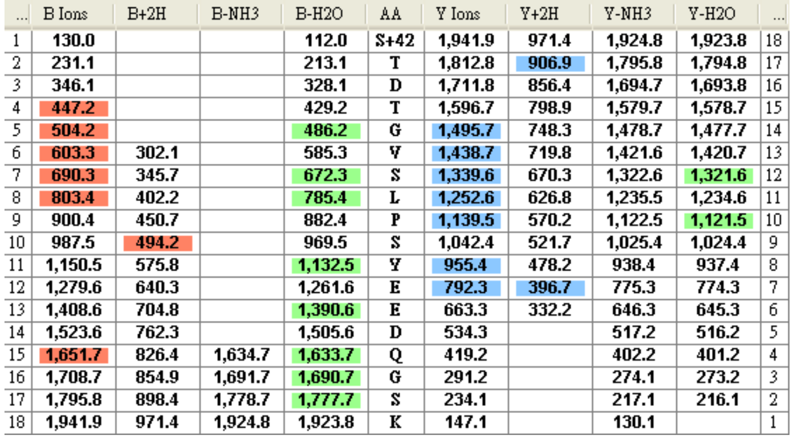


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	1,244.7	622.9	1,227.7	1,226.7	11
2	211.1				P	1,131.6	566.3	1,114.6	1,113.6	10
3	371.2				C+57	1,034.6	517.8	1,017.5	1,016.6	9
4	484.3				L	874.5	437.8	857.5	856.5	8
5	597.3				L	761.5	381.2	744.4	743.4	7
6	668.4	334.7			A	648.4	324.7	631.3	630.4	6
7	765.4	383.2			P	577.3		560.3	559.3	5
8	852.5	426.7		834.5	S	480.3		463.3	462.3	4
9	951.5	476.3		933.5	V	393.2		376.2		3
10	1,098.6	549.8		1,080.6	F	294.2		277.2		2
11	1,244.7	622.9	1,227.7	1,226.7	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-122	sp|Q9Y241|HIG1A_HUMAN	STDTGVSLPSYEEDQGSK	30.56	Acetyl (Protein N-term)	Light	2	971.43163

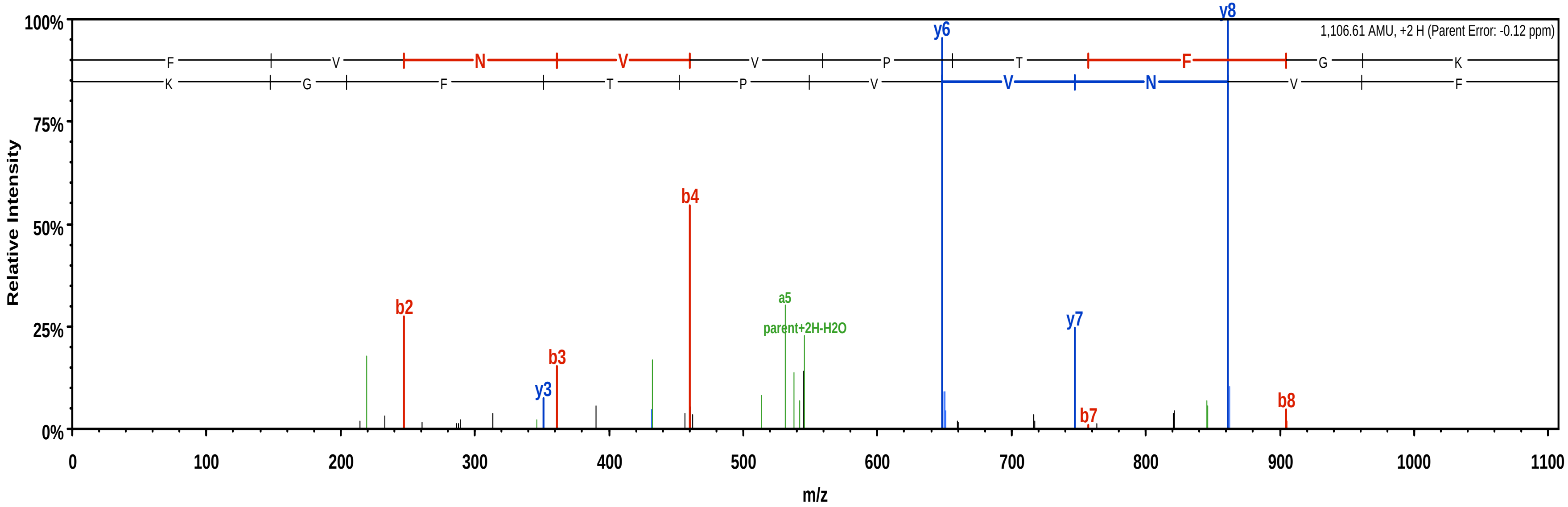


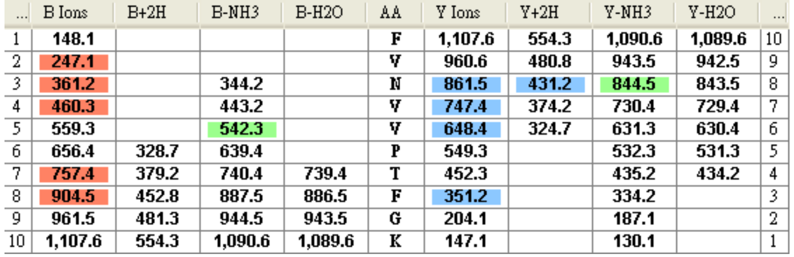


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	130.0			112.0	S+42	1,941.9	971.4	1,924.8	1,923.8	18
2	231.1			213.1	T	1,812.8	906.9	1,795.8	1,794.8	17
3	346.1			328.1	D	1,711.8	856.4	1,694.7	1,693.8	16
4	447.2			429.2	T	1,596.7	798.9	1,579.7	1,578.7	15
5	504.2			486.2	G	1,495.7	748.3	1,478.7	1,477.7	14
6	603.3	302.1		585.3	V	1,438.7	719.8	1,421.6	1,420.7	13
7	690.3	345.7		672.3	S	1,339.6	670.3	1,322.6	1,321.6	12
8	803.4	402.2		785.4	L	1,252.6	626.8	1,235.5	1,234.6	11
9	900.4	450.7		882.4	P	1,139.5	570.2	1,122.5	1,121.5	10
10	987.5	494.2		969.5	S	1,042.4	521.7	1,025.4	1,024.4	9
11	1,150.5	575.8		1,132.5	Y	955.4	478.2	938.4	937.4	8
12	1,279.6	640.3		1,261.6	E	792.3	396.7	775.3	774.3	7
13	1,408.6	704.8		1,390.6	E	663.3	332.2	646.3	645.3	6
14	1,523.6	762.3		1,505.6	D	534.3		517.2	516.2	5
15	1,651.7	826.4	1,634.7	1,633.7	Q	419.2		402.2	401.2	4
16	1,708.7	854.9	1,691.7	1,690.7	G	291.2		274.1	273.2	3
17	1,795.8	898.4	1,778.7	1,777.7	S	234.1		217.1	216.1	2
18	1,941.9	971.4	1,924.8	1,923.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-123	splP62861lRS30_HUMAN	FVNVVPTFGK	30.3	Unmodified	Light	2	554.31349

