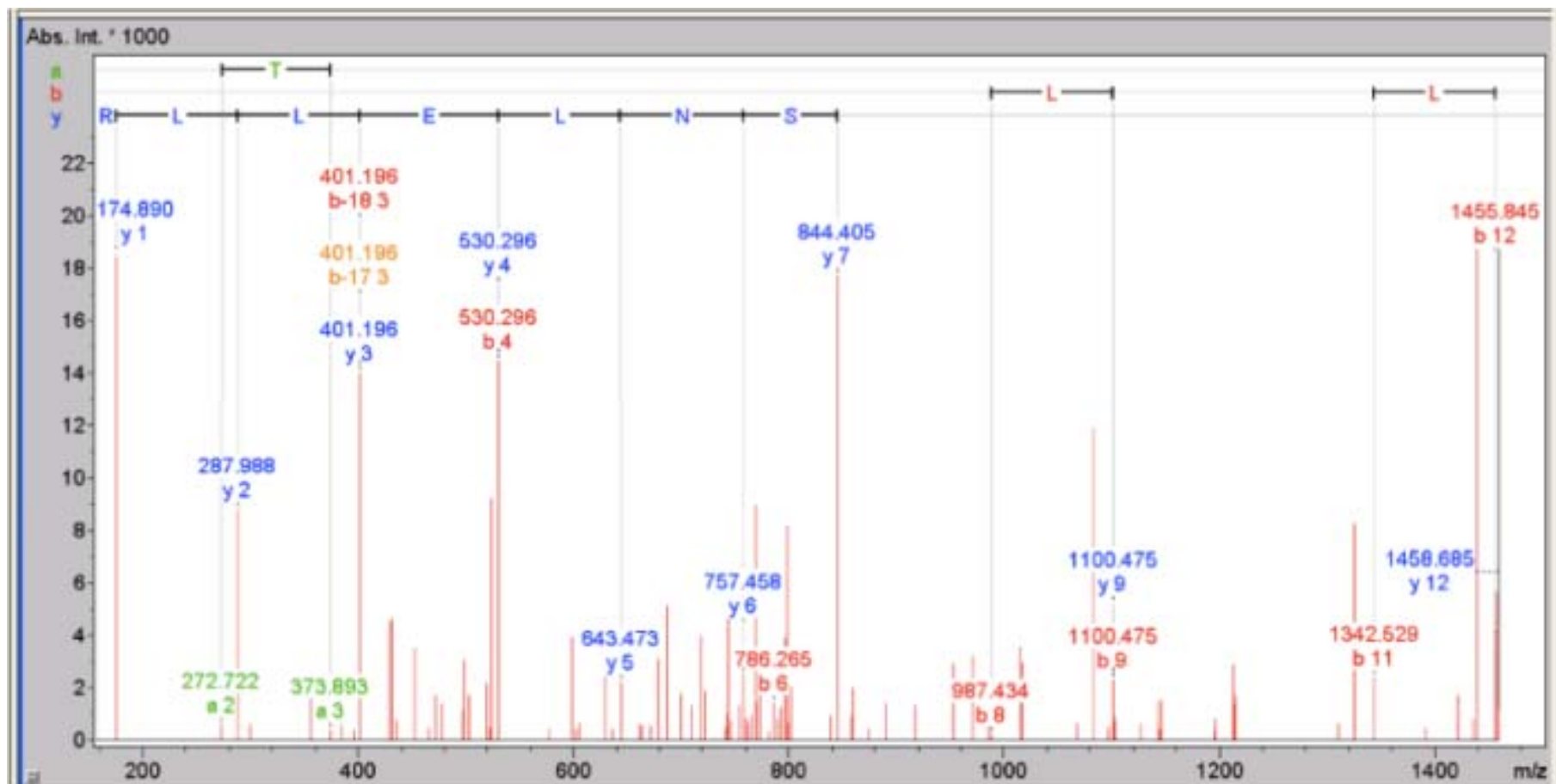


Supplemental Figure 1 : MS/MS spectra of modified peptides.

Spectra of all modifications shown in table 2 are presented.

