Supplemental Materials and Methods

Cells, antibodies and reagents

KG-1 cells were cultured in RPMI 1640 supplemented with 10% fetal calf serum and antibiotics. For SILAC labeling of KG-1 cells $^{13}C_6{}^{15}N_4$ L-arginine and $^{13}C_6{}^{15}N_2$ L-Lysine (both Cambridge Isotopes, Andover, USA) were used.

Regarding the primary AML cells all patients gave written informed consent. Baseline morphology, cytogenetics and cell surface antigen analysis were performed as part of the routine clinical evaluation. Immunomagnetically enriched CD34$^+$ cells were maintained in liquid culture (X-Vivo 10, Lonza, Basel, Switzerland) supplemented with 10% FBS (HyClone, Perbio, Aalst, Belgium), 1% L-Glutamin (Gibco, Darmstadt, Germany), interleukin-3, thrombopoietin (25 ng/mL each), stem cell factor and flt-3 ligand (50 ng/mL each, Peprotech, Hamburg, Germany) with medium changes to 2 x 10^5 cells/ml every 7 days.

Antibodies for western-blot analyses recognized (p)Syk(Tyr525/526), SLP65, pTyr(4G10), (p)STAT3(Tyr705), (p)STAT5(Tyr694), Pim1, Socs3 and actin (all from Cell Signaling Technology (Danvers, USA) or Santa Cruz Biotechnology (Santa Cruz, USA)). Antibodies recognizing FcRγ were purchased from Millipore (Billerica, USA), the antibodies recognizing CD18 and Mac-1 were purchased from Novus Biologicals (Littleton, USA). For immobilization of antibodies Protein A/G Sepharose was used (Santa Cruz Biotechnology).

The Syk inhibitor Bay 61-3606 (Merck, Darmstadt, Germany) was resuspended in H_2O and was stored at -20°C; it was used in a final concentration of 250nM. Calf intestinal alkaline phosphatase (CIP (New England Biolabs, Ipswich, USA)) was subjected to cleared cellular lysates for 30 min at 37 °C for dephosphorylation of proteins *in vitro*.

Vectors and cell transduction

Sequences targeted by each Syk shRNA were described previously[4]. shRNAs targeting Syk, FcRγ-, Mac-1- or CD18 were purchased from Sigma-Aldrich and the shRNA encoding sequences were cloned into pLKO.1 vectors for lentiviral transduction.

The following shRNA constructs were used: shRNA specific for FcRγ: Sigma-TRCN 0000057454. shRNA specific for Mac-1: Sigma-TRCN 0000414619. shRNA specific for CD18: Sigma-TRCN 0000029643. Cloning of the oligonucleotides and cell infections were performed as described previously[4]. The retroviral vectors pMSCV-iGFP, pMSCV-iGFP-caSTAT3 and pMSCV-iGFP-caSTAT5A were kindly provided by C. Wichmann and R. Moriggl. The STAT3 cDNA was manipulated by site-directed mutagenesis in a way that upon expression cysteine residues substituted A661 and N663 of STAT3[22]. The cDNA encoding for constitutively active STAT5A harbors point mutations resulting in the replacement of S711 by phenylalanine on the protein level[23]. Retroviral transductions were performed as described previously[24].

Mass spectrometric analysis, database search and MaxQuant-based protein quantification

All slices were reduced with 10mM DTT for 55 min at 56°C, alkylated with 55mM IAA for 20 min at 26°C and digested with modified trypsin (Promega, Madison, USA) overnight at 37°C. Tryptic peptides were injected into a C_{18} precolumn (1.5cm, 360μm o.d., 150μm i.d., Reprosil-Pur 120A°, 3μm, C_{18}-AQ, Dr Maisch GmbH) at a flow rate of 10 ml/min. Bound peptides were eluted and separated on a C_{18} capillary column (15cm, 360μm o.d., 75μm i.d., Reprosil-Pur 120A°, 3μm, C_{18}-AQ, Dr Maisch GmbH) at a flow rate of 300 nl/min, with a gradient from 7.5 to 37.5% ACN in 0.1% formic acid for 50 min using an Agilent 1100 nano-flow LC system (Agilent Technologies, Böblingen, Germany) coupled to an LTQ-Orbitrap XL hybrid mass spectrometer (Thermo Fisher Scientific, Waltham, USA). MS conditions were as followed: spray voltage, 1.6kV; heated capillary temperature, 150°C; normalized collision-induced dissociation (CID) collision energy 37.5% for MS/MS in LTQ. An activation q=0.25 and activation time of 30 ms were used. The mass spectrometer was operated in the data-dependent mode to automatically switch between MS and MS/MS acquisition. Survey MS spectra were acquired in the Orbitrap (m/z 350–1600) with the resolution set to 30000 at m/z 400 and automatic gain control target at $5x10^5$. The five most intense ions were sequentially isolated for CID MS/MS fragmentation and detection in the linear ion trap. Ions with single and unrecognized charge states were excluded. Raw data were analysed with MaxQuant software (Version 1.0.13.13) in combination with Mascot search engine for peptide and protein identifications (Version 2.2.07, Matrix Science). IPI human database (Version 3.87) was used as human sequence database. MS/MS peak lists were filtered to contain at most six peaks per 100 Da interval and searched against Mascot server. The MS mass tolerance was set to 7 ppm and MS/MS mass tolerance was set to 0.6 Da. Up to three missed cleavages of trypsin were allowed. Oxidized methionine and cysteine carbamido-methylation were searched as variable modifications. The modifications corresponding to arginine and lysine labeled with heavy stable isotopes were handled as fixed modifications in the Mascot search, if applicable, after identification of SILAC pairs by MaxQuant. The false positive rate was set to 1% at the peptide level, the false discovery rate was set to 1% at the protein level and the minimum required peptide length was set to six amino acids.

Mass spectrometric phosphopeptide analysis

The Syk band was excised, reduced, alkylated, in-gel digested with trypsin, and then extracted from the gel, as described above. The tryptic peptides were re-dissolved in 20µl

DHB solution (200mg 2,5-dihydroxybenzoic acid (Sigma, USA) in 1 ml of 80% acetonitrile, 5% trifluoroacetic acid and loaded onto a TiO_2 microcolumn (GL Sciences Inc.), as described[19].The columns were washed three times with 20μl DHB solution and five times with 20μl of a solution of 5% trifluoroacetic acid and 80% acetonitrile to remove non-specific binding peptides and DHB. The bound peptides were then eluted with 3 x 20μl of 0.3N NH_4OH (pH > 10.5) and evaporated to dryness in a SpeedVac for further MS analysis. The LTQ-Orbitrap Velos hybrid mass spectrometer (Thermo Fisher Scientific, Waltham, USA) was used in place of LTQ-Orbitrap XL hybrid mass spectrometer. The multistage activation of neutral loss of phosphoric acid was used in all CID MS/MS events to improve the fragmentation spectra of the phosphopeptides. All MS/MS spectra were searched using MASCOT v2.2.07 against the IPI human database (Version 3.87) with the following criteria: peptide mass tolerance, 10 ppm; MS/MS ion mass tolerance, 0.6 Da; number of missed cleavages allowed, up to three. The variable modifications considered were phosphorylation of serine, threonine and tyrosine, methionine oxidation, and cysteine carboxyamidomethylation. All phosphorylated sites were examined manually by the presence of a mass difference of 69 Da between fragment ions for phosphoserine and a difference of 83 Da for phosphothreonine (supplementary table 1, supplementary figure 1).

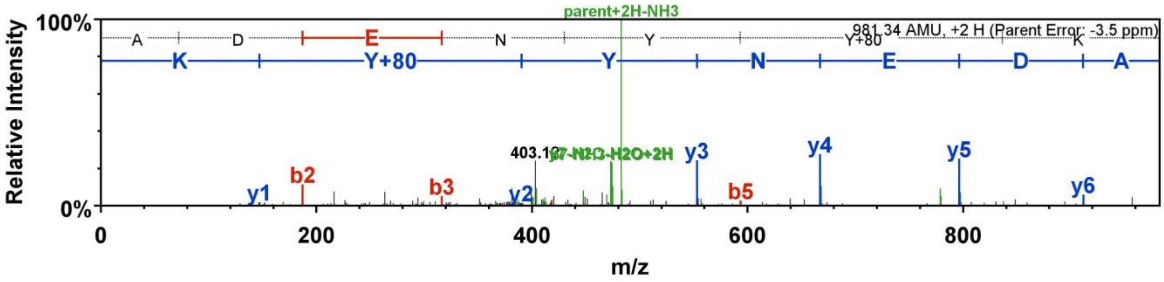
Cell proliferation assay

$5 \cdot 10^3$ FFM05 or FFM12, or 10^3 KG-1 cells were seeded into the wells of a 96-well plate on day zero. The cells were cultured in the respective growth media outlined above. At given time points the cells were treated using a mixture consisting of the XTT-labeling reagent and the electron coupling reagent according to the protocol of the cell proliferation kit II (Roche). Four hours later the XTT-derived signals that are proportional to the cell numbers were monitored by an Elisa-Reader (Spectra Fluor Plus, specific absorbance filter: 475nm, non-specific absorbance filter: 660nm) (Tecan). Wells containing groth media served as background controls in all experiments. In case of AML cell/stroma co-culture experiments, wells containing stroma cells and growth media were used as background controls.

In vitro kinase assays

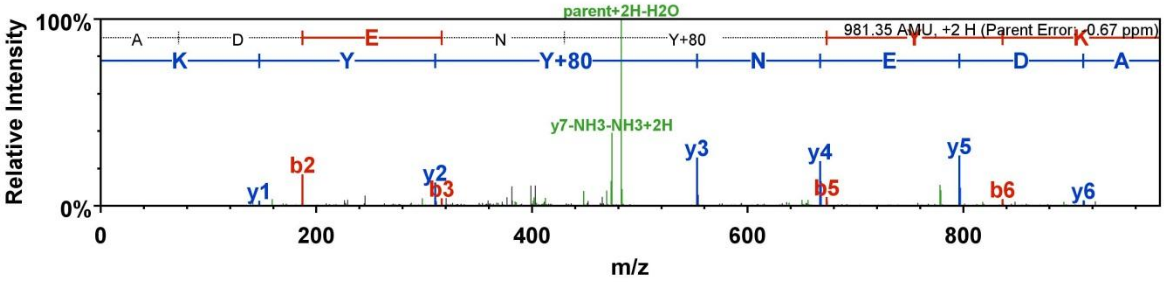
For phosphorylation the recombinant catalytic domain of Syk (Biomol, Germany) was used or Syk was purified by immunopurification as described above and resuspended in kinase buffer containing 60mM HEPES pH7.5; 5mM $MgCL_2$; 5mM $MnCL_2$; 3μM Na_3VO_4; 1.25mM DTT. Protein A/G beads only served as negative control for the immunopurification. 1.5μM biotinylated substrate peptide and 20μM ATP were added, incubated for 15min at 37°C, and the reaction was stopped by adding EDTA to a final concentration of 25mM. Peptides were immobilized on streptavidine-coated 96well plates (Millipore, Billerica, USA) and phosphorylation efficiency was determined by ELISA using 1μg/ml anti-pTyr (Millipore, Billerica, USA) and 1:1000 HRPO-conjugated anti-mouse IgG antibodies (Pierce, Rockford, USA). The mean value and standard deviation (SD) of quadruplicates was determined by calculating the difference of absorption at 405nm and background absorption at 490nm.

Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(R)ADENYyK(A)	pY	491.6796	981.345	2	-0.003	27.0



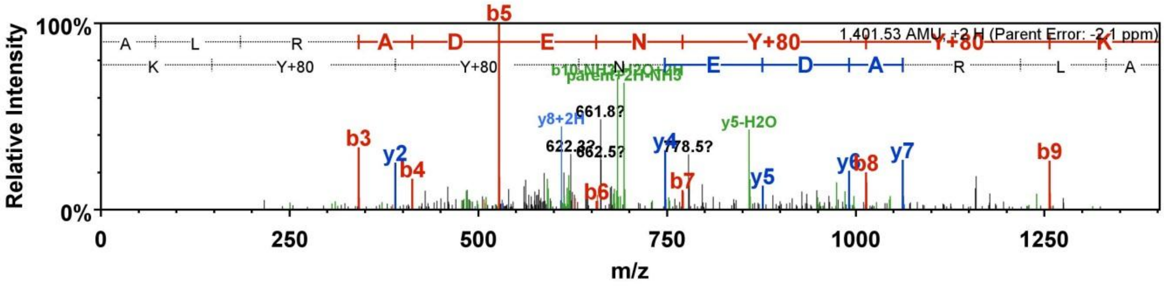
B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	982.4	491.7	965.3	964.3	7
2	187.1			169.1	D	911.3	456.2	894.3	893.3	6
3	316.1			298.1	E	796.3		779.3	778.3	5
4	430.2		413.1	412.1	N	667.2		650.2		4
5	593.2		576.2	575.2	Y	553.2		536.2		3
6	836.2	418.6	819.2	818.2	Y+80	390.1		373.1		2
7	982.4	491.7	965.3	964.3	K	147.1		130.1		1

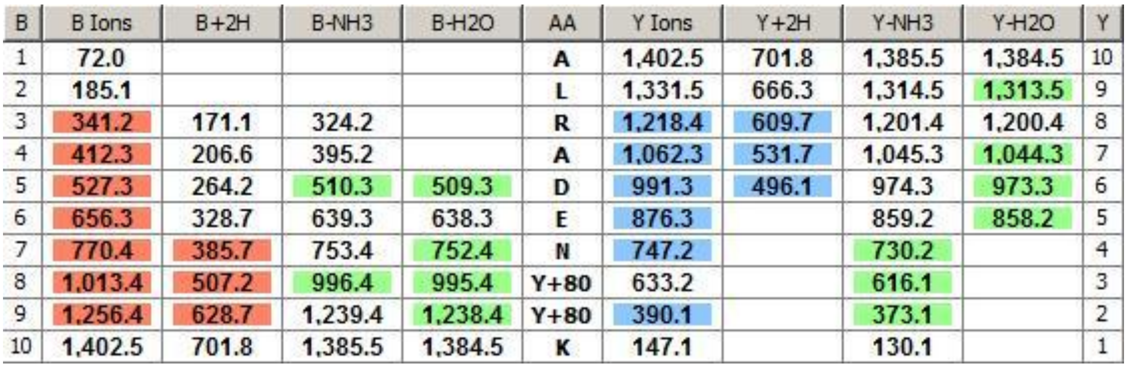
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(R)ADENyYK(A)	pY	491.6810	981.347	2	-0.001	33.0



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	982.4	491.7	965.3	964.3	7
2	187.1			169.1	D	911.3	456.2	894.3	893.3	6
3	316.1			298.1	E	796.3		779.3	778.3	5
4	430.2		413.1	412.1	N	667.2		650.2		4
5	673.2		656.2	655.2	Y+80	553.2		536.2		3
6	836.2	418.6	819.2	818.2	Y	310.2		293.1		2
7	982.4	491.7	965.3	964.3	K	147.1		130.1		1

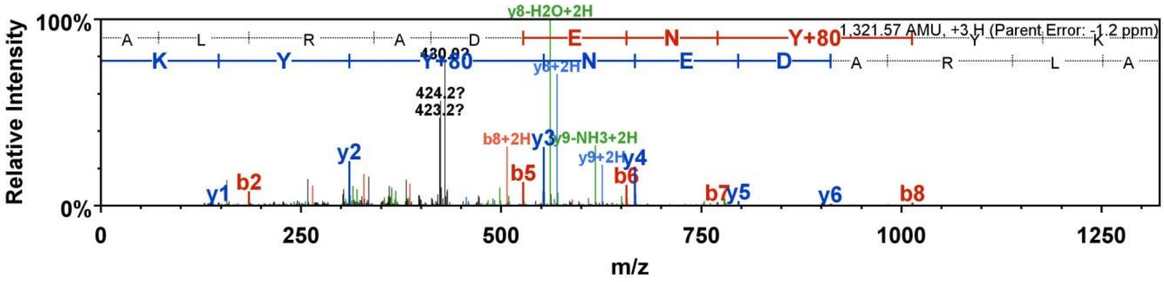
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(K)ALRADENyyK(A)	pY, pY	701.7742	1401.534	2	-0.003	28.2

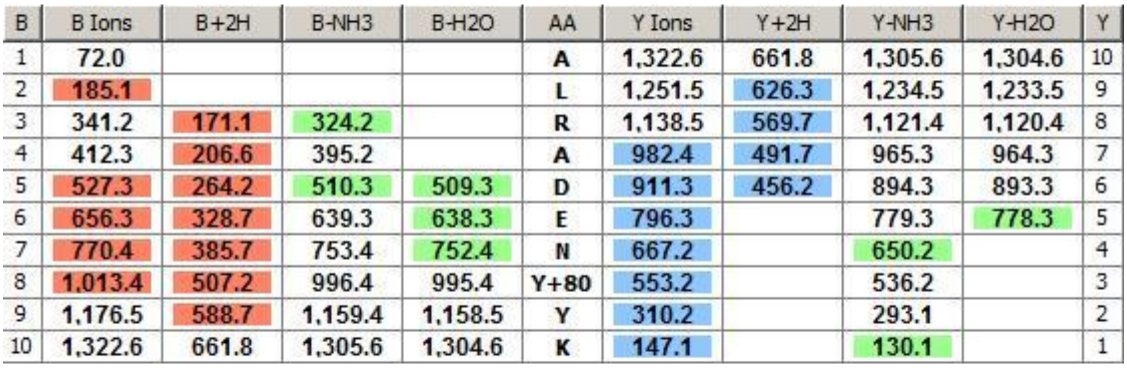




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1,402.5	701.8	1,385.5	1,384.5	10
2	185.1				L	1,331.5	666.3	1,314.5	1,313.5	9
3	341.2	171.1	324.2		R	1,218.4	609.7	1,201.4	1,200.4	8
4	412.3	206.6	395.2		A	1,062.3	531.7	1,045.3	1,044.3	7
5	527.3	264.2	510.3	509.3	D	991.3	496.1	974.3	973.3	6
6	656.3	328.7	639.3	638.3	E	876.3		859.2	858.2	5
7	770.4	385.7	753.4	752.4	N	747.2		730.2		4
8	1,013.4	507.2	996.4	995.4	Y+80	633.2		616.1		3
9	1,256.4	628.7	1,239.4	1,238.4	Y+80	390.1		373.1		2
10	1,402.5	701.8	1,385.5	1,384.5	K	147.1		130.1		1

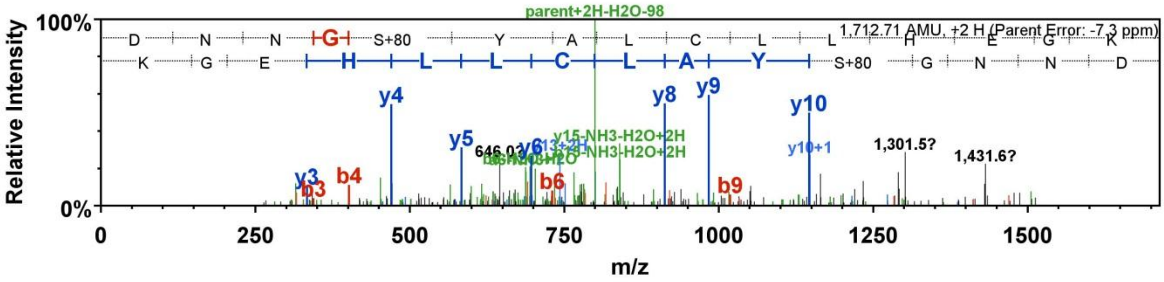
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(K)ALRADENyYK(A)	pY	441.5302	1321.569	3	-0.002	25.7

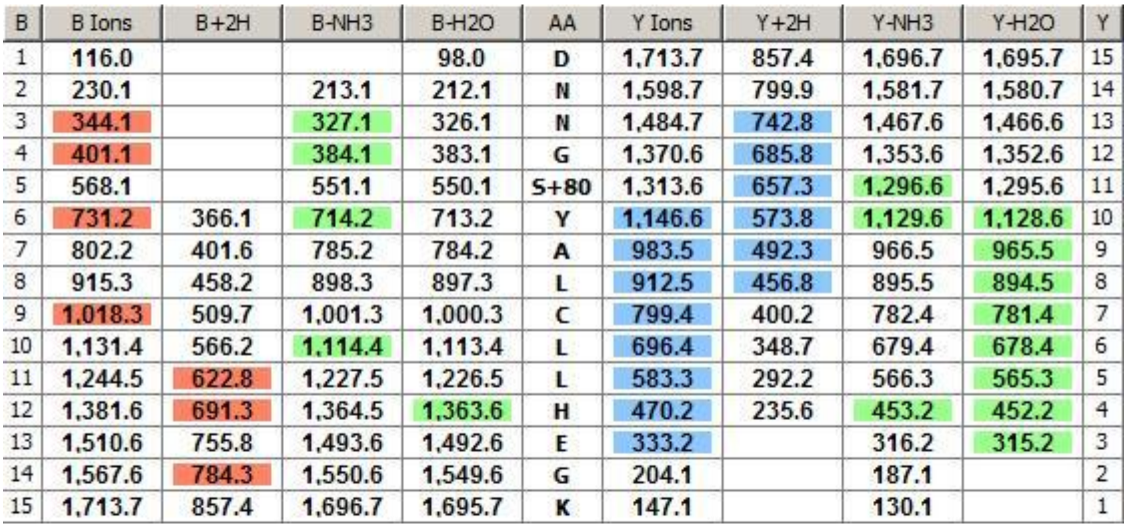




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1,322.6	661.8	1,305.6	1,304.6	10
2	185.1				L	1,251.5	626.3	1,234.5	1,233.5	9
3	341.2	171.1	324.2		R	1,138.5	569.7	1,121.4	1,120.4	8
4	412.3	206.6	395.2		A	982.4	491.7	965.3	964.3	7
5	527.3	264.2	510.3	509.3	D	911.3	456.2	894.3	893.3	6
6	656.3	328.7	639.3	638.3	E	796.3		779.3	778.3	5
7	770.4	385.7	753.4	752.4	N	667.2		650.2		4
8	1,013.4	507.2	996.4	995.4	Y+80	553.2		536.2		3
9	1,176.5	588.7	1,159.4	1,158.5	Y	310.2		293.1		2
10	1,322.6	661.8	1,305.6	1,304.6	K	147.1		130.1		1

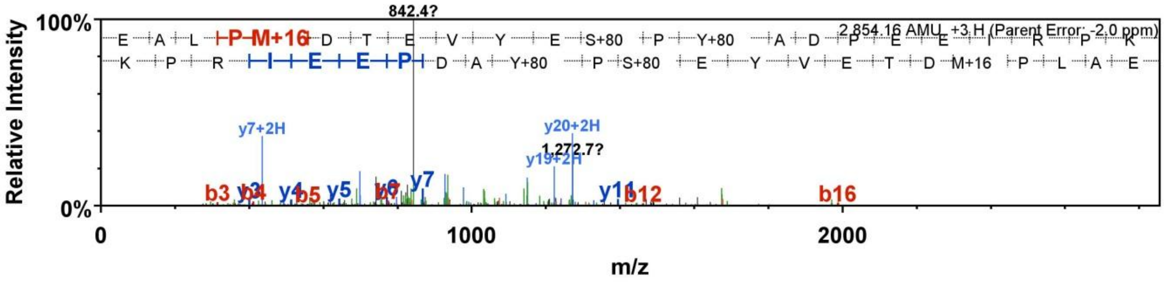
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(R)DNNGsYALCLLHEGK(V)	pS	857.3626	1712.711	2	-0.012	43.2





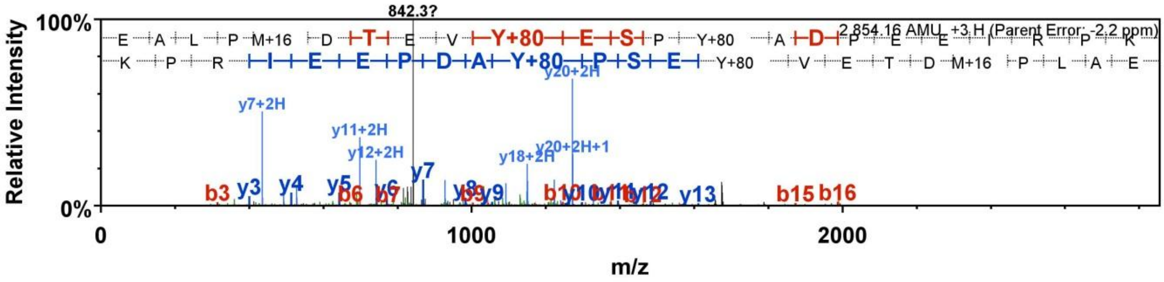
B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	116.0			98.0	D	1,713.7	857.4	1,696.7	1,695.7	15
2	230.1		213.1	212.1	N	1,598.7	799.9	1,581.7	1,580.7	14
3	344.1		327.1	326.1	N	1,484.7	742.8	1,467.6	1,466.6	13
4	401.1		384.1	383.1	G	1,370.6	685.8	1,353.6	1,352.6	12
5	568.1		551.1	550.1	S+80	1,313.6	657.3	1,296.6	1,295.6	11
6	731.2	366.1	714.2	713.2	Y	1,146.6	573.8	1,129.6	1,128.6	10
7	802.2	401.6	785.2	784.2	A	983.5	492.3	966.5	965.5	9
8	915.3	458.2	898.3	897.3	L	912.5	456.8	895.5	894.5	8
9	1,018.3	509.7	1,001.3	1,000.3	C	799.4	400.2	782.4	781.4	7
10	1,131.4	566.2	1,114.4	1,113.4	L	696.4	348.7	679.4	678.4	6
11	1,244.5	622.8	1,227.5	1,226.5	L	583.3	292.2	566.3	565.3	5
12	1,381.6	691.3	1,364.5	1,363.6	H	470.2	235.6	453.2	452.2	4
13	1,510.6	755.8	1,493.6	1,492.6	E	333.2		316.2	315.2	3
14	1,567.6	784.3	1,550.6	1,549.6	G	204.1		187.1		2
15	1,713.7	857.4	1,696.7	1,695.7	K	147.1		130.1		1

Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(R)EALPmDTEVYEsPyADPEEIRPK(E)	Mox, pS, pY	952.3954	2854.164	3	-0.006	34.0



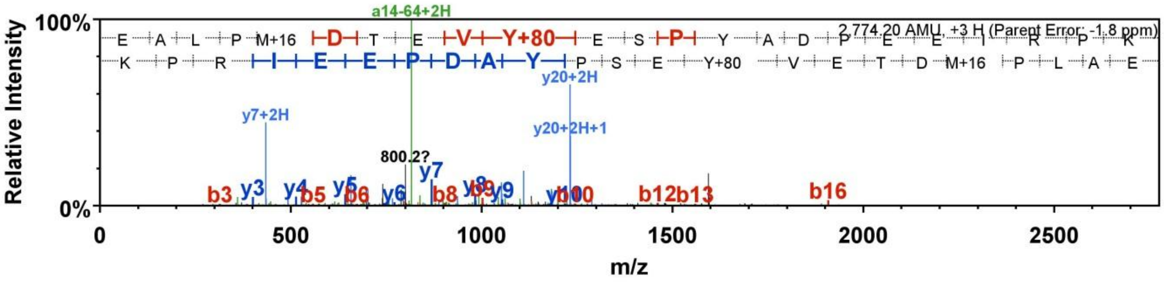
B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	2,855.2	1,428.1	2,838.2	2,837.2	23
2	201.1			183.1	A	2,726.1	1,363.6	2,709.1	2,708.1	22
3	314.2			296.2	L	2,655.1	1,328.1	2,638.1	2,637.1	21
4	411.2			393.2	P	2,542.0	1,271.5	2,525.0	2,524.0	20
5	558.3			540.2	M+16	2,445.0	1,223.0	2,427.9	2,427.0	19
6	673.3	337.1		655.3	D	2,297.9	1,149.5	2,280.9	2,279.9	18
7	774.3	387.7		756.3	T	2,182.9	1,092.0	2,165.9	2,164.9	17
8	903.4	452.2		885.4	E	2,081.9	1,041.4	2,064.8	2,063.8	16
9	1,002.4	501.7		984.4	V	1,952.8	976.9	1,935.8	1,934.8	15
10	1,165.5	583.3		1,147.5	Y	1,853.7	927.4	1,836.7	1,835.7	14
11	1,294.6	647.8		1,276.5	E	1,690.7	845.8	1,673.6	1,672.7	13
12	1,461.5	731.3		1,443.5	S+80	1,561.6	781.3	1,544.6	1,543.6	12
13	1,558.6	779.8		1,540.6	P	1,394.6	697.8	1,377.6	1,376.6	11
14	1,801.6	901.3		1,783.6	Y+80	1,297.6	649.3	1,280.6	1,279.6	10
15	1,872.7	936.8		1,854.7	A	1,054.6	527.8	1,037.5	1,036.5	9
16	1,987.7	994.4		1,969.7	D	983.5	492.3	966.5	965.5	8
17	2,084.7	1,042.9		2,066.7	P	868.5	434.7	851.5	850.5	7
18	2,213.8	1,107.4		2,195.8	E	771.4	386.2	754.4	753.4	6
19	2,342.8	1,171.9		2,324.8	E	642.4	321.7	625.4	624.4	5
20	2,455.9	1,228.5		2,437.9	I	513.4	257.2	496.3		4
21	2,612.0	1,306.5	2,595.0	2,594.0	R	400.3	200.6	383.2		3
22	2,709.1	1,355.0	2,692.0	2,691.1	P	244.2		227.1		2
23	2,855.2	1,428.1	2,838.2	2,837.2	K	147.1		130.1		1

Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(R)EALPmDTEVyESPyADPEEIRPK(E)	Mox, pY, pY	952.3952	2854.164	3	-0.006	53.5



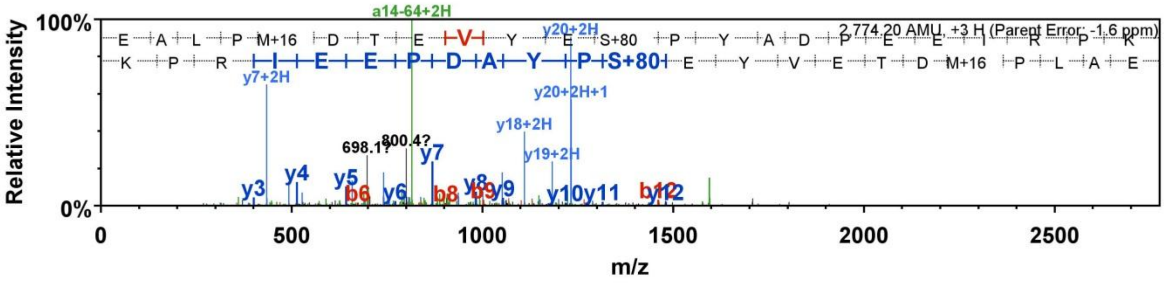
B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	2,855.2	1,428.1	2,838.2	2,837.2	23
2	201.1			183.1	A	2,726.1	1,363.6	2,709.1	2,708.1	22
3	314.2			296.2	L	2,655.1	1,328.1	2,638.1	2,637.1	21
4	411.2			393.2	P	2,542.0	1,271.5	2,525.0	2,524.0	20
5	558.3			540.2	M+16	2,445.0	1,223.0	2,427.9	2,427.0	19
6	673.3	337.1		655.3	D	2,297.9	1,149.5	2,280.9	2,279.9	18
7	774.3	387.7		756.3	T	2,182.9	1,092.0	2,165.9	2,164.9	17
8	903.4	452.2		885.4	E	2,081.9	1,041.4	2,064.8	2,063.8	16
9	1,002.4	501.7		984.4	V	1,952.8	976.9	1,935.8	1,934.8	15
10	1,245.5	623.2		1,227.5	Y+80	1,853.7	927.4	1,836.7	1,835.7	14
11	1,374.5	687.8		1,356.5	E	1,610.7	805.9	1,593.7	1,592.7	13
12	1,461.5	731.3		1,443.5	S	1,481.7	741.3	1,464.6	1,463.7	12
13	1,558.6	779.8		1,540.6	P	1,394.6	697.8	1,377.6	1,376.6	11
14	1,801.6	901.3		1,783.6	Y+80	1,297.6	649.3	1,280.6	1,279.6	10
15	1,872.7	936.8		1,854.7	A	1,054.6	527.8	1,037.5	1,036.5	9
16	1,987.7	994.4		1,969.7	D	983.5	492.3	966.5	965.5	8
17	2,084.7	1,042.9		2,066.7	P	868.5	434.7	851.5	850.5	7
18	2,213.8	1,107.4		2,195.8	E	771.4	386.2	754.4	753.4	6
19	2,342.8	1,171.9		2,324.8	E	642.4	321.7	625.4	624.4	5
20	2,455.9	1,228.5		2,437.9	I	513.4	257.2	496.3		4
21	2,612.0	1,306.5	2,595.0	2,594.0	R	400.3	200.6	383.2		3
22	2,709.1	1,355.0	2,692.0	2,691.1	P	244.2		227.1		2
23	2,855.2	1,428.1	2,838.2	2,837.2	K	147.1		130.1		1

Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(R)EALPmDTEVyESPYADPEEIRPK(E)	Mox, pY	925.7402	2774.199	3	-0.005	58.6