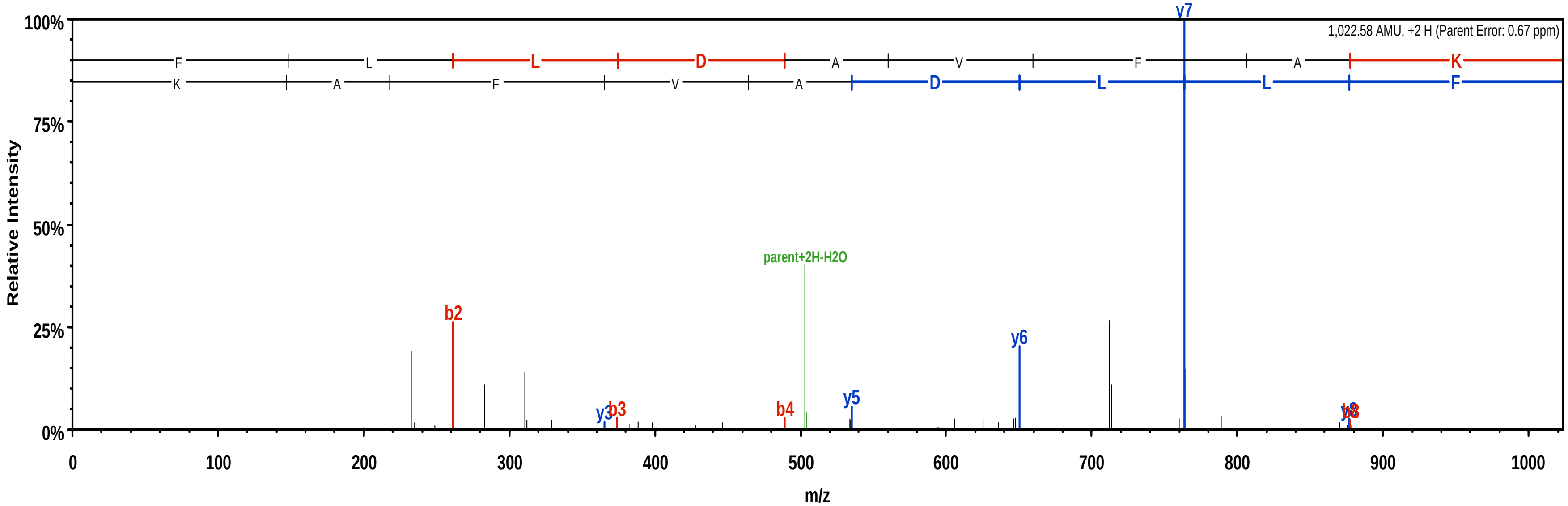


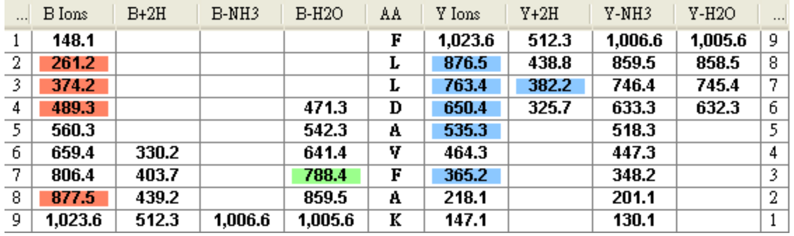


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.1				F	1,107.6	554.3	1,090.6	1,089.6	10
2	247.1				V	960.6	480.8	943.5	942.5	9
3	361.2		344.2		N	861.5	431.2	844.5	843.5	8
4	460.3		443.2		V	747.4	374.2	730.4	729.4	7
5	559.3		542.3		V	648.4	324.7	631.3	630.4	6
6	656.4	328.7	639.4		P	549.3		532.3	531.3	5
7	757.4	379.2	740.4	739.4	T	452.3		435.2	434.2	4
8	904.5	452.8	887.5	886.5	F	351.2		334.2		3
9	961.5	481.3	944.5	943.5	G	204.1		187.1		2
10	1,107.6	554.3	1,090.6	1,089.6	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-124	sp|Q96K76|UBP47_HUMAN	FLLDAVFAK	30.29	Unmodified	Light	2	512.29731

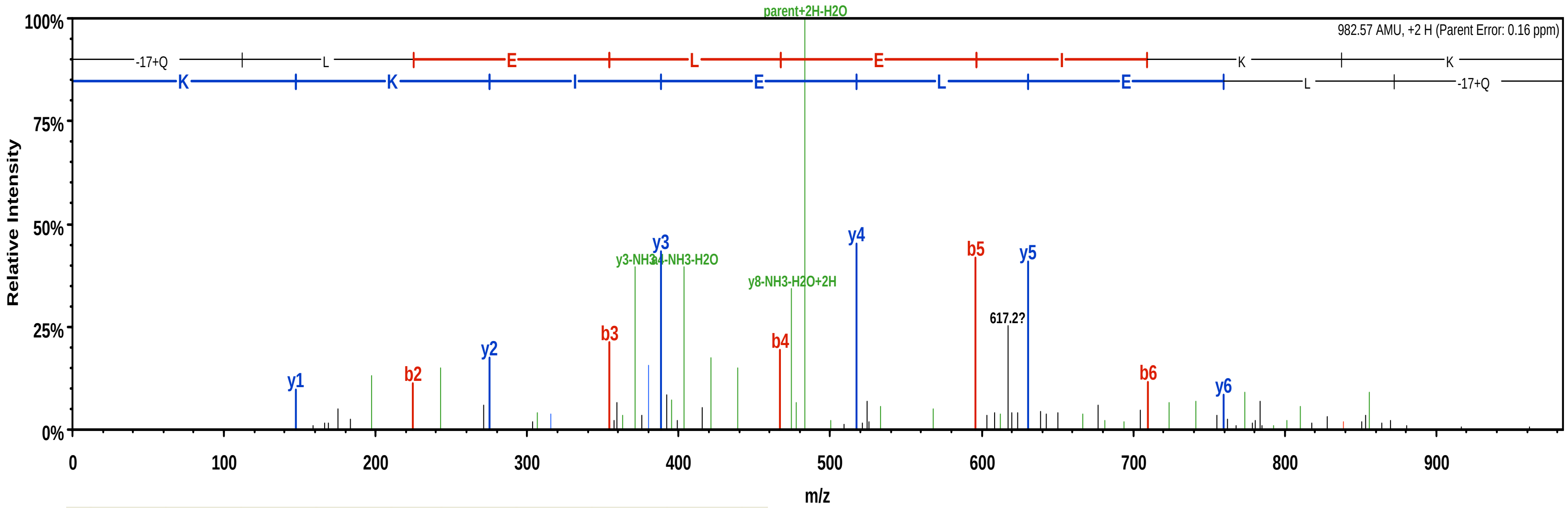


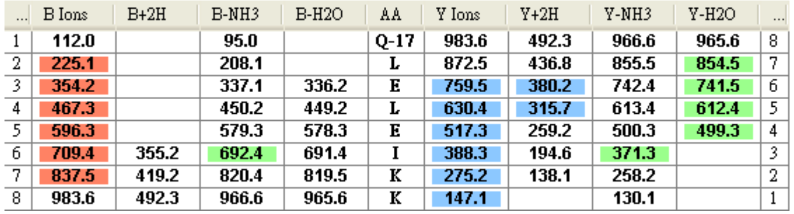


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.1				F	1,023.6	512.3	1,006.6	1,005.6	9
2	261.2				L	876.5	438.8	859.5	858.5	8
3	374.2				L	763.4	382.2	746.4	745.4	7
4	489.3			471.3	D	650.4	325.7	633.3	632.3	6
5	560.3			542.3	A	535.3		518.3		5
6	659.4	330.2		641.4	V	464.3		447.3		4
7	806.4	403.7		788.4	F	365.2		348.2		3
8	877.5	439.2		859.5	A	218.1		201.1		2
9	1,023.6	512.3	1,006.6	1,005.6	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-125	sp|Q9UQN3|CHM2B_HUMAN	QLELEIKK	29.07	Gln->pyro-Glu (N-term Q)	Light	2	492.29223

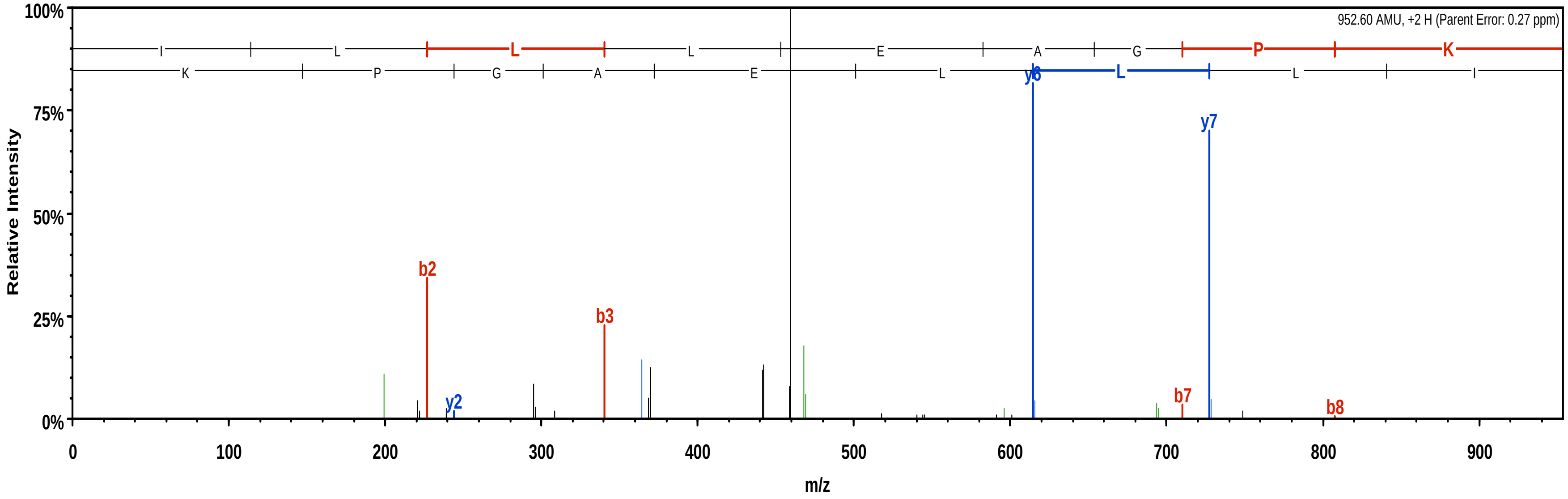


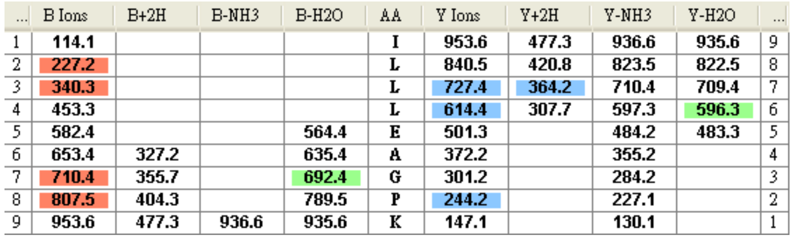


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	983.6	492.3	966.6	965.6	8
2	225.1		208.1		L	872.5	436.8	855.5	854.5	7
3	354.2		337.1	336.2	E	759.5	380.2	742.4	741.5	6
4	467.3		450.2	449.2	L	630.4	315.7	613.4	612.4	5
5	596.3		579.3	578.3	E	517.3	259.2	500.3	499.3	4
6	709.4	355.2	692.4	691.4	I	388.3	194.6	371.3		3
7	837.5	419.2	820.4	819.5	K	275.2	138.1	258.2		2
8	983.6	492.3	966.6	965.6	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-126	sp|Q9Y2Z9|COQ6_HUMAN	ILLLEAGPK	28.19	Unmodified	Light	2	477.30514