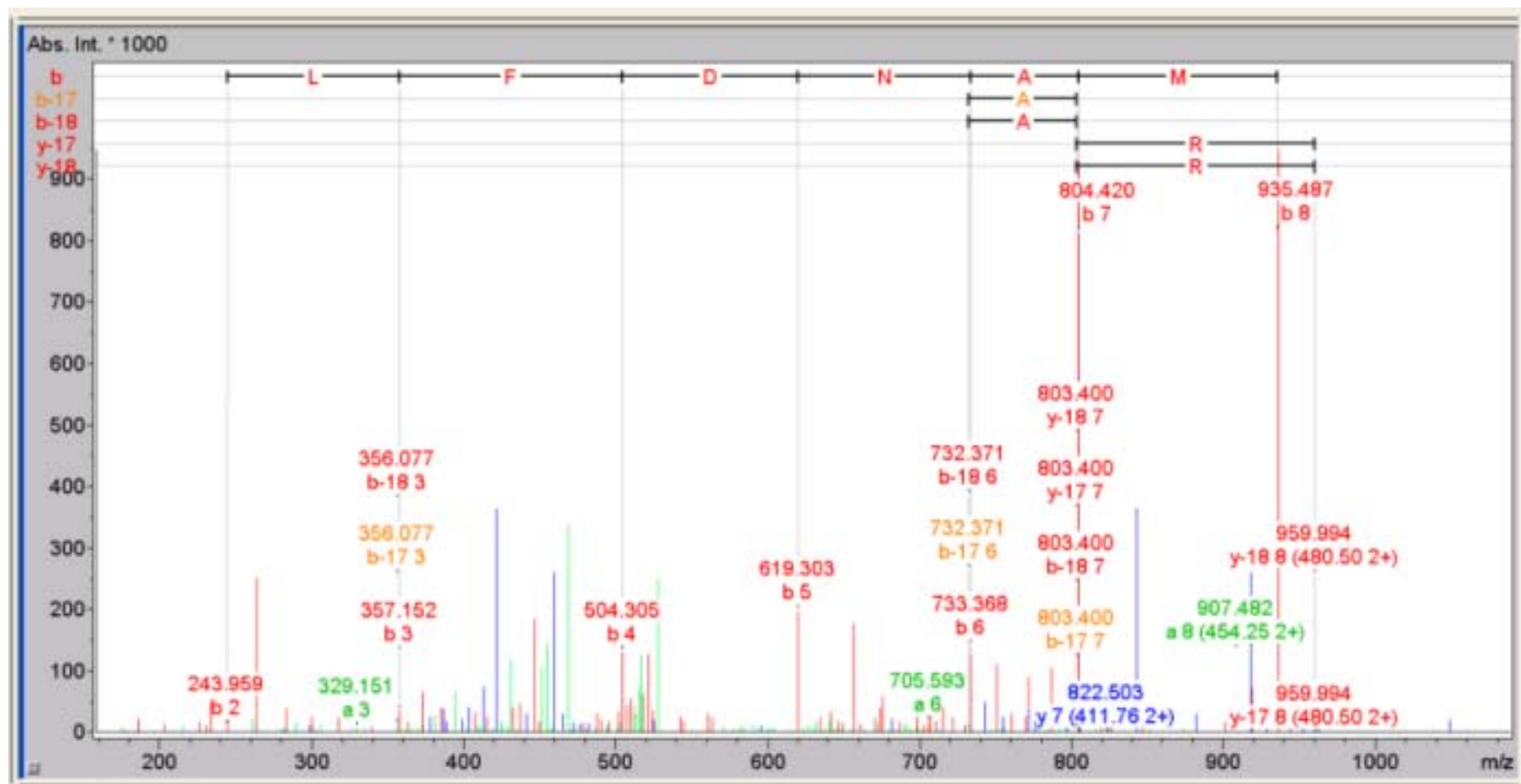
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 lower band	Mascot	Acetylation: E91	815.4321	2+
sequence (enzyme/ion score/mass error)				
91 R.E*ETQQKSNLELLR.I Acetylation(E) 103 (Try/49/0.0127)				



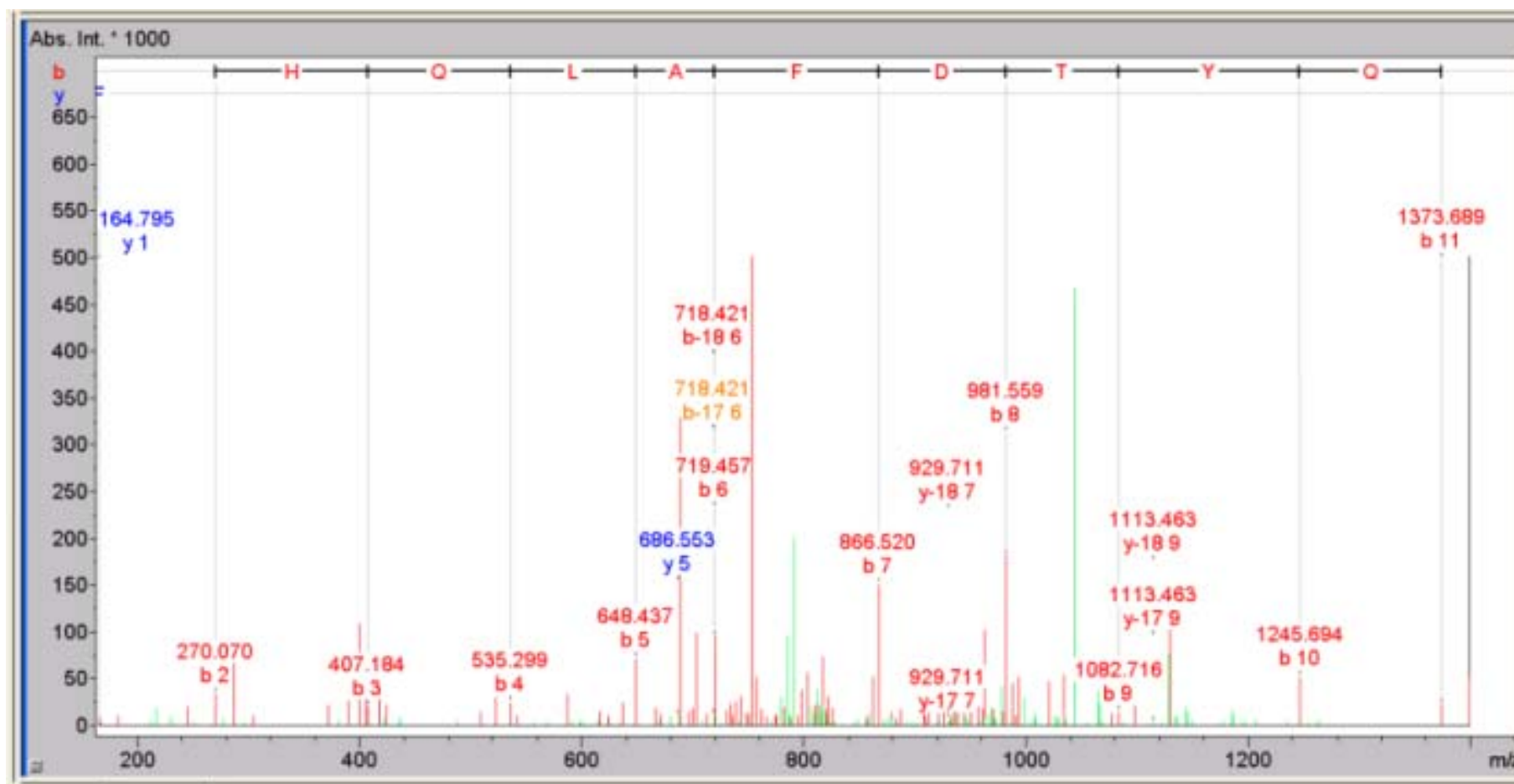