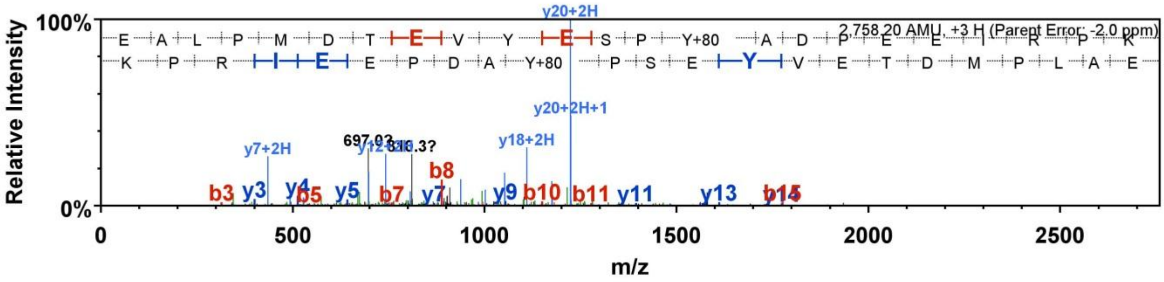
B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	2,775.2	1,388.1	2,758.2	2,757.2	23
2	201.1			183.1	A	2,646.2	1,323.6	2,629.1	2,628.2	22
3	314.2			296.2	L	2,575.1	1,288.1	2,558.1	2,557.1	21
4	411.2			393.2	P	2,462.0	1,231.5	2,445.0	2,444.0	20
5	558.3			540.2	M+16	2,365.0	1,183.0	2,348.0	2,347.0	19
6	673.3	337.1		655.3	D	2,218.0	1,109.5	2,200.9	2,199.9	18
7	774.3	387.7		756.3	T	2,102.9	1,052.0	2,085.9	2,084.9	17
8	903.4	452.2		885.4	E	2,001.9	1,001.4	1,984.9	1,983.9	16
9	1,002.4	501.7		984.4	V	1,872.8	936.9	1,855.8	1,854.8	15
10	1,245.5	623.2		1,227.5	Y+80	1,773.8	887.4	1,756.7	1,755.8	14
11	1,374.5	687.8		1,356.5	E	1,530.7	765.9	1,513.7	1,512.7	13
12	1,461.5	731.3		1,443.5	S	1,401.7	701.4	1,384.7	1,383.7	12
13	1,558.6	779.8		1,540.6	P	1,314.7	657.8	1,297.6	1,296.7	11
14	1,721.7	861.3		1,703.7	Y	1,217.6	609.3	1,200.6	1,199.6	10
15	1,792.7	896.9		1,774.7	A	1,054.6	527.8	1,037.5	1,036.5	9
16	1,907.7	954.4		1,889.7	D	983.5	492.3	966.5	965.5	8
17	2,004.8	1,002.9		1,986.8	P	868.5	434.7	851.5	850.5	7
18	2,133.8	1,067.4		2,115.8	E	771.4	386.2	754.4	753.4	6
19	2,262.9	1,131.9		2,244.9	E	642.4	321.7	625.4	624.4	5
20	2,376.0	1,188.5		2,357.9	I	513.4	257.2	496.3		4
21	2,532.1	1,266.5	2,515.0	2,514.0	R	400.3	200.6	383.2		3
22	2,629.1	1,315.1	2,612.1	2,611.1	P	244.2		227.1		2
23	2,775.2	1,388.1	2,758.2	2,757.2	K	147.1		130.1		1

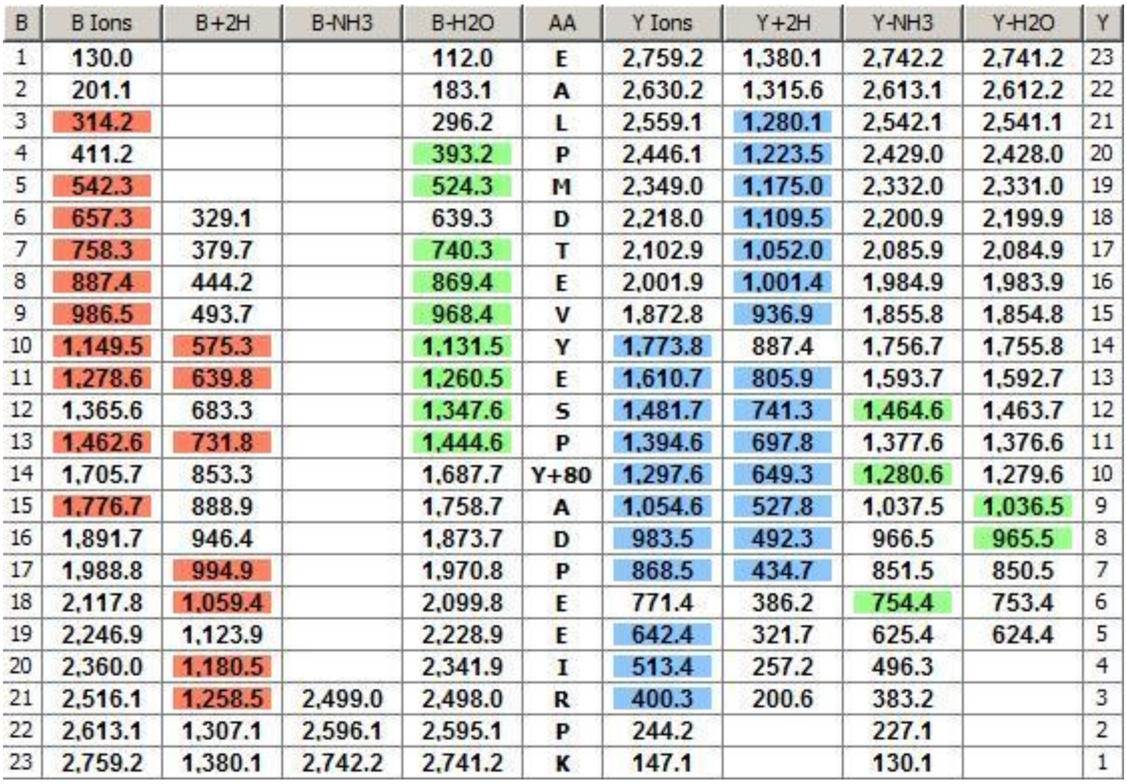
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(R)EALPmDTEVYEsPYADPEEIRPK(E)	Mox, pS	925.7404	2774.199	3	-0.004	61.4



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	2,775.2	1,388.1	2,758.2	2,757.2	23
2	201.1			183.1	A	2,646.2	1,323.6	2,629.1	2,628.2	22
3	314.2			296.2	L	2,575.1	1,288.1	2,558.1	2,557.1	21
4	411.2			393.2	P	2,462.0	1,231.5	2,445.0	2,444.0	20
5	558.3			540.2	M+16	2,365.0	1,183.0	2,348.0	2,347.0	19
6	673.3	337.1		655.3	D	2,218.0	1,109.5	2,200.9	2,199.9	18
7	774.3	387.7		756.3	T	2,102.9	1,052.0	2,085.9	2,084.9	17
8	903.4	452.2		885.4	E	2,001.9	1,001.4	1,984.9	1,983.9	16
9	1,002.4	501.7		984.4	V	1,872.8	936.9	1,855.8	1,854.8	15
10	1,165.5	583.3		1,147.5	Y	1,773.8	887.4	1,756.7	1,755.8	14
11	1,294.6	647.8		1,276.5	E	1,610.7	805.9	1,593.7	1,592.7	13
12	1,461.5	731.3		1,443.5	S+80	1,481.7	741.3	1,464.6	1,463.7	12
13	1,558.6	779.8		1,540.6	P	1,314.7	657.8	1,297.6	1,296.7	11
14	1,721.7	861.3		1,703.7	Y	1,217.6	609.3	1,200.6	1,199.6	10
15	1,792.7	896.9		1,774.7	A	1,054.6	527.8	1,037.5	1,036.5	9
16	1,907.7	954.4		1,889.7	D	983.5	492.3	966.5	965.5	8
17	2,004.8	1,002.9		1,986.8	P	868.5	434.7	851.5	850.5	7
18	2,133.8	1,067.4		2,115.8	E	771.4	386.2	754.4	753.4	6
19	2,262.9	1,131.9		2,244.9	E	642.4	321.7	625.4	624.4	5
20	2,376.0	1,188.5		2,357.9	I	513.4	257.2	496.3		4
21	2,532.1	1,266.5	2,515.0	2,514.0	R	400.3	200.6	383.2		3
22	2,629.1	1,315.1	2,612.1	2,611.1	P	244.2		227.1		2
23	2,775.2	1,388.1	2,758.2	2,757.2	K	147.1		130.1		1

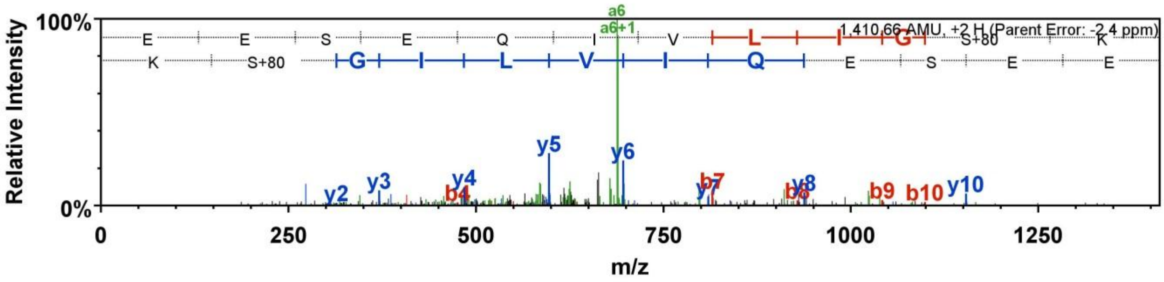
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(R)EALPMDTEVYESPyADPEEIRPK(E)	pY	920.4084	2758.203	3	-0.005	72.4





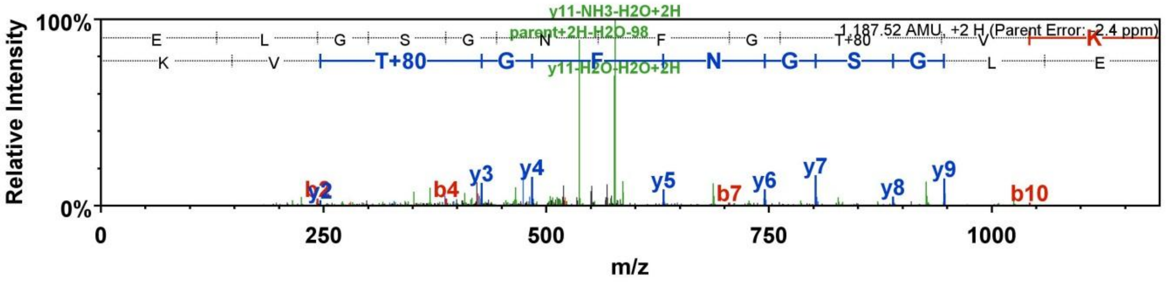
B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	2,759.2	1,380.1	2,742.2	2,741.2	23
2	201.1			183.1	A	2,630.2	1,315.6	2,613.1	2,612.2	22
3	314.2			296.2	L	2,559.1	1,280.1	2,542.1	2,541.1	21
4	411.2			393.2	P	2,446.1	1,223.5	2,429.0	2,428.0	20
5	542.3			524.3	M	2,349.0	1,175.0	2,332.0	2,331.0	19
6	657.3	329.1		639.3	D	2,218.0	1,109.5	2,200.9	2,199.9	18
7	758.3	379.7		740.3	T	2,102.9	1,052.0	2,085.9	2,084.9	17
8	887.4	444.2		869.4	E	2,001.9	1,001.4	1,984.9	1,983.9	16
9	986.5	493.7		968.4	V	1,872.8	936.9	1,855.8	1,854.8	15
10	1,149.5	575.3		1,131.5	Y	1,773.8	887.4	1,756.7	1,755.8	14
11	1,278.6	639.8		1,260.5	E	1,610.7	805.9	1,593.7	1,592.7	13
12	1,365.6	683.3		1,347.6	S	1,481.7	741.3	1,464.6	1,463.7	12
13	1,462.6	731.8		1,444.6	P	1,394.6	697.8	1,377.6	1,376.6	11
14	1,705.7	853.3		1,687.7	Y+80	1,297.6	649.3	1,280.6	1,279.6	10
15	1,776.7	888.9		1,758.7	A	1,054.6	527.8	1,037.5	1,036.5	9
16	1,891.7	946.4		1,873.7	D	983.5	492.3	966.5	965.5	8
17	1,988.8	994.9		1,970.8	P	868.5	434.7	851.5	850.5	7
18	2,117.8	1,059.4		2,099.8	E	771.4	386.2	754.4	753.4	6
19	2,246.9	1,123.9		2,228.9	E	642.4	321.7	625.4	624.4	5
20	2,360.0	1,180.5		2,341.9	I	513.4	257.2	496.3		4
21	2,516.1	1,258.5	2,499.0	2,498.0	R	400.3	200.6	383.2		3
22	2,613.1	1,307.1	2,596.1	2,595.1	P	244.2		227.1		2
23	2,759.2	1,380.1	2,742.2	2,741.2	K	147.1		130.1		1

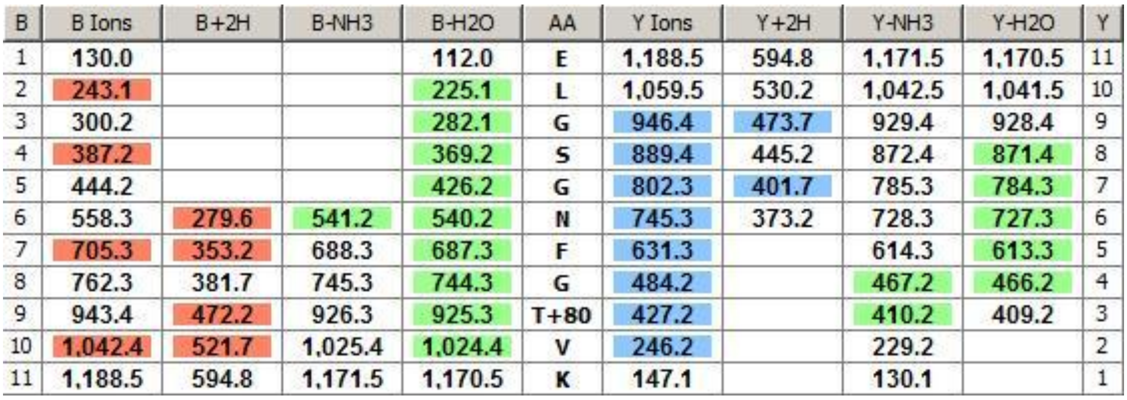
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(R)EESEQIVLIGsK(T)	pS	706.3378	1410.661	2	-0.003	30.3



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	1,411.7	706.3	1,394.6	1,393.7	12
2	259.1			241.1	E	1,282.6	641.8	1,265.6	1,264.6	11
3	346.1			328.1	S	1,153.6	577.3	1,136.6	1,135.6	10
4	475.2			457.2	E	1,066.6	533.8	1,049.5	1,048.5	9
5	603.2		586.2	585.2	Q	937.5	469.3	920.5	919.5	8
6	716.3	358.7	699.3	698.3	I	809.5	405.2	792.4	791.4	7
7	815.4	408.2	798.4	797.4	V	696.4	348.7	679.3	678.4	6
8	928.5	464.7	911.4	910.5	L	597.3		580.3	579.3	5
9	1,041.5	521.3	1,024.5	1,023.5	I	484.2		467.2	466.2	4
10	1,098.6	549.8	1,081.5	1,080.6	G	371.1		354.1	353.1	3
11	1,265.6	633.3	1,248.5	1,247.6	S+80	314.1		297.1	296.1	2
12	1,411.7	706.3	1,394.6	1,393.7	K	147.1		130.1		1

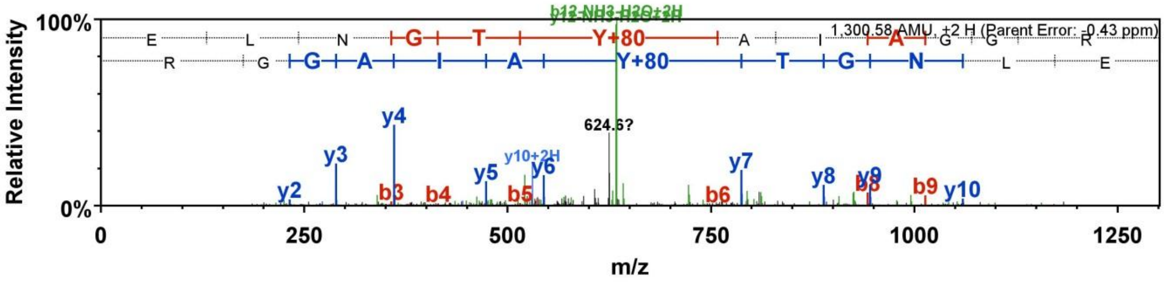
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(K)ELGSGNFGtVK(K)	pT	594.7671	1187.520	2	-0.003	35.4





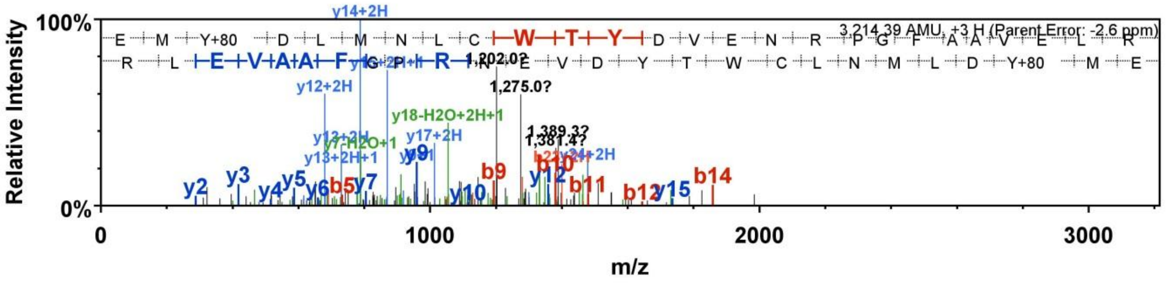
B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	1,188.5	594.8	1,171.5	1,170.5	11
2	243.1			225.1	L	1,059.5	530.2	1,042.5	1,041.5	10
3	300.2			282.1	G	946.4	473.7	929.4	928.4	9
4	387.2			369.2	S	889.4	445.2	872.4	871.4	8
5	444.2			426.2	G	802.3	401.7	785.3	784.3	7
6	558.3	279.6	541.2	540.2	N	745.3	373.2	728.3	727.3	6
7	705.3	353.2	688.3	687.3	F	631.3		614.3	613.3	5
8	762.3	381.7	745.3	744.3	G	484.2		467.2	466.2	4
9	943.4	472.2	926.3	925.3	T+80	427.2		410.2	409.2	3
10	1,042.4	521.7	1,025.4	1,024.4	V	246.2		229.2		2
11	1,188.5	594.8	1,171.5	1,170.5	K	147.1		130.1		1

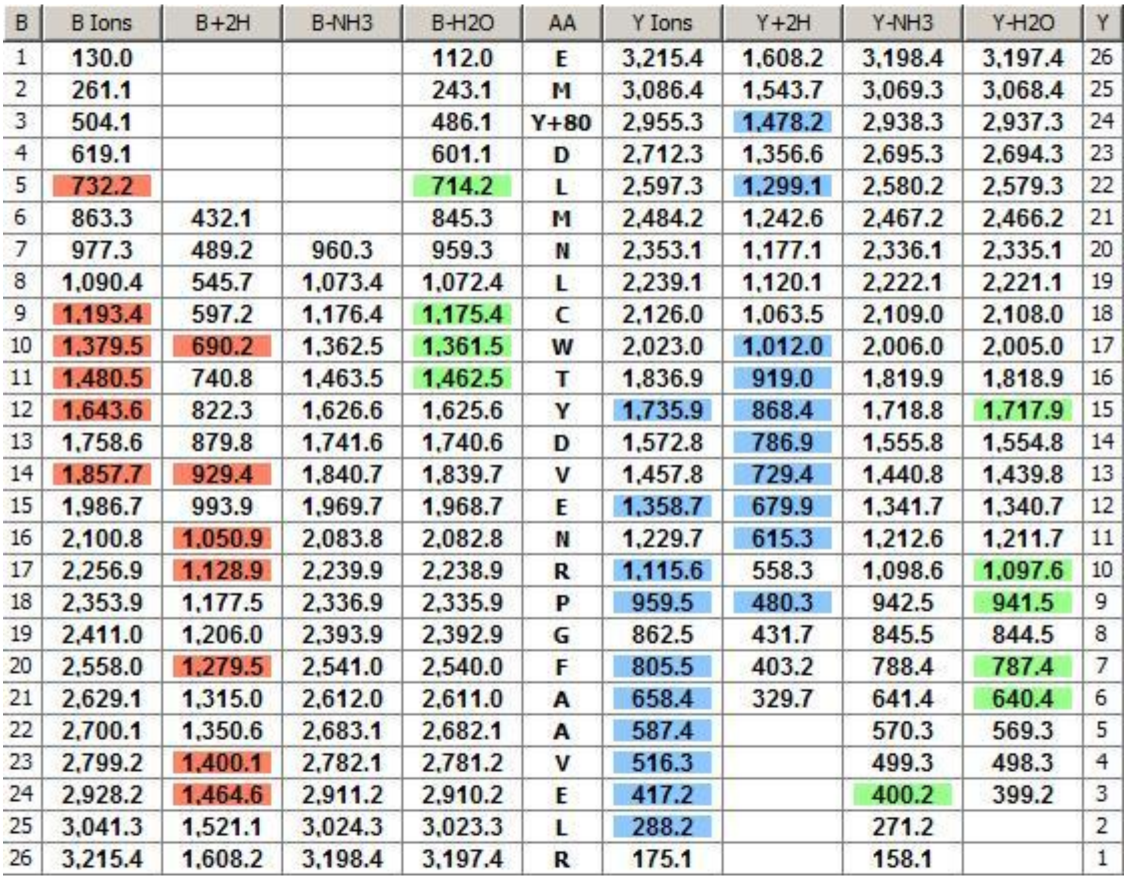
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(R)ELNGTyAIAGGR(T)	pY	651.2977	1300.581	2	-0.001	53.7



B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	1,301.6	651.3	1,284.6	1,283.6	12
2	243.1			225.1	L	1,172.5	586.8	1,155.5	1,154.5	11
3	357.2		340.2	339.2	N	1,059.5	530.2	1,042.4	1,041.5	10
4	414.2		397.2	396.2	G	945.4	473.2	928.4	927.4	9
5	515.2		498.2	497.2	T	888.4	444.7	871.4	870.4	8
6	758.3	379.6	741.2	740.3	Y+80	787.3	394.2	770.3		7
7	829.3	415.2	812.3	811.3	A	544.3	272.7	527.3		6
8	942.4	471.7	925.4	924.4	I	473.3		456.3		5
9	1,013.4	507.2	996.4	995.4	A	360.2		343.2		4
10	1,070.5	535.7	1,053.4	1,052.4	G	289.2		272.1		3
11	1,127.5	564.2	1,110.5	1,109.5	G	232.1		215.1		2
12	1,301.6	651.3	1,284.6	1,283.6	R	175.1		158.1		1

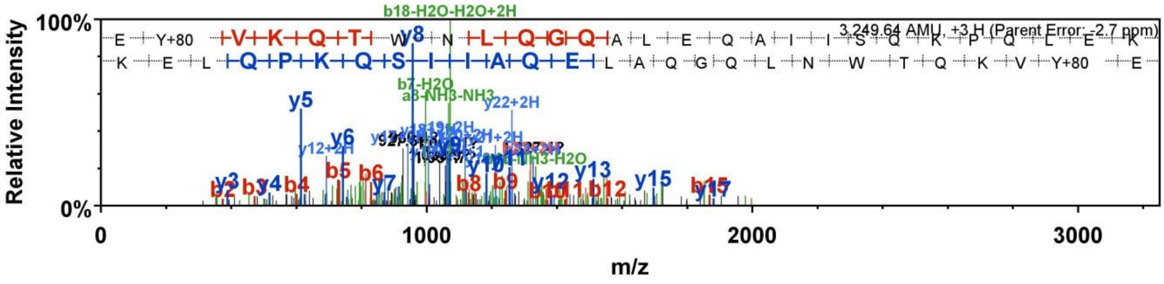
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(R)EMyDLMNLCWTYDVENRPGFAAVELR(L)	pY	1072.4700	3214.388	3	-0.008	29.3

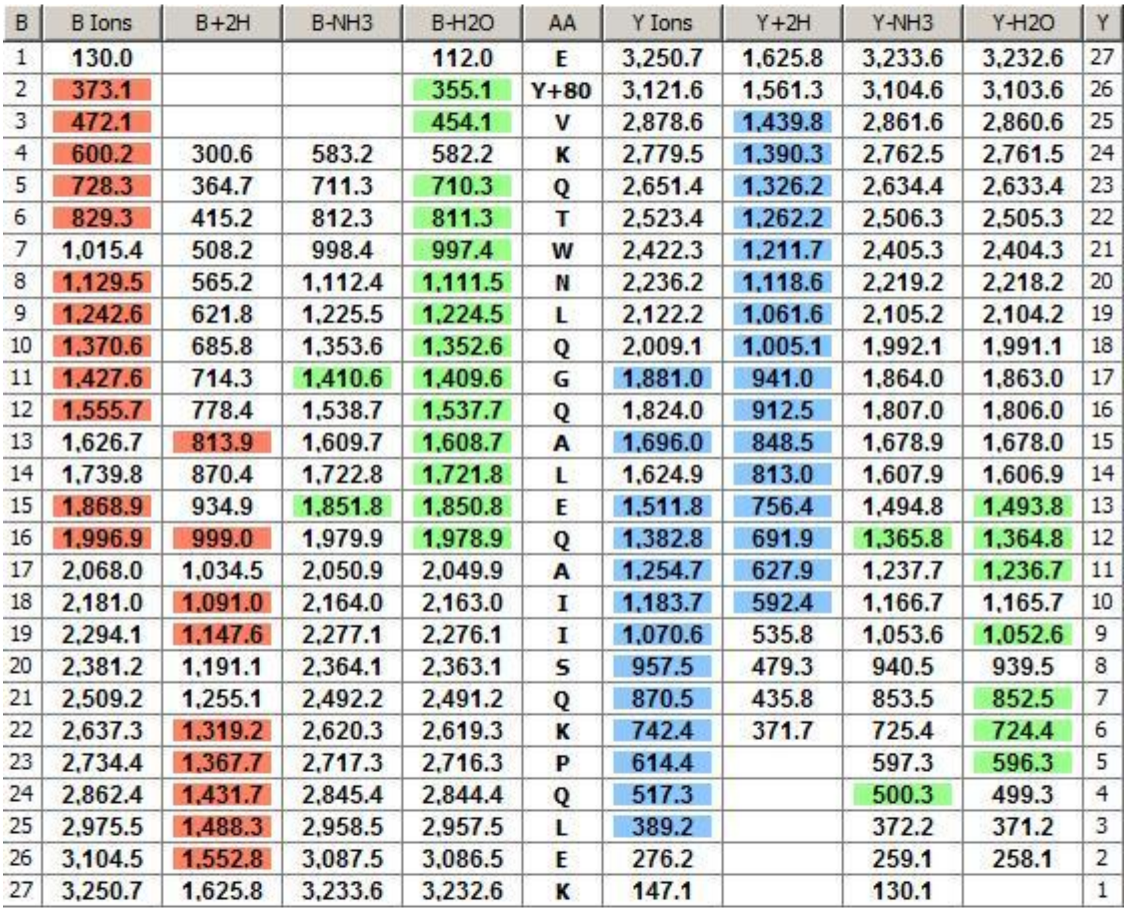




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	3,215.4	1,608.2	3,198.4	3,197.4	26
2	261.1			243.1	M	3,086.4	1,543.7	3,069.3	3,068.4	25
3	504.1			486.1	Y+80	2,955.3	1,478.2	2,938.3	2,937.3	24
4	619.1			601.1	D	2,712.3	1,356.6	2,695.3	2,694.3	23
5	732.2			714.2	L	2,597.3	1,299.1	2,580.2	2,579.3	22
6	863.3	432.1		845.3	M	2,484.2	1,242.6	2,467.2	2,466.2	21
7	977.3	489.2	960.3	959.3	N	2,353.1	1,177.1	2,336.1	2,335.1	20
8	1,090.4	545.7	1,073.4	1,072.4	L	2,239.1	1,120.1	2,222.1	2,221.1	19
9	1,193.4	597.2	1,176.4	1,175.4	C	2,126.0	1,063.5	2,109.0	2,108.0	18
10	1,379.5	690.2	1,362.5	1,361.5	W	2,023.0	1,012.0	2,006.0	2,005.0	17
11	1,480.5	740.8	1,463.5	1,462.5	T	1,836.9	919.0	1,819.9	1,818.9	16
12	1,643.6	822.3	1,626.6	1,625.6	Y	1,735.9	868.4	1,718.8	1,717.9	15
13	1,758.6	879.8	1,741.6	1,740.6	D	1,572.8	786.9	1,555.8	1,554.8	14
14	1,857.7	929.4	1,840.7	1,839.7	V	1,457.8	729.4	1,440.8	1,439.8	13
15	1,986.7	993.9	1,969.7	1,968.7	E	1,358.7	679.9	1,341.7	1,340.7	12
16	2,100.8	1,050.9	2,083.8	2,082.8	N	1,229.7	615.3	1,212.6	1,211.7	11
17	2,256.9	1,128.9	2,239.9	2,238.9	R	1,115.6	558.3	1,098.6	1,097.6	10
18	2,353.9	1,177.5	2,336.9	2,335.9	P	959.5	480.3	942.5	941.5	9
19	2,411.0	1,206.0	2,393.9	2,392.9	G	862.5	431.7	845.5	844.5	8
20	2,558.0	1,279.5	2,541.0	2,540.0	F	805.5	403.2	788.4	787.4	7
21	2,629.1	1,315.0	2,612.0	2,611.0	A	658.4	329.7	641.4	640.4	6
22	2,700.1	1,350.6	2,683.1	2,682.1	A	587.4		570.3	569.3	5
23	2,799.2	1,400.1	2,782.1	2,781.2	V	516.3		499.3	498.3	4
24	2,928.2	1,464.6	2,911.2	2,910.2	E	417.2		400.2	399.2	3
25	3,041.3	1,521.1	3,024.3	3,023.3	L	288.2		271.2		2
26	3,215.4	1,608.2	3,198.4	3,197.4	R	175.1		158.1		1

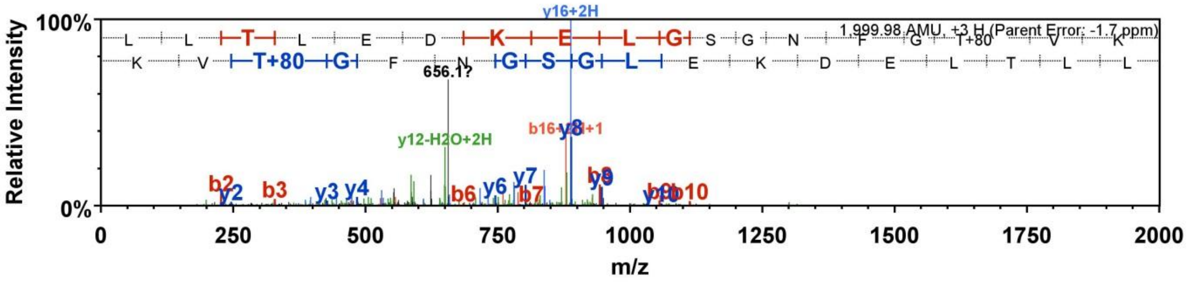
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(R)EyVKQTWNLQGQALEQAIISQKPQLEK(L)	pY	1084.2190	3249.635	3	-0.009	66.8

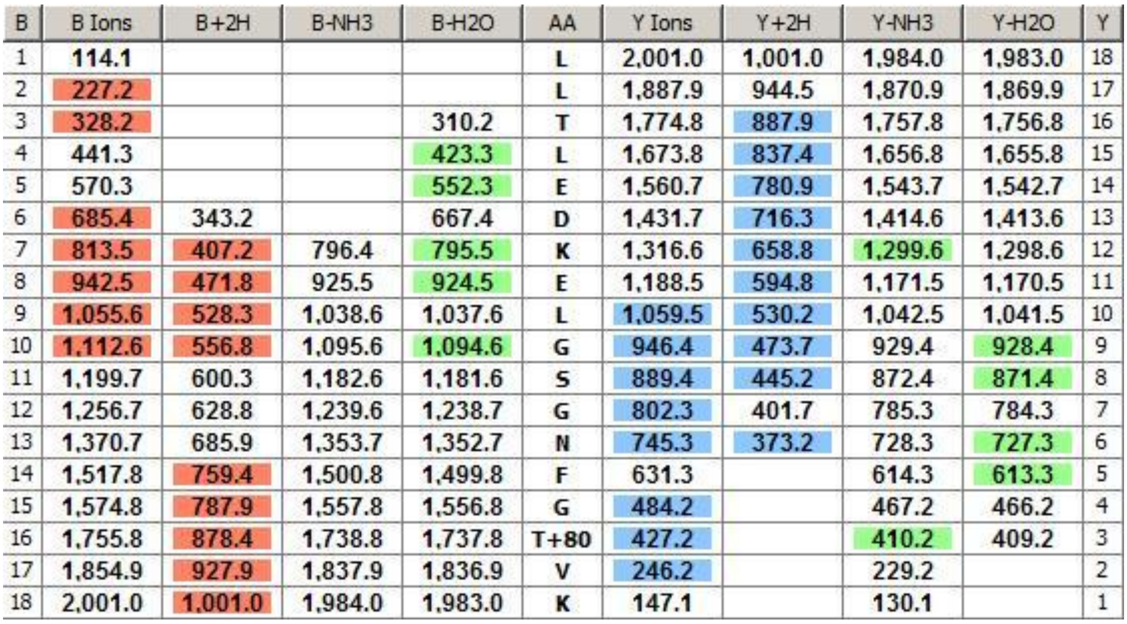




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	3,250.7	1,625.8	3,233.6	3,232.6	27
2	373.1			355.1	Y+80	3,121.6	1,561.3	3,104.6	3,103.6	26
3	472.1			454.1	V	2,878.6	1,439.8	2,861.6	2,860.6	25
4	600.2	300.6	583.2	582.2	K	2,779.5	1,390.3	2,762.5	2,761.5	24
5	728.3	364.7	711.3	710.3	Q	2,651.4	1,326.2	2,634.4	2,633.4	23
6	829.3	415.2	812.3	811.3	T	2,523.4	1,262.2	2,506.3	2,505.3	22
7	1,015.4	508.2	998.4	997.4	W	2,422.3	1,211.7	2,405.3	2,404.3	21
8	1,129.5	565.2	1,112.4	1,111.5	N	2,236.2	1,118.6	2,219.2	2,218.2	20
9	1,242.6	621.8	1,225.5	1,224.5	L	2,122.2	1,061.6	2,105.2	2,104.2	19
10	1,370.6	685.8	1,353.6	1,352.6	Q	2,009.1	1,005.1	1,992.1	1,991.1	18
11	1,427.6	714.3	1,410.6	1,409.6	G	1,881.0	941.0	1,864.0	1,863.0	17
12	1,555.7	778.4	1,538.7	1,537.7	Q	1,824.0	912.5	1,807.0	1,806.0	16
13	1,626.7	813.9	1,609.7	1,608.7	A	1,696.0	848.5	1,678.9	1,678.0	15
14	1,739.8	870.4	1,722.8	1,721.8	L	1,624.9	813.0	1,607.9	1,606.9	14
15	1,868.9	934.9	1,851.8	1,850.8	E	1,511.8	756.4	1,494.8	1,493.8	13
16	1,996.9	999.0	1,979.9	1,978.9	Q	1,382.8	691.9	1,365.8	1,364.8	12
17	2,068.0	1,034.5	2,050.9	2,049.9	A	1,254.7	627.9	1,237.7	1,236.7	11
18	2,181.0	1,091.0	2,164.0	2,163.0	I	1,183.7	592.4	1,166.7	1,165.7	10
19	2,294.1	1,147.6	2,277.1	2,276.1	I	1,070.6	535.8	1,053.6	1,052.6	9
20	2,381.2	1,191.1	2,364.1	2,363.1	S	957.5	479.3	940.5	939.5	8
21	2,509.2	1,255.1	2,492.2	2,491.2	Q	870.5	435.8	853.5	852.5	7
22	2,637.3	1,319.2	2,620.3	2,619.3	K	742.4	371.7	725.4	724.4	6
23	2,734.4	1,367.7	2,717.3	2,716.3	P	614.4		597.3	596.3	5
24	2,862.4	1,431.7	2,845.4	2,844.4	Q	517.3		500.3	499.3	4
25	2,975.5	1,488.3	2,958.5	2,957.5	L	389.2		372.2	371.2	3
26	3,104.5	1,552.8	3,087.5	3,086.5	E	276.2		259.1	258.1	2
27	3,250.7	1,625.8	3,233.6	3,232.6	K	147.1		130.1		1