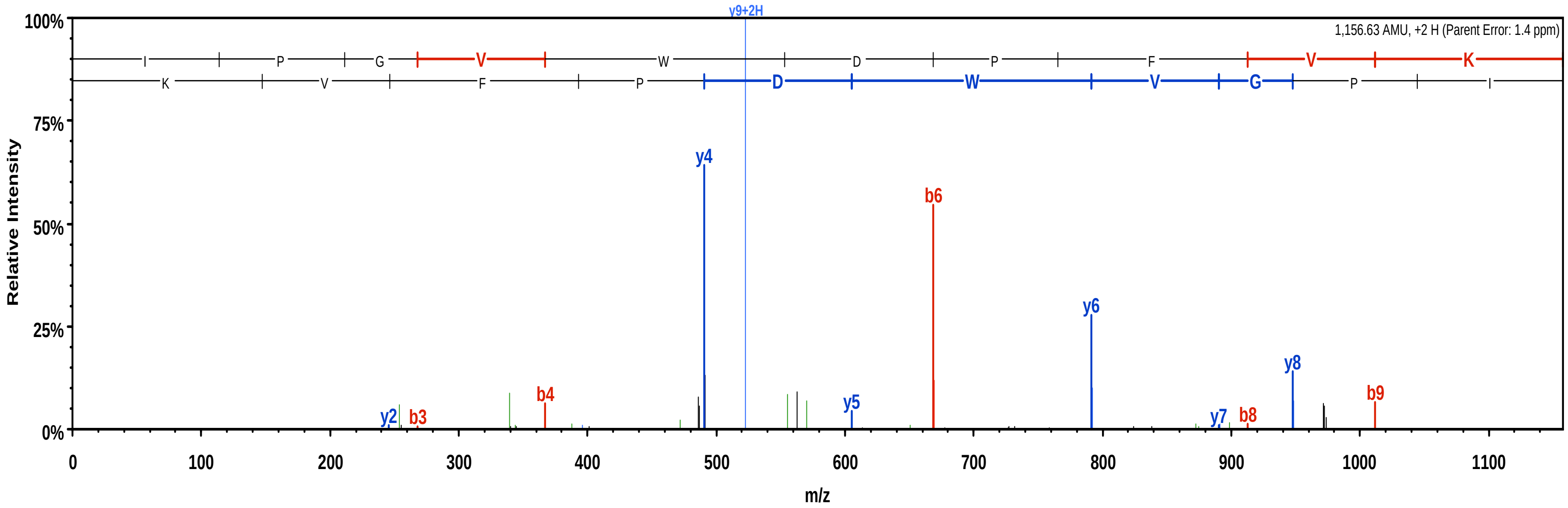


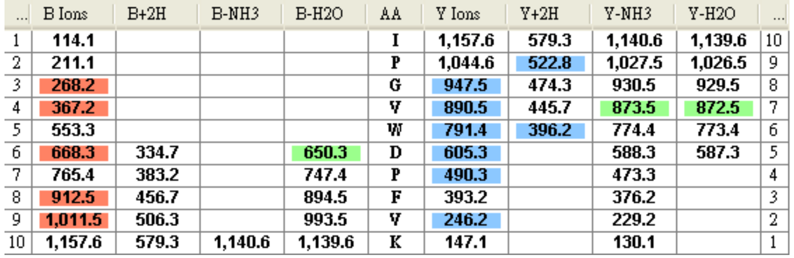


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	953.6	477.3	936.6	935.6	9
2	227.2				L	840.5	420.8	823.5	822.5	8
3	340.3				L	727.4	364.2	710.4	709.4	7
4	453.3				L	614.4	307.7	597.3	596.3	6
5	582.4			564.4	E	501.3		484.2	483.3	5
6	653.4	327.2		635.4	A	372.2		355.2		4
7	710.4	355.7		692.4	G	301.2		284.2		3
8	807.5	404.3		789.5	P	244.2		227.1		2
9	953.6	477.3	936.6	935.6	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-127	sp|Q15573|TAF1A_HUMAN	IPGVWDPFVK	26.92	Unmodified	Light	2	579.32132

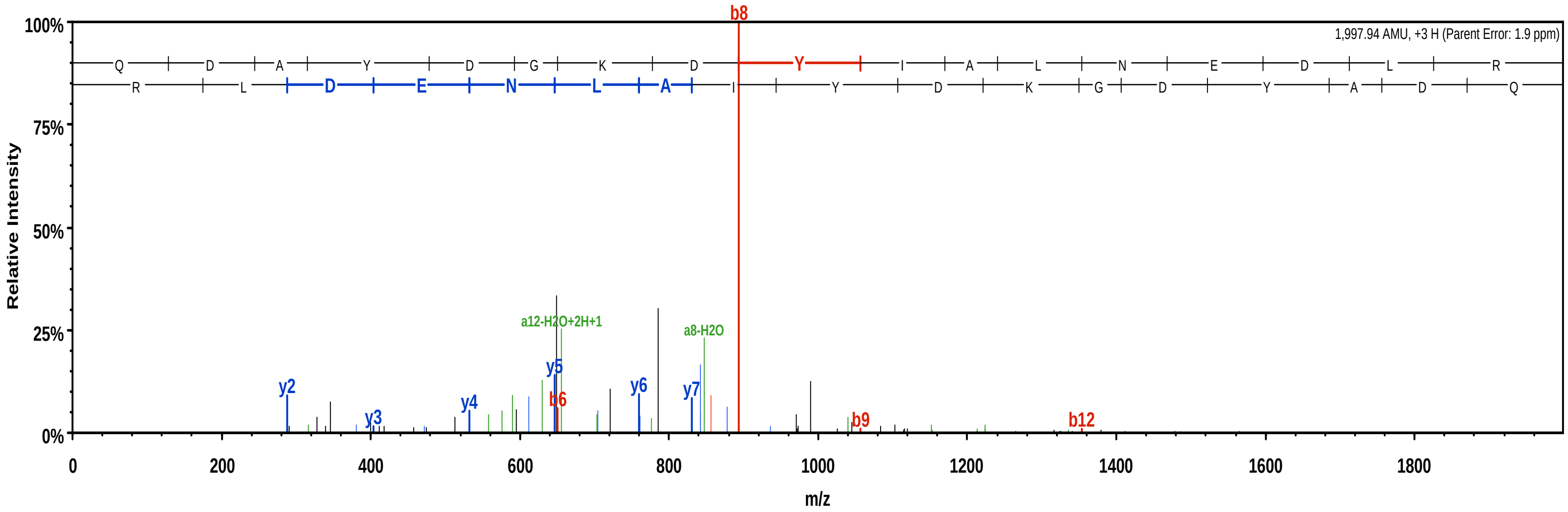


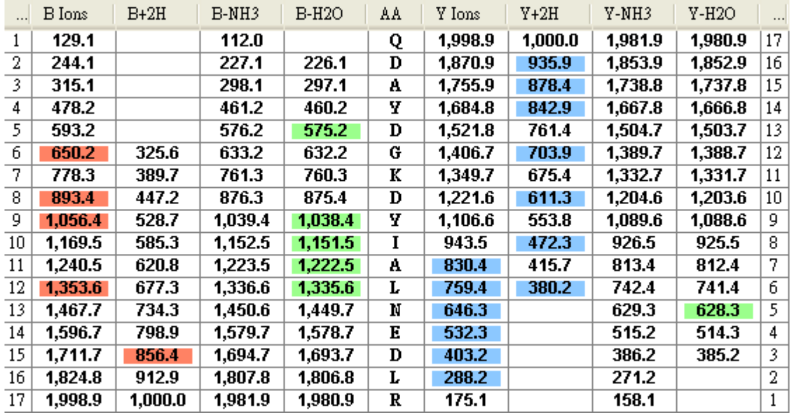


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	1,157.6	579.3	1,140.6	1,139.6	10
2	211.1				P	1,044.6	522.8	1,027.5	1,026.5	9
3	268.2				G	947.5	474.3	930.5	929.5	8
4	367.2				V	890.5	445.7	873.5	872.5	7
5	553.3				W	791.4	396.2	774.4	773.4	6
6	668.3	334.7		650.3	D	605.3		588.3	587.3	5
7	765.4	383.2		747.4	P	490.3		473.3		4
8	912.5	456.7		894.5	F	393.2		376.2		3
9	1,011.5	506.3		993.5	V	246.2		229.2		2
10	1,157.6	579.3	1,140.6	1,139.6	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-128	sp|P04439|1A03_HUMAN	QDAYDGKDYIALNEDLR	26.56	Unmodified	Light	3	666.98496