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Mascot	Amidation: L41	533.241	2+
sequence (enzyme/ion score/mass error)				
33 L.SRLFDNAML*.R Amidation(L) 41 (Chy/34/-0.0762)				



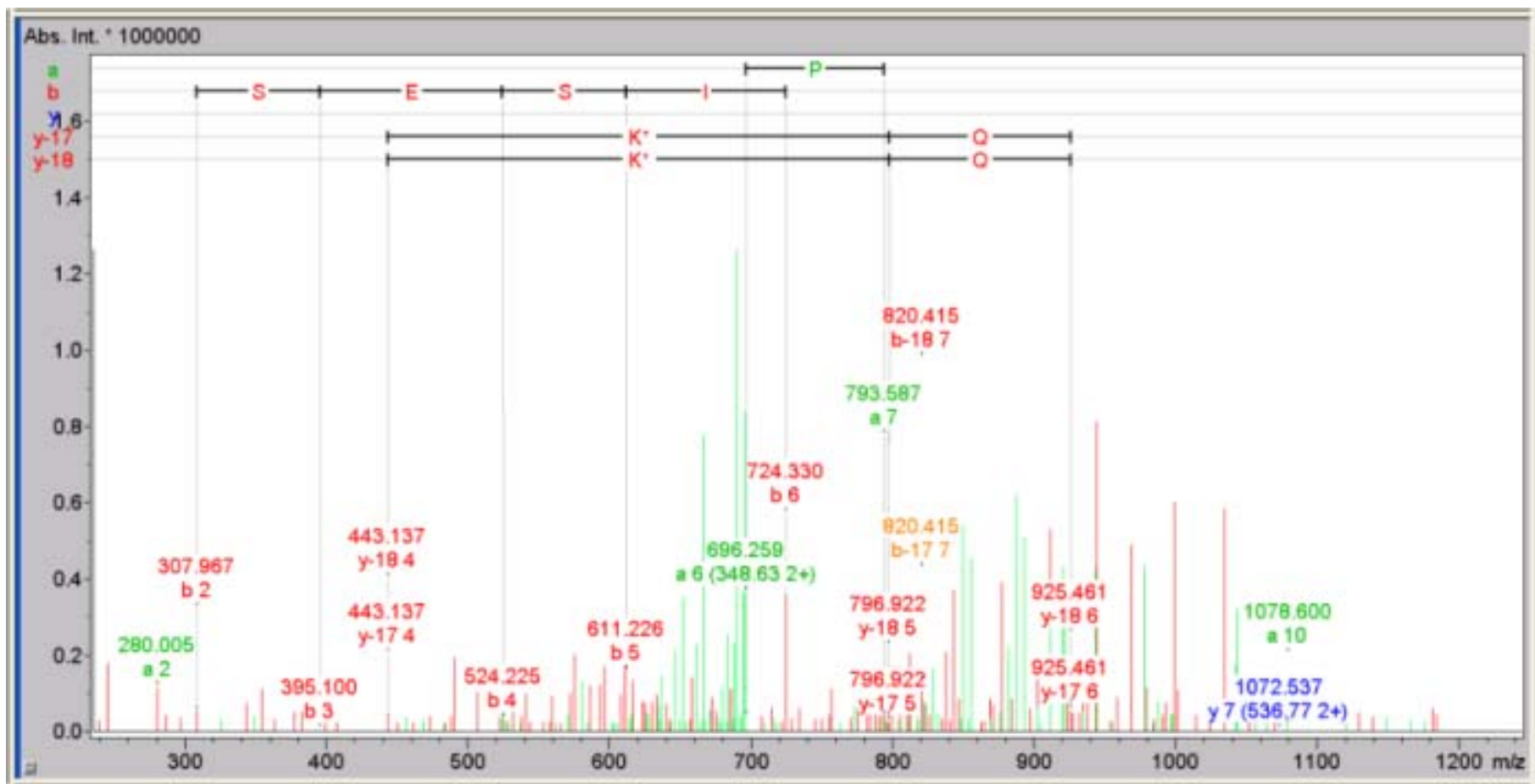
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Mascot	Amidation: F57	833.9581	2+