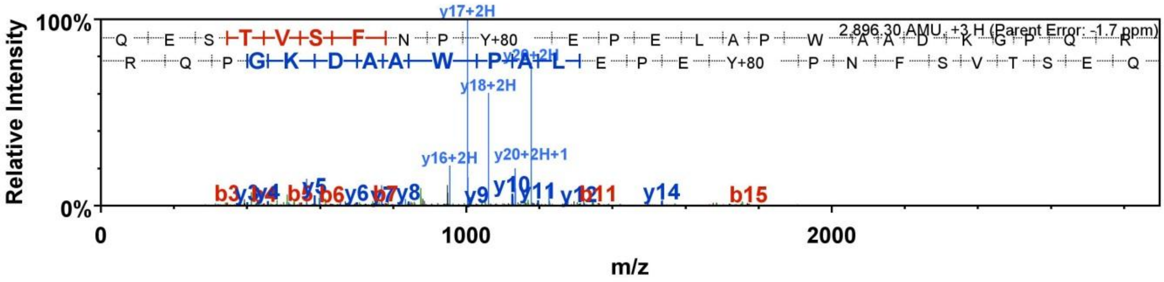
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(K)LLTLEDKELGSGNFGtVK(K)	pT	667.6685	1999.984	3	-0.003	43.6

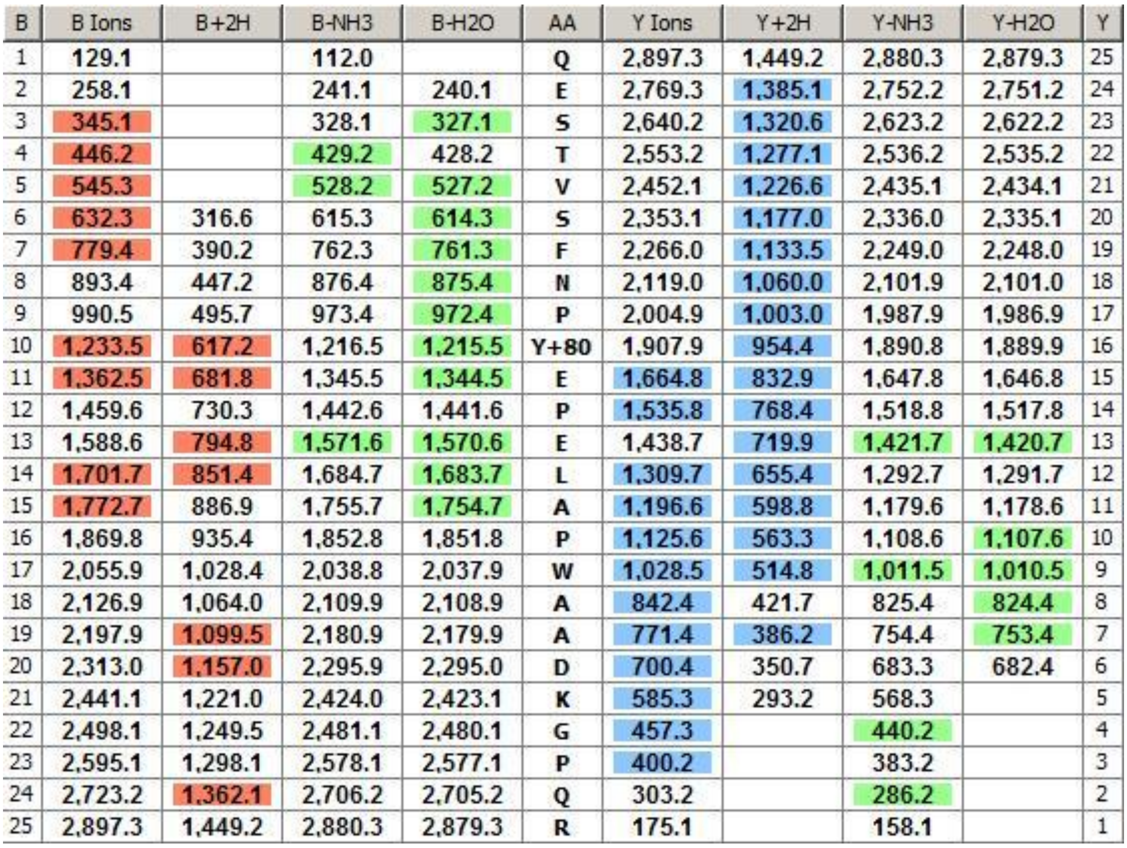




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	2,001.0	1,001.0	1,984.0	1,983.0	18
2	227.2				L	1,887.9	944.5	1,870.9	1,869.9	17
3	328.2			310.2	T	1,774.8	887.9	1,757.8	1,756.8	16
4	441.3			423.3	L	1,673.8	837.4	1,656.8	1,655.8	15
5	570.3			552.3	E	1,560.7	780.9	1,543.7	1,542.7	14
6	685.4	343.2		667.4	D	1,431.7	716.3	1,414.6	1,413.6	13
7	813.5	407.2	796.4	795.5	K	1,316.6	658.8	1,299.6	1,298.6	12
8	942.5	471.8	925.5	924.5	E	1,188.5	594.8	1,171.5	1,170.5	11
9	1,055.6	528.3	1,038.6	1,037.6	L	1,059.5	530.2	1,042.5	1,041.5	10
10	1,112.6	556.8	1,095.6	1,094.6	G	946.4	473.7	929.4	928.4	9
11	1,199.7	600.3	1,182.6	1,181.6	S	889.4	445.2	872.4	871.4	8
12	1,256.7	628.8	1,239.6	1,238.7	G	802.3	401.7	785.3	784.3	7
13	1,370.7	685.9	1,353.7	1,352.7	N	745.3	373.2	728.3	727.3	6
14	1,517.8	759.4	1,500.8	1,499.8	F	631.3		614.3	613.3	5
15	1,574.8	787.9	1,557.8	1,556.8	G	484.2		467.2	466.2	4
16	1,755.8	878.4	1,738.8	1,737.8	T+80	427.2		410.2	409.2	3
17	1,854.9	927.9	1,837.9	1,836.9	V	246.2		229.2		2
18	2,001.0	1,001.0	1,984.0	1,983.0	K	147.1		130.1		1

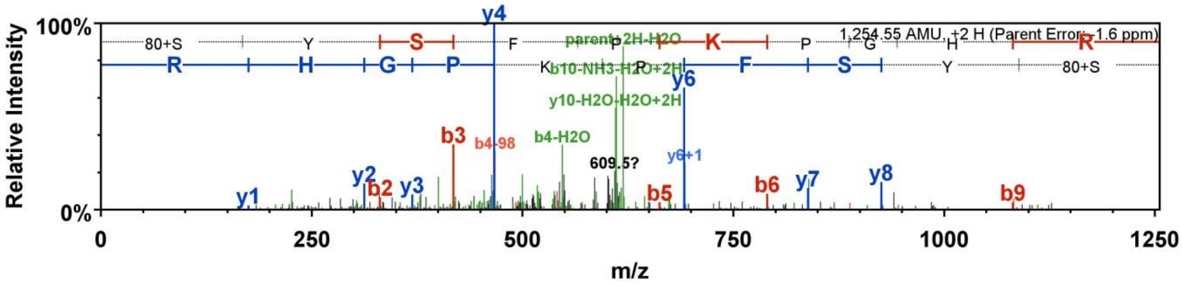
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(R)QESTVSFNPyEPELAPWAADKGPQR(E)	pY	966.4413	2896.302	3	-0.005	62.7

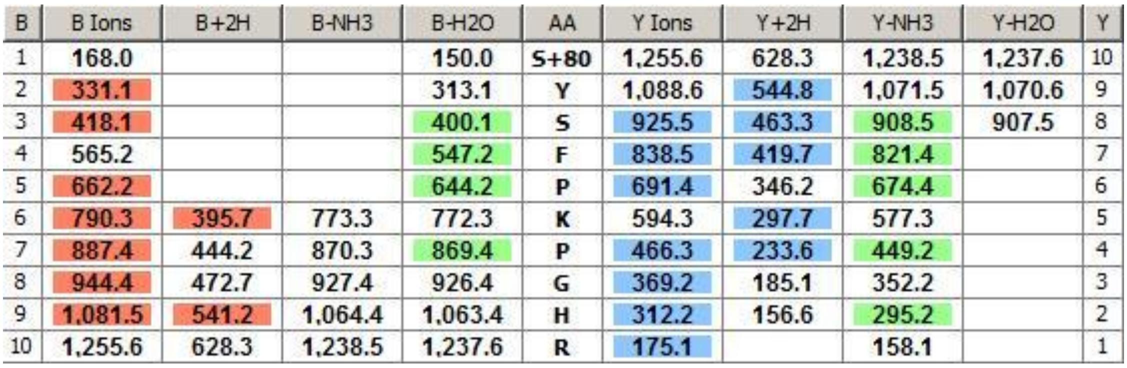




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	129.1		112.0		Q	2,897.3	1,449.2	2,880.3	2,879.3	25
2	258.1		241.1	240.1	E	2,769.3	1,385.1	2,752.2	2,751.2	24
3	345.1		328.1	327.1	S	2,640.2	1,320.6	2,623.2	2,622.2	23
4	446.2		429.2	428.2	T	2,553.2	1,277.1	2,536.2	2,535.2	22
5	545.3		528.2	527.2	V	2,452.1	1,226.6	2,435.1	2,434.1	21
6	632.3	316.6	615.3	614.3	S	2,353.1	1,177.0	2,336.0	2,335.1	20
7	779.4	390.2	762.3	761.3	F	2,266.0	1,133.5	2,249.0	2,248.0	19
8	893.4	447.2	876.4	875.4	N	2,119.0	1,060.0	2,101.9	2,101.0	18
9	990.5	495.7	973.4	972.4	P	2,004.9	1,003.0	1,987.9	1,986.9	17
10	1,233.5	617.2	1,216.5	1,215.5	Y+80	1,907.9	954.4	1,890.8	1,889.9	16
11	1,362.5	681.8	1,345.5	1,344.5	E	1,664.8	832.9	1,647.8	1,646.8	15
12	1,459.6	730.3	1,442.6	1,441.6	P	1,535.8	768.4	1,518.8	1,517.8	14
13	1,588.6	794.8	1,571.6	1,570.6	E	1,438.7	719.9	1,421.7	1,420.7	13
14	1,701.7	851.4	1,684.7	1,683.7	L	1,309.7	655.4	1,292.7	1,291.7	12
15	1,772.7	886.9	1,755.7	1,754.7	A	1,196.6	598.8	1,179.6	1,178.6	11
16	1,869.8	935.4	1,852.8	1,851.8	P	1,125.6	563.3	1,108.6	1,107.6	10
17	2,055.9	1,028.4	2,038.8	2,037.9	W	1,028.5	514.8	1,011.5	1,010.5	9
18	2,126.9	1,064.0	2,109.9	2,108.9	A	842.4	421.7	825.4	824.4	8
19	2,197.9	1,099.5	2,180.9	2,179.9	A	771.4	386.2	754.4	753.4	7
20	2,313.0	1,157.0	2,295.9	2,295.0	D	700.4	350.7	683.3	682.4	6
21	2,441.1	1,221.0	2,424.0	2,423.1	K	585.3	293.2	568.3		5
22	2,498.1	1,249.5	2,481.1	2,480.1	G	457.3		440.2		4
23	2,595.1	1,298.1	2,578.1	2,577.1	P	400.2		383.2		3
24	2,723.2	1,362.1	2,706.2	2,705.2	Q	303.2		286.2		2
25	2,897.3	1,449.2	2,880.3	2,879.3	R	175.1		158.1		1

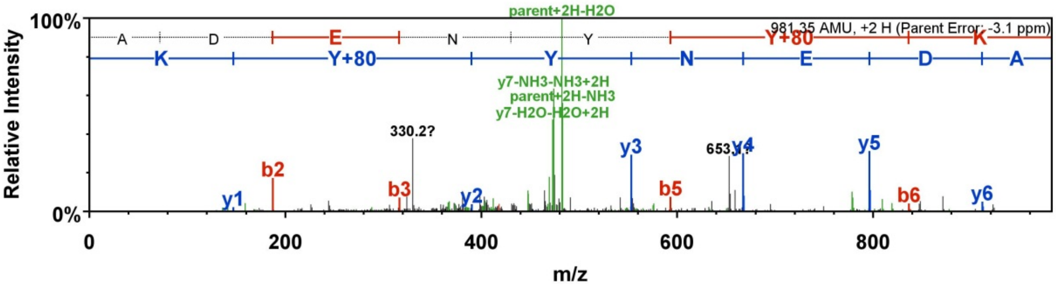
Sequence	Modification	Exp. m/z	Exp M.W.	Charge	Delta	Mascot Ion score
(K)sYSFPKPGHR(K)	pS	628.2836	1254.553	2	-0.002	30.2

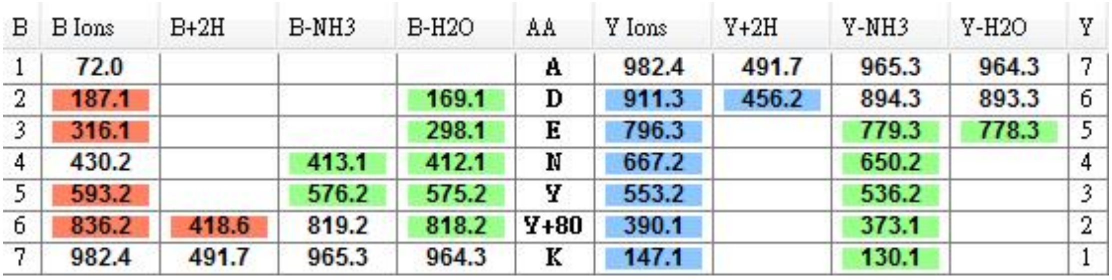




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	168.0			150.0	S+80	1,255.6	628.3	1,238.5	1,237.6	10
2	331.1			313.1	Y	1,088.6	544.8	1,071.5	1,070.6	9
3	418.1			400.1	S	925.5	463.3	908.5	907.5	8
4	565.2			547.2	F	838.5	419.7	821.4		7
5	662.2			644.2	P	691.4	346.2	674.4		6
6	790.3	395.7	773.3	772.3	K	594.3	297.7	577.3		5
7	887.4	444.2	870.3	869.4	P	466.3	233.6	449.2		4
8	944.4	472.7	927.4	926.4	G	369.2	185.1	352.2		3
9	1,081.5	541.2	1,064.4	1,063.4	H	312.2	156.6	295.2		2
10	1,255.6	628.3	1,238.5	1,237.6	R	175.1		158.1		1

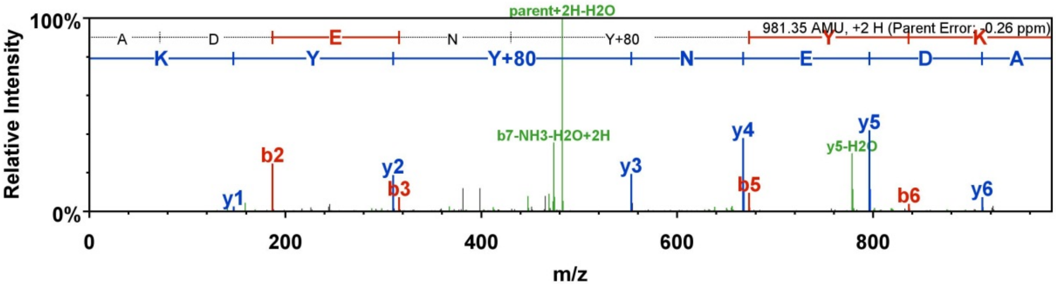
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
ADENY**Y**K	pY	491.6798	981.345	2	981.3481	-0.003	17.4

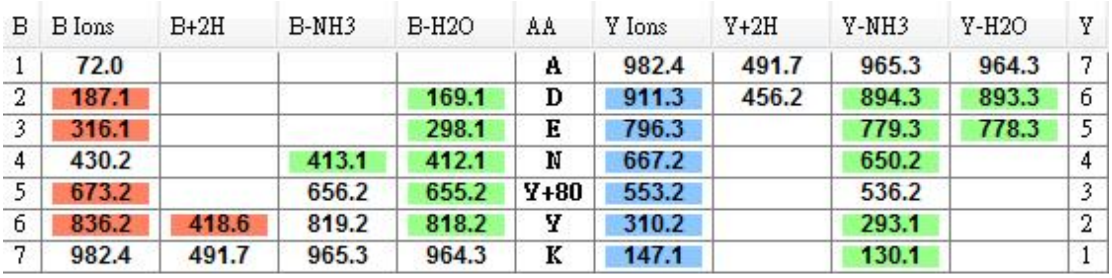




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	982.4	491.7	965.3	964.3	7
2	187.1			169.1	D	911.3	456.2	894.3	893.3	6
3	316.1			298.1	E	796.3		779.3	778.3	5
4	430.2		413.1	412.1	N	667.2		650.2		4
5	593.2		576.2	575.2	Y	553.2		536.2		3
6	836.2	418.6	819.2	818.2	Y+80	390.1		373.1		2
7	982.4	491.7	965.3	964.3	K	147.1		130.1		1

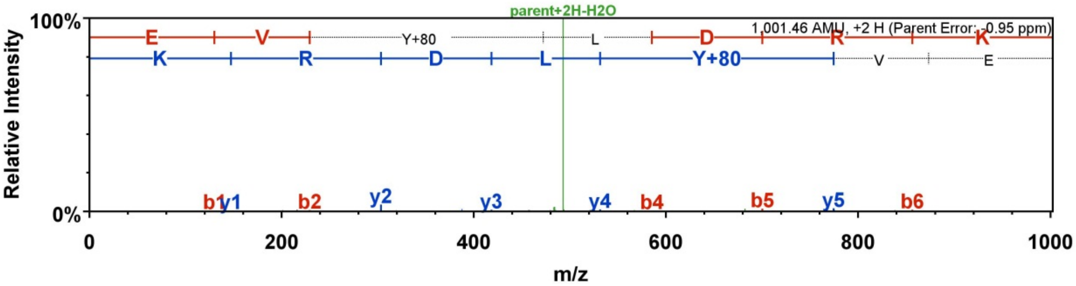
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
ADENYYK	pY	491.6812	981.3478	2	981.3481	-0.0002	38.99

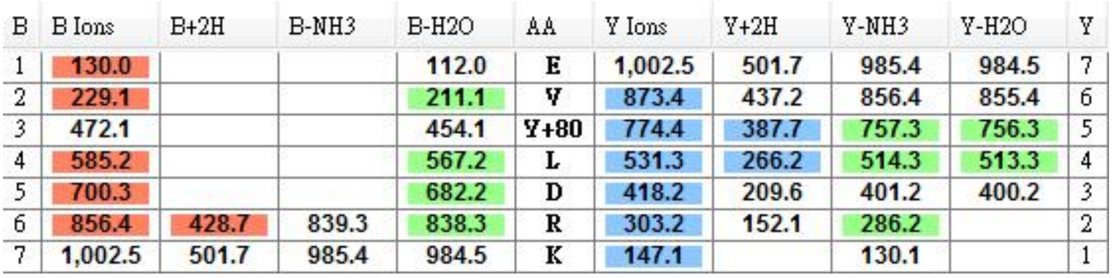




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	982.4	491.7	965.3	964.3	7
2	187.1			169.1	D	911.3	456.2	894.3	893.3	6
3	316.1			298.1	E	796.3		779.3	778.3	5
4	430.2		413.1	412.1	N	667.2		650.2		4
5	673.2		656.2	655.2	Y+80	553.2		536.2		3
6	836.2	418.6	819.2	818.2	Y	310.2		293.1		2
7	982.4	491.7	965.3	964.3	K	147.1		130.1		1

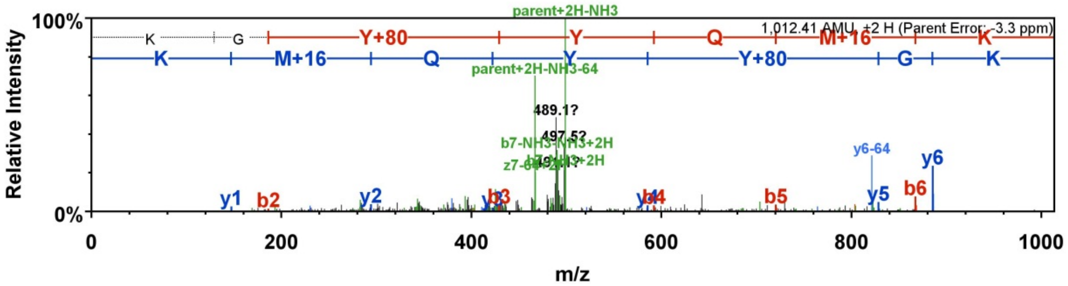
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
EV**Y**LDRK	pY	501.736	1001.4574	2	1001.4583	-0.0008	26.19

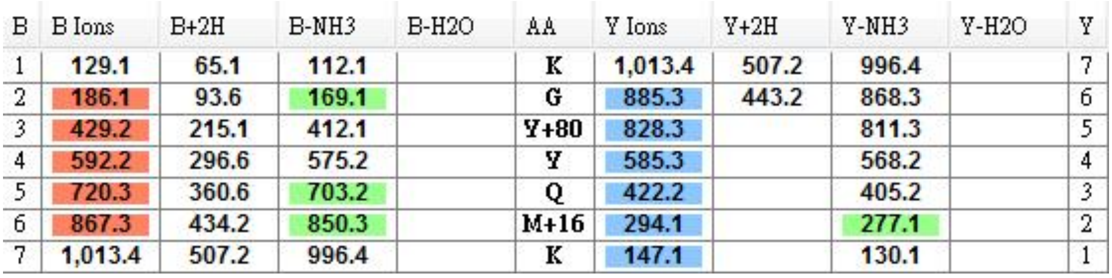




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	1,002.5	501.7	985.4	984.5	7
2	229.1			211.1	V	873.4	437.2	856.4	855.4	6
3	472.1			454.1	Y+80	774.4	387.7	757.3	756.3	5
4	585.2			567.2	L	531.3	266.2	514.3	513.3	4
5	700.3			682.2	D	418.2	209.6	401.2	400.2	3
6	856.4	428.7	839.3	838.3	R	303.2	152.1	286.2		2
7	1,002.5	501.7	985.4	984.5	K	147.1		130.1		1

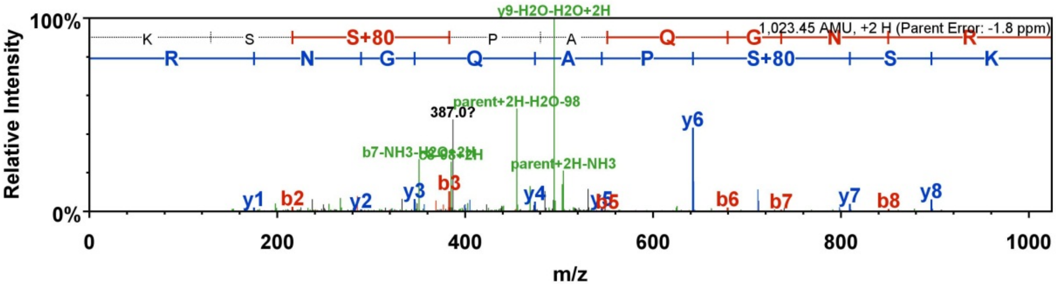
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
KGYYQMK	Mox; pY	507.2101	1012.4056	2	1012.4089	-0.0032	14.54

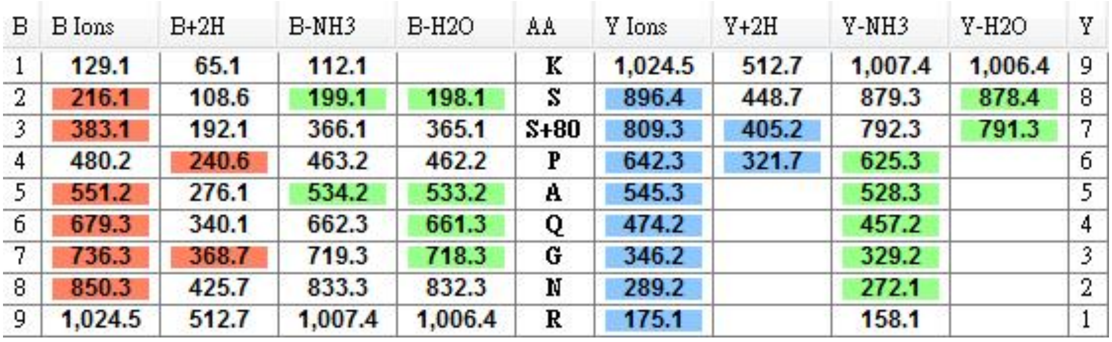




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	129.1	65.1	112.1		K	1,013.4	507.2	996.4		7
2	186.1	93.6	169.1		G	885.3	443.2	868.3		6
3	429.2	215.1	412.1		Y+80	828.3		811.3		5
4	592.2	296.6	575.2		Y	585.3		568.2		4
5	720.3	360.6	703.2		Q	422.2		405.2		3
6	867.3	434.2	850.3		M+16	294.1		277.1		2
7	1,013.4	507.2	996.4		K	147.1		130.1		1

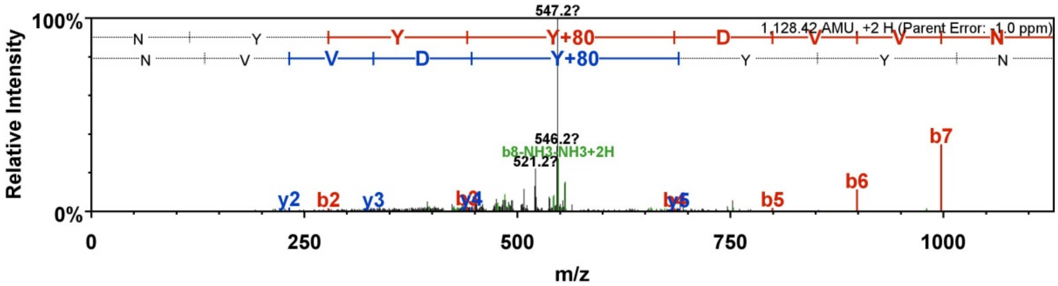
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
KSSPAQGNR	pS	512.7313	1023.448	2	1023.4498	-0.0018	21.24

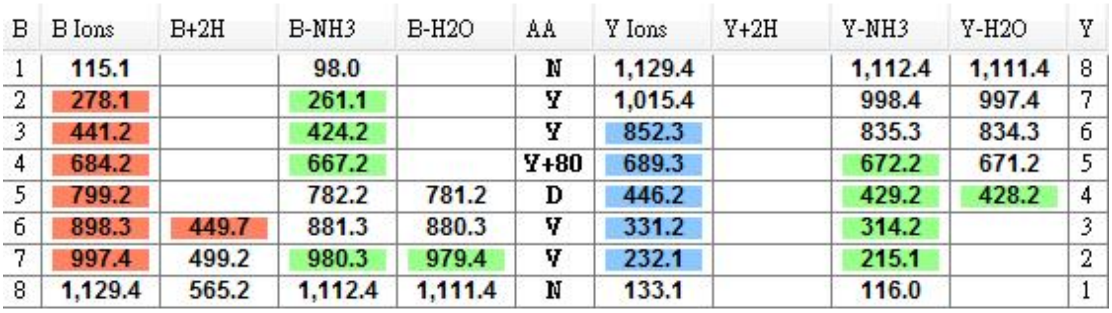




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	129.1	65.1	112.1		K	1,024.5	512.7	1,007.4	1,006.4	9
2	216.1	108.6	199.1	198.1	S	896.4	448.7	879.3	878.4	8
3	383.1	192.1	366.1	365.1	S+80	809.3	405.2	792.3	791.3	7
4	480.2	240.6	463.2	462.2	P	642.3	321.7	625.3		6
5	551.2	276.1	534.2	533.2	A	545.3		528.3		5
6	679.3	340.1	662.3	661.3	Q	474.2		457.2		4
7	736.3	368.7	719.3	718.3	G	346.2		329.2		3
8	850.3	425.7	833.3	832.3	N	289.2		272.1		2
9	1,024.5	512.7	1,007.4	1,006.4	R	175.1		158.1		1

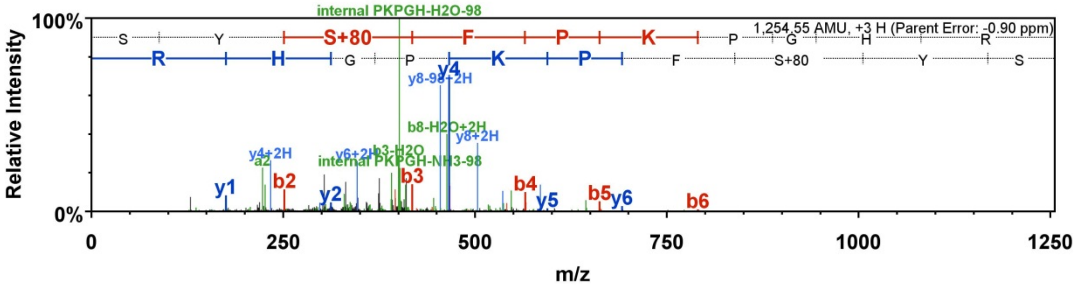
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
NyyyDVVN	pY	565.2149	1128.4152	2	1128.4165	-0.0012	10.88

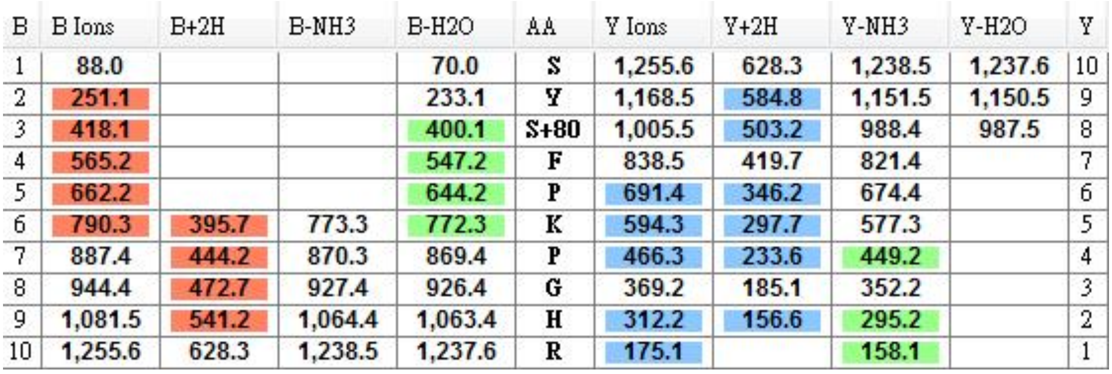




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	115.1		98.0		N	1,129.4		1,112.4	1,111.4	8
2	278.1		261.1		Y	1,015.4		998.4	997.4	7
3	441.2		424.2		Y	852.3		835.3	834.3	6
4	684.2		667.2		Y+80	689.3		672.2	671.2	5
5	799.2		782.2	781.2	D	446.2		429.2	428.2	4
6	898.3	449.7	881.3	880.3	V	331.2		314.2		3
7	997.4	499.2	980.3	979.4	V	232.1		215.1		2
8	1,129.4	565.2	1,112.4	1,111.4	N	133.1		116.0		1

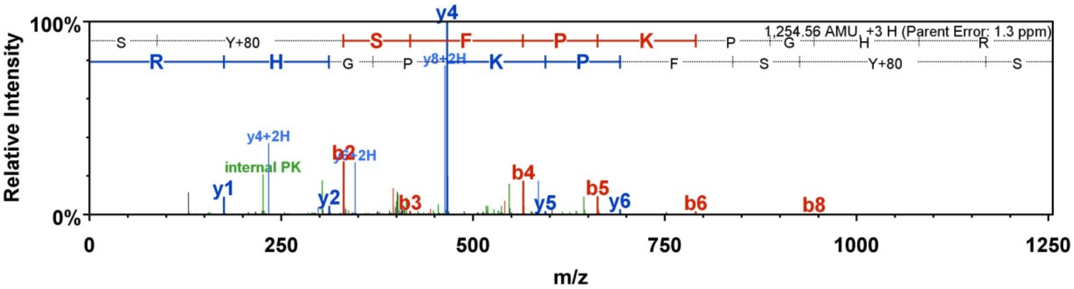
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
SY**S**FPKPGHR	pS	419.1918	1254.5536	3	1254.5547	-0.0011	19.84