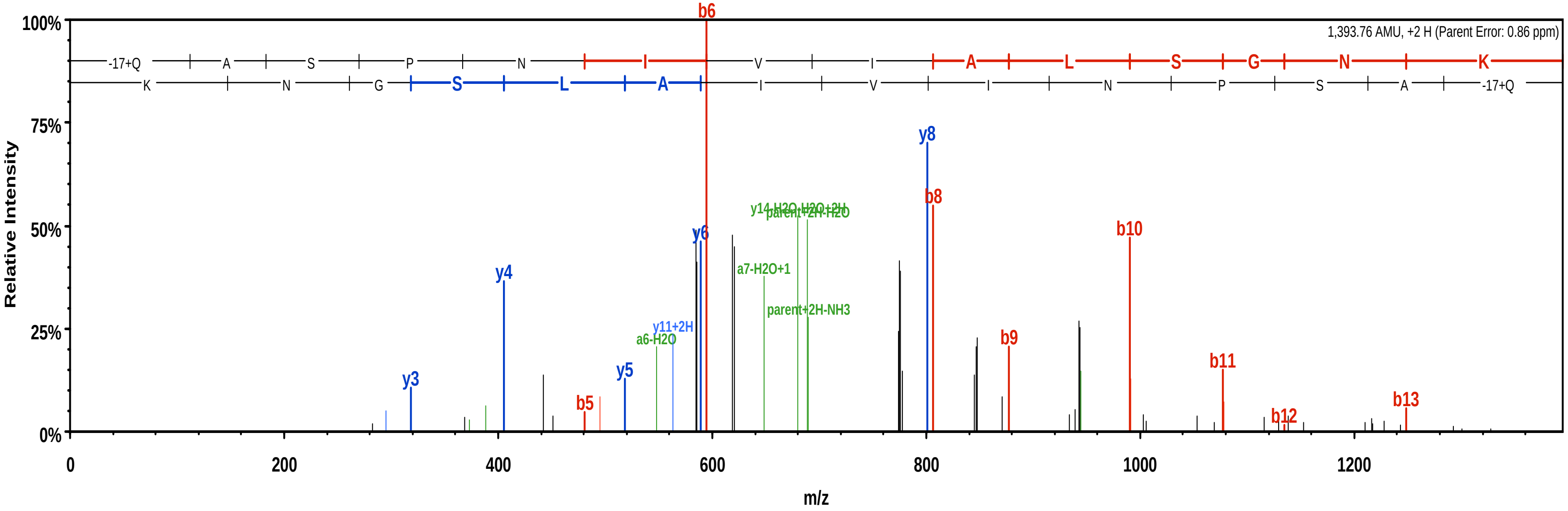


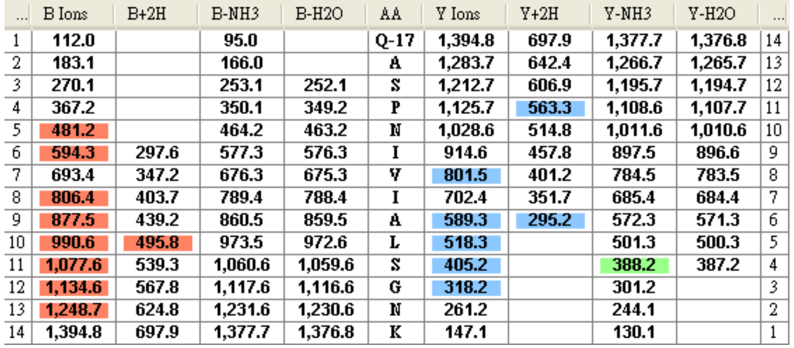


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	129.1		112.0		Q	1,998.9	1,000.0	1,981.9	1,980.9	17
2	244.1		227.1	226.1	D	1,870.9	935.9	1,853.9	1,852.9	16
3	315.1		298.1	297.1	A	1,755.9	878.4	1,738.8	1,737.8	15
4	478.2		461.2	460.2	Y	1,684.8	842.9	1,667.8	1,666.8	14
5	593.2		576.2	575.2	D	1,521.8	761.4	1,504.7	1,503.7	13
6	650.2	325.6	633.2	632.2	G	1,406.7	703.9	1,389.7	1,388.7	12
7	778.3	389.7	761.3	760.3	K	1,349.7	675.4	1,332.7	1,331.7	11
8	893.4	447.2	876.3	875.4	D	1,221.6	611.3	1,204.6	1,203.6	10
9	1,056.4	528.7	1,039.4	1,038.4	Y	1,106.6	553.8	1,089.6	1,088.6	9
10	1,169.5	585.3	1,152.5	1,151.5	I	943.5	472.3	926.5	925.5	8
11	1,240.5	620.8	1,223.5	1,222.5	A	830.4	415.7	813.4	812.4	7
12	1,353.6	677.3	1,336.6	1,335.6	L	759.4	380.2	742.4	741.4	6
13	1,467.7	734.3	1,450.6	1,449.7	N	646.3		629.3	628.3	5
14	1,596.7	798.9	1,579.7	1,578.7	E	532.3		515.2	514.3	4
15	1,711.7	856.4	1,694.7	1,693.7	D	403.2		386.2	385.2	3
16	1,824.8	912.9	1,807.8	1,806.8	L	288.2		271.2		2
17	1,998.9	1,000.0	1,981.9	1,980.9	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-129	sp|P20339|RAB5A_HUMAN	QASPNIVIALSGNK	26.43	Gln->pyro-Glu (N-term Q)	Light	2	697.88554