sequence (enzyme/ion score/mass error)				
45 H.RLHQLAFDTYQEF*.E Amidation(F) 57 (Chy/36/0.0753)				



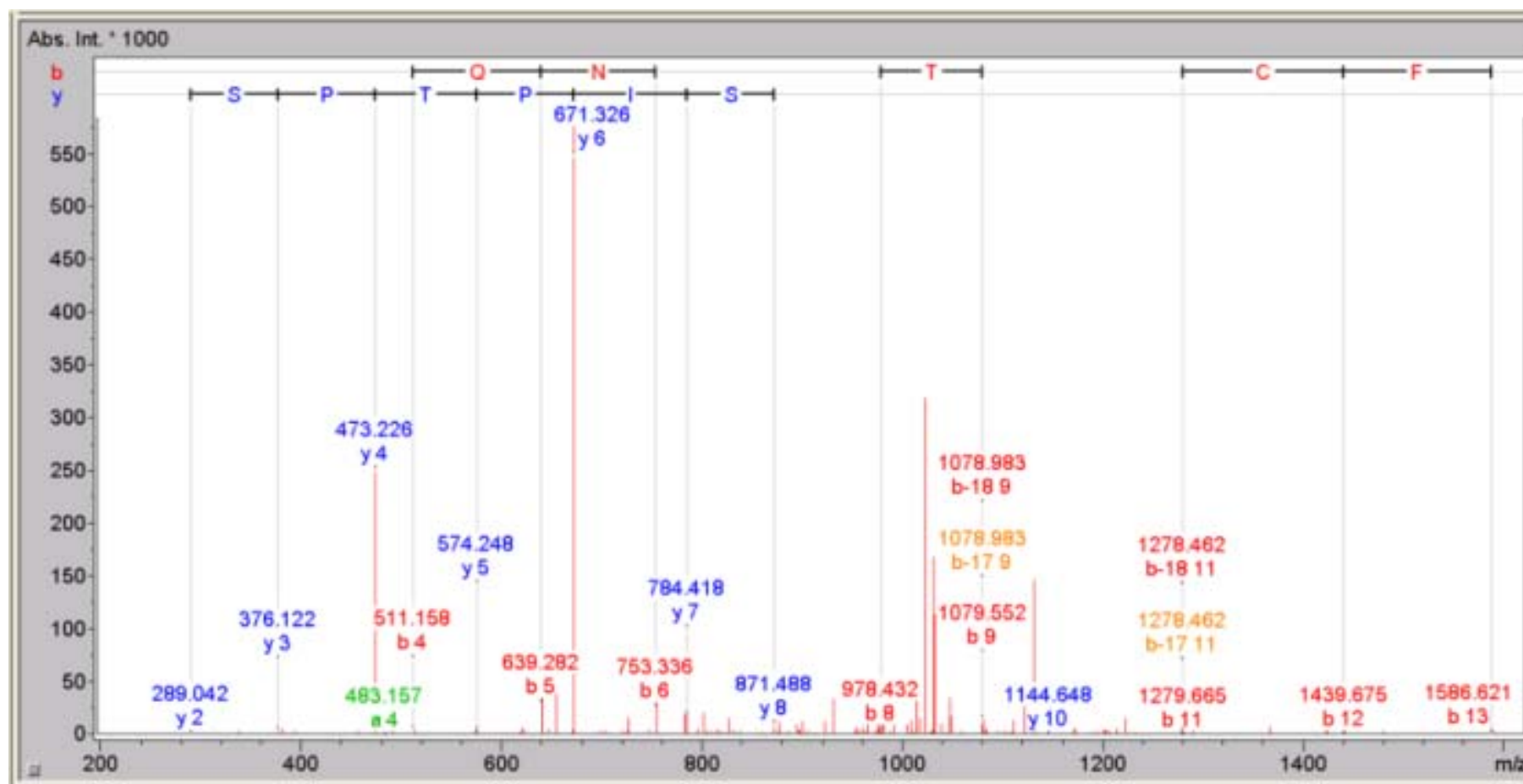
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Mascot	Biotinylation: K96	702.6032	3+