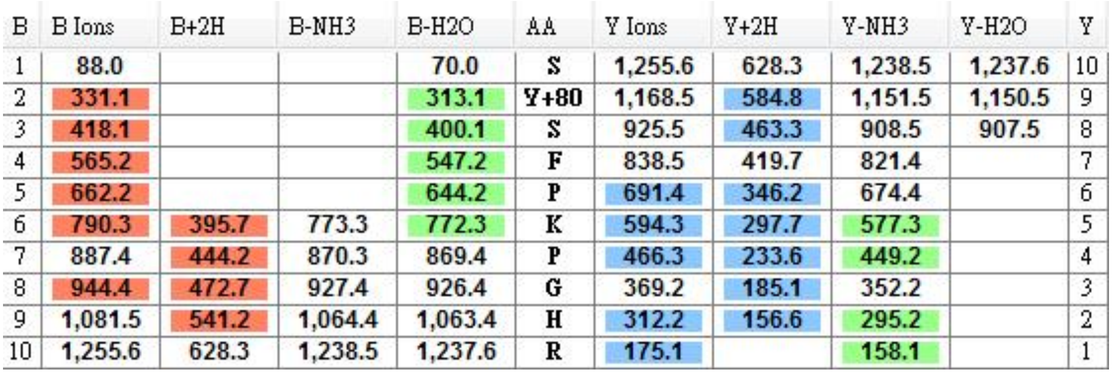




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	88.0			70.0	S	1,255.6	628.3	1,238.5	1,237.6	10
2	251.1			233.1	Y	1,168.5	584.8	1,151.5	1,150.5	9
3	418.1			400.1	S+80	1,005.5	503.2	988.4	987.5	8
4	565.2			547.2	F	838.5	419.7	821.4		7
5	662.2			644.2	P	691.4	346.2	674.4		6
6	790.3	395.7	773.3	772.3	K	594.3	297.7	577.3		5
7	887.4	444.2	870.3	869.4	P	466.3	233.6	449.2		4
8	944.4	472.7	927.4	926.4	G	369.2	185.1	352.2		3
9	1,081.5	541.2	1,064.4	1,063.4	H	312.2	156.6	295.2		2
10	1,255.6	628.3	1,238.5	1,237.6	R	175.1		158.1		1

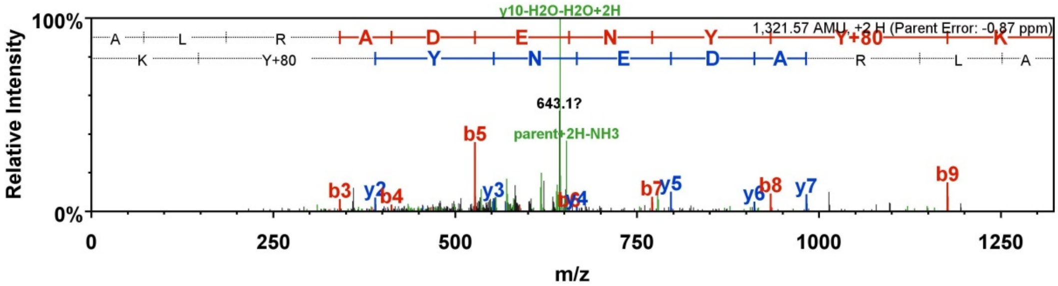
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
SYSFPKPGHR	pY	419.1927	1254.5563	3	1254.5547	0.0016	33.78

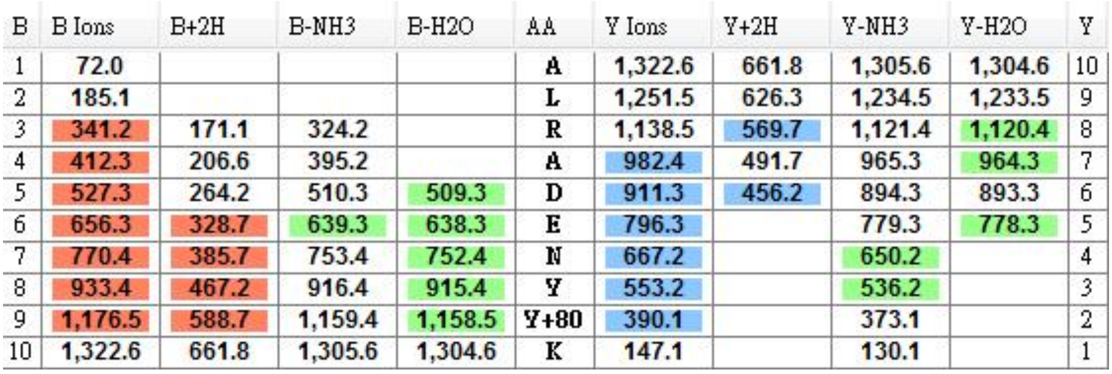




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	88.0			70.0	S	1,255.6	628.3	1,238.5	1,237.6	10
2	331.1			313.1	Y+80	1,168.5	584.8	1,151.5	1,150.5	9
3	418.1			400.1	S	925.5	463.3	908.5	907.5	8
4	565.2			547.2	F	838.5	419.7	821.4		7
5	662.2			644.2	P	691.4	346.2	674.4		6
6	790.3	395.7	773.3	772.3	K	594.3	297.7	577.3		5
7	887.4	444.2	870.3	869.4	P	466.3	233.6	449.2		4
8	944.4	472.7	927.4	926.4	G	369.2	185.1	352.2		3
9	1,081.5	541.2	1,064.4	1,063.4	H	312.2	156.6	295.2		2
10	1,255.6	628.3	1,238.5	1,237.6	R	175.1		158.1		1

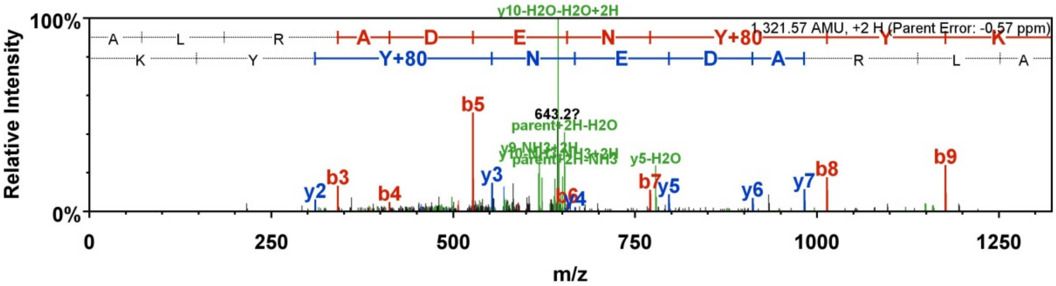
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
ALRADENY**Y**K	pY	661.7919	1321.5692	2	1321.5703	-0.0011	21.5

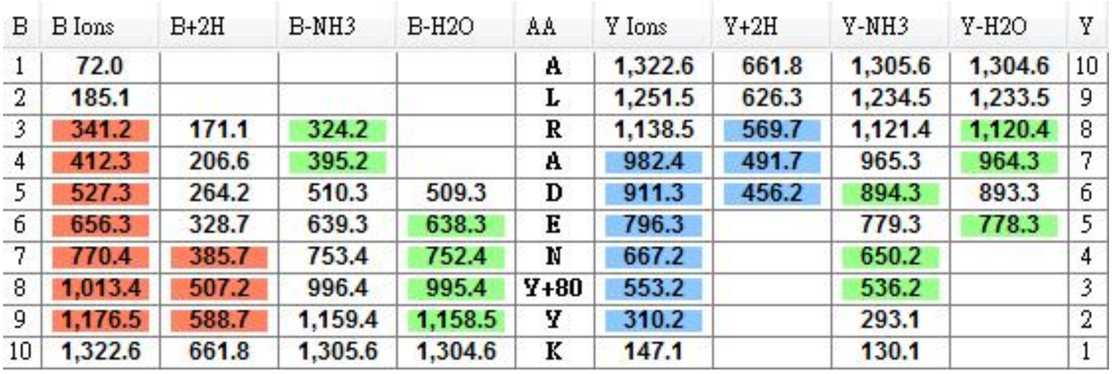




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1,322.6	661.8	1,305.6	1,304.6	10
2	185.1				L	1,251.5	626.3	1,234.5	1,233.5	9
3	341.2	171.1	324.2		R	1,138.5	569.7	1,121.4	1,120.4	8
4	412.3	206.6	395.2		A	982.4	491.7	965.3	964.3	7
5	527.3	264.2	510.3	509.3	D	911.3	456.2	894.3	893.3	6
6	656.3	328.7	639.3	638.3	E	796.3		779.3	778.3	5
7	770.4	385.7	753.4	752.4	N	667.2		650.2		4
8	933.4	467.2	916.4	915.4	Y	553.2		536.2		3
9	1,176.5	588.7	1,159.4	1,158.5	Y+80	390.1		373.1		2
10	1,322.6	661.8	1,305.6	1,304.6	K	147.1		130.1		1

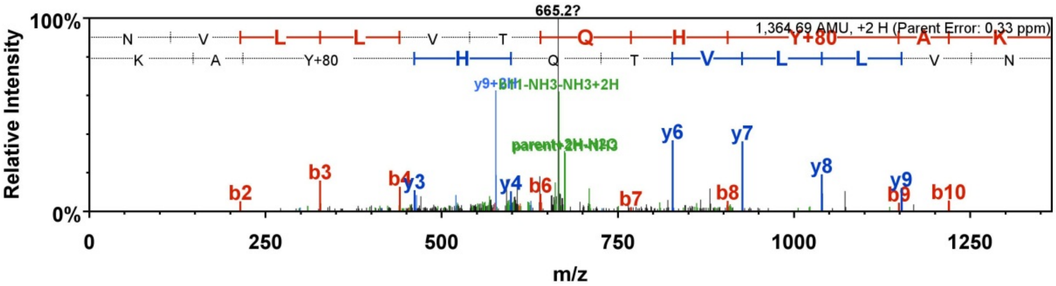
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
ALRADENYYK	pY	661.7921	1321.5696	2	1321.5703	-0.0007	30.3

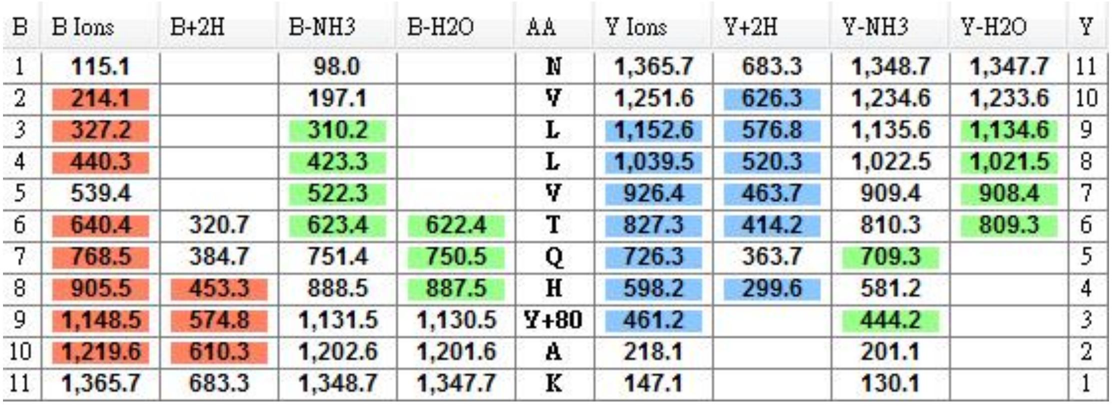




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1,322.6	661.8	1,305.6	1,304.6	10
2	185.1				L	1,251.5	626.3	1,234.5	1,233.5	9
3	341.2	171.1	324.2		R	1,138.5	569.7	1,121.4	1,120.4	8
4	412.3	206.6	395.2		A	982.4	491.7	965.3	964.3	7
5	527.3	264.2	510.3	509.3	D	911.3	456.2	894.3	893.3	6
6	656.3	328.7	639.3	638.3	E	796.3		779.3	778.3	5
7	770.4	385.7	753.4	752.4	N	667.2		650.2		4
8	1,013.4	507.2	996.4	995.4	Y+80	553.2		536.2		3
9	1,176.5	588.7	1,159.4	1,158.5	Y	310.2		293.1		2
10	1,322.6	661.8	1,305.6	1,304.6	K	147.1		130.1		1

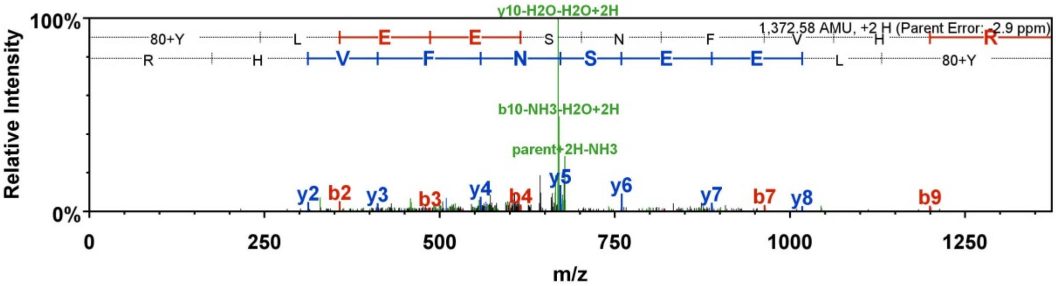
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
NVLLVTQHYAK	pY	683.3502	1364.6858	2	1364.6853	0.0005	33.17

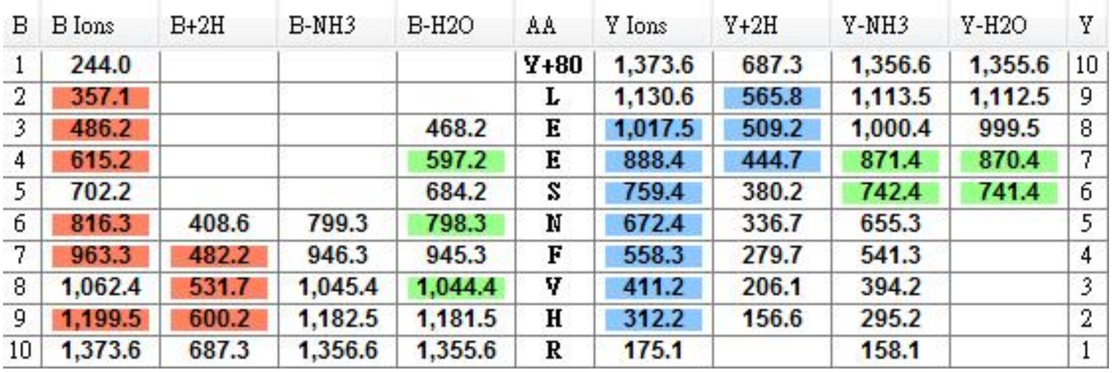




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	115.1		98.0		N	1,365.7	683.3	1,348.7	1,347.7	11
2	214.1		197.1		V	1,251.6	626.3	1,234.6	1,233.6	10
3	327.2		310.2		L	1,152.6	576.8	1,135.6	1,134.6	9
4	440.3		423.3		L	1,039.5	520.3	1,022.5	1,021.5	8
5	539.4		522.3		V	926.4	463.7	909.4	908.4	7
6	640.4	320.7	623.4	622.4	T	827.3	414.2	810.3	809.3	6
7	768.5	384.7	751.4	750.5	Q	726.3	363.7	709.3		5
8	905.5	453.3	888.5	887.5	H	598.2	299.6	581.2		4
9	1,148.5	574.8	1,131.5	1,130.5	Y+80	461.2		444.2		3
10	1,219.6	610.3	1,202.6	1,201.6	A	218.1		201.1		2
11	1,365.7	683.3	1,348.7	1,347.7	K	147.1		130.1		1

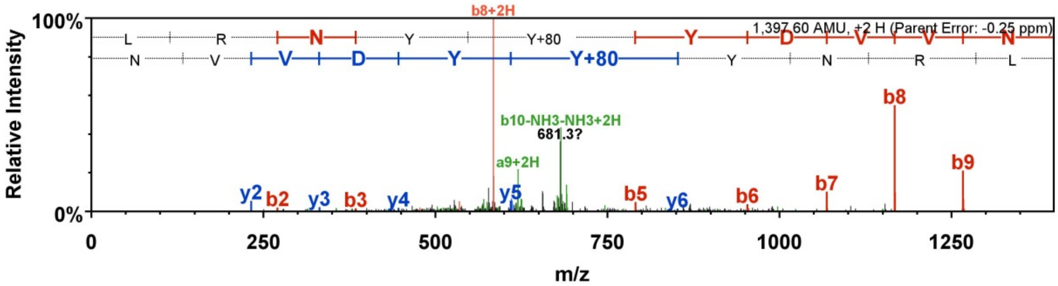
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
YLEESNFVHR	pY	687.2959	1372.5772	2	1372.5813	-0.004	18.66

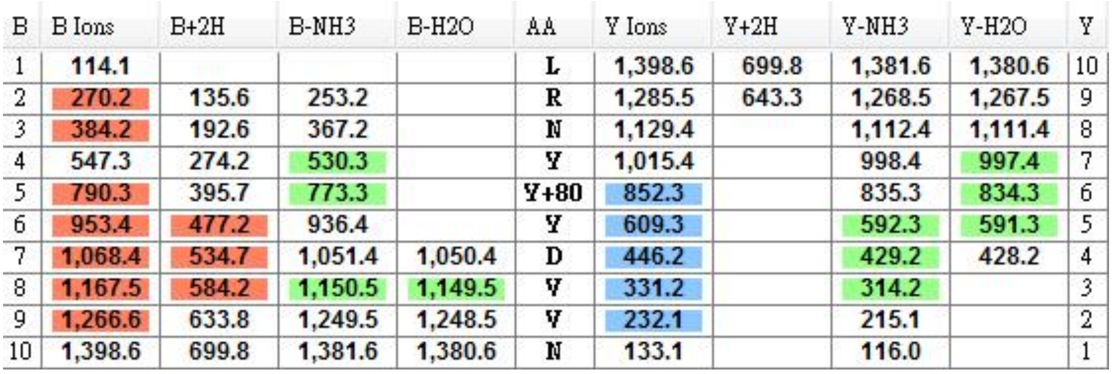




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	244.0				**Y+80**	1,373.6	687.3	1,356.6	1,355.6	10
2	357.1				**L**	1,130.6	565.8	1,113.5	1,112.5	9
3	486.2			468.2	**E**	1,017.5	509.2	1,000.4	999.5	8
4	615.2			597.2	**E**	888.4	444.7	871.4	870.4	7
5	702.2			684.2	**S**	759.4	380.2	742.4	741.4	6
6	816.3	408.6	799.3	798.3	**N**	672.4	336.7	655.3		5
7	963.3	482.2	946.3	945.3	**F**	558.3	279.7	541.3		4
8	1,062.4	531.7	1,045.4	1,044.4	**V**	411.2	206.1	394.2		3
9	1,199.5	600.2	1,182.5	1,181.5	**H**	312.2	156.6	295.2		2
10	1,373.6	687.3	1,356.6	1,355.6	**R**	175.1		158.1		1

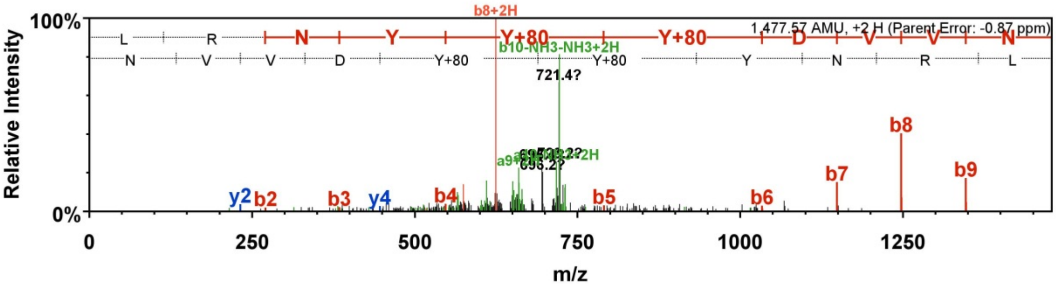
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
LRNYYYDVVN	pY	699.8079	1397.6012	2	1397.6017	-0.0004	32.61

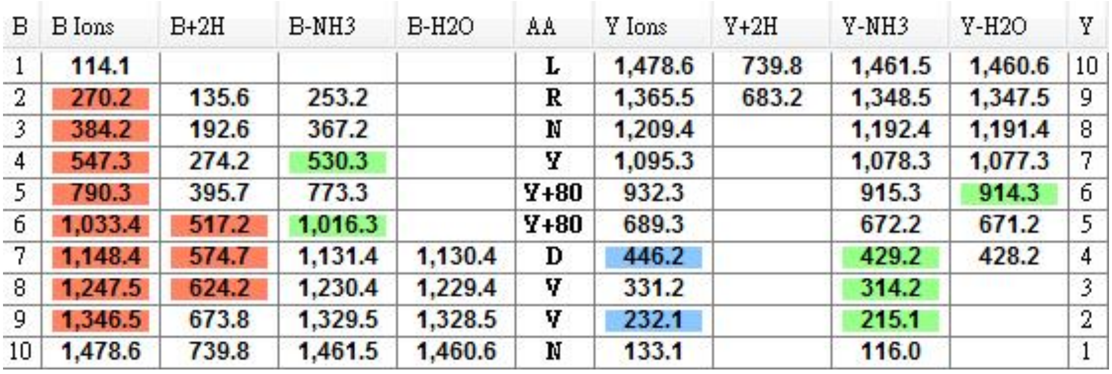




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1,398.6	699.8	1,381.6	1,380.6	10
2	270.2	135.6	253.2		R	1,285.5	643.3	1,268.5	1,267.5	9
3	384.2	192.6	367.2		N	1,129.4		1,112.4	1,111.4	8
4	547.3	274.2	530.3		Y	1,015.4		998.4	997.4	7
5	790.3	395.7	773.3		Y+80	852.3		835.3	834.3	6
6	953.4	477.2	936.4		Y	609.3		592.3	591.3	5
7	1,068.4	534.7	1,051.4	1,050.4	D	446.2		429.2	428.2	4
8	1,167.5	584.2	1,150.5	1,149.5	V	331.2		314.2		3
9	1,266.6	633.8	1,249.5	1,248.5	V	232.1		215.1		2
10	1,398.6	699.8	1,381.6	1,380.6	N	133.1		116.0		1

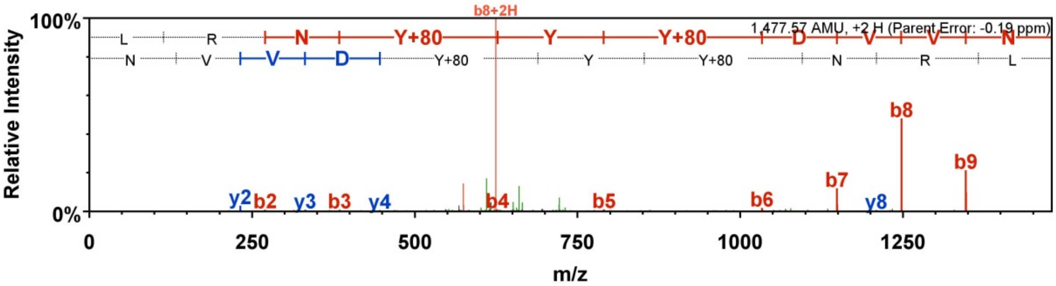
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
LRNY<u>YY</u>DVVN	2 pY	739.7906	1477.5666	2	1477.568	-0.0013	10.17

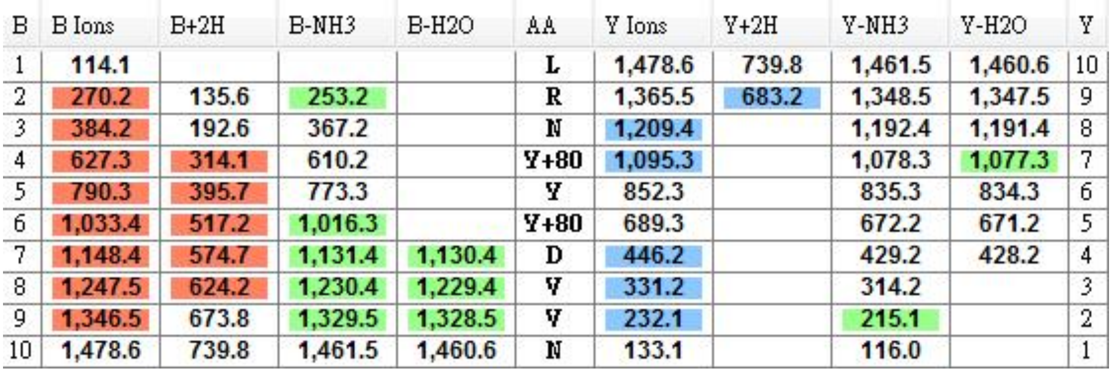




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1,478.6	739.8	1,461.5	1,460.6	10
2	270.2	135.6	253.2		R	1,365.5	683.2	1,348.5	1,347.5	9
3	384.2	192.6	367.2		N	1,209.4		1,192.4	1,191.4	8
4	547.3	274.2	530.3		Y	1,095.3		1,078.3	1,077.3	7
5	790.3	395.7	773.3		Y+80	932.3		915.3	914.3	6
6	1,033.4	517.2	1,016.3		Y+80	689.3		672.2	671.2	5
7	1,148.4	574.7	1,131.4	1,130.4	D	446.2		429.2	428.2	4
8	1,247.5	624.2	1,230.4	1,229.4	V	331.2		314.2		3
9	1,346.5	673.8	1,329.5	1,328.5	V	232.1		215.1		2
10	1,478.6	739.8	1,461.5	1,460.6	N	133.1		116.0		1

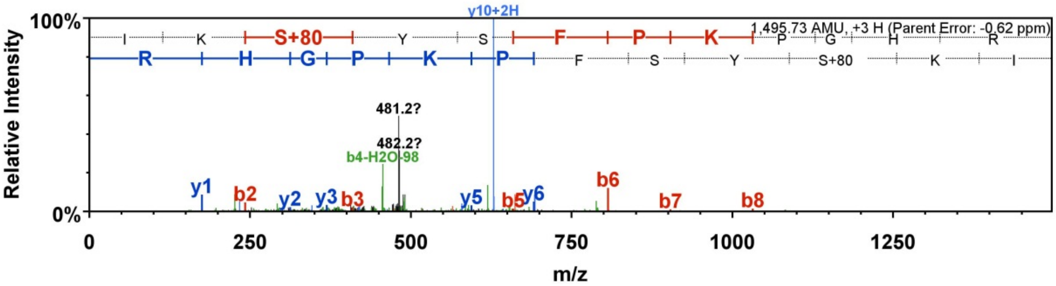
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
LRNYYYDVVN	2 pY	739.7911	1477.5676	2	1477.568	-0.0003	21.12

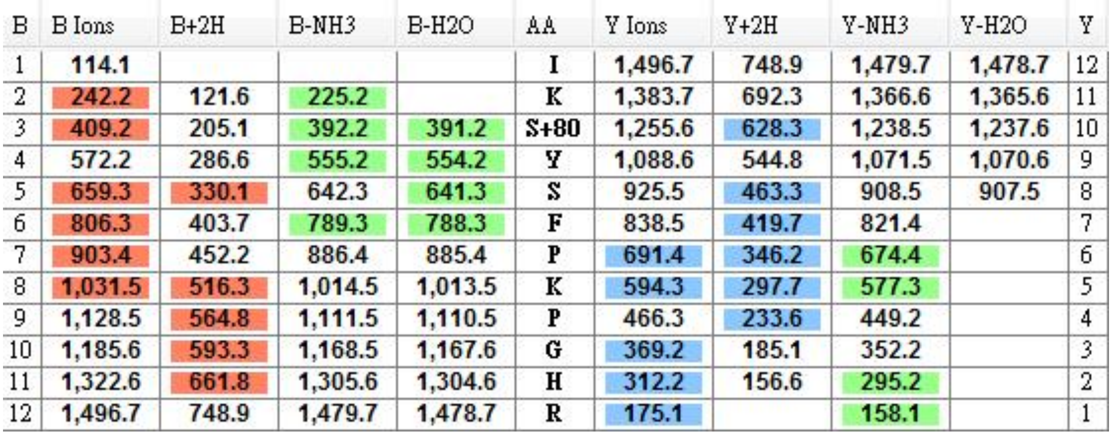




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				L	1,478.6	739.8	1,461.5	1,460.6	10
2	270.2	135.6	253.2		R	1,365.5	683.2	1,348.5	1,347.5	9
3	384.2	192.6	367.2		N	1,209.4		1,192.4	1,191.4	8
4	627.3	314.1	610.2		Y+80	1,095.3		1,078.3	1,077.3	7
5	790.3	395.7	773.3		Y	852.3		835.3	834.3	6
6	1,033.4	517.2	1,016.3		Y+80	689.3		672.2	671.2	5
7	1,148.4	574.7	1,131.4	1,130.4	D	446.2		429.2	428.2	4
8	1,247.5	624.2	1,230.4	1,229.4	V	331.2		314.2		3
9	1,346.5	673.8	1,329.5	1,328.5	V	232.1		215.1		2
10	1,478.6	739.8	1,461.5	1,460.6	N	133.1		116.0		1

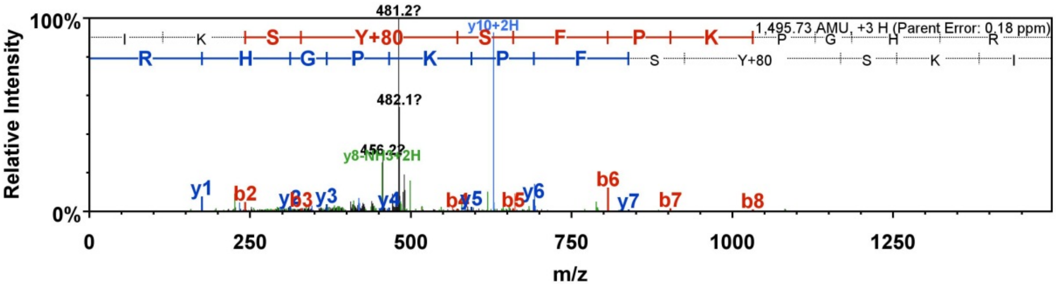
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
IK**S**YSFPKPGHR	pS	499.5849	1495.7329	3	1495.7337	-0.0008	31.6

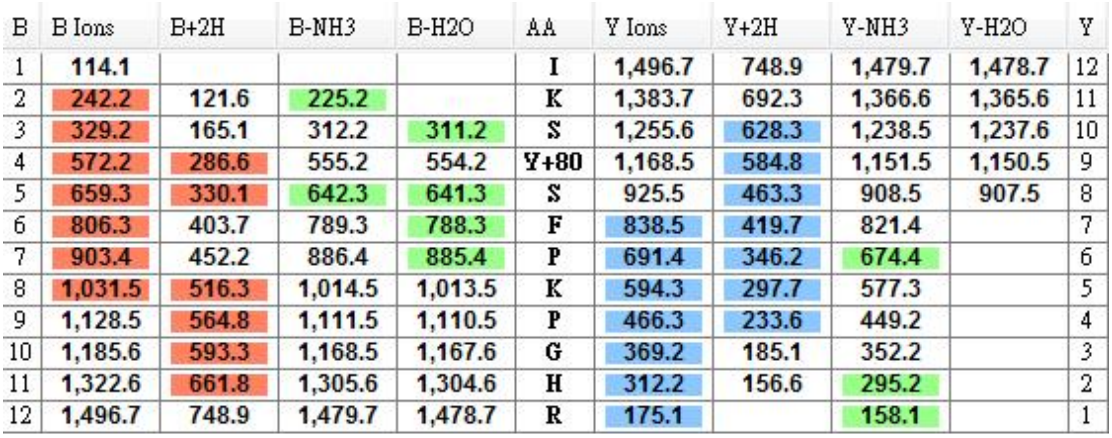




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	1,496.7	748.9	1,479.7	1,478.7	12
2	242.2	121.6	225.2		K	1,383.7	692.3	1,366.6	1,365.6	11
3	409.2	205.1	392.2	391.2	S+80	1,255.6	628.3	1,238.5	1,237.6	10
4	572.2	286.6	555.2	554.2	Y	1,088.6	544.8	1,071.5	1,070.6	9
5	659.3	330.1	642.3	641.3	S	925.5	463.3	908.5	907.5	8
6	806.3	403.7	789.3	788.3	F	838.5	419.7	821.4		7
7	903.4	452.2	886.4	885.4	P	691.4	346.2	674.4		6
8	1,031.5	516.3	1,014.5	1,013.5	K	594.3	297.7	577.3		5
9	1,128.5	564.8	1,111.5	1,110.5	P	466.3	233.6	449.2		4
10	1,185.6	593.3	1,168.5	1,167.6	G	369.2	185.1	352.2		3
11	1,322.6	661.8	1,305.6	1,304.6	H	312.2	156.6	295.2		2
12	1,496.7	748.9	1,479.7	1,478.7	R	175.1		158.1		1

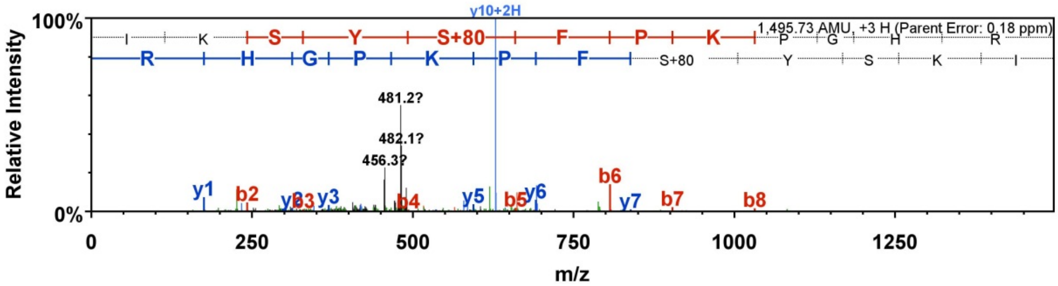
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
IKSYSFPKPGHR	pY	499.5853	1495.7341	3	1495.7337	0.0004	23.85