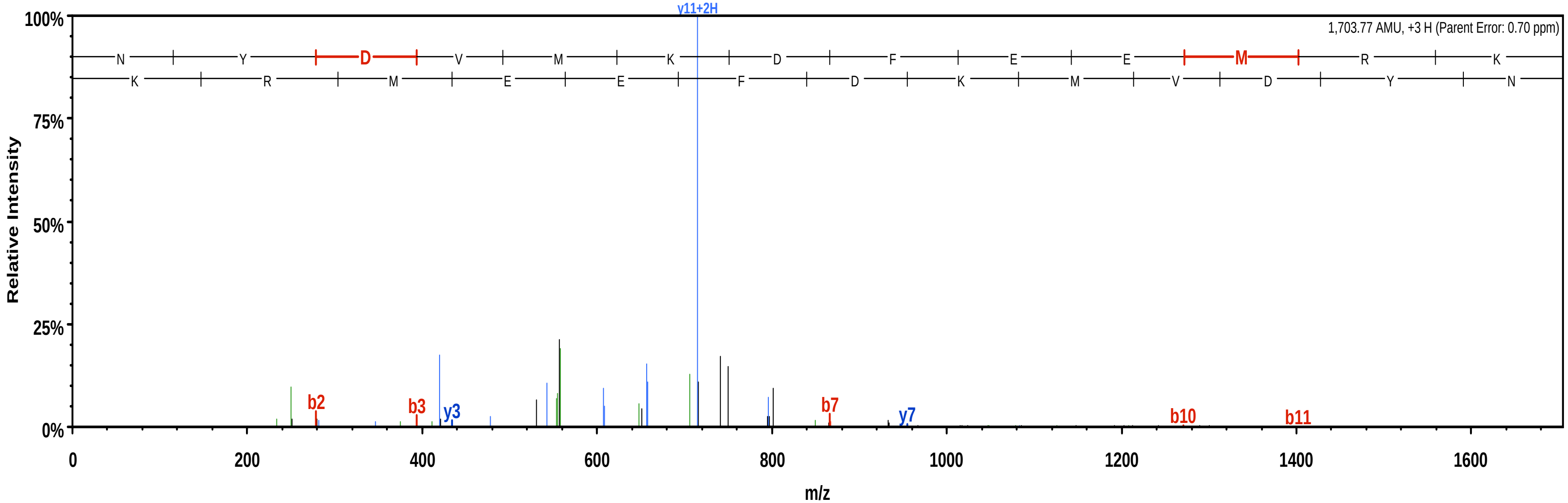


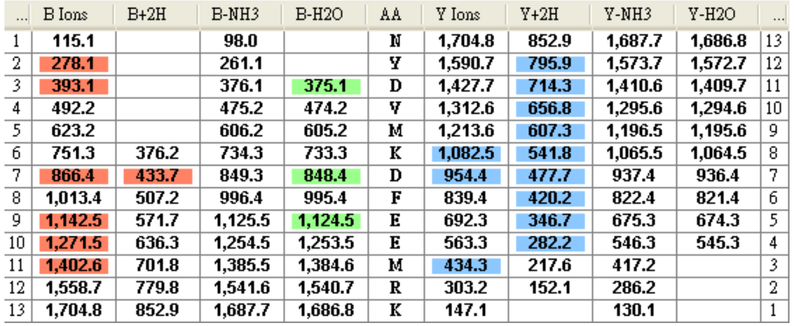


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	112.0		95.0		Q-17	1,394.8	697.9	1,377.7	1,376.8	14
2	183.1		166.0		A	1,283.7	642.4	1,266.7	1,265.7	13
3	270.1		253.1	252.1	S	1,212.7	606.9	1,195.7	1,194.7	12
4	367.2		350.1	349.2	P	1,125.7	563.3	1,108.6	1,107.7	11
5	481.2		464.2	463.2	N	1,028.6	514.8	1,011.6	1,010.6	10
6	594.3	297.6	577.3	576.3	I	914.6	457.8	897.5	896.6	9
7	693.4	347.2	676.3	675.3	V	801.5	401.2	784.5	783.5	8
8	806.4	403.7	789.4	788.4	I	702.4	351.7	685.4	684.4	7
9	877.5	439.2	860.5	859.5	A	589.3	295.2	572.3	571.3	6
10	990.6	495.8	973.5	972.6	L	518.3		501.3	500.3	5
11	1,077.6	539.3	1,060.6	1,059.6	S	405.2		388.2	387.2	4
12	1,134.6	567.8	1,117.6	1,116.6	G	318.2		301.2		3
13	1,248.7	624.8	1,231.6	1,230.6	N	261.2		244.1		2
14	1,394.8	697.9	1,377.7	1,376.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-130	sp|P09669|COX6C_HUMAN	NYDVMKDFEEMRK	26.36	Unmodified	Light	3	568.92885

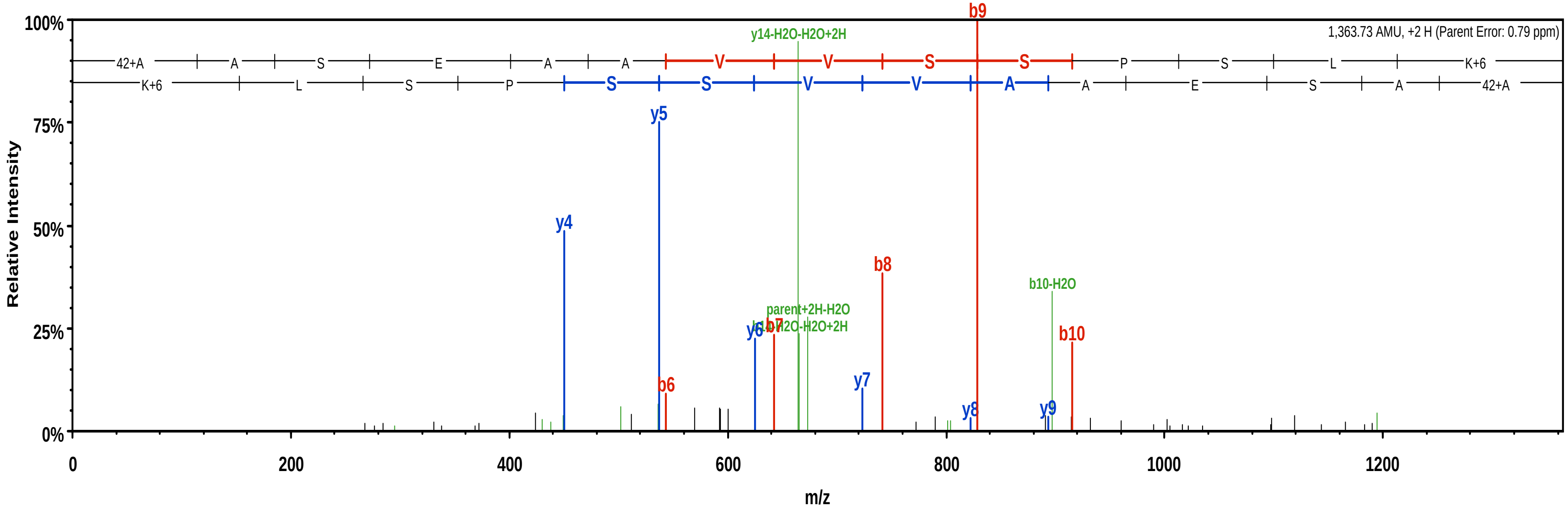


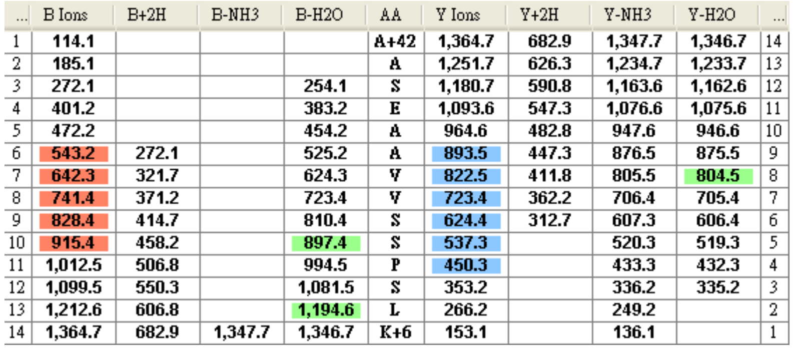


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	115.1		98.0		N	1,704.8	852.9	1,687.7	1,686.8	13
2	278.1		261.1		Y	1,590.7	795.9	1,573.7	1,572.7	12
3	393.1		376.1	375.1	D	1,427.7	714.3	1,410.6	1,409.7	11
4	492.2		475.2	474.2	V	1,312.6	656.8	1,295.6	1,294.6	10
5	623.2		606.2	605.2	M	1,213.6	607.3	1,196.5	1,195.6	9
6	751.3	376.2	734.3	733.3	K	1,082.5	541.8	1,065.5	1,064.5	8
7	866.4	433.7	849.3	848.4	D	954.4	477.7	937.4	936.4	7
8	1,013.4	507.2	996.4	995.4	F	839.4	420.2	822.4	821.4	6
9	1,142.5	571.7	1,125.5	1,124.5	E	692.3	346.7	675.3	674.3	5
10	1,271.5	636.3	1,254.5	1,253.5	E	563.3	282.2	546.3	545.3	4
11	1,402.6	701.8	1,385.5	1,384.6	M	434.3	217.6	417.2		3
12	1,558.7	779.8	1,541.6	1,540.7	R	303.2	152.1	286.2		2
13	1,704.8	852.9	1,687.7	1,686.8	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-131	sp|Q8WWH5|TRUB1_HUMAN	AASEAAVVSSPSLK	25.04	Acetyl (Protein N-term)	Heavy	2	679.86173