sequence (enzyme/ion score/mass error)				
79 L.CFSESIPTPSNREETQK*SNLE.L Biotinylation(K) 100 (Chy/57/0.1299)				



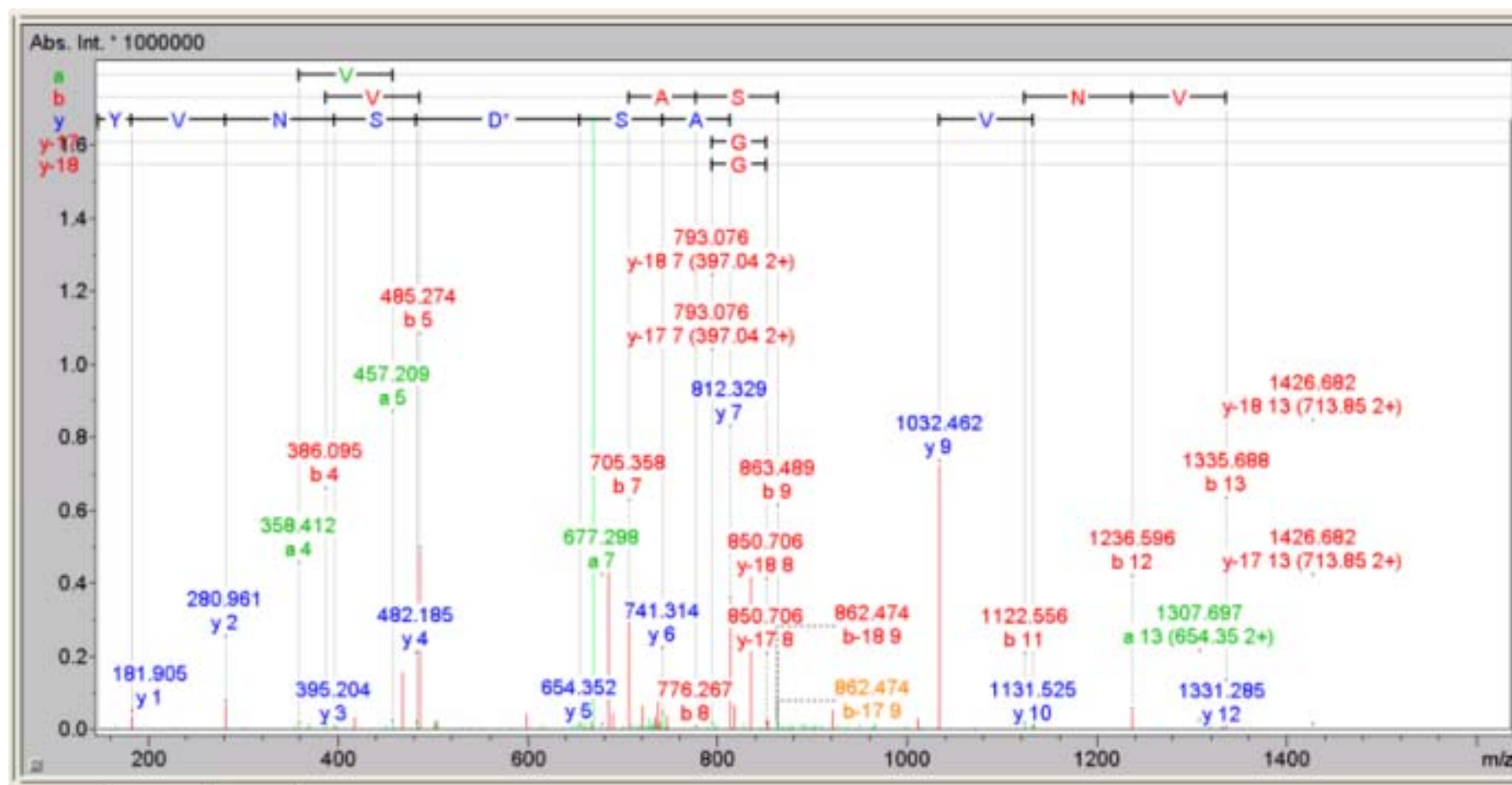
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Mascot	Carbamidomethylation: E82	910.7377	3+
sequence (enzyme/ion score/mass error)				