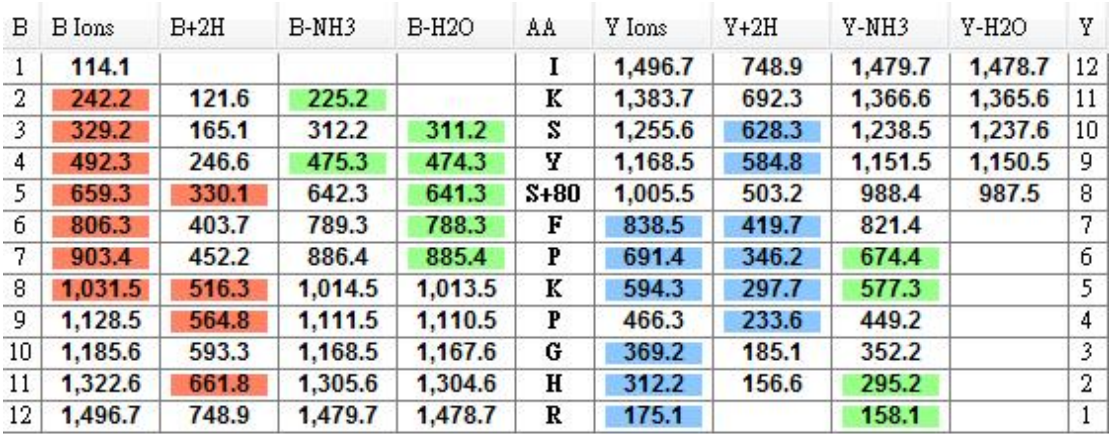




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	1,496.7	748.9	1,479.7	1,478.7	12
2	242.2	121.6	225.2		K	1,383.7	692.3	1,366.6	1,365.6	11
3	329.2	165.1	312.2	311.2	S	1,255.6	628.3	1,238.5	1,237.6	10
4	572.2	286.6	555.2	554.2	Y+80	1,168.5	584.8	1,151.5	1,150.5	9
5	659.3	330.1	642.3	641.3	S	925.5	463.3	908.5	907.5	8
6	806.3	403.7	789.3	788.3	F	838.5	419.7	821.4		7
7	903.4	452.2	886.4	885.4	P	691.4	346.2	674.4		6
8	1,031.5	516.3	1,014.5	1,013.5	K	594.3	297.7	577.3		5
9	1,128.5	564.8	1,111.5	1,110.5	P	466.3	233.6	449.2		4
10	1,185.6	593.3	1,168.5	1,167.6	G	369.2	185.1	352.2		3
11	1,322.6	661.8	1,305.6	1,304.6	H	312.2	156.6	295.2		2
12	1,496.7	748.9	1,479.7	1,478.7	R	175.1		158.1		1

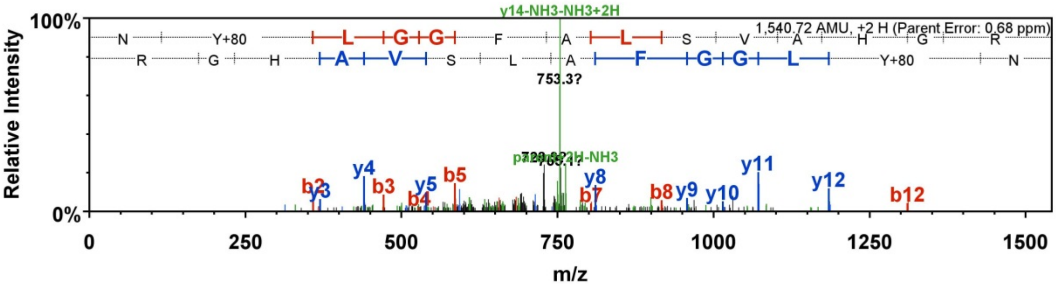
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
IKSY**S**FPKPGHR	pS	499.5853	1495.7341	3	1495.7337	0.0004	30.79

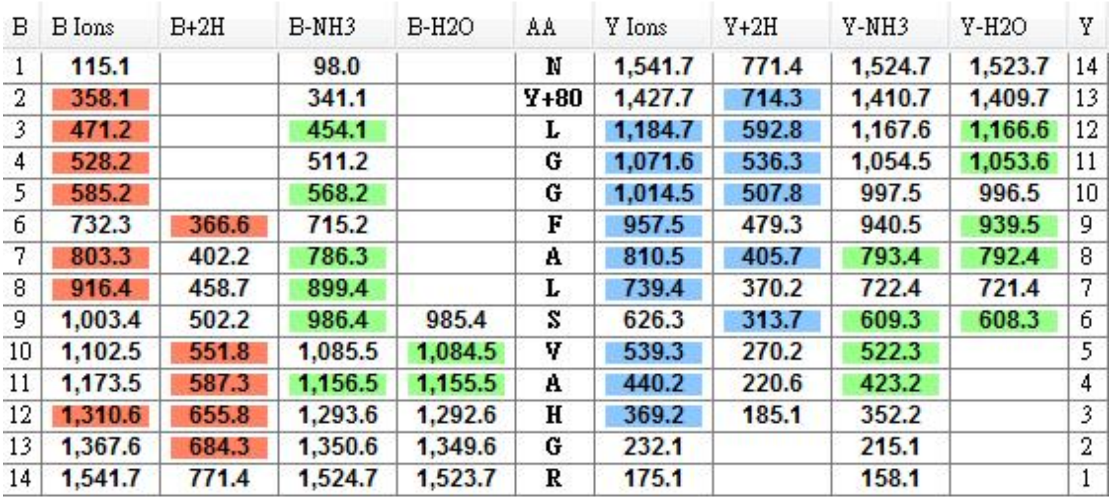




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	114.1				I	1,496.7	748.9	1,479.7	1,478.7	12
2	242.2	121.6	225.2		K	1,383.7	692.3	1,366.6	1,365.6	11
3	329.2	165.1	312.2	311.2	S	1,255.6	628.3	1,238.5	1,237.6	10
4	492.3	246.6	475.3	474.3	Y	1,168.5	584.8	1,151.5	1,150.5	9
5	659.3	330.1	642.3	641.3	S+80	1,005.5	503.2	988.4	987.5	8
6	806.3	403.7	789.3	788.3	F	838.5	419.7	821.4		7
7	903.4	452.2	886.4	885.4	P	691.4	346.2	674.4		6
8	1,031.5	516.3	1,014.5	1,013.5	K	594.3	297.7	577.3		5
9	1,128.5	564.8	1,111.5	1,110.5	P	466.3	233.6	449.2		4
10	1,185.6	593.3	1,168.5	1,167.6	G	369.2	185.1	352.2		3
11	1,322.6	661.8	1,305.6	1,304.6	H	312.2	156.6	295.2		2
12	1,496.7	748.9	1,479.7	1,478.7	R	175.1		158.1		1

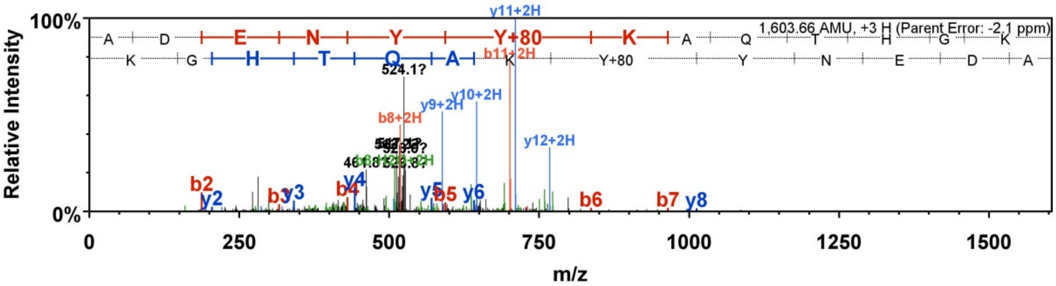
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
NYLGGFALSVAHGR	pY	771.3672	1540.7198	2	1540.7188	0.0011	39.23

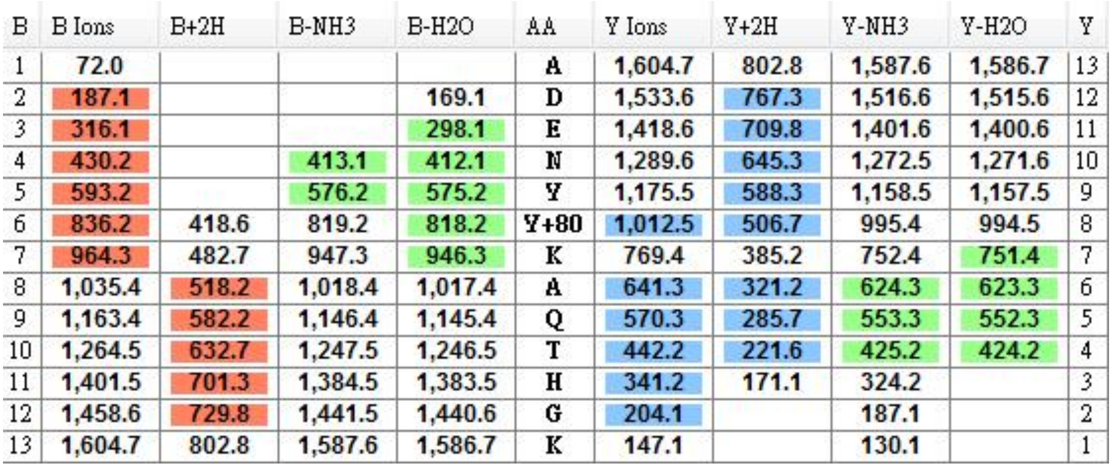




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	115.1		98.0		N	1,541.7	771.4	1,524.7	1,523.7	14
2	358.1		341.1		Y+80	1,427.7	714.3	1,410.7	1,409.7	13
3	471.2		454.1		L	1,184.7	592.8	1,167.6	1,166.6	12
4	528.2		511.2		G	1,071.6	536.3	1,054.5	1,053.6	11
5	585.2		568.2		G	1,014.5	507.8	997.5	996.5	10
6	732.3	366.6	715.2		F	957.5	479.3	940.5	939.5	9
7	803.3	402.2	786.3		A	810.5	405.7	793.4	792.4	8
8	916.4	458.7	899.4		L	739.4	370.2	722.4	721.4	7
9	1,003.4	502.2	986.4	985.4	S	626.3	313.7	609.3	608.3	6
10	1,102.5	551.8	1,085.5	1,084.5	V	539.3	270.2	522.3		5
11	1,173.5	587.3	1,156.5	1,155.5	A	440.2	220.6	423.2		4
12	1,310.6	655.8	1,293.6	1,292.6	H	369.2	185.1	352.2		3
13	1,367.6	684.3	1,350.6	1,349.6	G	232.1		215.1		2
14	1,541.7	771.4	1,524.7	1,523.7	R	175.1		158.1		1

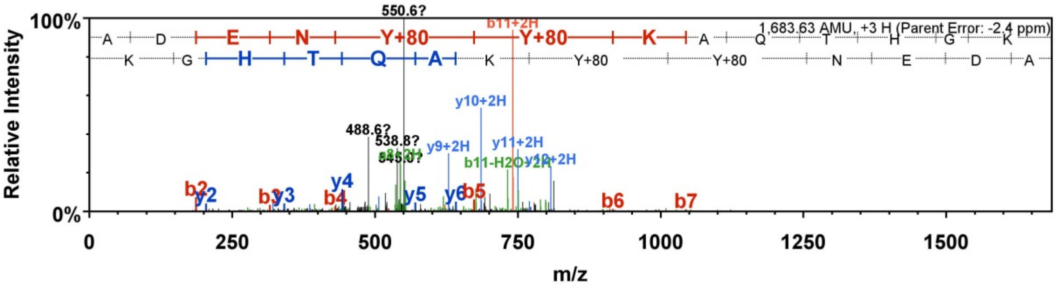
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
ADENYYKAQTHGK	pY	535.5618	1603.6636	3	1603.6668	-0.0032	24.94

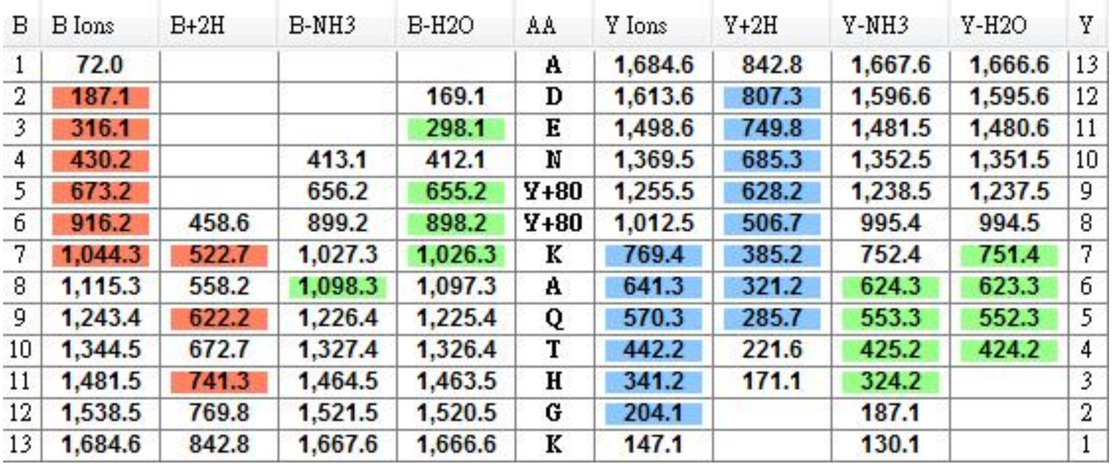




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1,604.7	802.8	1,587.6	1,586.7	13
2	187.1			169.1	D	1,533.6	767.3	1,516.6	1,515.6	12
3	316.1			298.1	E	1,418.6	709.8	1,401.6	1,400.6	11
4	430.2		413.1	412.1	N	1,289.6	645.3	1,272.5	1,271.6	10
5	593.2		576.2	575.2	Y	1,175.5	588.3	1,158.5	1,157.5	9
6	836.2	418.6	819.2	818.2	Y+80	1,012.5	506.7	995.4	994.5	8
7	964.3	482.7	947.3	946.3	K	769.4	385.2	752.4	751.4	7
8	1,035.4	518.2	1,018.4	1,017.4	A	641.3	321.2	624.3	623.3	6
9	1,163.4	582.2	1,146.4	1,145.4	Q	570.3	285.7	553.3	552.3	5
10	1,264.5	632.7	1,247.5	1,246.5	T	442.2	221.6	425.2	424.2	4
11	1,401.5	701.3	1,384.5	1,383.5	H	341.2	171.1	324.2		3
12	1,458.6	729.8	1,441.5	1,440.6	G	204.1		187.1		2
13	1,604.7	802.8	1,587.6	1,586.7	K	147.1		130.1		1

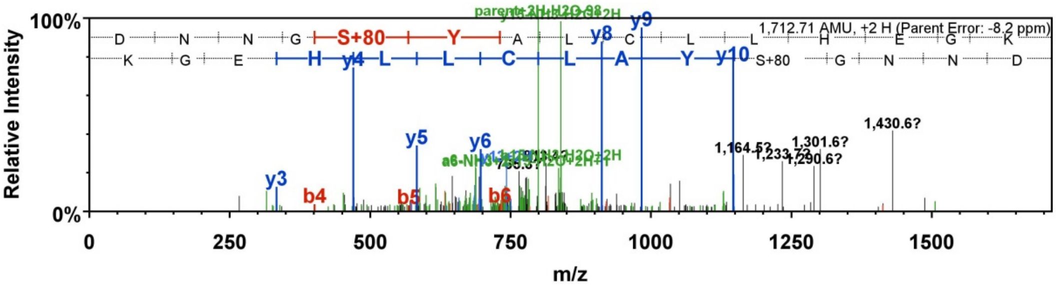
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
ADEN<u>YY</u>KAQTHGK	2 pY	562.217	1683.6292	3	1683.6331	-0.0039	29.2

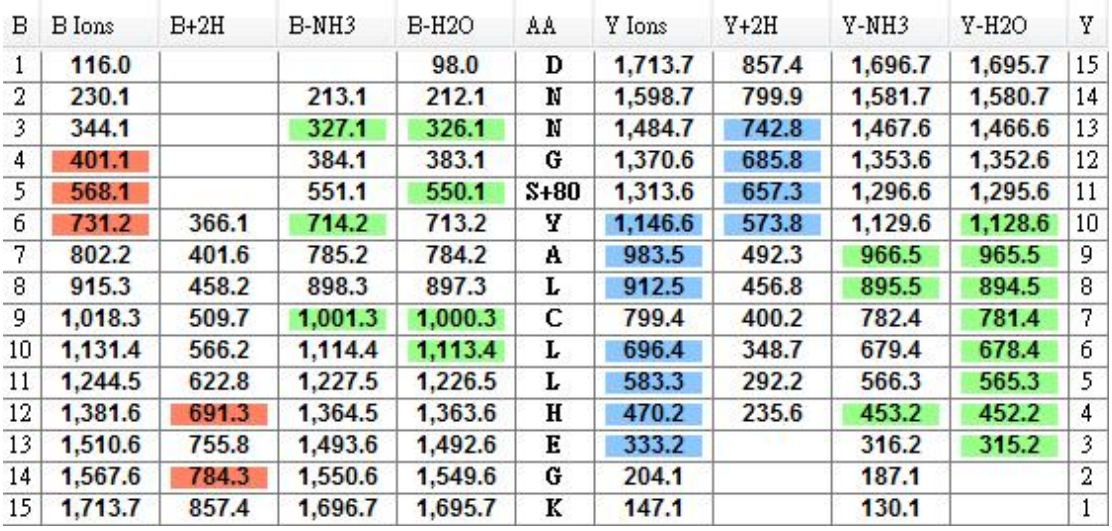




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	1,684.6	842.8	1,667.6	1,666.6	13
2	187.1			169.1	D	1,613.6	807.3	1,596.6	1,595.6	12
3	316.1			298.1	E	1,498.6	749.8	1,481.5	1,480.6	11
4	430.2		413.1	412.1	N	1,369.5	685.3	1,352.5	1,351.5	10
5	673.2		656.2	655.2	Y+80	1,255.5	628.2	1,238.5	1,237.5	9
6	916.2	458.6	899.2	898.2	Y+80	1,012.5	506.7	995.4	994.5	8
7	1,044.3	522.7	1,027.3	1,026.3	K	769.4	385.2	752.4	751.4	7
8	1,115.3	558.2	1,098.3	1,097.3	A	641.3	321.2	624.3	623.3	6
9	1,243.4	622.2	1,226.4	1,225.4	Q	570.3	285.7	553.3	552.3	5
10	1,344.5	672.7	1,327.4	1,326.4	T	442.2	221.6	425.2	424.2	4
11	1,481.5	741.3	1,464.5	1,463.5	H	341.2	171.1	324.2		3
12	1,538.5	769.8	1,521.5	1,520.5	G	204.1		187.1		2
13	1,684.6	842.8	1,667.6	1,666.6	K	147.1		130.1		1

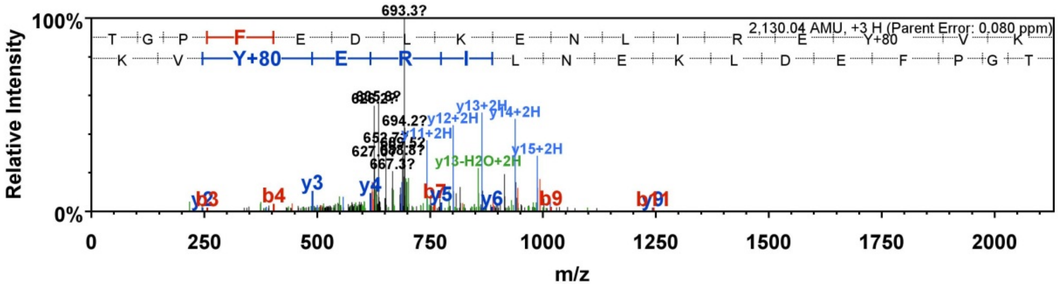
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
DNNG**S**YALCLLHEGK	pS	857.3618	1712.709	2	1712.7229	-0.0139	40.03

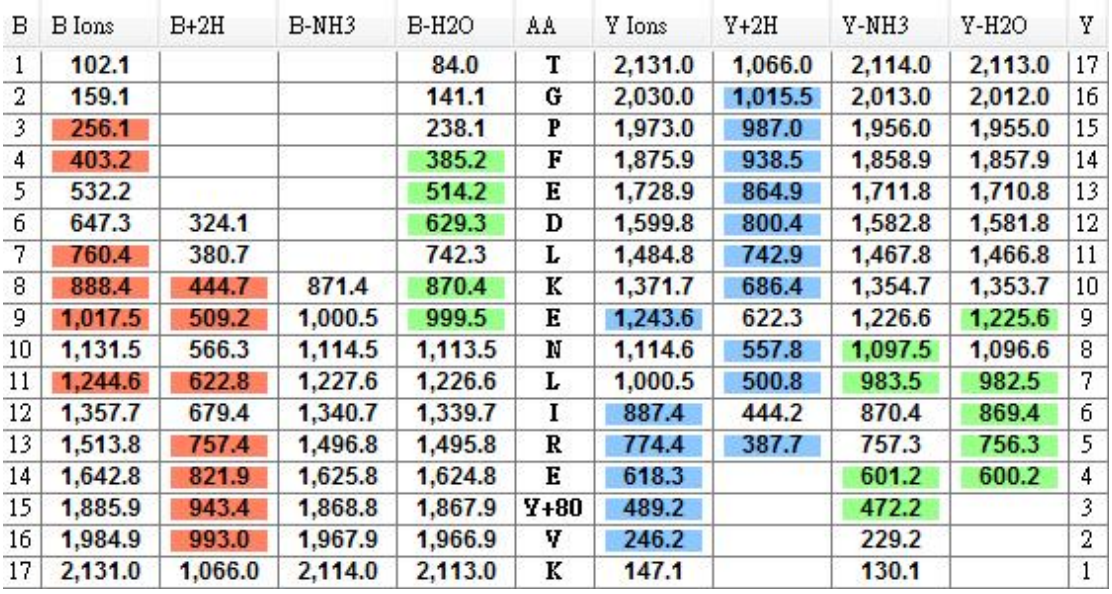




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	116.0			98.0	D	1,713.7	857.4	1,696.7	1,695.7	15
2	230.1		213.1	212.1	N	1,598.7	799.9	1,581.7	1,580.7	14
3	344.1		327.1	326.1	N	1,484.7	742.8	1,467.6	1,466.6	13
4	401.1		384.1	383.1	G	1,370.6	685.8	1,353.6	1,352.6	12
5	568.1		551.1	550.1	S+80	1,313.6	657.3	1,296.6	1,295.6	11
6	731.2	366.1	714.2	713.2	Y	1,146.6	573.8	1,129.6	1,128.6	10
7	802.2	401.6	785.2	784.2	A	983.5	492.3	966.5	965.5	9
8	915.3	458.2	898.3	897.3	L	912.5	456.8	895.5	894.5	8
9	1,018.3	509.7	1,001.3	1,000.3	C	799.4	400.2	782.4	781.4	7
10	1,131.4	566.2	1,114.4	1,113.4	L	696.4	348.7	679.4	678.4	6
11	1,244.5	622.8	1,227.5	1,226.5	L	583.3	292.2	566.3	565.3	5
12	1,381.6	691.3	1,364.5	1,363.6	H	470.2	235.6	453.2	452.2	4
13	1,510.6	755.8	1,493.6	1,492.6	E	333.2		316.2	315.2	3
14	1,567.6	784.3	1,550.6	1,549.6	G	204.1		187.1		2
15	1,713.7	857.4	1,696.7	1,695.7	K	147.1		130.1		1

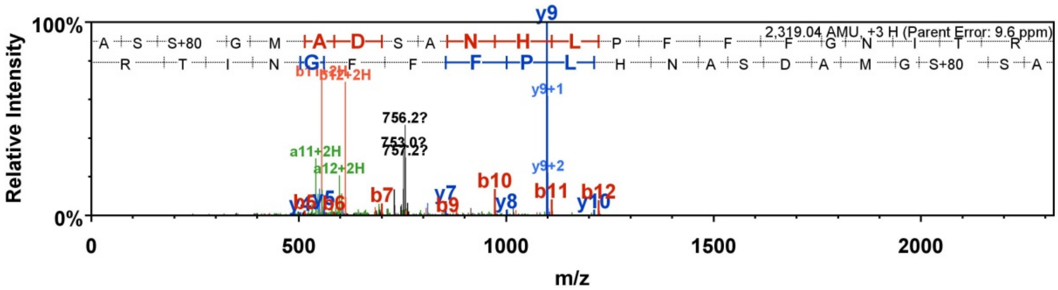
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
TGPFEDLKENLIREYVK	pY	711.0207	2130.0403	3	2130.0398	0.0005	34.17

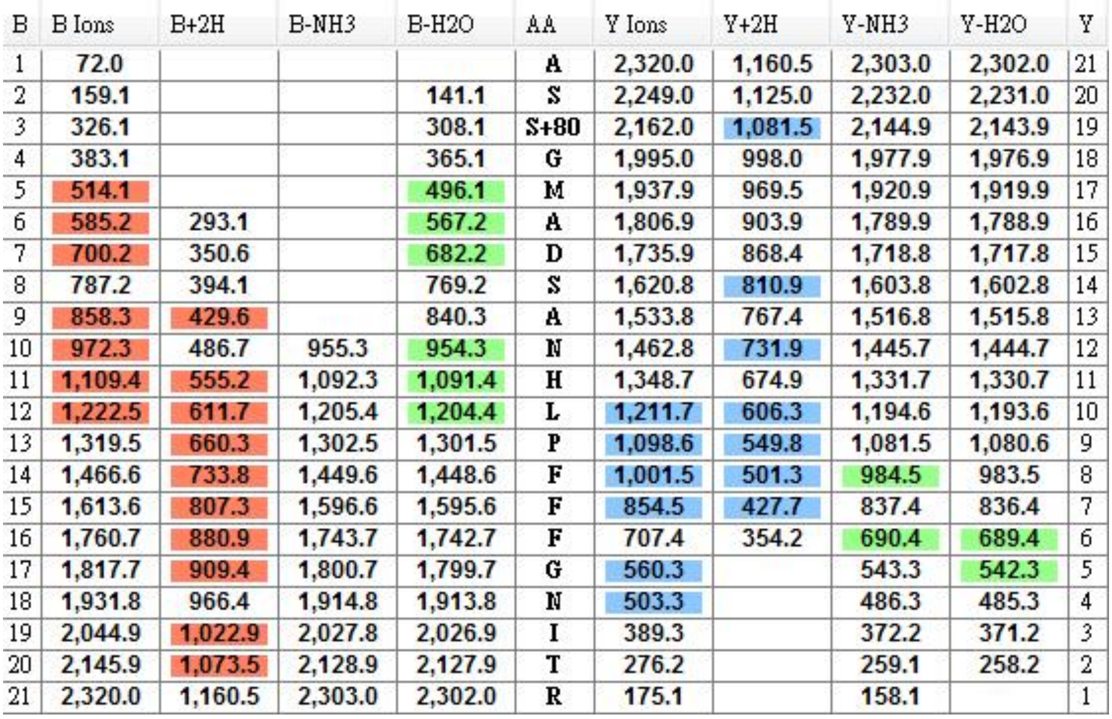




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	102.1			84.0	T	2,131.0	1,066.0	2,114.0	2,113.0	17
2	159.1			141.1	G	2,030.0	1,015.5	2,013.0	2,012.0	16
3	256.1			238.1	P	1,973.0	987.0	1,956.0	1,955.0	15
4	403.2			385.2	F	1,875.9	938.5	1,858.9	1,857.9	14
5	532.2			514.2	E	1,728.9	864.9	1,711.8	1,710.8	13
6	647.3	324.1		629.3	D	1,599.8	800.4	1,582.8	1,581.8	12
7	760.4	380.7		742.3	L	1,484.8	742.9	1,467.8	1,466.8	11
8	888.4	444.7	871.4	870.4	K	1,371.7	686.4	1,354.7	1,353.7	10
9	1,017.5	509.2	1,000.5	999.5	E	1,243.6	622.3	1,226.6	1,225.6	9
10	1,131.5	566.3	1,114.5	1,113.5	N	1,114.6	557.8	1,097.5	1,096.6	8
11	1,244.6	622.8	1,227.6	1,226.6	L	1,000.5	500.8	983.5	982.5	7
12	1,357.7	679.4	1,340.7	1,339.7	I	887.4	444.2	870.4	869.4	6
13	1,513.8	757.4	1,496.8	1,495.8	R	774.4	387.7	757.3	756.3	5
14	1,642.8	821.9	1,625.8	1,624.8	E	618.3		601.2	600.2	4
15	1,885.9	943.4	1,868.8	1,867.9	Y+80	489.2		472.2		3
16	1,984.9	993.0	1,967.9	1,966.9	V	246.2		229.2		2
17	2,131.0	1,066.0	2,114.0	2,113.0	K	147.1		130.1		1

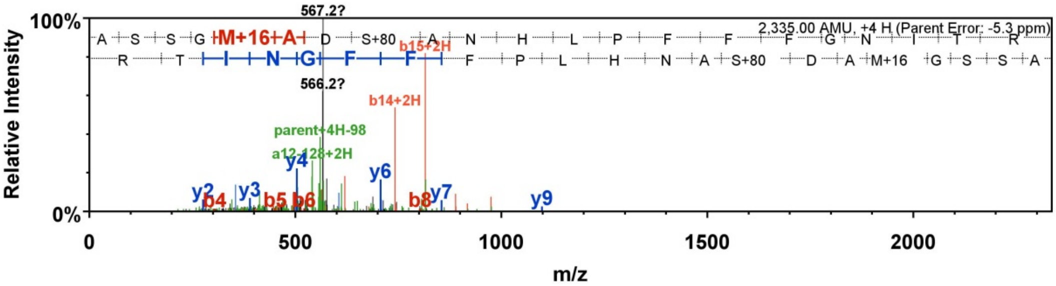
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
AssGMADSANHLPFFFGNITR	pS	774.0195	2319.0367	3	2319.0144	0.0223	11.65

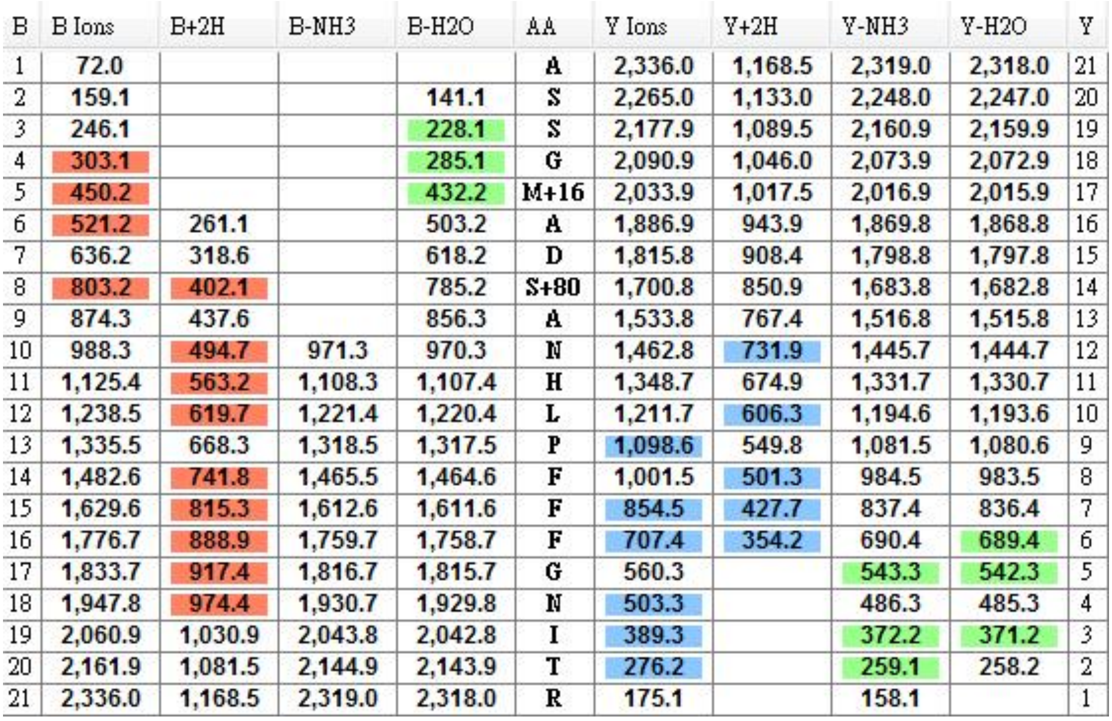




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	2,320.0	1,160.5	2,303.0	2,302.0	21
2	159.1			141.1	S	2,249.0	1,125.0	2,232.0	2,231.0	20
3	326.1			308.1	S+80	2,162.0	1,081.5	2,144.9	2,143.9	19
4	383.1			365.1	G	1,995.0	998.0	1,977.9	1,976.9	18
5	514.1			496.1	M	1,937.9	969.5	1,920.9	1,919.9	17
6	585.2	293.1		567.2	A	1,806.9	903.9	1,789.9	1,788.9	16
7	700.2	350.6		682.2	D	1,735.9	868.4	1,718.8	1,717.8	15
8	787.2	394.1		769.2	S	1,620.8	810.9	1,603.8	1,602.8	14
9	858.3	429.6		840.3	A	1,533.8	767.4	1,516.8	1,515.8	13
10	972.3	486.7	955.3	954.3	N	1,462.8	731.9	1,445.7	1,444.7	12
11	1,109.4	555.2	1,092.3	1,091.4	H	1,348.7	674.9	1,331.7	1,330.7	11
12	1,222.5	611.7	1,205.4	1,204.4	L	1,211.7	606.3	1,194.6	1,193.6	10
13	1,319.5	660.3	1,302.5	1,301.5	P	1,098.6	549.8	1,081.5	1,080.6	9
14	1,466.6	733.8	1,449.6	1,448.6	F	1,001.5	501.3	984.5	983.5	8
15	1,613.6	807.3	1,596.6	1,595.6	F	854.5	427.7	837.4	836.4	7
16	1,760.7	880.9	1,743.7	1,742.7	F	707.4	354.2	690.4	689.4	6
17	1,817.7	909.4	1,800.7	1,799.7	G	560.3		543.3	542.3	5
18	1,931.8	966.4	1,914.8	1,913.8	N	503.3		486.3	485.3	4
19	2,044.9	1,022.9	2,027.8	2,026.9	I	389.3		372.2	371.2	3
20	2,145.9	1,073.5	2,128.9	2,127.9	T	276.2		259.1	258.2	2
21	2,320.0	1,160.5	2,303.0	2,302.0	R	175.1		158.1		1