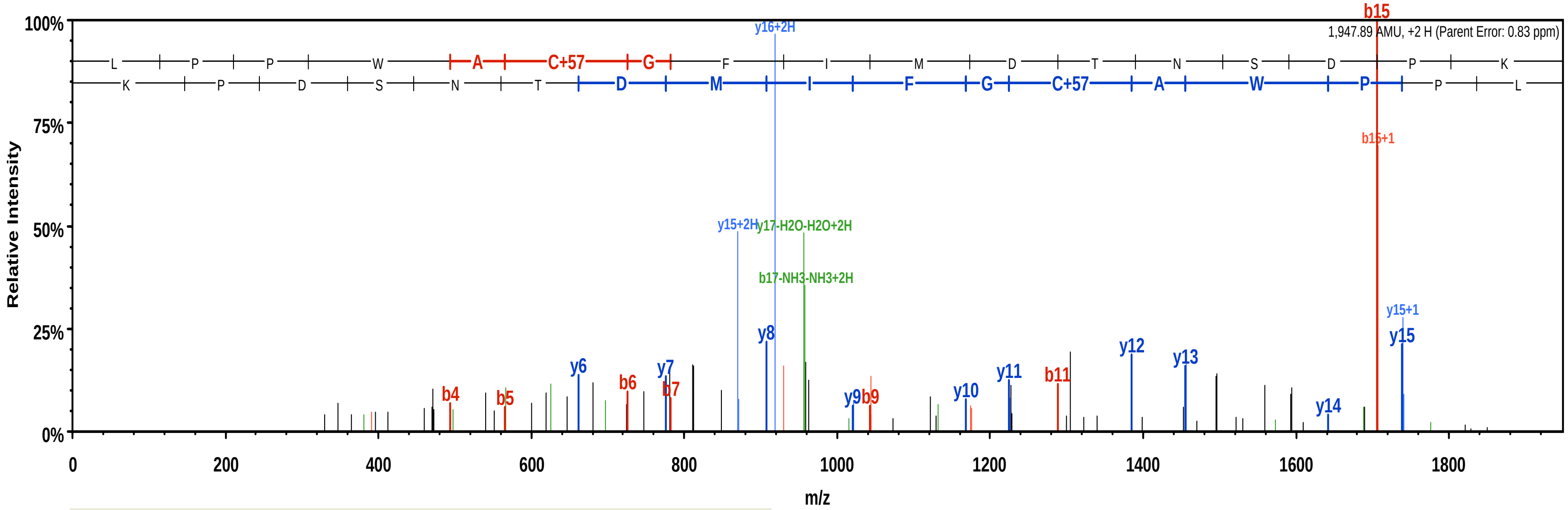


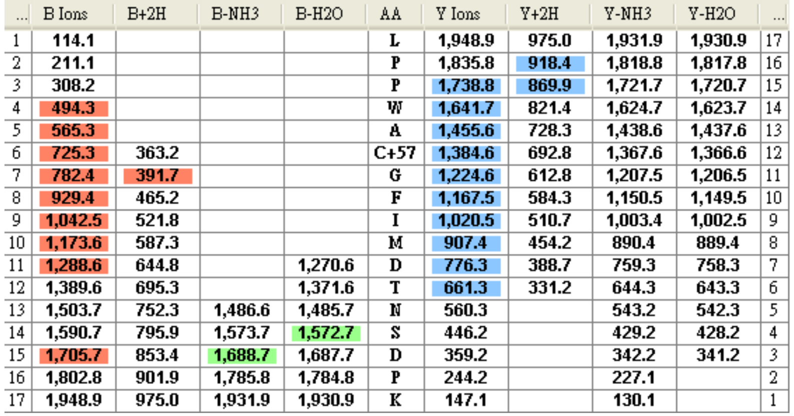


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				A+42	1,364.7	682.9	1,347.7	1,346.7	14
2	185.1				A	1,251.7	626.3	1,234.7	1,233.7	13
3	272.1			254.1	S	1,180.7	590.8	1,163.6	1,162.6	12
4	401.2			383.2	E	1,093.6	547.3	1,076.6	1,075.6	11
5	472.2			454.2	A	964.6	482.8	947.6	946.6	10
6	543.2	272.1		525.2	A	893.5	447.3	876.5	875.5	9
7	642.3	321.7		624.3	V	822.5	411.8	805.5	804.5	8
8	741.4	371.2		723.4	V	723.4	362.2	706.4	705.4	7
9	828.4	414.7		810.4	S	624.4	312.7	607.3	606.4	6
10	915.4	458.2		897.4	S	537.3		520.3	519.3	5
11	1,012.5	506.8		994.5	P	450.3		433.3	432.3	4
12	1,099.5	550.3		1,081.5	S	353.2		336.2	335.2	3
13	1,212.6	606.8		1,194.6	L	266.2		249.2		2
14	1,364.7	682.9	1,347.7	1,346.7	K+6	153.1		136.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-132	sp|Q4J6C6|PPCEL_HUMAN	LPPWACGFIMDTNSDPK	22.54	Unmodified	Light	2	974.95023

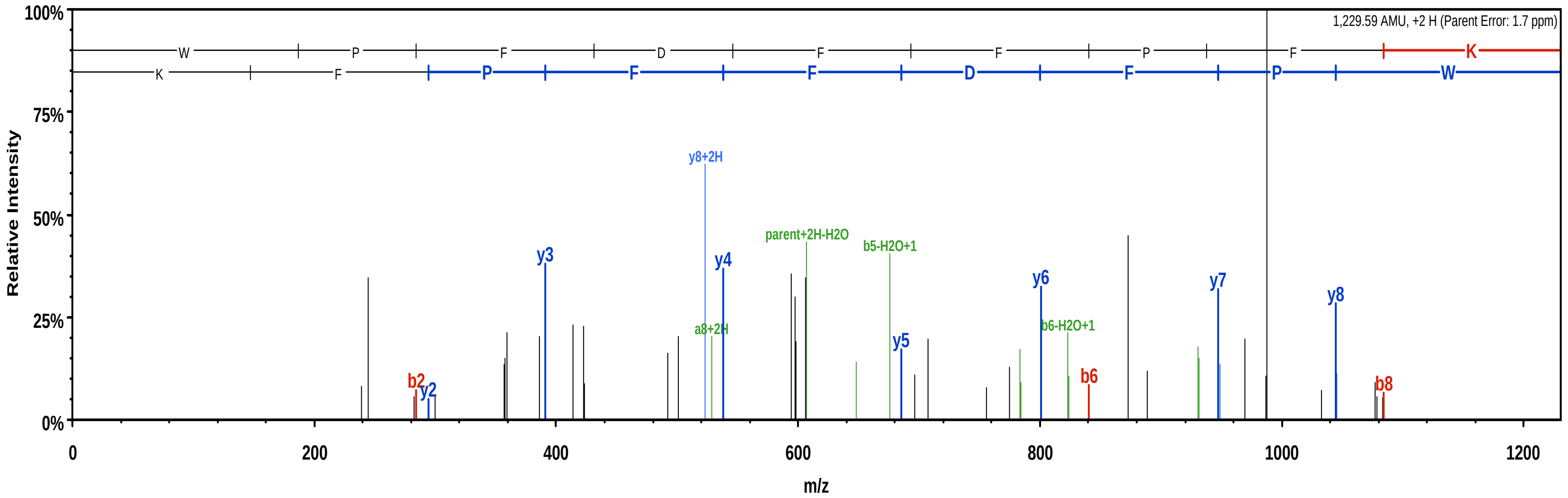


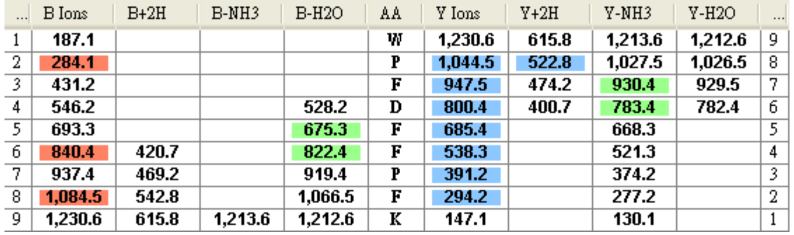


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				L	1,948.9	975.0	1,931.9	1,930.9	17
2	211.1				P	1,835.8	918.4	1,818.8	1,817.8	16
3	308.2				P	1,738.8	869.9	1,721.7	1,720.7	15
4	494.3				W	1,641.7	821.4	1,624.7	1,623.7	14
5	565.3				A	1,455.6	728.3	1,438.6	1,437.6	13
6	725.3	363.2			C+57	1,384.6	692.8	1,367.6	1,366.6	12
7	782.4	391.7			G	1,224.6	612.8	1,207.5	1,206.5	11
8	929.4	465.2			F	1,167.5	584.3	1,150.5	1,149.5	10
9	1,042.5	521.8			I	1,020.5	510.7	1,003.4	1,002.5	9
10	1,173.6	587.3			M	907.4	454.2	890.4	889.4	8
11	1,288.6	644.8		1,270.6	D	776.3	388.7	759.3	758.3	7
12	1,389.6	695.3		1,371.6	T	661.3	331.2	644.3	643.3	6
13	1,503.7	752.3	1,486.6	1,485.7	N	560.3		543.2	542.3	5
14	1,590.7	795.9	1,573.7	1,572.7	S	446.2		429.2	428.2	4
15	1,705.7	853.4	1,688.7	1,687.7	D	359.2		342.2	341.2	3
16	1,802.8	901.9	1,785.8	1,784.8	P	244.2		227.1		2
17	1,948.9	975.0	1,931.9	1,930.9	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-133	sp|Q6NUS6|TECT3_HUMAN	WPFDFFPFK	21.83	Unmodified	Light	2	615.80276