68 K.YSFLQNPQTSLCFSE*SIPTPSNR.E Carbamidomethylation(E) 90 (Try/46/-0.0843)				



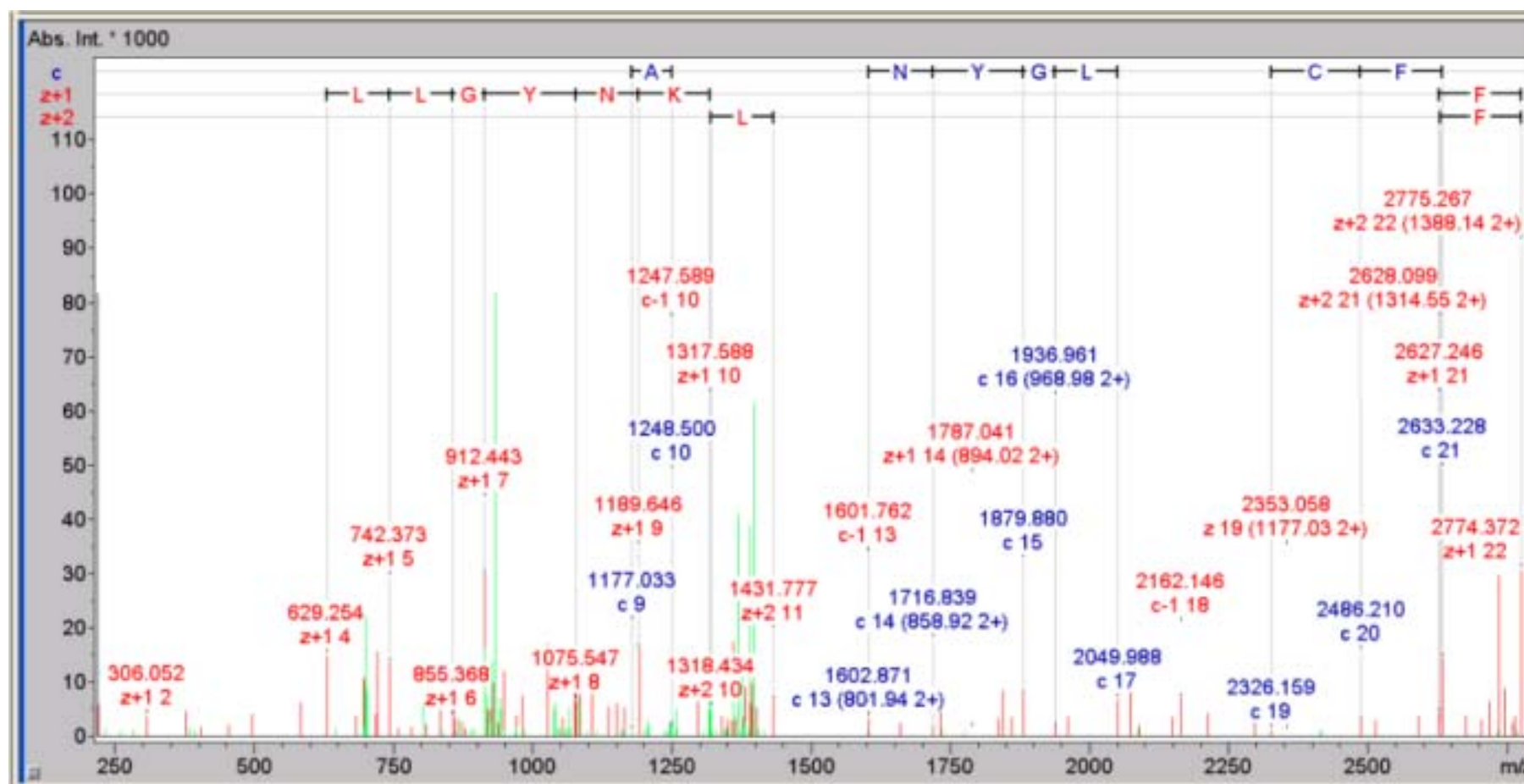
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Mascot	Carbamidomethylation: D133	758.856	2+
sequence (enzyme/ion score/mass error)				