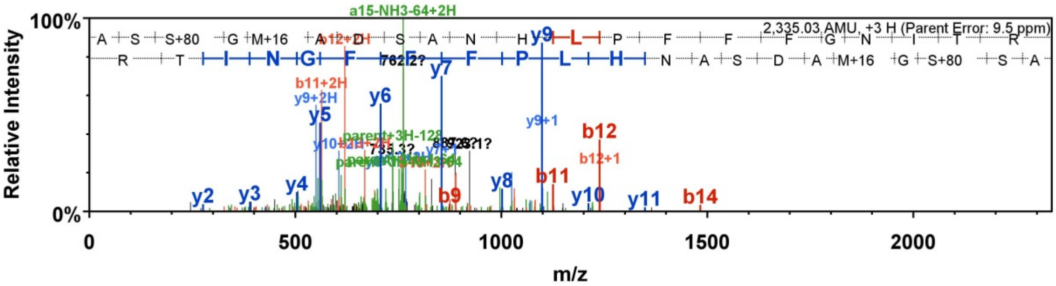
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
ASSGMAD**S**ANHLPFFFGNITR	Mox; pS	584.7565	2334.9969	4	2335.0093	-0.0124	33.5

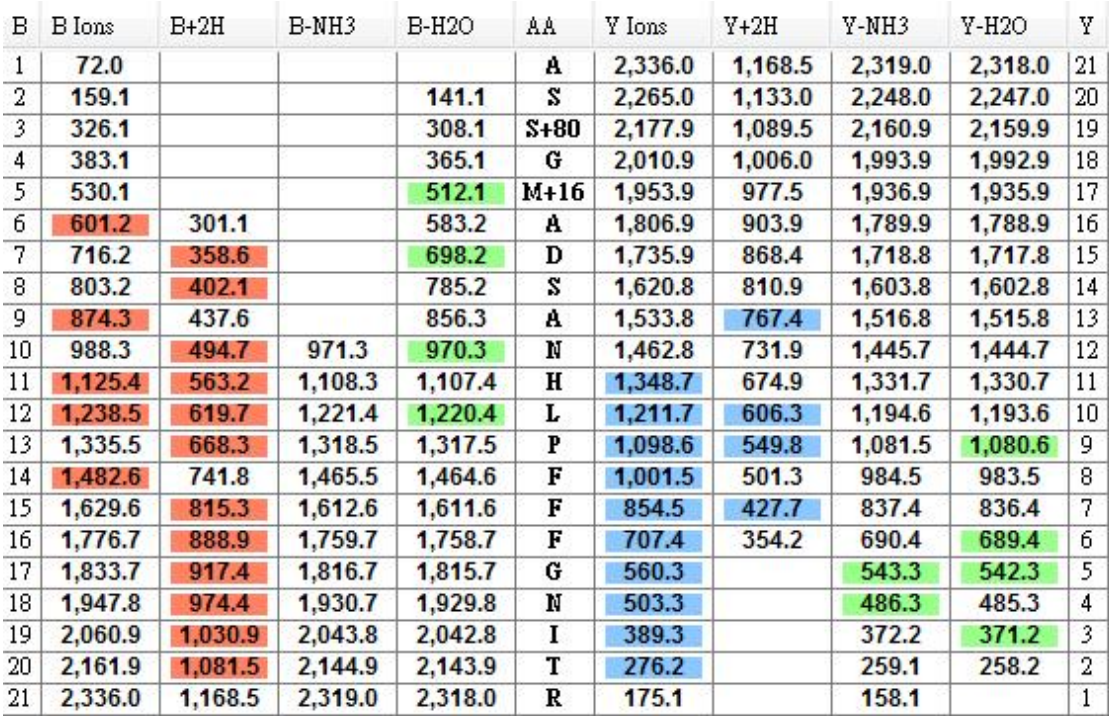




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	2,336.0	1,168.5	2,319.0	2,318.0	21
2	159.1			141.1	S	2,265.0	1,133.0	2,248.0	2,247.0	20
3	246.1			228.1	S	2,177.9	1,089.5	2,160.9	2,159.9	19
4	303.1			285.1	G	2,090.9	1,046.0	2,073.9	2,072.9	18
5	450.2			432.2	M+16	2,033.9	1,017.5	2,016.9	2,015.9	17
6	521.2	261.1		503.2	A	1,886.9	943.9	1,869.8	1,868.8	16
7	636.2	318.6		618.2	D	1,815.8	908.4	1,798.8	1,797.8	15
8	803.2	402.1		785.2	S+80	1,700.8	850.9	1,683.8	1,682.8	14
9	874.3	437.6		856.3	A	1,533.8	767.4	1,516.8	1,515.8	13
10	988.3	494.7	971.3	970.3	N	1,462.8	731.9	1,445.7	1,444.7	12
11	1,125.4	563.2	1,108.3	1,107.4	H	1,348.7	674.9	1,331.7	1,330.7	11
12	1,238.5	619.7	1,221.4	1,220.4	L	1,211.7	606.3	1,194.6	1,193.6	10
13	1,335.5	668.3	1,318.5	1,317.5	P	1,098.6	549.8	1,081.5	1,080.6	9
14	1,482.6	741.8	1,465.5	1,464.6	F	1,001.5	501.3	984.5	983.5	8
15	1,629.6	815.3	1,612.6	1,611.6	F	854.5	427.7	837.4	836.4	7
16	1,776.7	888.9	1,759.7	1,758.7	F	707.4	354.2	690.4	689.4	6
17	1,833.7	917.4	1,816.7	1,815.7	G	560.3		543.3	542.3	5
18	1,947.8	974.4	1,930.7	1,929.8	N	503.3		486.3	485.3	4
19	2,060.9	1,030.9	2,043.8	2,042.8	I	389.3		372.2	371.2	3
20	2,161.9	1,081.5	2,144.9	2,143.9	T	276.2		259.1	258.2	2
21	2,336.0	1,168.5	2,319.0	2,318.0	R	175.1		158.1		1

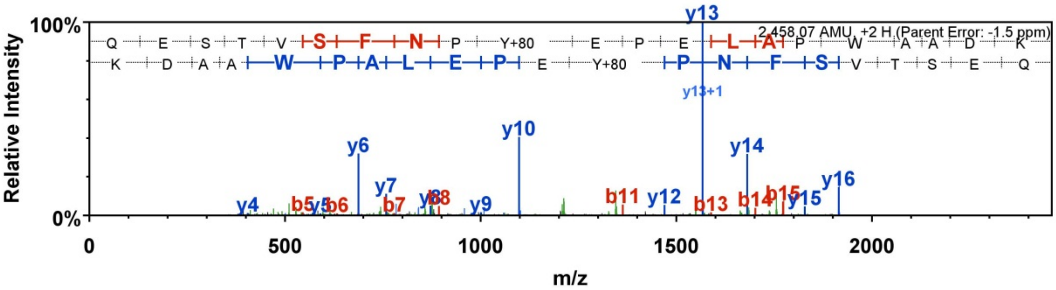
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
AssGMADSANHLPFFFGNITR	Mox; pS	779.3511	2335.0315	3	2335.0093	0.0222	32.38

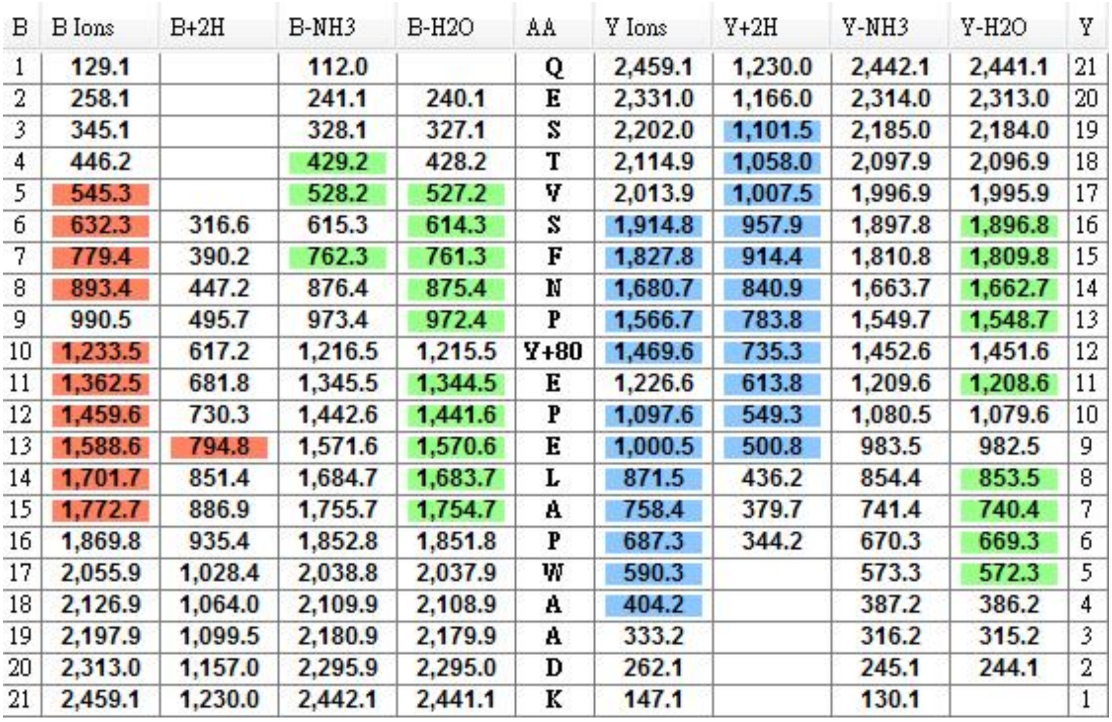




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	72.0				A	2,336.0	1,168.5	2,319.0	2,318.0	21
2	159.1			141.1	S	2,265.0	1,133.0	2,248.0	2,247.0	20
3	326.1			308.1	S+80	2,177.9	1,089.5	2,160.9	2,159.9	19
4	383.1			365.1	G	2,010.9	1,006.0	1,993.9	1,992.9	18
5	530.1			512.1	M+16	1,953.9	977.5	1,936.9	1,935.9	17
6	601.2	301.1		583.2	A	1,806.9	903.9	1,789.9	1,788.9	16
7	716.2	358.6		698.2	D	1,735.9	868.4	1,718.8	1,717.8	15
8	803.2	402.1		785.2	S	1,620.8	810.9	1,603.8	1,602.8	14
9	874.3	437.6		856.3	A	1,533.8	767.4	1,516.8	1,515.8	13
10	988.3	494.7	971.3	970.3	N	1,462.8	731.9	1,445.7	1,444.7	12
11	1,125.4	563.2	1,108.3	1,107.4	H	1,348.7	674.9	1,331.7	1,330.7	11
12	1,238.5	619.7	1,221.4	1,220.4	L	1,211.7	606.3	1,194.6	1,193.6	10
13	1,335.5	668.3	1,318.5	1,317.5	P	1,098.6	549.8	1,081.5	1,080.6	9
14	1,482.6	741.8	1,465.5	1,464.6	F	1,001.5	501.3	984.5	983.5	8
15	1,629.6	815.3	1,612.6	1,611.6	F	854.5	427.7	837.4	836.4	7
16	1,776.7	888.9	1,759.7	1,758.7	F	707.4	354.2	690.4	689.4	6
17	1,833.7	917.4	1,816.7	1,815.7	G	560.3		543.3	542.3	5
18	1,947.8	974.4	1,930.7	1,929.8	N	503.3		486.3	485.3	4
19	2,060.9	1,030.9	2,043.8	2,042.8	I	389.3		372.2	371.2	3
20	2,161.9	1,081.5	2,144.9	2,143.9	T	276.2		259.1	258.2	2
21	2,336.0	1,168.5	2,319.0	2,318.0	R	175.1		158.1		1

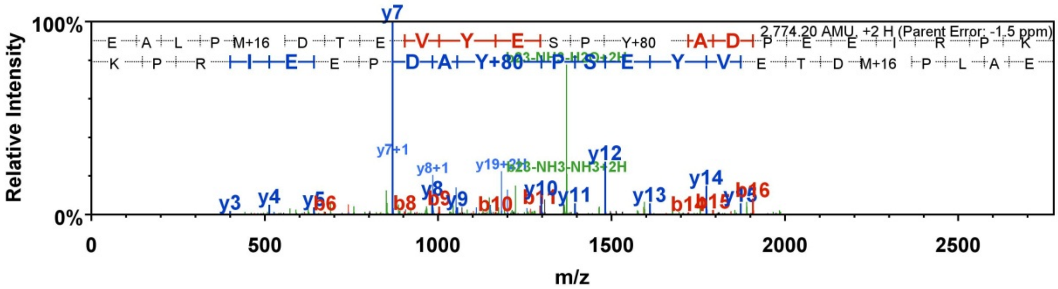
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
QESTVSFNPYEPELAPWAADK	pY	1230.042	2458.0694	2	2458.073	-0.0035	48.39

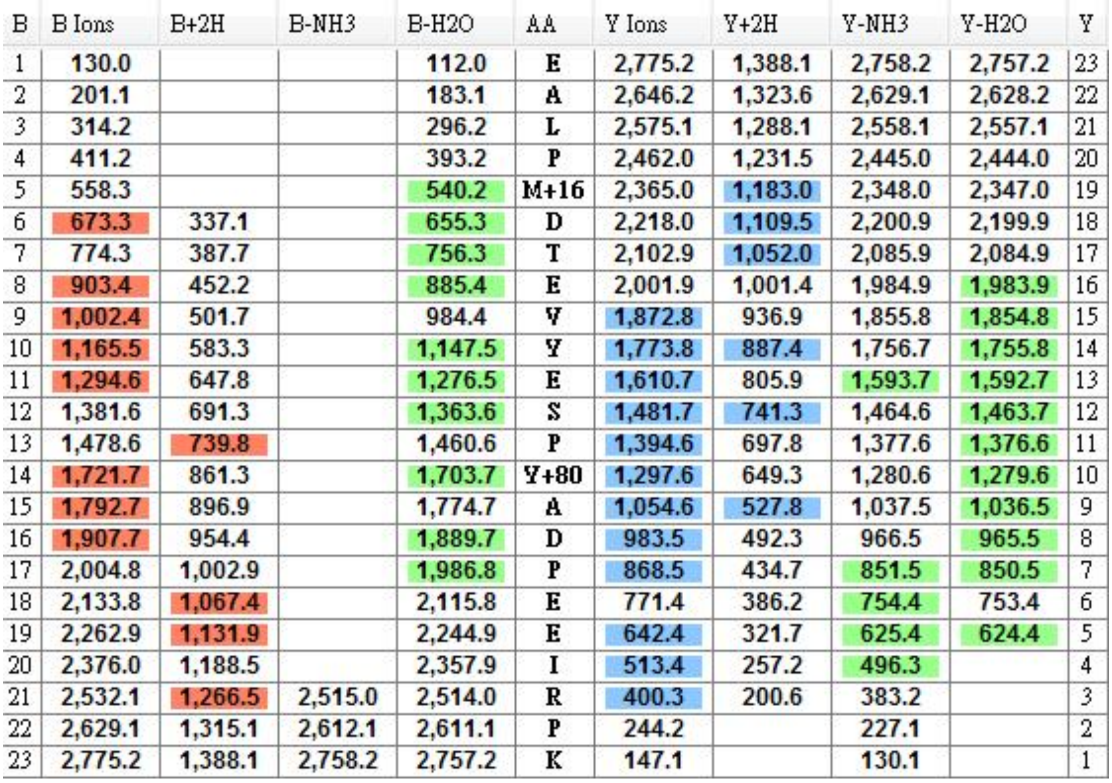




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	129.1		112.0		Q	2,459.1	1,230.0	2,442.1	2,441.1	21
2	258.1		241.1	240.1	E	2,331.0	1,166.0	2,314.0	2,313.0	20
3	345.1		328.1	327.1	S	2,202.0	1,101.5	2,185.0	2,184.0	19
4	446.2		429.2	428.2	T	2,114.9	1,058.0	2,097.9	2,096.9	18
5	545.3		528.2	527.2	V	2,013.9	1,007.5	1,996.9	1,995.9	17
6	632.3	316.6	615.3	614.3	S	1,914.8	957.9	1,897.8	1,896.8	16
7	779.4	390.2	762.3	761.3	F	1,827.8	914.4	1,810.8	1,809.8	15
8	893.4	447.2	876.4	875.4	N	1,680.7	840.9	1,663.7	1,662.7	14
9	990.5	495.7	973.4	972.4	P	1,566.7	783.8	1,549.7	1,548.7	13
10	1,233.5	617.2	1,216.5	1,215.5	Y+80	1,469.6	735.3	1,452.6	1,451.6	12
11	1,362.5	681.8	1,345.5	1,344.5	E	1,226.6	613.8	1,209.6	1,208.6	11
12	1,459.6	730.3	1,442.6	1,441.6	P	1,097.6	549.3	1,080.5	1,079.6	10
13	1,588.6	794.8	1,571.6	1,570.6	E	1,000.5	500.8	983.5	982.5	9
14	1,701.7	851.4	1,684.7	1,683.7	L	871.5	436.2	854.4	853.5	8
15	1,772.7	886.9	1,755.7	1,754.7	A	758.4	379.7	741.4	740.4	7
16	1,869.8	935.4	1,852.8	1,851.8	P	687.3	344.2	670.3	669.3	6
17	2,055.9	1,028.4	2,038.8	2,037.9	W	590.3		573.3	572.3	5
18	2,126.9	1,064.0	2,109.9	2,108.9	A	404.2		387.2	386.2	4
19	2,197.9	1,099.5	2,180.9	2,179.9	A	333.2		316.2	315.2	3
20	2,313.0	1,157.0	2,295.9	2,295.0	D	262.1		245.1	244.1	2
21	2,459.1	1,230.0	2,442.1	2,441.1	K	147.1		130.1		1

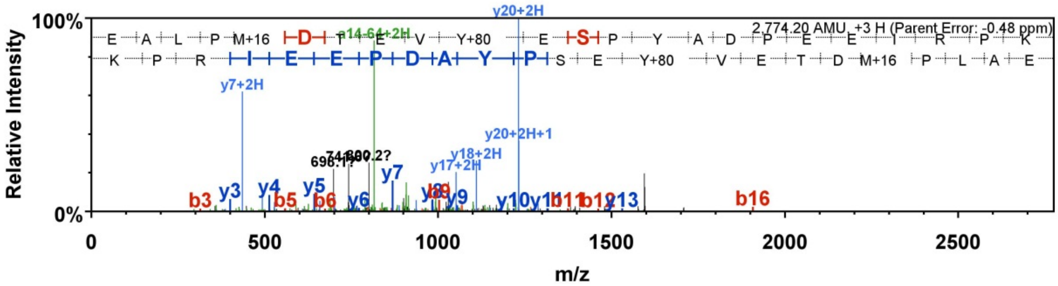
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
EALPMDTEVYESP**Y**ADPEEIRPK	Mox; pY	1388.107	2774.1994	2	2774.2034	-0.0039	49.52

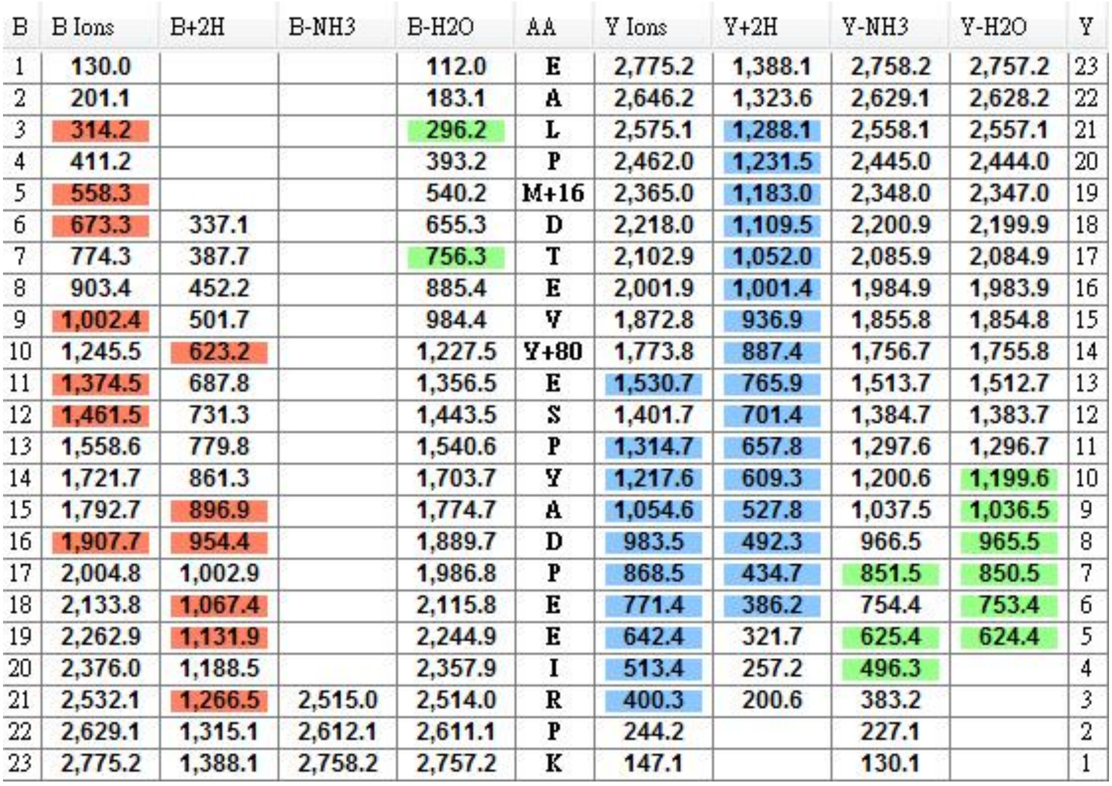




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	2,775.2	1,388.1	2,758.2	2,757.2	23
2	201.1			183.1	A	2,646.2	1,323.6	2,629.1	2,628.2	22
3	314.2			296.2	L	2,575.1	1,288.1	2,558.1	2,557.1	21
4	411.2			393.2	P	2,462.0	1,231.5	2,445.0	2,444.0	20
5	558.3			540.2	M+16	2,365.0	1,183.0	2,348.0	2,347.0	19
6	673.3	337.1		655.3	D	2,218.0	1,109.5	2,200.9	2,199.9	18
7	774.3	387.7		756.3	T	2,102.9	1,052.0	2,085.9	2,084.9	17
8	903.4	452.2		885.4	E	2,001.9	1,001.4	1,984.9	1,983.9	16
9	1,002.4	501.7		984.4	V	1,872.8	936.9	1,855.8	1,854.8	15
10	1,165.5	583.3		1,147.5	Y	1,773.8	887.4	1,756.7	1,755.8	14
11	1,294.6	647.8		1,276.5	E	1,610.7	805.9	1,593.7	1,592.7	13
12	1,381.6	691.3		1,363.6	S	1,481.7	741.3	1,464.6	1,463.7	12
13	1,478.6	739.8		1,460.6	P	1,394.6	697.8	1,377.6	1,376.6	11
14	1,721.7	861.3		1,703.7	Y+80	1,297.6	649.3	1,280.6	1,279.6	10
15	1,792.7	896.9		1,774.7	A	1,054.6	527.8	1,037.5	1,036.5	9
16	1,907.7	954.4		1,889.7	D	983.5	492.3	966.5	965.5	8
17	2,004.8	1,002.9		1,986.8	P	868.5	434.7	851.5	850.5	7
18	2,133.8	1,067.4		2,115.8	E	771.4	386.2	754.4	753.4	6
19	2,262.9	1,131.9		2,244.9	E	642.4	321.7	625.4	624.4	5
20	2,376.0	1,188.5		2,357.9	I	513.4	257.2	496.3		4
21	2,532.1	1,266.5	2,515.0	2,514.0	R	400.3	200.6	383.2		3
22	2,629.1	1,315.1	2,612.1	2,611.1	P	244.2		227.1		2
23	2,775.2	1,388.1	2,758.2	2,757.2	K	147.1		130.1		1

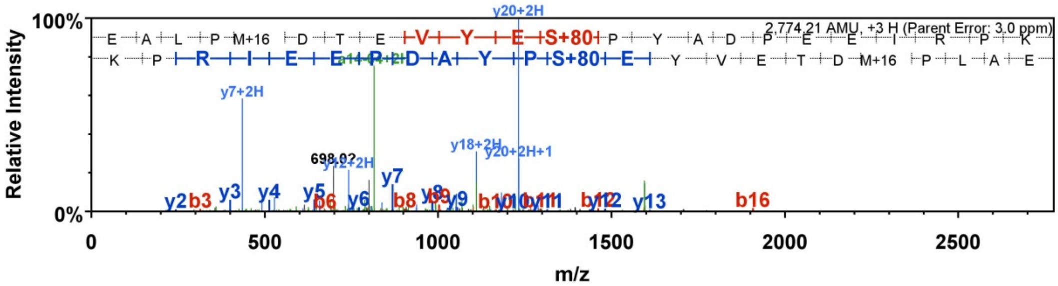
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
EALPMDTEVYESPYADPEEIRPK	Mox; pY	925.7414	2774.2024	3	2774.2034	-0.001	36.85

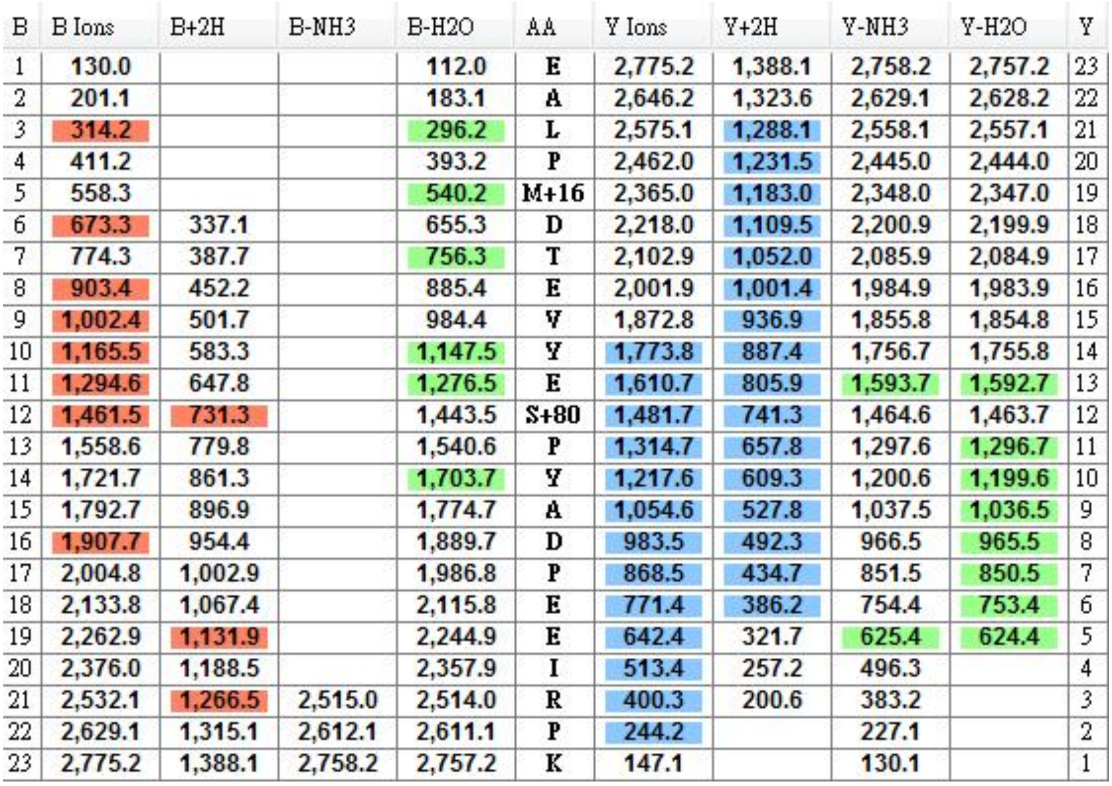




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	2,775.2	1,388.1	2,758.2	2,757.2	23
2	201.1			183.1	A	2,646.2	1,323.6	2,629.1	2,628.2	22
3	314.2			296.2	L	2,575.1	1,288.1	2,558.1	2,557.1	21
4	411.2			393.2	P	2,462.0	1,231.5	2,445.0	2,444.0	20
5	558.3			540.2	M+16	2,365.0	1,183.0	2,348.0	2,347.0	19
6	673.3	337.1		655.3	D	2,218.0	1,109.5	2,200.9	2,199.9	18
7	774.3	387.7		756.3	T	2,102.9	1,052.0	2,085.9	2,084.9	17
8	903.4	452.2		885.4	E	2,001.9	1,001.4	1,984.9	1,983.9	16
9	1,002.4	501.7		984.4	V	1,872.8	936.9	1,855.8	1,854.8	15
10	1,245.5	623.2		1,227.5	Y+80	1,773.8	887.4	1,756.7	1,755.8	14
11	1,374.5	687.8		1,356.5	E	1,530.7	765.9	1,513.7	1,512.7	13
12	1,461.5	731.3		1,443.5	S	1,401.7	701.4	1,384.7	1,383.7	12
13	1,558.6	779.8		1,540.6	P	1,314.7	657.8	1,297.6	1,296.7	11
14	1,721.7	861.3		1,703.7	Y	1,217.6	609.3	1,200.6	1,199.6	10
15	1,792.7	896.9		1,774.7	A	1,054.6	527.8	1,037.5	1,036.5	9
16	1,907.7	954.4		1,889.7	D	983.5	492.3	966.5	965.5	8
17	2,004.8	1,002.9		1,986.8	P	868.5	434.7	851.5	850.5	7
18	2,133.8	1,067.4		2,115.8	E	771.4	386.2	754.4	753.4	6
19	2,262.9	1,131.9		2,244.9	E	642.4	321.7	625.4	624.4	5
20	2,376.0	1,188.5		2,357.9	I	513.4	257.2	496.3		4
21	2,532.1	1,266.5	2,515.0	2,514.0	R	400.3	200.6	383.2		3
22	2,629.1	1,315.1	2,612.1	2,611.1	P	244.2		227.1		2
23	2,775.2	1,388.1	2,758.2	2,757.2	K	147.1		130.1		1

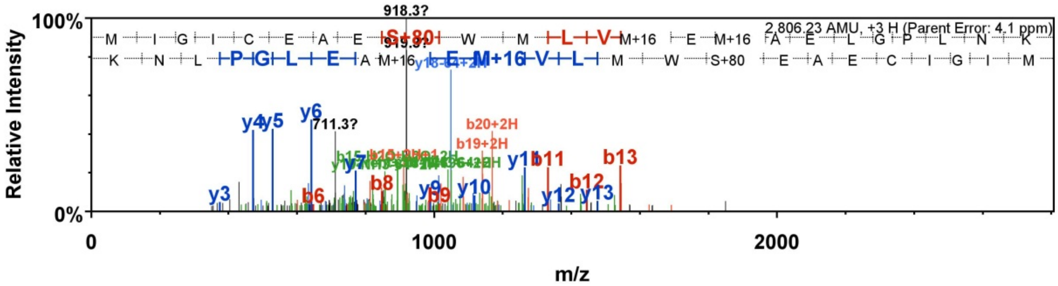
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
EALPMDTEVYESPYADPEEIRPK	Mox; pS	925.7446	2774.212	3	2774.2034	0.0086	59.18

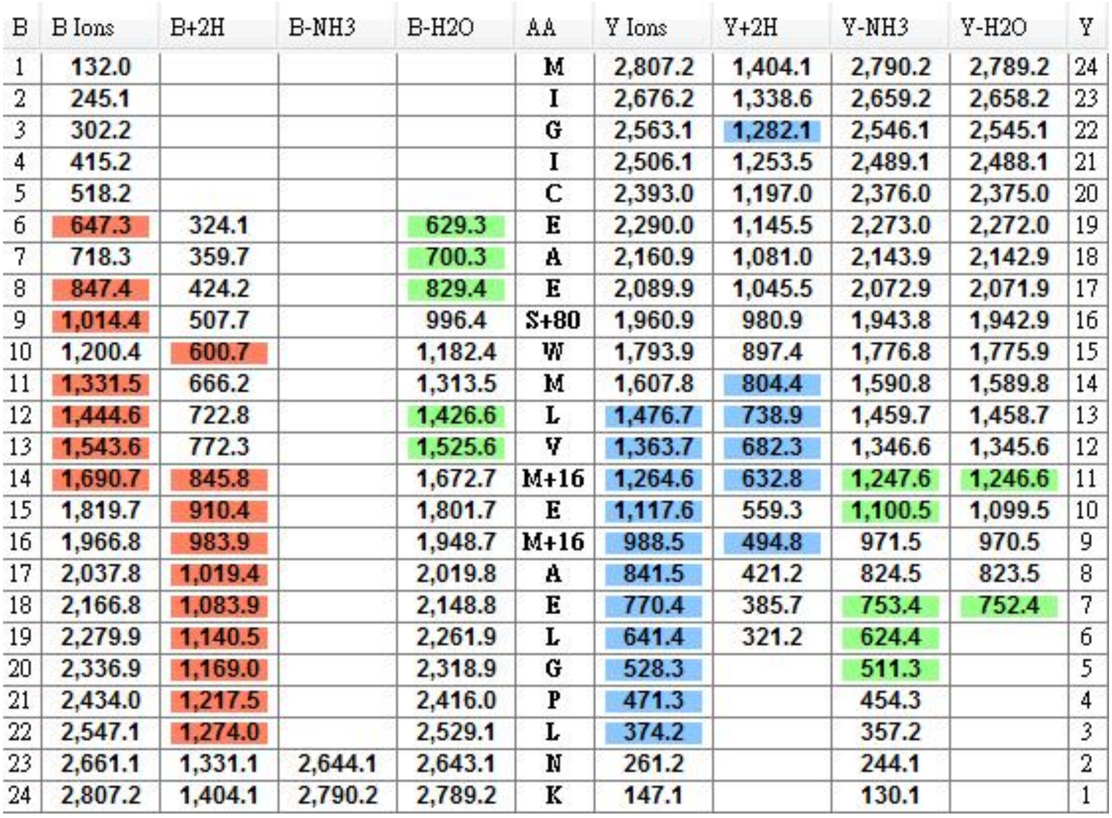




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	2,775.2	1,388.1	2,758.2	2,757.2	23
2	201.1			183.1	A	2,646.2	1,323.6	2,629.1	2,628.2	22
3	314.2			296.2	L	2,575.1	1,288.1	2,558.1	2,557.1	21
4	411.2			393.2	P	2,462.0	1,231.5	2,445.0	2,444.0	20
5	558.3			540.2	M+16	2,365.0	1,183.0	2,348.0	2,347.0	19
6	673.3	337.1		655.3	D	2,218.0	1,109.5	2,200.9	2,199.9	18
7	774.3	387.7		756.3	T	2,102.9	1,052.0	2,085.9	2,084.9	17
8	903.4	452.2		885.4	E	2,001.9	1,001.4	1,984.9	1,983.9	16
9	1,002.4	501.7		984.4	V	1,872.8	936.9	1,855.8	1,854.8	15
10	1,165.5	583.3		1,147.5	Y	1,773.8	887.4	1,756.7	1,755.8	14
11	1,294.6	647.8		1,276.5	E	1,610.7	805.9	1,593.7	1,592.7	13
12	1,461.5	731.3		1,443.5	S+80	1,481.7	741.3	1,464.6	1,463.7	12
13	1,558.6	779.8		1,540.6	P	1,314.7	657.8	1,297.6	1,296.7	11
14	1,721.7	861.3		1,703.7	Y	1,217.6	609.3	1,200.6	1,199.6	10
15	1,792.7	896.9		1,774.7	A	1,054.6	527.8	1,037.5	1,036.5	9
16	1,907.7	954.4		1,889.7	D	983.5	492.3	966.5	965.5	8
17	2,004.8	1,002.9		1,986.8	P	868.5	434.7	851.5	850.5	7
18	2,133.8	1,067.4		2,115.8	E	771.4	386.2	754.4	753.4	6
19	2,262.9	1,131.9		2,244.9	E	642.4	321.7	625.4	624.4	5
20	2,376.0	1,188.5		2,357.9	I	513.4	257.2	496.3		4
21	2,532.1	1,266.5	2,515.0	2,514.0	R	400.3	200.6	383.2		3
22	2,629.1	1,315.1	2,612.1	2,611.1	P	244.2		227.1		2
23	2,775.2	1,388.1	2,758.2	2,757.2	K	147.1		130.1		1