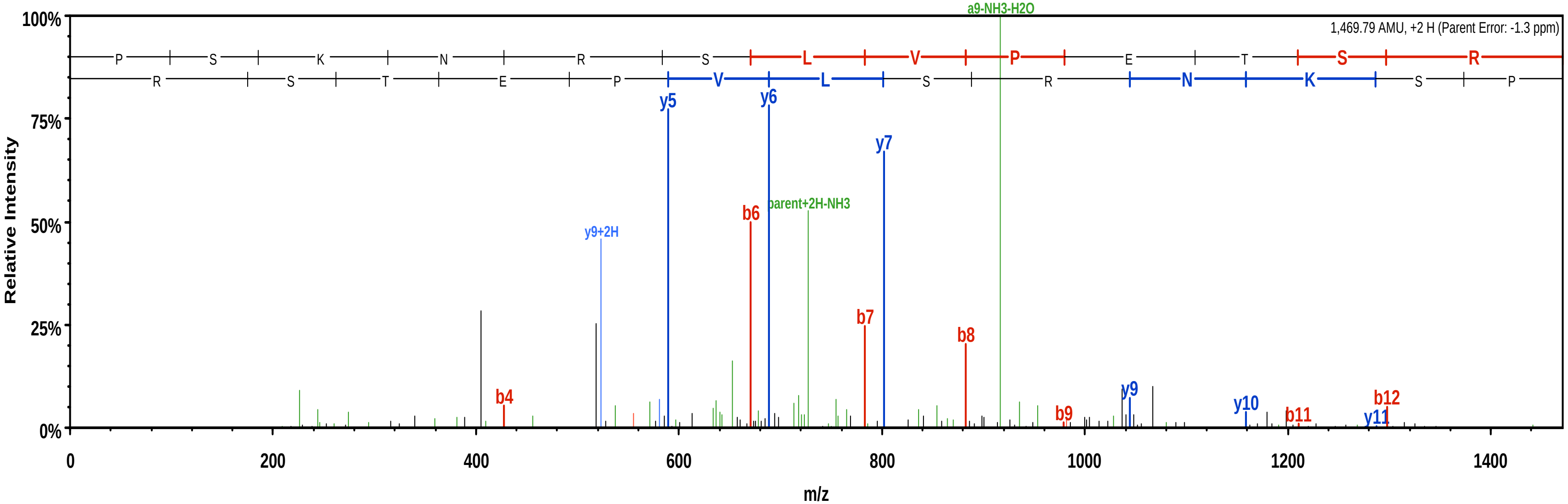


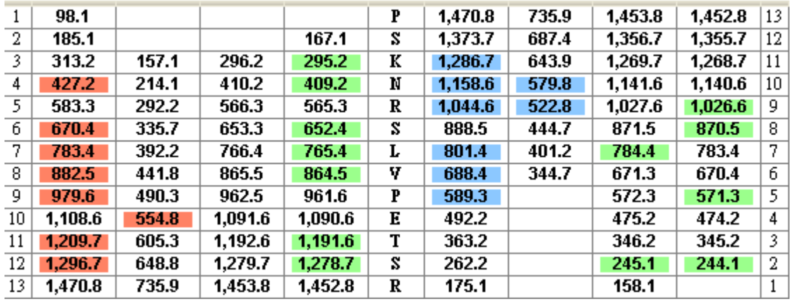


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	187.1				W	1,230.6	615.8	1,213.6	1,212.6	9
2	284.1				P	1,044.5	522.8	1,027.5	1,026.5	8
3	431.2				F	947.5	474.2	930.4	929.5	7
4	546.2			528.2	D	800.4	400.7	783.4	782.4	6
5	693.3			675.3	F	685.4		668.3		5
6	840.4	420.7		822.4	F	538.3		521.3		4
7	937.4	469.2		919.4	P	391.2		374.2		3
8	1,084.5	542.8		1,066.5	F	294.2		277.2		2
9	1,230.6	615.8	1,213.6	1,212.6	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-134	sp|O14607|UTY_HUMAN	PSKNRSLVPETSR	18.64	Unmodified	Light	2	735.9048

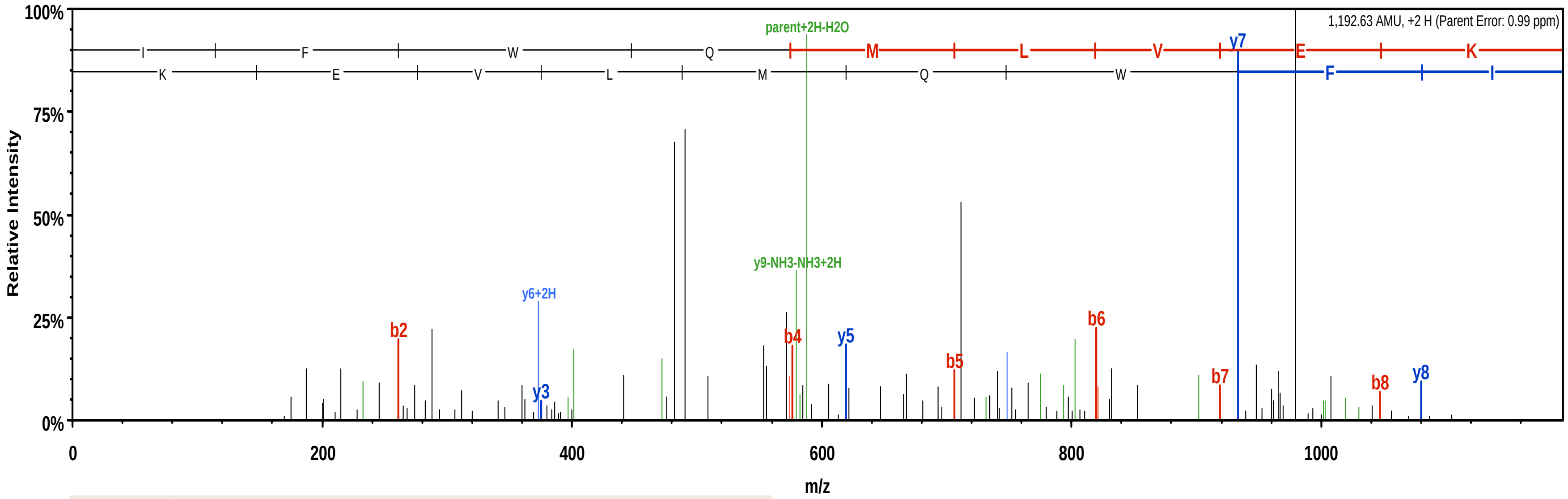


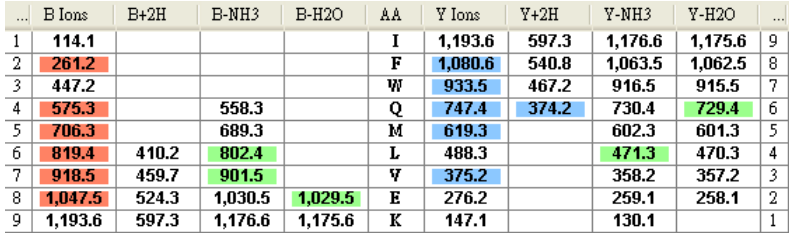


1	98.1				P	1,470.8	735.9	1,453.8	1,452.8	13
2	185.1			167.1	S	1,373.7	687.4	1,356.7	1,355.7	12
3	313.2	157.1	296.2	295.2	K	1,286.7	643.9	1,269.7	1,268.7	11
4	427.2	214.1	410.2	409.2	N	1,158.6	579.8	1,141.6	1,140.6	10
5	583.3	292.2	566.3	565.3	R	1,044.6	522.8	1,027.6	1,026.6	9
6	670.4	335.7	653.3	652.4	S	888.5	444.7	871.5	870.5	8
7	783.4	392.2	766.4	765.4	L	801.4	401.2	784.4	783.4	7
8	882.5	441.8	865.5	864.5	V	688.4	344.7	671.3	670.4	6
9	979.6	490.3	962.5	961.6	P	589.3		572.3	571.3	5
10	1,108.6	554.8	1,091.6	1,090.6	E	492.2		475.2	474.2	4
11	1,209.7	605.3	1,192.6	1,191.6	T	363.2		346.2	345.2	3
12	1,296.7	648.8	1,279.7	1,278.7	S	262.2		245.1	244.1	2
13	1,470.8	735.9	1,453.8	1,452.8	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-135	sp|Q6NUQ1|RINT1_HUMAN	IFWQMLVEK	15.95	Unmodified	Light	2	597.323