124 F.ANSLVYGASD*SNVY.D Carbamidomethylation(D) 137 (Chy/35/0.0133)				



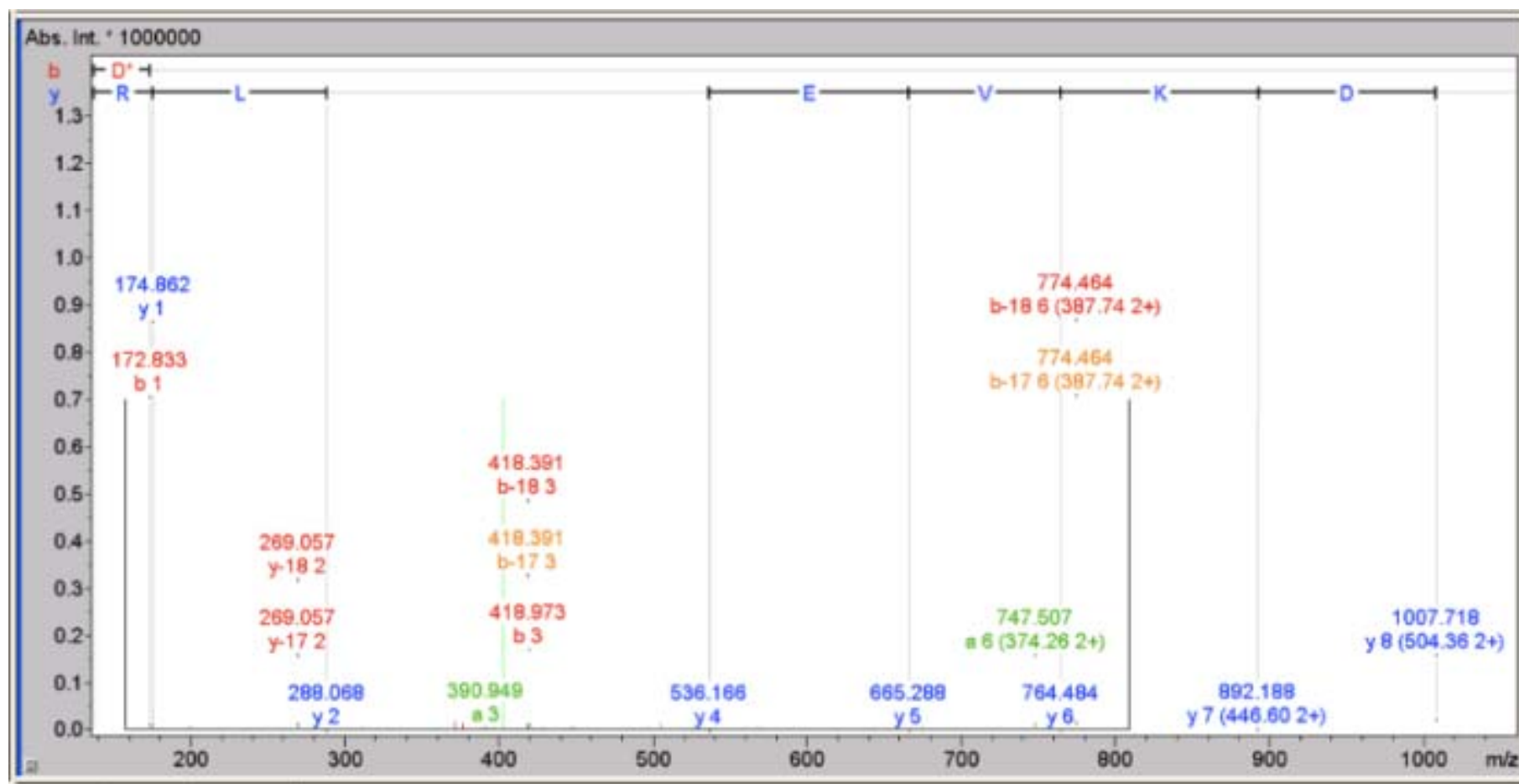
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Mascot	Carbamidomethylation: D180	698.3457	4+
sequence (enzyme/ion score/mass error)				
172 K.FD*TNSHNDD*ALLKNYGLLYCFR.K 2 Carbamidomethylation(D) 193 (Try/45/0.0669)				