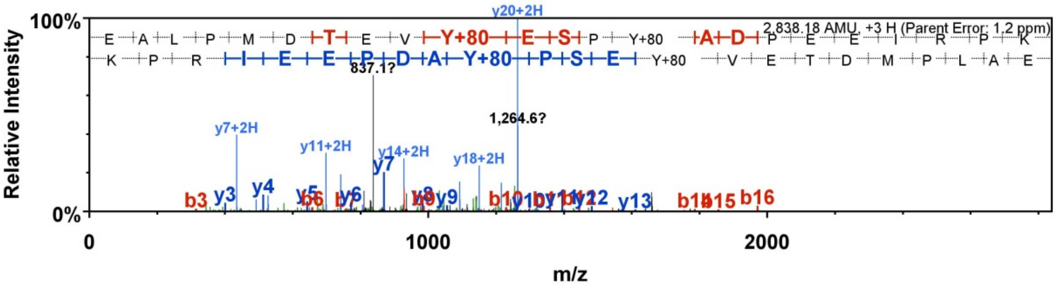
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
MIGICEAESWMLVMEMAELGPLNK	2 Mox; pS	936.4166	2806.228	3	2806.216	0.0119	20.16

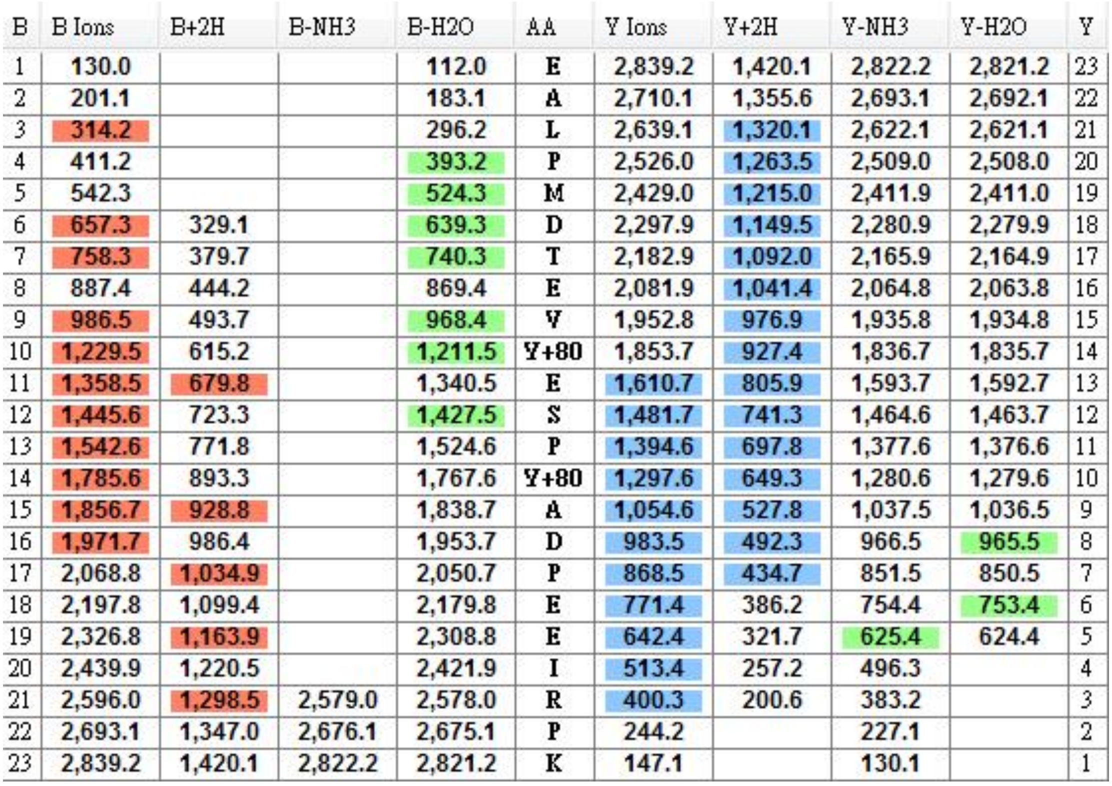




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	132.0				M	2,807.2	1,404.1	2,790.2	2,789.2	24
2	245.1				I	2,676.2	1,338.6	2,659.2	2,658.2	23
3	302.2				G	2,563.1	1,282.1	2,546.1	2,545.1	22
4	415.2				I	2,506.1	1,253.5	2,489.1	2,488.1	21
5	518.2				C	2,393.0	1,197.0	2,376.0	2,375.0	20
6	647.3	324.1		629.3	E	2,290.0	1,145.5	2,273.0	2,272.0	19
7	718.3	359.7		700.3	A	2,160.9	1,081.0	2,143.9	2,142.9	18
8	847.4	424.2		829.4	E	2,089.9	1,045.5	2,072.9	2,071.9	17
9	1,014.4	507.7		996.4	S+80	1,960.9	980.9	1,943.8	1,942.9	16
10	1,200.4	600.7		1,182.4	W	1,793.9	897.4	1,776.8	1,775.9	15
11	1,331.5	666.2		1,313.5	M	1,607.8	804.4	1,590.8	1,589.8	14
12	1,444.6	722.8		1,426.6	L	1,476.7	738.9	1,459.7	1,458.7	13
13	1,543.6	772.3		1,525.6	V	1,363.7	682.3	1,346.6	1,345.6	12
14	1,690.7	845.8		1,672.7	M+16	1,264.6	632.8	1,247.6	1,246.6	11
15	1,819.7	910.4		1,801.7	E	1,117.6	559.3	1,100.5	1,099.5	10
16	1,966.8	983.9		1,948.7	M+16	988.5	494.8	971.5	970.5	9
17	2,037.8	1,019.4		2,019.8	A	841.5	421.2	824.5	823.5	8
18	2,166.8	1,083.9		2,148.8	E	770.4	385.7	753.4	752.4	7
19	2,279.9	1,140.5		2,261.9	L	641.4	321.2	624.4		6
20	2,336.9	1,169.0		2,318.9	G	528.3		511.3		5
21	2,434.0	1,217.5		2,416.0	P	471.3		454.3		4
22	2,547.1	1,274.0		2,529.1	L	374.2		357.2		3
23	2,661.1	1,331.1	2,644.1	2,643.1	N	261.2		244.1		2
24	2,807.2	1,404.1	2,790.2	2,789.2	K	147.1		130.1		1

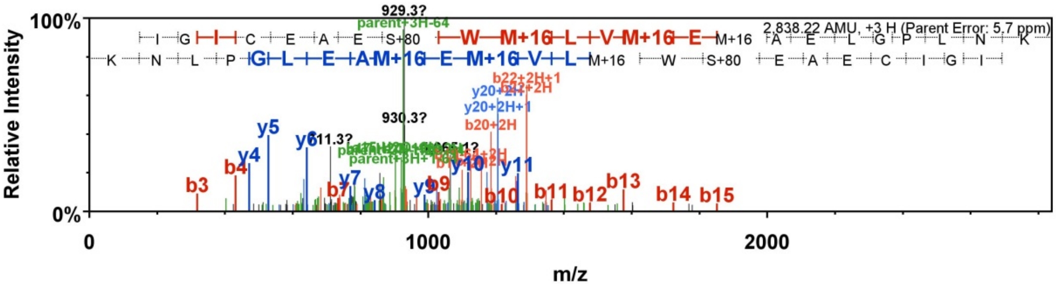
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
EALPMDTEVYESPYADPEEIRPK	2 pY	947.0668	2838.1786	3	2838.1748	0.0038	61.19

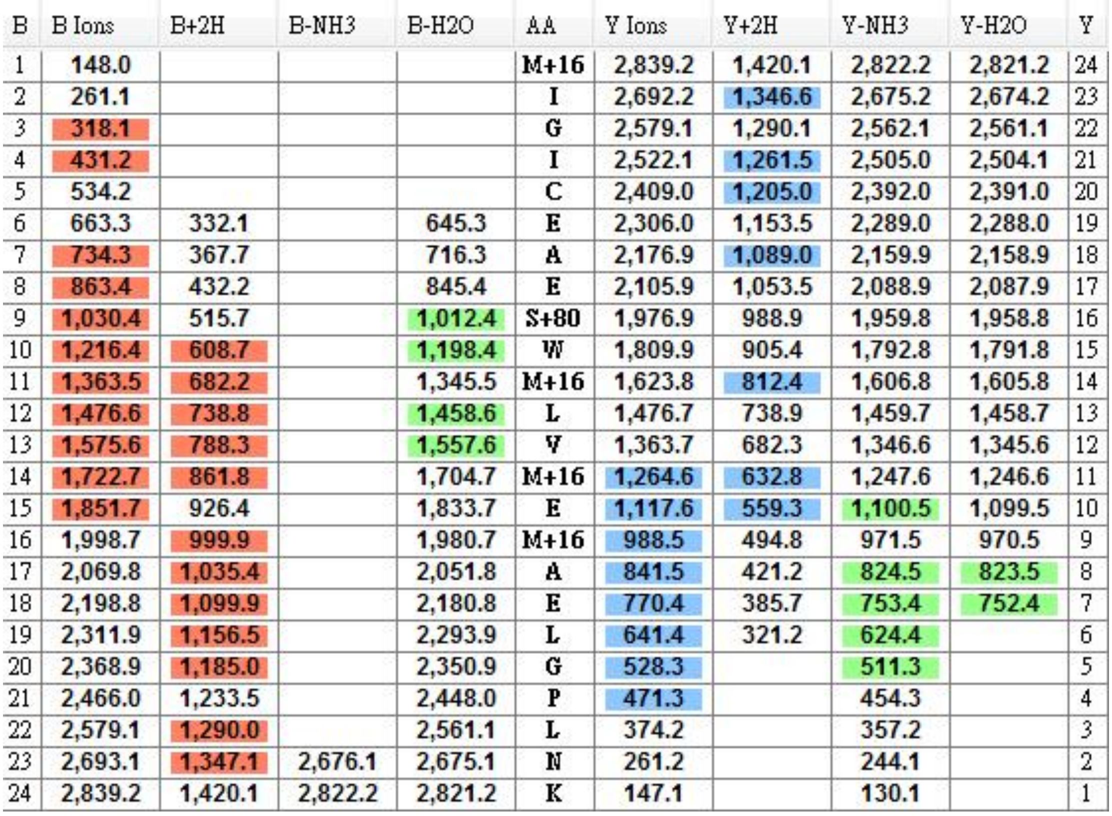




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	2,839.2	1,420.1	2,822.2	2,821.2	23
2	201.1			183.1	A	2,710.1	1,355.6	2,693.1	2,692.1	22
3	314.2			296.2	L	2,639.1	1,320.1	2,622.1	2,621.1	21
4	411.2			393.2	P	2,526.0	1,263.5	2,509.0	2,508.0	20
5	542.3			524.3	M	2,429.0	1,215.0	2,411.9	2,411.0	19
6	657.3	329.1		639.3	D	2,297.9	1,149.5	2,280.9	2,279.9	18
7	758.3	379.7		740.3	T	2,182.9	1,092.0	2,165.9	2,164.9	17
8	887.4	444.2		869.4	E	2,081.9	1,041.4	2,064.8	2,063.8	16
9	986.5	493.7		968.4	V	1,952.8	976.9	1,935.8	1,934.8	15
10	1,229.5	615.2		1,211.5	Y+80	1,853.7	927.4	1,836.7	1,835.7	14
11	1,358.5	679.8		1,340.5	E	1,610.7	805.9	1,593.7	1,592.7	13
12	1,445.6	723.3		1,427.5	S	1,481.7	741.3	1,464.6	1,463.7	12
13	1,542.6	771.8		1,524.6	P	1,394.6	697.8	1,377.6	1,376.6	11
14	1,785.6	893.3		1,767.6	Y+80	1,297.6	649.3	1,280.6	1,279.6	10
15	1,856.7	928.8		1,838.7	A	1,054.6	527.8	1,037.5	1,036.5	9
16	1,971.7	986.4		1,953.7	D	983.5	492.3	966.5	965.5	8
17	2,068.8	1,034.9		2,050.7	P	868.5	434.7	851.5	850.5	7
18	2,197.8	1,099.4		2,179.8	E	771.4	386.2	754.4	753.4	6
19	2,326.8	1,163.9		2,308.8	E	642.4	321.7	625.4	624.4	5
20	2,439.9	1,220.5		2,421.9	I	513.4	257.2	496.3		4
21	2,596.0	1,298.5	2,579.0	2,578.0	R	400.3	200.6	383.2		3
22	2,693.1	1,347.0	2,676.1	2,675.1	P	244.2		227.1		2
23	2,839.2	1,420.1	2,822.2	2,821.2	K	147.1		130.1		1

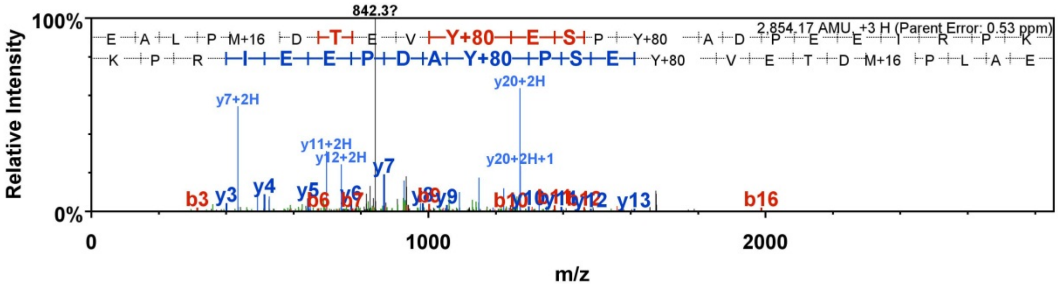
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
MIGICEAE**S**WMLVMEMAELGPLNK	4 Mox; pS	947.0814	2838.2224	3	2838.2059	0.0165	26.19

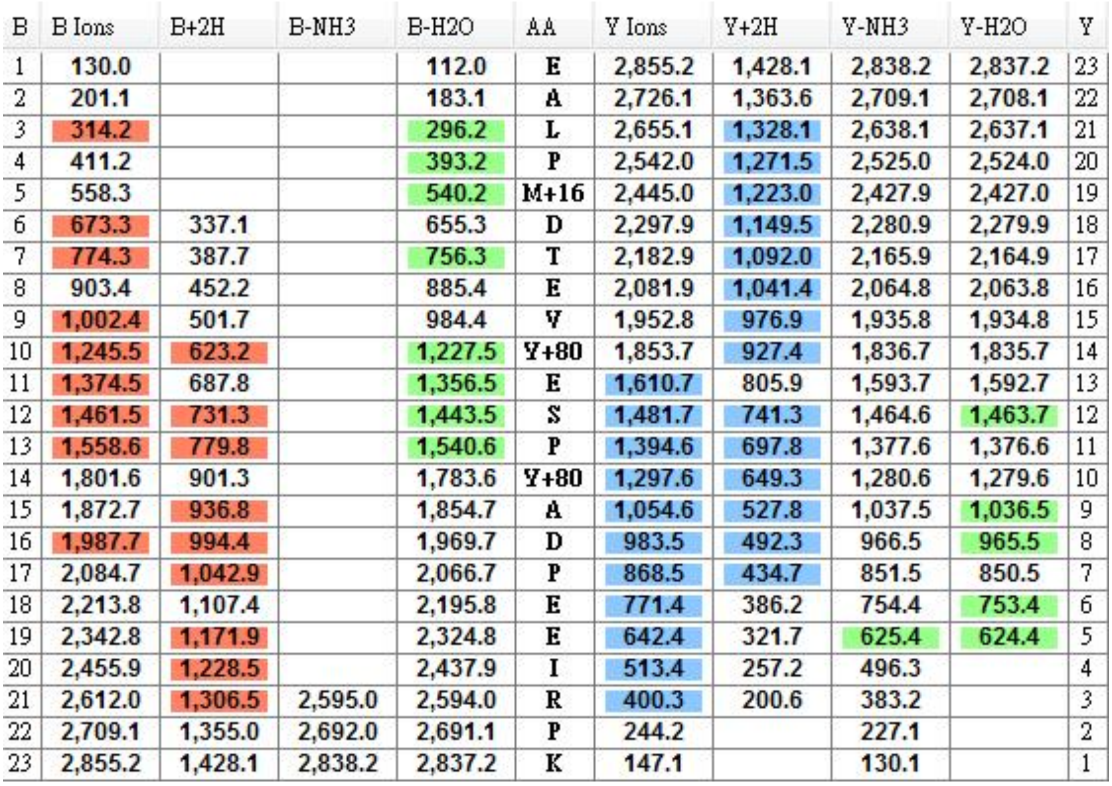




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	148.0				M+16	2,839.2	1,420.1	2,822.2	2,821.2	24
2	261.1				I	2,692.2	1,346.6	2,675.2	2,674.2	23
3	318.1				G	2,579.1	1,290.1	2,562.1	2,561.1	22
4	431.2				I	2,522.1	1,261.5	2,505.0	2,504.1	21
5	534.2				C	2,409.0	1,205.0	2,392.0	2,391.0	20
6	663.3	332.1		645.3	E	2,306.0	1,153.5	2,289.0	2,288.0	19
7	734.3	367.7		716.3	A	2,176.9	1,089.0	2,159.9	2,158.9	18
8	863.4	432.2		845.4	E	2,105.9	1,053.5	2,088.9	2,087.9	17
9	1,030.4	515.7		1,012.4	S+80	1,976.9	988.9	1,959.8	1,958.8	16
10	1,216.4	608.7		1,198.4	W	1,809.9	905.4	1,792.8	1,791.8	15
11	1,363.5	682.2		1,345.5	M+16	1,623.8	812.4	1,606.8	1,605.8	14
12	1,476.6	738.8		1,458.6	L	1,476.7	738.9	1,459.7	1,458.7	13
13	1,575.6	788.3		1,557.6	V	1,363.7	682.3	1,346.6	1,345.6	12
14	1,722.7	861.8		1,704.7	M+16	1,264.6	632.8	1,247.6	1,246.6	11
15	1,851.7	926.4		1,833.7	E	1,117.6	559.3	1,100.5	1,099.5	10
16	1,998.7	999.9		1,980.7	M+16	988.5	494.8	971.5	970.5	9
17	2,069.8	1,035.4		2,051.8	A	841.5	421.2	824.5	823.5	8
18	2,198.8	1,099.9		2,180.8	E	770.4	385.7	753.4	752.4	7
19	2,311.9	1,156.5		2,293.9	L	641.4	321.2	624.4		6
20	2,368.9	1,185.0		2,350.9	G	528.3		511.3		5
21	2,466.0	1,233.5		2,448.0	P	471.3		454.3		4
22	2,579.1	1,290.0		2,561.1	L	374.2		357.2		3
23	2,693.1	1,347.1	2,676.1	2,675.1	N	261.2		244.1		2
24	2,839.2	1,420.1	2,822.2	2,821.2	K	147.1		130.1		1

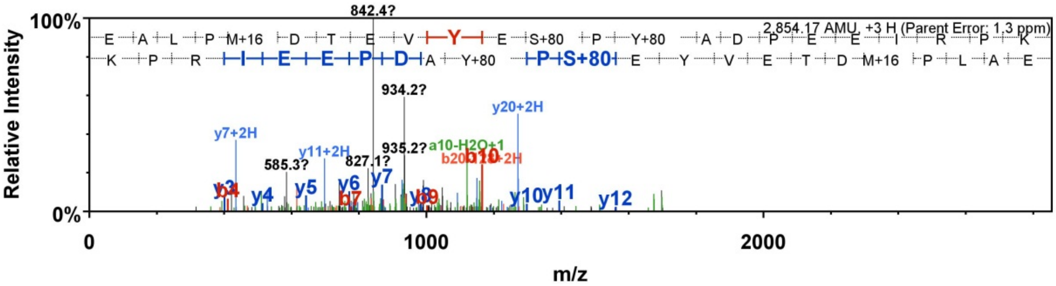
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
EALPMDTEVYESPYADPEEIRPK	Mox; 2 pY	952.3978	2854.1716	3	2854.1697	0.0019	59.45

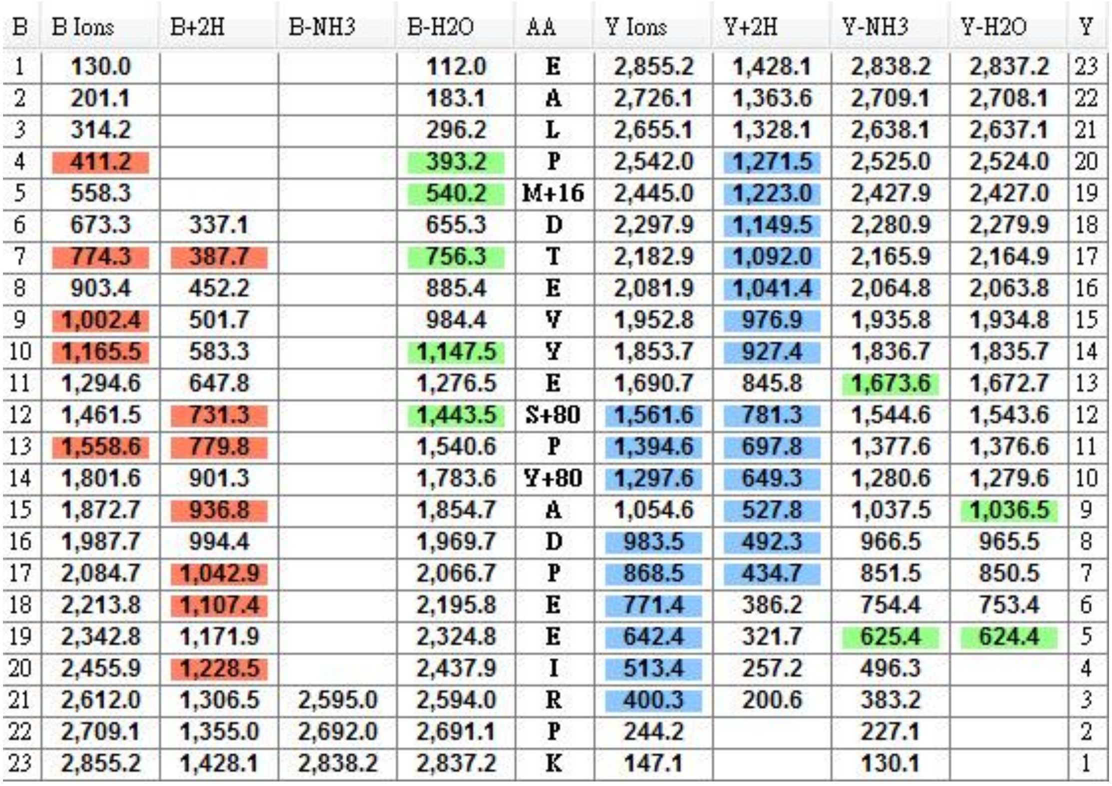




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	2,855.2	1,428.1	2,838.2	2,837.2	23
2	201.1			183.1	A	2,726.1	1,363.6	2,709.1	2,708.1	22
3	314.2			296.2	L	2,655.1	1,328.1	2,638.1	2,637.1	21
4	411.2			393.2	P	2,542.0	1,271.5	2,525.0	2,524.0	20
5	558.3			540.2	M+16	2,445.0	1,223.0	2,427.9	2,427.0	19
6	673.3	337.1		655.3	D	2,297.9	1,149.5	2,280.9	2,279.9	18
7	774.3	387.7		756.3	T	2,182.9	1,092.0	2,165.9	2,164.9	17
8	903.4	452.2		885.4	E	2,081.9	1,041.4	2,064.8	2,063.8	16
9	1,002.4	501.7		984.4	V	1,952.8	976.9	1,935.8	1,934.8	15
10	1,245.5	623.2		1,227.5	Y+80	1,853.7	927.4	1,836.7	1,835.7	14
11	1,374.5	687.8		1,356.5	E	1,610.7	805.9	1,593.7	1,592.7	13
12	1,461.5	731.3		1,443.5	S	1,481.7	741.3	1,464.6	1,463.7	12
13	1,558.6	779.8		1,540.6	P	1,394.6	697.8	1,377.6	1,376.6	11
14	1,801.6	901.3		1,783.6	Y+80	1,297.6	649.3	1,280.6	1,279.6	10
15	1,872.7	936.8		1,854.7	A	1,054.6	527.8	1,037.5	1,036.5	9
16	1,987.7	994.4		1,969.7	D	983.5	492.3	966.5	965.5	8
17	2,084.7	1,042.9		2,066.7	P	868.5	434.7	851.5	850.5	7
18	2,213.8	1,107.4		2,195.8	E	771.4	386.2	754.4	753.4	6
19	2,342.8	1,171.9		2,324.8	E	642.4	321.7	625.4	624.4	5
20	2,455.9	1,228.5		2,437.9	I	513.4	257.2	496.3		4
21	2,612.0	1,306.5	2,595.0	2,594.0	R	400.3	200.6	383.2		3
22	2,709.1	1,355.0	2,692.0	2,691.1	P	244.2		227.1		2
23	2,855.2	1,428.1	2,838.2	2,837.2	K	147.1		130.1		1

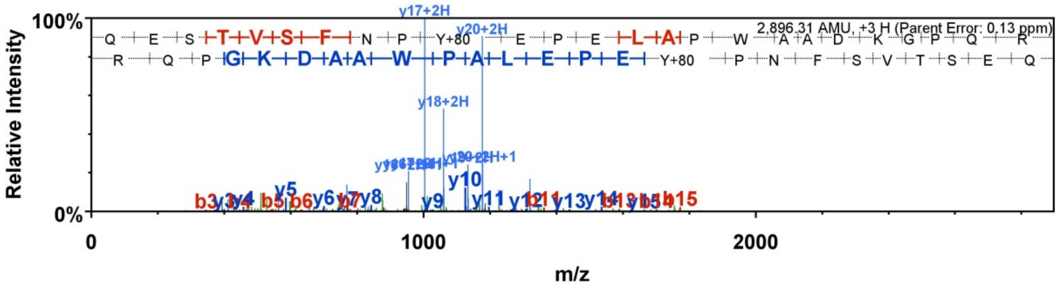
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
EALPMDTEVYESPYADPEEIRPK	Mox; pS; pY	952.3985	2854.1737	3	2854.1697	0.004	21.26

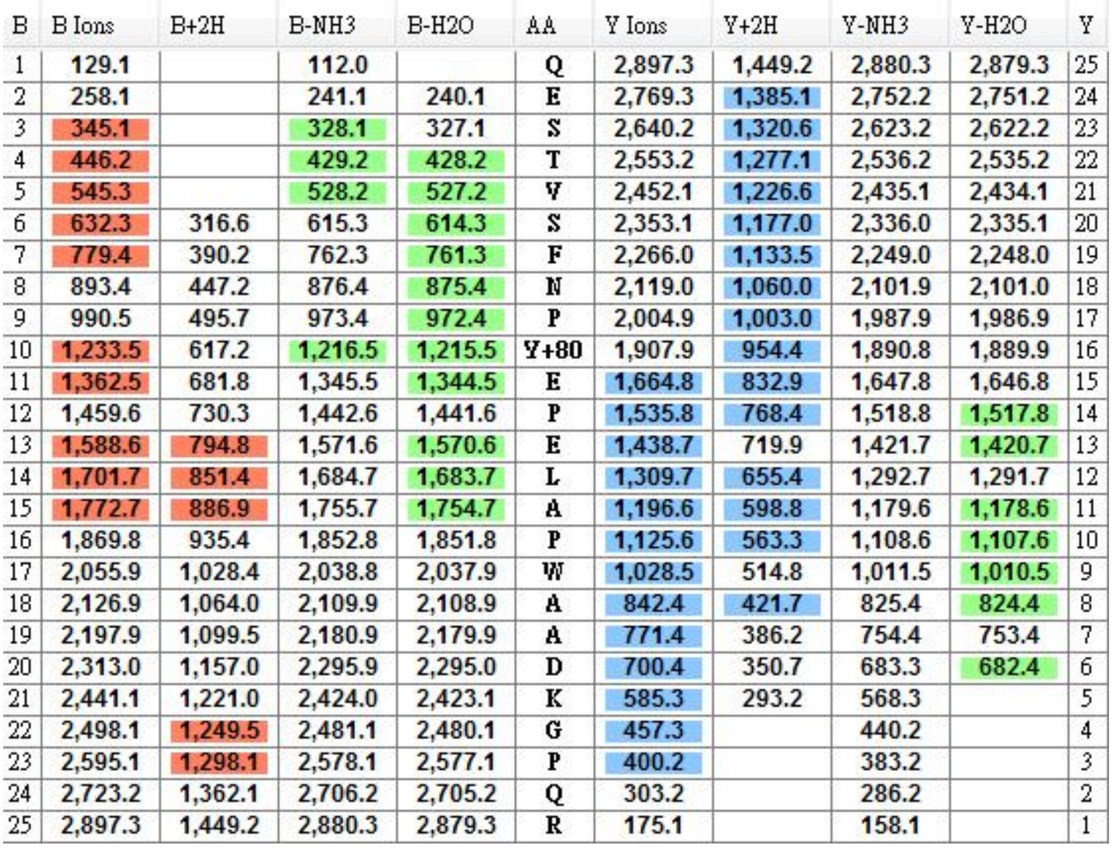




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	2,855.2	1,428.1	2,838.2	2,837.2	23
2	201.1			183.1	A	2,726.1	1,363.6	2,709.1	2,708.1	22
3	314.2			296.2	L	2,655.1	1,328.1	2,638.1	2,637.1	21
4	411.2			393.2	P	2,542.0	1,271.5	2,525.0	2,524.0	20
5	558.3			540.2	M+16	2,445.0	1,223.0	2,427.9	2,427.0	19
6	673.3	337.1		655.3	D	2,297.9	1,149.5	2,280.9	2,279.9	18
7	774.3	387.7		756.3	T	2,182.9	1,092.0	2,165.9	2,164.9	17
8	903.4	452.2		885.4	E	2,081.9	1,041.4	2,064.8	2,063.8	16
9	1,002.4	501.7		984.4	V	1,952.8	976.9	1,935.8	1,934.8	15
10	1,165.5	583.3		1,147.5	Y	1,853.7	927.4	1,836.7	1,835.7	14
11	1,294.6	647.8		1,276.5	E	1,690.7	845.8	1,673.6	1,672.7	13
12	1,461.5	731.3		1,443.5	S+80	1,561.6	781.3	1,544.6	1,543.6	12
13	1,558.6	779.8		1,540.6	P	1,394.6	697.8	1,377.6	1,376.6	11
14	1,801.6	901.3		1,783.6	Y+80	1,297.6	649.3	1,280.6	1,279.6	10
15	1,872.7	936.8		1,854.7	A	1,054.6	527.8	1,037.5	1,036.5	9
16	1,987.7	994.4		1,969.7	D	983.5	492.3	966.5	965.5	8
17	2,084.7	1,042.9		2,066.7	P	868.5	434.7	851.5	850.5	7
18	2,213.8	1,107.4		2,195.8	E	771.4	386.2	754.4	753.4	6
19	2,342.8	1,171.9		2,324.8	E	642.4	321.7	625.4	624.4	5
20	2,455.9	1,228.5		2,437.9	I	513.4	257.2	496.3		4
21	2,612.0	1,306.5	2,595.0	2,594.0	R	400.3	200.6	383.2		3
22	2,709.1	1,355.0	2,692.0	2,691.1	P	244.2		227.1		2
23	2,855.2	1,428.1	2,838.2	2,837.2	K	147.1		130.1		1