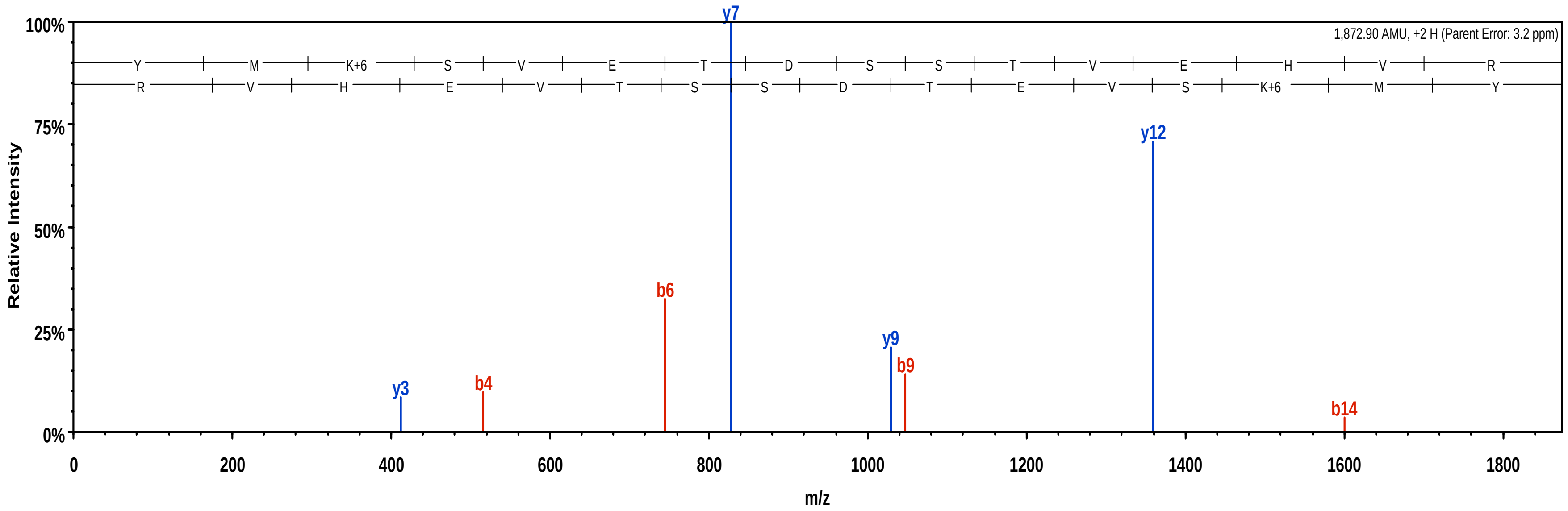


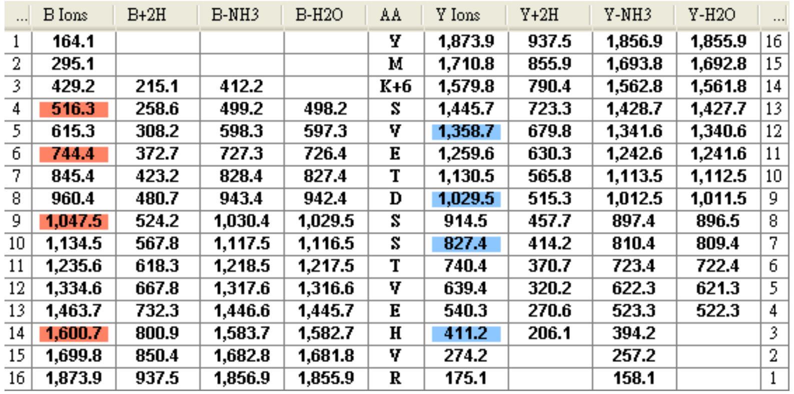


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	114.1				I	1,193.6	597.3	1,176.6	1,175.6	9
2	261.2				F	1,080.6	540.8	1,063.5	1,062.5	8
3	447.2				W	933.5	467.2	916.5	915.5	7
4	575.3		558.3		Q	747.4	374.2	730.4	729.4	6
5	706.3		689.3		M	619.3		602.3	601.3	5
6	819.4	410.2	802.4		L	488.3		471.3	470.3	4
7	918.5	459.7	901.5		V	375.2		358.2	357.2	3
8	1,047.5	524.3	1,030.5	1,029.5	E	276.2		259.1	258.1	2
9	1,193.6	597.3	1,176.6	1,175.6	K	147.1		130.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-136	sp|Q96F07|CYFP2_HUMAN	YMKSVETDSSTVEHVR	6.99	Unmodified	Heavy	2	934.44636

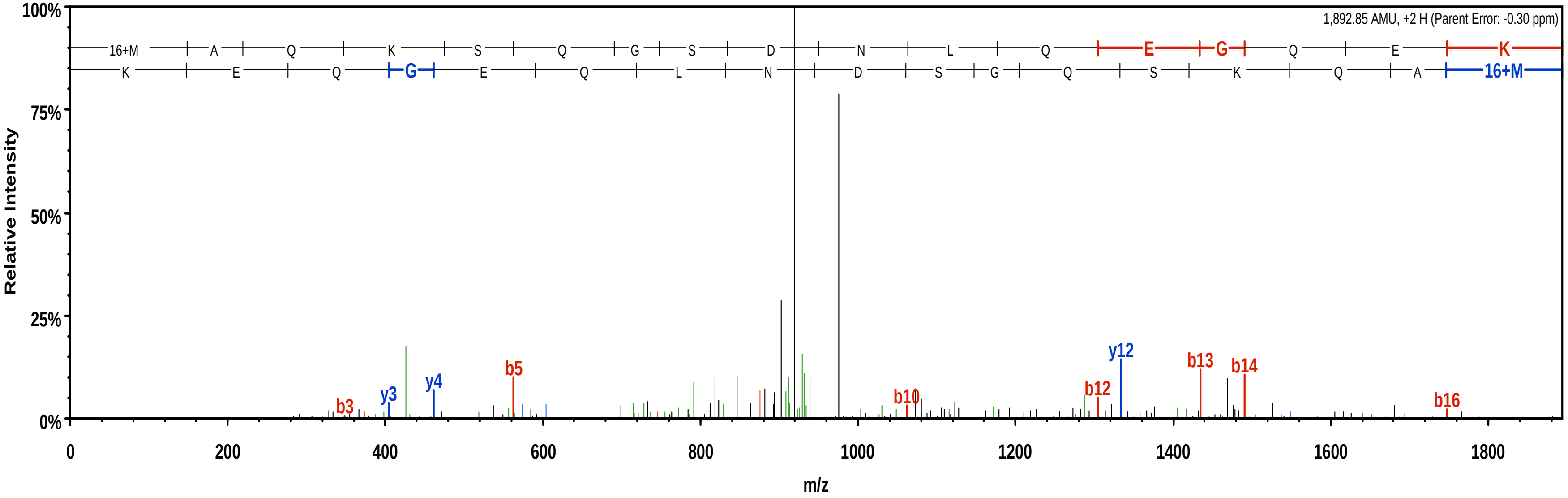


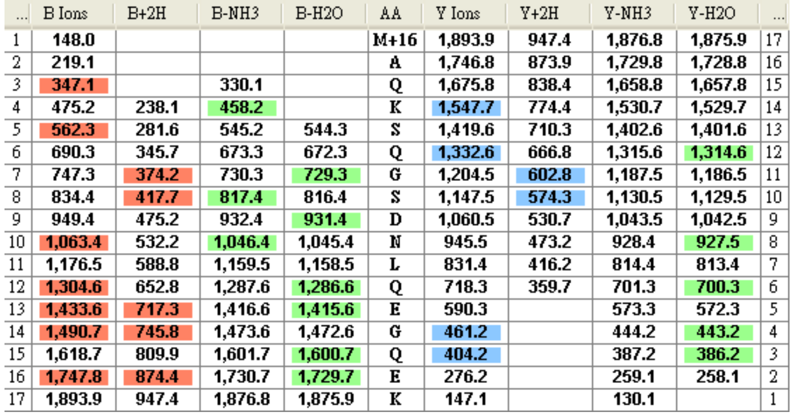


...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	164.1				Y	1,873.9	937.5	1,856.9	1,855.9	16
2	295.1				M	1,710.8	855.9	1,693.8	1,692.8	15
3	429.2	215.1	412.2		K+6	1,579.8	790.4	1,562.8	1,561.8	14
4	516.3	258.6	499.2	498.2	S	1,445.7	723.3	1,428.7	1,427.7	13
5	615.3	308.2	598.3	597.3	V	1,358.7	679.8	1,341.6	1,340.6	12
6	744.4	372.7	727.3	726.4	E	1,259.6	630.3	1,242.6	1,241.6	11
7	845.4	423.2	828.4	827.4	T	1,130.5	565.8	1,113.5	1,112.5	10
8	960.4	480.7	943.4	942.4	D	1,029.5	515.3	1,012.5	1,011.5	9
9	1,047.5	524.2	1,030.4	1,029.5	S	914.5	457.7	897.4	896.5	8
10	1,134.5	567.8	1,117.5	1,116.5	S	827.4	414.2	810.4	809.4	7
11	1,235.6	618.3	1,218.5	1,217.5	T	740.4	370.7	723.4	722.4	6
12	1,334.6	667.8	1,317.6	1,316.6	V	639.4	320.2	622.3	621.3	5
13	1,463.7	732.3	1,446.6	1,445.7	E	540.3	270.6	523.3	522.3	4
14	1,600.7	800.9	1,583.7	1,582.7	H	411.2	206.1	394.2		3
15	1,699.8	850.4	1,682.8	1,681.8	V	274.2		257.2		2
16	1,873.9	937.5	1,856.9	1,855.9	R	175.1		158.1		1

Nuclear proteome

Protein No.	Leading protein name	Sequence	Mascot Score	Variable Modifications	SILAC State	Charge	m/z
N-137	sp|Q6ZRS4|CC129_HUMAN	MAQKSQGSDNLQEGQEK	6.16	Oxidation (M)	Light	2	947.43399





...	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	...
1	148.0				M+16	1,893.9	947.4	1,876.8	1,875.9	17
2	219.1				A	1,746.8	873.9	1,729.8	1,728.8	16
3	347.1		330.1		Q	1,675.8	838.4	1,658.8	1,657.8	15
4	475.2	238.1	458.2		K	1,547.7	774.4	1,530.7	1,529.7	14
5	562.3	281.6	545.2	544.3	S	1,419.6	710.3	1,402.6	1,401.6	13
6	690.3	345.7	673.3	672.3	Q	1,332.6	666.8	1,315.6	1,314.6	12
7	747.3	374.2	730.3	729.3	G	1,204.5	602.8	1,187.5	1,186.5	11
8	834.4	417.7	817.4	816.4	S	1,147.5	574.3	1,130.5	1,129.5	10
9	949.4	475.2	932.4	931.4	D	1,060.5	530.7	1,043.5	1,042.5	9
10	1,063.4	532.2	1,046.4	1,045.4	N	945.5	473.2	928.4	927.5	8
11	1,176.5	588.8	1,159.5	1,158.5	L	831.4	416.2	814.4	813.4	7
12	1,304.6	652.8	1,287.6	1,286.6	Q	718.3	359.7	701.3	700.3	6
13	1,433.6	717.3	1,416.6	1,415.6	E	590.3		573.3	572.3	5
14	1,490.7	745.8	1,473.6	1,472.6	G	461.2		444.2	443.2	4
15	1,618.7	809.9	1,601.7	1,600.7	Q	404.2		387.2	386.2	3
16	1,747.8	874.4	1,730.7	1,729.7	E	276.2		259.1	258.1	2
17	1,893.9	947.4	1,876.8	1,875.9	K	147.1		130.1		1