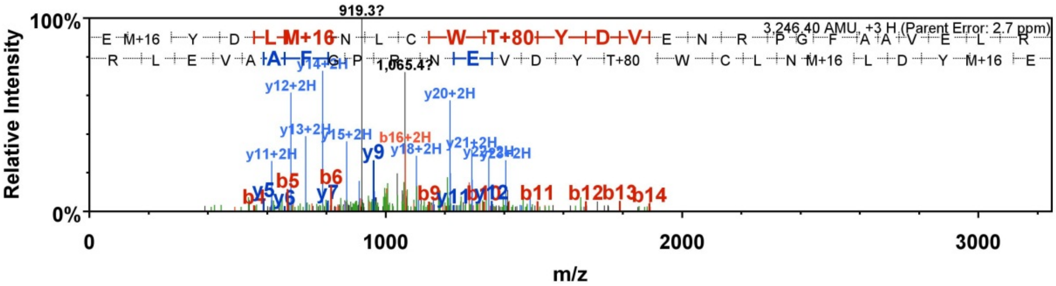
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
QESTVSFNPYEPELAPWAADKGPQR	pY	966.4431	2896.3075	3	2896.3069	0.0006	82.45

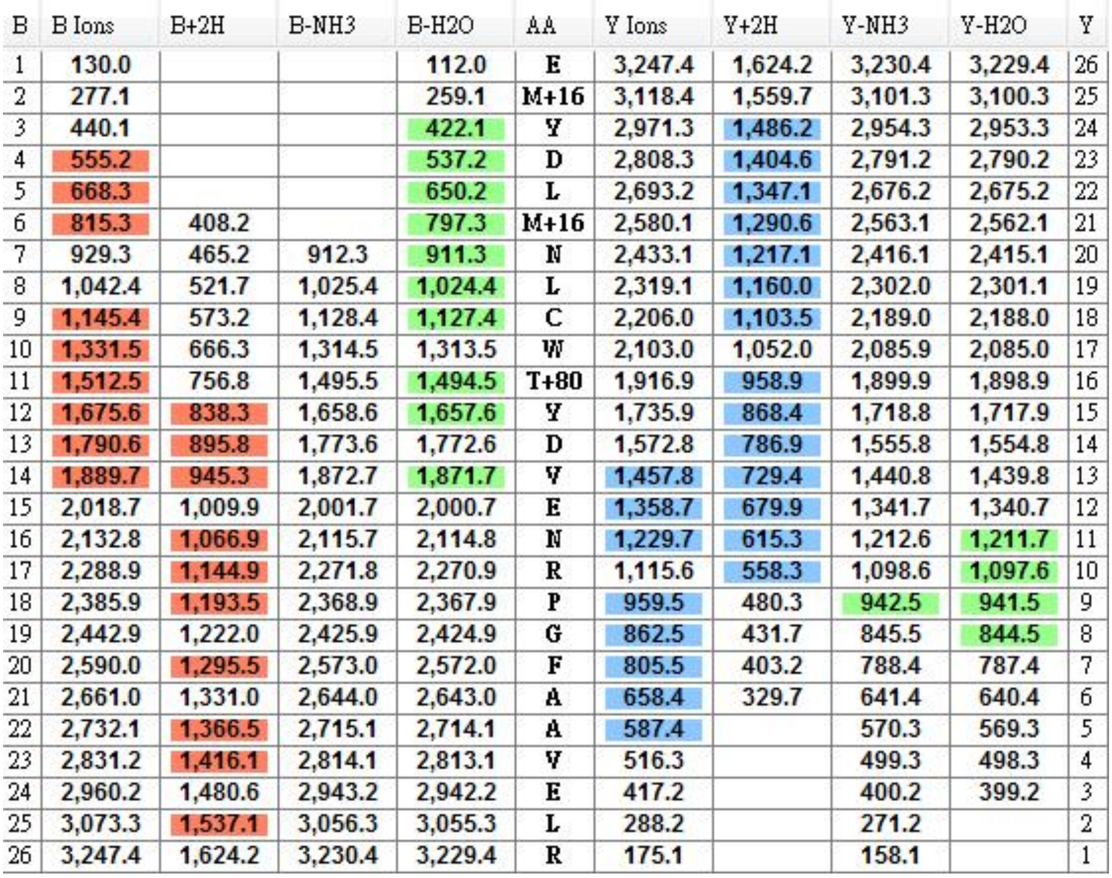




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	129.1		112.0		Q	2,897.3	1,449.2	2,880.3	2,879.3	25
2	258.1		241.1	240.1	E	2,769.3	1,385.1	2,752.2	2,751.2	24
3	345.1		328.1	327.1	S	2,640.2	1,320.6	2,623.2	2,622.2	23
4	446.2		429.2	428.2	T	2,553.2	1,277.1	2,536.2	2,535.2	22
5	545.3		528.2	527.2	V	2,452.1	1,226.6	2,435.1	2,434.1	21
6	632.3	316.6	615.3	614.3	S	2,353.1	1,177.0	2,336.0	2,335.1	20
7	779.4	390.2	762.3	761.3	F	2,266.0	1,133.5	2,249.0	2,248.0	19
8	893.4	447.2	876.4	875.4	N	2,119.0	1,060.0	2,101.9	2,101.0	18
9	990.5	495.7	973.4	972.4	P	2,004.9	1,003.0	1,987.9	1,986.9	17
10	1,233.5	617.2	1,216.5	1,215.5	Y+80	1,907.9	954.4	1,890.8	1,889.9	16
11	1,362.5	681.8	1,345.5	1,344.5	E	1,664.8	832.9	1,647.8	1,646.8	15
12	1,459.6	730.3	1,442.6	1,441.6	P	1,535.8	768.4	1,518.8	1,517.8	14
13	1,588.6	794.8	1,571.6	1,570.6	E	1,438.7	719.9	1,421.7	1,420.7	13
14	1,701.7	851.4	1,684.7	1,683.7	L	1,309.7	655.4	1,292.7	1,291.7	12
15	1,772.7	886.9	1,755.7	1,754.7	A	1,196.6	598.8	1,179.6	1,178.6	11
16	1,869.8	935.4	1,852.8	1,851.8	P	1,125.6	563.3	1,108.6	1,107.6	10
17	2,055.9	1,028.4	2,038.8	2,037.9	W	1,028.5	514.8	1,011.5	1,010.5	9
18	2,126.9	1,064.0	2,109.9	2,108.9	A	842.4	421.7	825.4	824.4	8
19	2,197.9	1,099.5	2,180.9	2,179.9	A	771.4	386.2	754.4	753.4	7
20	2,313.0	1,157.0	2,295.9	2,295.0	D	700.4	350.7	683.3	682.4	6
21	2,441.1	1,221.0	2,424.0	2,423.1	K	585.3	293.2	568.3		5
22	2,498.1	1,249.5	2,481.1	2,480.1	G	457.3		440.2		4
23	2,595.1	1,298.1	2,578.1	2,577.1	P	400.2		383.2		3
24	2,723.2	1,362.1	2,706.2	2,705.2	Q	303.2		286.2		2
25	2,897.3	1,449.2	2,880.3	2,879.3	R	175.1		158.1		1

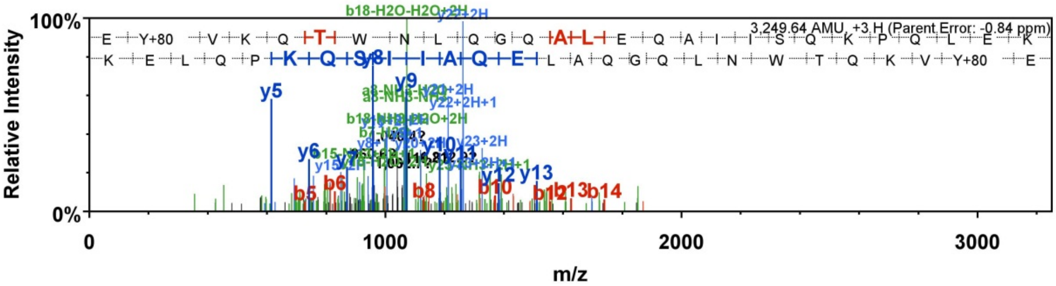
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
EMYDLMNLCWTYDVENRPGFAAVELR	2 Mox; pT	1083.139	3246.3952	3	3246.3861	0.009	49.45

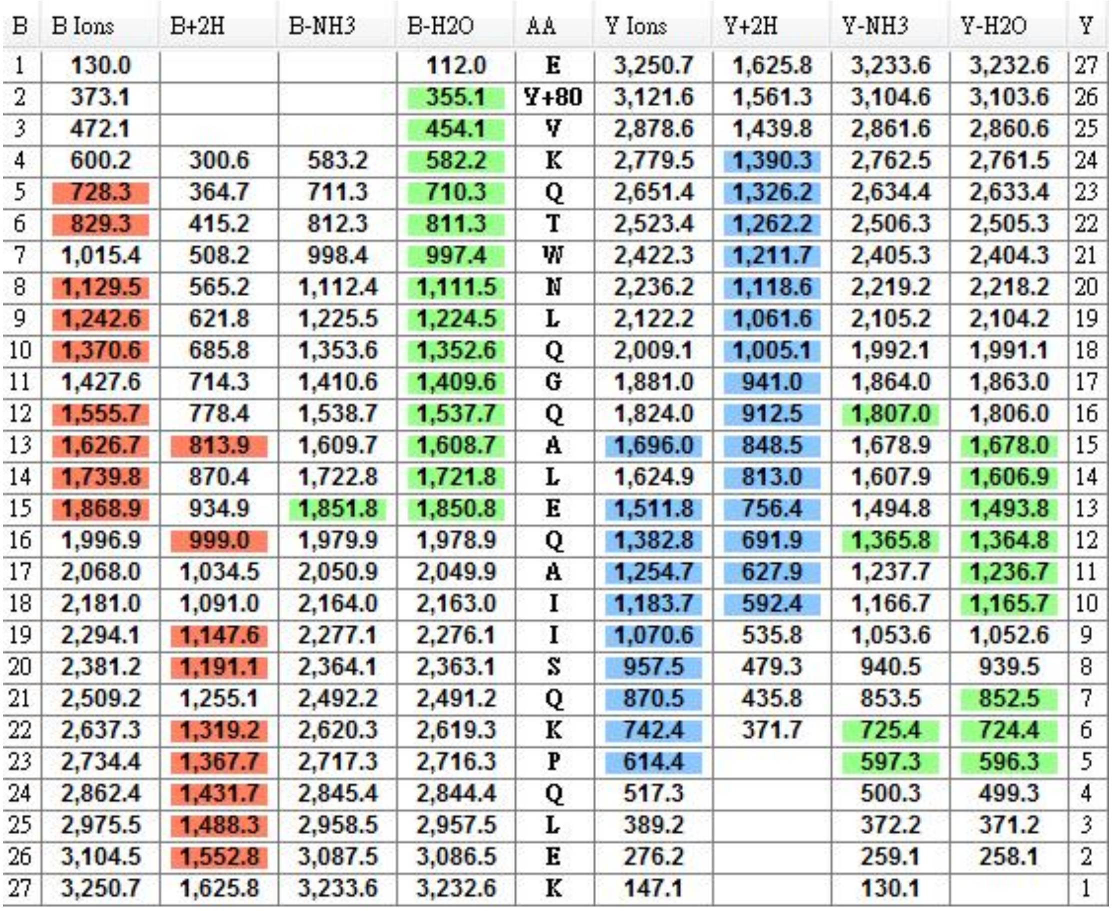




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	3,247.4	1,624.2	3,230.4	3,229.4	26
2	277.1			259.1	M+16	3,118.4	1,559.7	3,101.3	3,100.3	25
3	440.1			422.1	Y	2,971.3	1,486.2	2,954.3	2,953.3	24
4	555.2			537.2	D	2,808.3	1,404.6	2,791.2	2,790.2	23
5	668.3			650.2	L	2,693.2	1,347.1	2,676.2	2,675.2	22
6	815.3	408.2		797.3	M+16	2,580.1	1,290.6	2,563.1	2,562.1	21
7	929.3	465.2	912.3	911.3	N	2,433.1	1,217.1	2,416.1	2,415.1	20
8	1,042.4	521.7	1,025.4	1,024.4	L	2,319.1	1,160.0	2,302.0	2,301.1	19
9	1,145.4	573.2	1,128.4	1,127.4	C	2,206.0	1,103.5	2,189.0	2,188.0	18
10	1,331.5	666.3	1,314.5	1,313.5	W	2,103.0	1,052.0	2,085.9	2,085.0	17
11	1,512.5	756.8	1,495.5	1,494.5	T+80	1,916.9	958.9	1,899.9	1,898.9	16
12	1,675.6	838.3	1,658.6	1,657.6	Y	1,735.9	868.4	1,718.8	1,717.9	15
13	1,790.6	895.8	1,773.6	1,772.6	D	1,572.8	786.9	1,555.8	1,554.8	14
14	1,889.7	945.3	1,872.7	1,871.7	V	1,457.8	729.4	1,440.8	1,439.8	13
15	2,018.7	1,009.9	2,001.7	2,000.7	E	1,358.7	679.9	1,341.7	1,340.7	12
16	2,132.8	1,066.9	2,115.7	2,114.8	N	1,229.7	615.3	1,212.6	1,211.7	11
17	2,288.9	1,144.9	2,271.8	2,270.9	R	1,115.6	558.3	1,098.6	1,097.6	10
18	2,385.9	1,193.5	2,368.9	2,367.9	P	959.5	480.3	942.5	941.5	9
19	2,442.9	1,222.0	2,425.9	2,424.9	G	862.5	431.7	845.5	844.5	8
20	2,590.0	1,295.5	2,573.0	2,572.0	F	805.5	403.2	788.4	787.4	7
21	2,661.0	1,331.0	2,644.0	2,643.0	A	658.4	329.7	641.4	640.4	6
22	2,732.1	1,366.5	2,715.1	2,714.1	A	587.4		570.3	569.3	5
23	2,831.2	1,416.1	2,814.1	2,813.1	V	516.3		499.3	498.3	4
24	2,960.2	1,480.6	2,943.2	2,942.2	E	417.2		400.2	399.2	3
25	3,073.3	1,537.1	3,056.3	3,055.3	L	288.2		271.2		2
26	3,247.4	1,624.2	3,230.4	3,229.4	R	175.1		158.1		1

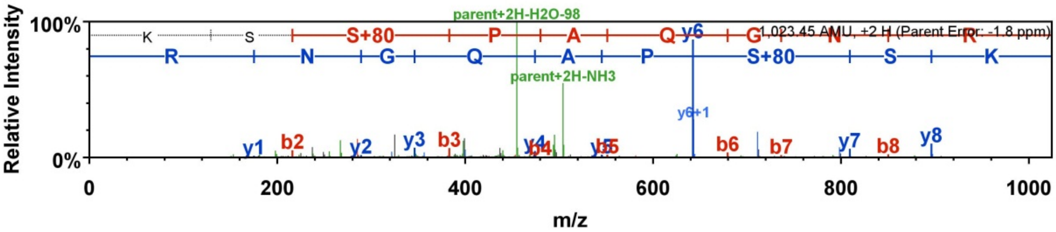
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
EYVKQTWNLQGQALEQAIISQKPQLEK	pY	1084.221	3249.6412	3	3249.6434	-0.0023	45.43

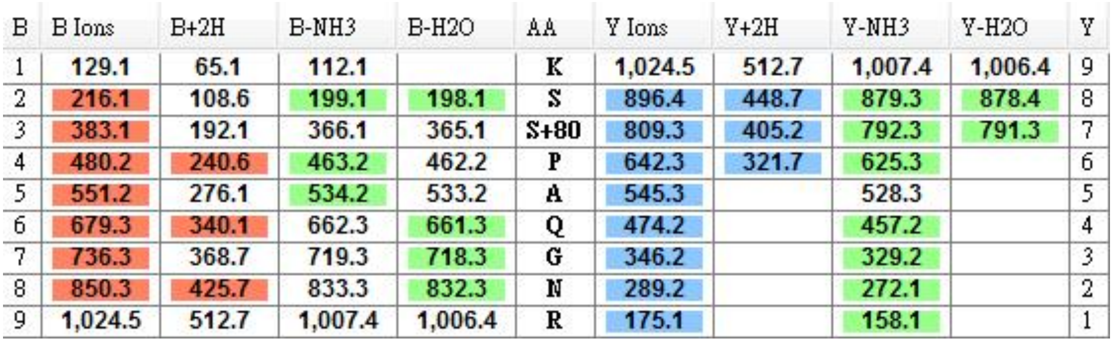




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	3,250.7	1,625.8	3,233.6	3,232.6	27
2	373.1			355.1	Y+80	3,121.6	1,561.3	3,104.6	3,103.6	26
3	472.1			454.1	V	2,878.6	1,439.8	2,861.6	2,860.6	25
4	600.2	300.6	583.2	582.2	K	2,779.5	1,390.3	2,762.5	2,761.5	24
5	728.3	364.7	711.3	710.3	Q	2,651.4	1,326.2	2,634.4	2,633.4	23
6	829.3	415.2	812.3	811.3	T	2,523.4	1,262.2	2,506.3	2,505.3	22
7	1,015.4	508.2	998.4	997.4	W	2,422.3	1,211.7	2,405.3	2,404.3	21
8	1,129.5	565.2	1,112.4	1,111.5	N	2,236.2	1,118.6	2,219.2	2,218.2	20
9	1,242.6	621.8	1,225.5	1,224.5	L	2,122.2	1,061.6	2,105.2	2,104.2	19
10	1,370.6	685.8	1,353.6	1,352.6	Q	2,009.1	1,005.1	1,992.1	1,991.1	18
11	1,427.6	714.3	1,410.6	1,409.6	G	1,881.0	941.0	1,864.0	1,863.0	17
12	1,555.7	778.4	1,538.7	1,537.7	Q	1,824.0	912.5	1,807.0	1,806.0	16
13	1,626.7	813.9	1,609.7	1,608.7	A	1,696.0	848.5	1,678.9	1,678.0	15
14	1,739.8	870.4	1,722.8	1,721.8	L	1,624.9	813.0	1,607.9	1,606.9	14
15	1,868.9	934.9	1,851.8	1,850.8	E	1,511.8	756.4	1,494.8	1,493.8	13
16	1,996.9	999.0	1,979.9	1,978.9	Q	1,382.8	691.9	1,365.8	1,364.8	12
17	2,068.0	1,034.5	2,050.9	2,049.9	A	1,254.7	627.9	1,237.7	1,236.7	11
18	2,181.0	1,091.0	2,164.0	2,163.0	I	1,183.7	592.4	1,166.7	1,165.7	10
19	2,294.1	1,147.6	2,277.1	2,276.1	I	1,070.6	535.8	1,053.6	1,052.6	9
20	2,381.2	1,191.1	2,364.1	2,363.1	S	957.5	479.3	940.5	939.5	8
21	2,509.2	1,255.1	2,492.2	2,491.2	Q	870.5	435.8	853.5	852.5	7
22	2,637.3	1,319.2	2,620.3	2,619.3	K	742.4	371.7	725.4	724.4	6
23	2,734.4	1,367.7	2,717.3	2,716.3	P	614.4		597.3	596.3	5
24	2,862.4	1,431.7	2,845.4	2,844.4	Q	517.3		500.3	499.3	4
25	2,975.5	1,488.3	2,958.5	2,957.5	L	389.2		372.2	371.2	3
26	3,104.5	1,552.8	3,087.5	3,086.5	E	276.2		259.1	258.1	2
27	3,250.7	1,625.8	3,233.6	3,232.6	K	147.1		130.1		1

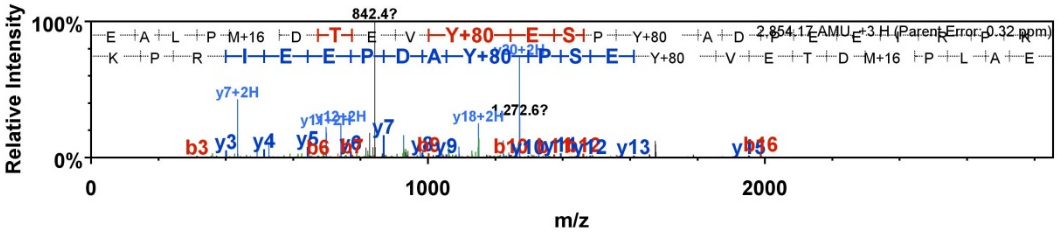
Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
KS**S**PAQGNR	pS	512.7313	1023.448	2	1023.4498	-0.0018	35.51

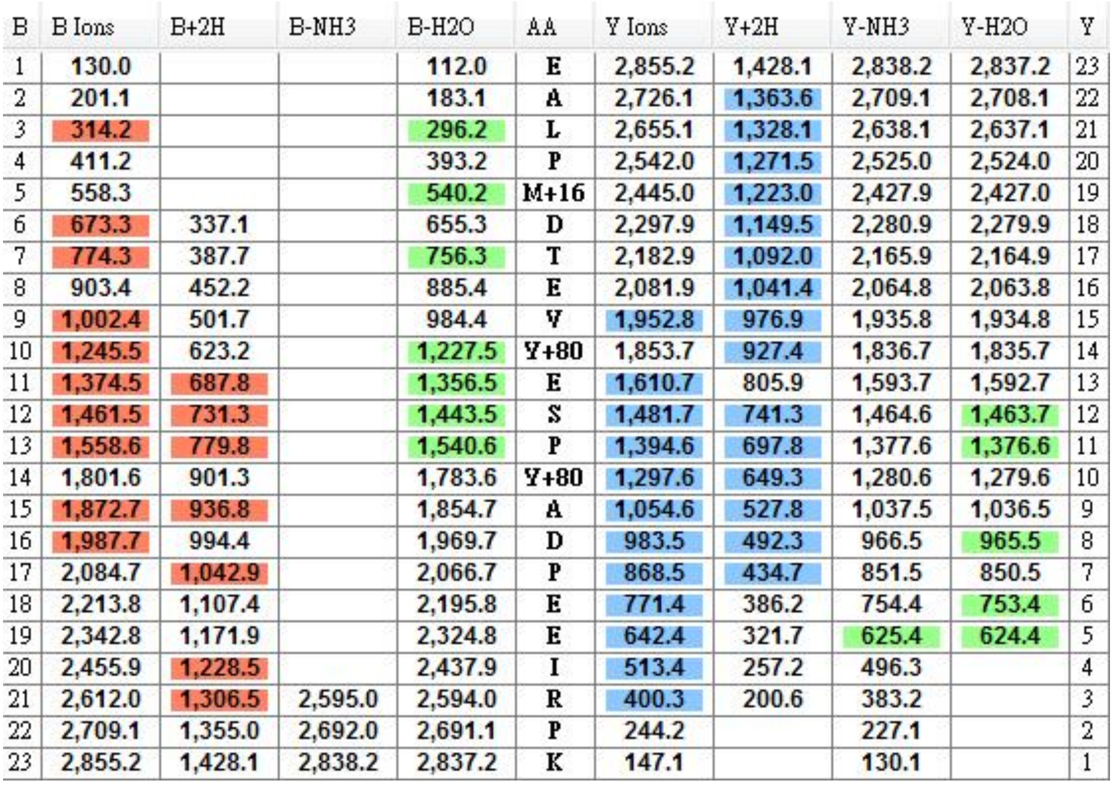




B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	129.1	65.1	112.1		K	1,024.5	512.7	1,007.4	1,006.4	9
2	216.1	108.6	199.1	198.1	S	896.4	448.7	879.3	878.4	8
3	383.1	192.1	366.1	365.1	S+80	809.3	405.2	792.3	791.3	7
4	480.2	240.6	463.2	462.2	P	642.3	321.7	625.3		6
5	551.2	276.1	534.2	533.2	A	545.3		528.3		5
6	679.3	340.1	662.3	661.3	Q	474.2		457.2		4
7	736.3	368.7	719.3	718.3	G	346.2		329.2		3
8	850.3	425.7	833.3	832.3	N	289.2		272.1		2
9	1,024.5	512.7	1,007.4	1,006.4	R	175.1		158.1		1

Sequence	Modification	Exp. m/z	Exp. M.W.	Charge	Cal. M.W.	Delta	Score
EALPMDTEVYESPYADPEEIRPK	Mox; 2 pY	952.3976	2854.171	3	2854.1697	0.0013	60.41



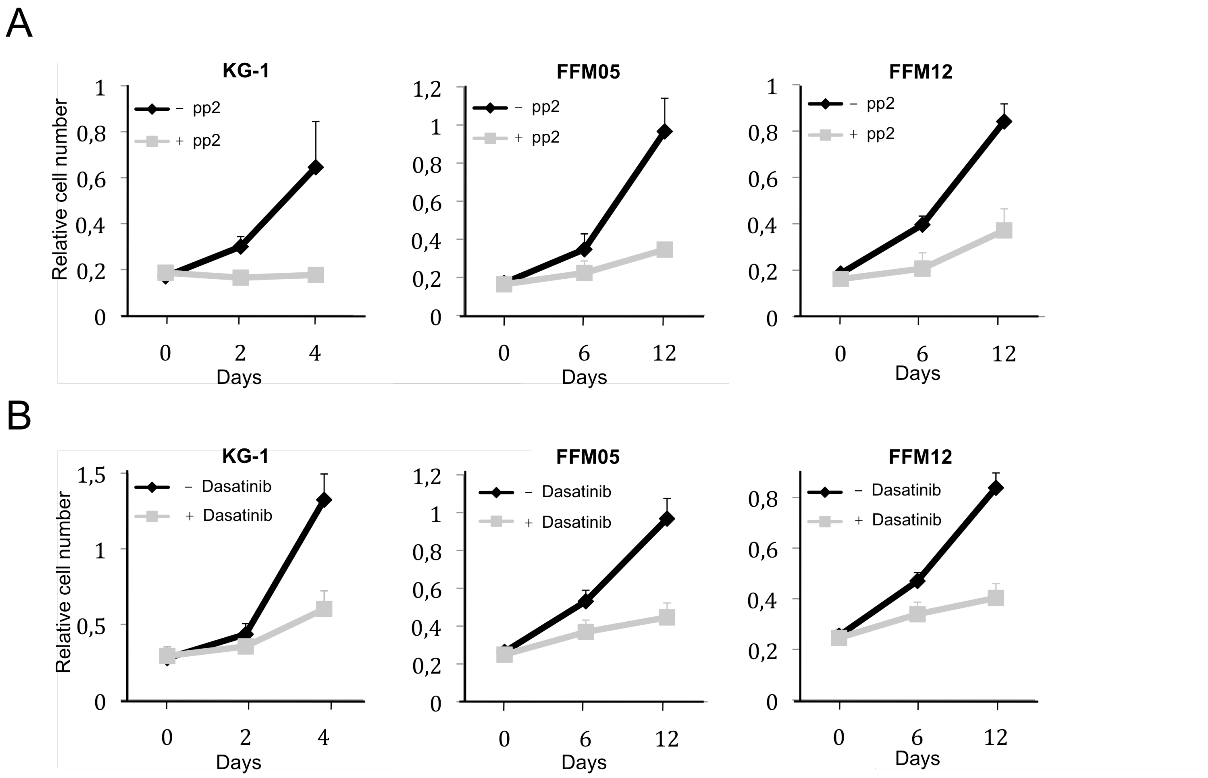


B	B Ions	B+2H	B-NH3	B-H2O	AA	Y Ions	Y+2H	Y-NH3	Y-H2O	Y
1	130.0			112.0	E	2,855.2	1,428.1	2,838.2	2,837.2	23
2	201.1			183.1	A	2,726.1	1,363.6	2,709.1	2,708.1	22
3	314.2			296.2	L	2,655.1	1,328.1	2,638.1	2,637.1	21
4	411.2			393.2	P	2,542.0	1,271.5	2,525.0	2,524.0	20
5	558.3			540.2	M+16	2,445.0	1,223.0	2,427.9	2,427.0	19
6	673.3	337.1		655.3	D	2,297.9	1,149.5	2,280.9	2,279.9	18
7	774.3	387.7		756.3	T	2,182.9	1,092.0	2,165.9	2,164.9	17
8	903.4	452.2		885.4	E	2,081.9	1,041.4	2,064.8	2,063.8	16
9	1,002.4	501.7		984.4	V	1,952.8	976.9	1,935.8	1,934.8	15
10	1,245.5	623.2		1,227.5	Y+80	1,853.7	927.4	1,836.7	1,835.7	14
11	1,374.5	687.8		1,356.5	E	1,610.7	805.9	1,593.7	1,592.7	13
12	1,461.5	731.3		1,443.5	S	1,481.7	741.3	1,464.6	1,463.7	12
13	1,558.6	779.8		1,540.6	P	1,394.6	697.8	1,377.6	1,376.6	11
14	1,801.6	901.3		1,783.6	Y+80	1,297.6	649.3	1,280.6	1,279.6	10
15	1,872.7	936.8		1,854.7	A	1,054.6	527.8	1,037.5	1,036.5	9
16	1,987.7	994.4		1,969.7	D	983.5	492.3	966.5	965.5	8
17	2,084.7	1,042.9		2,066.7	P	868.5	434.7	851.5	850.5	7
18	2,213.8	1,107.4		2,195.8	E	771.4	386.2	754.4	753.4	6
19	2,342.8	1,171.9		2,324.8	E	642.4	321.7	625.4	624.4	5
20	2,455.9	1,228.5		2,437.9	I	513.4	257.2	496.3		4
21	2,612.0	1,306.5	2,595.0	2,594.0	R	400.3	200.6	383.2		3
22	2,709.1	1,355.0	2,692.0	2,691.1	P	244.2		227.1		2
23	2,855.2	1,428.1	2,838.2	2,837.2	K	147.1		130.1		1

Supplementary figure 1

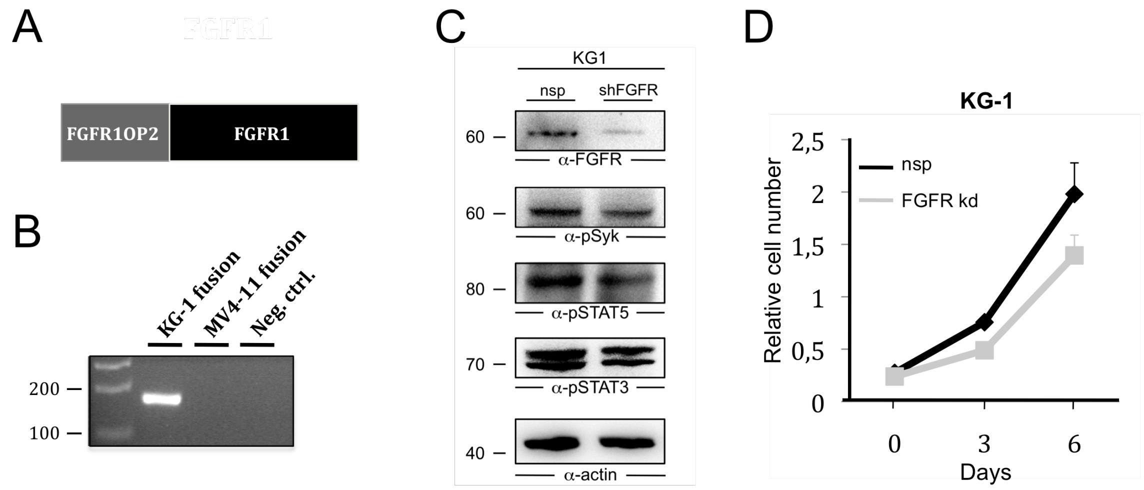
Annotated ESI-MSMS spectra of phosphorylated tryptic peptides derived from Syk.

Annotated Mascot MSMS spectra of phosphopeptides are shown and the corresponding assigned fragment ions. The table above the spectra lists the m/z values of the precursor ions, the charge state, the corresponding MW, the mass deviation, the peptide score (in MASCOT), the confirmed phosphorylation site, the identified sequence and the modification(s) of the sequenced peptide. Spectra were recorded on an Orbitrap MS (Thermo Fisher Scientific). The precursor in MS showed a mass accuracy of ≤ 2 ppm. At least one MSMS spectrum is shown for each p-site.



Supplementary figure 2

Growth curves of KG-1-, FFM05- and FFM12 cells that were left untreated/DMSO treated (black lines) or were treated **(A)** with the Src kinase inhibitor pp2 at a final concentration of 1μM (grey lines) or **(B)** with Dasatinib at a final concentration of 4nM (grey lines). Proliferation was monitored by an XTT-based assay as outlined in the *Methods* section.



Supplementary figure 3

(A) Schematic representation of the FGFR1OP2-FGFR1 fusion protein. **(B)** RT-PCR of the fusion region of the FGFR1OP2-FGFR1 fusion protein**.** The following primers were used: forward ATCAGTCGGCCTTGGAACTTA, reverse AGAAGAACCCCAGAGTTCATG **(C)** 48 hours after silencing of FGFR1, KG-1 cells were harvested and lysed. The respective lysates were subjected to immunoblot analysis using antibodies against FGFR1, pSTAT3, pSTAT5, pSyk and actin. **(D)** Growth curve of KG-1 cells that were treated with shRNAs against FGFR1 (grey line) or the respective control shRNAs (black line). Proliferation was monitored by an XTT-based assay.

UPN	Age	AML sec. to	WBC $^{x}10^9$/L (% blasts)	Karyotype	Molecular-genetic findings	Risk group
FFM05	60	MDS	2 (7%) BM: 25%	At onset: 44-45,XY,t(1;3)(q42;q27), del(5)(q14q33)-7,del(16)(q23),+MAI1,+Mar2	None (No FLT3-ITD mutations, no FLT3-kinase domain mutations, no Kit mutations)	HR
FFM12	24	-	7 (22%)	45,XX,-7[12]; 46,XX[8]	AML1/ETO; NRAS (No FLT3-ITD mutations, no FLT3-kinase domain mutations, no Kit mutations)	HR

Supplementary table 1:

Primary AML patient characteristics.

Primary AML cells of two patients were purified and cultured as outlined in the *Material and Methods* section and the respective primary AML cell lines are denominated as FFM05 and FFM12. Enlisted are the results of the cytogenetic and molecular-genetic analyses, the age of the patients, the initial white blood count (WBC) and the respective risk groups.

AML-specific p-sites	**B cell-specific p-sites**
S3/4	Y28
S9	S44
Y389	T256
S443	S306
T610	S316
-	T317
-	S319
-	S379
-	T384
-	T530
-	S579
-	T582

Supplementary table 3:

Cell type-specific phosphorylation patterns.

P-sites that were identified in AML cells and were not reported to be phosphorylated in B cells are outlined in the left column. P-sites that were previously identified in B cell antigen receptor stimulated B cells but not in AML cells are listed in the right column[26].