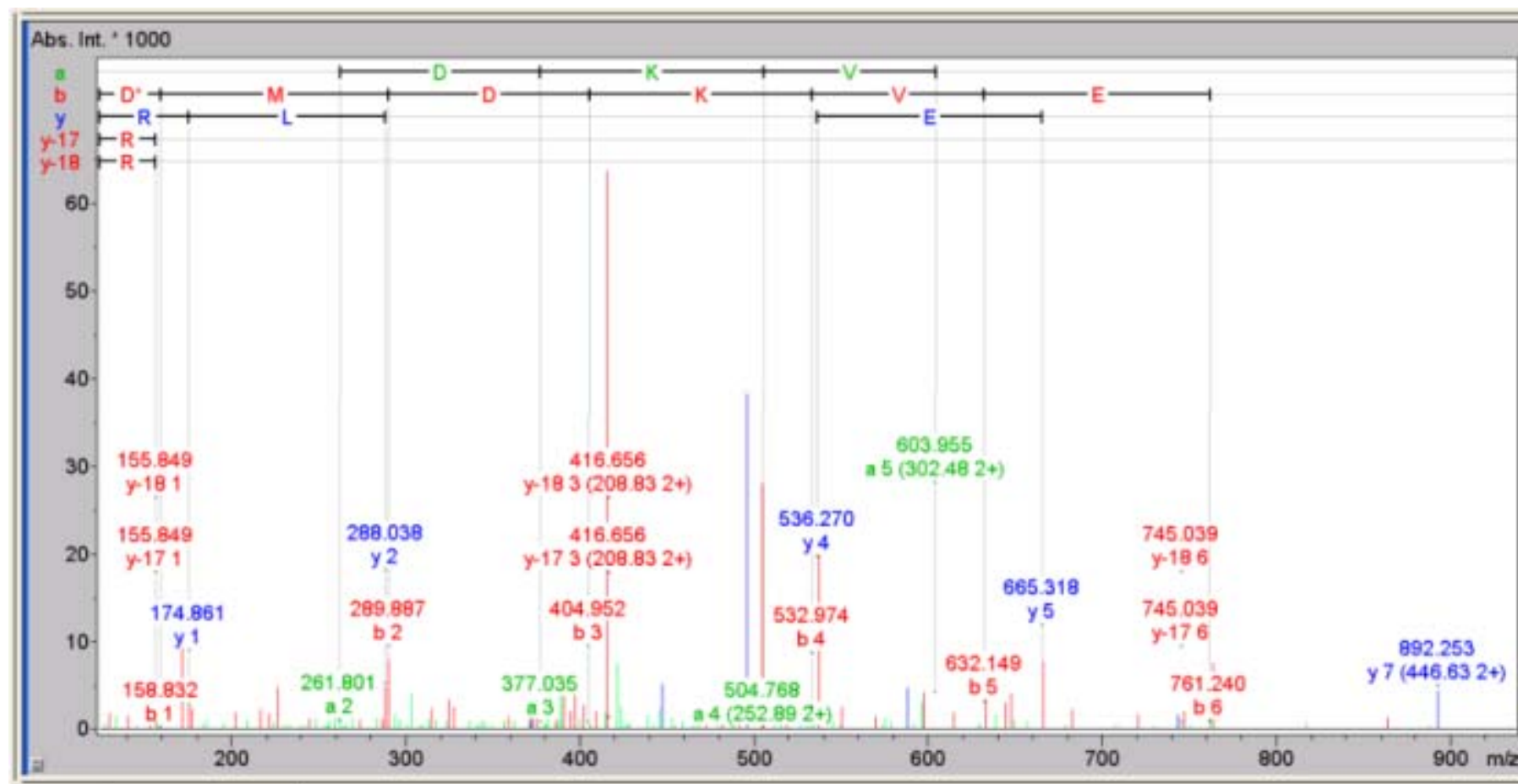
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Mascot	Carbamidomethylation: D195	437.5593	3+
sequence (enzyme/ion score/mass error)				
195 K.D*MDKVETFLR.I Carbamidomethylation(D) 204 (Try/37/0.0225)				



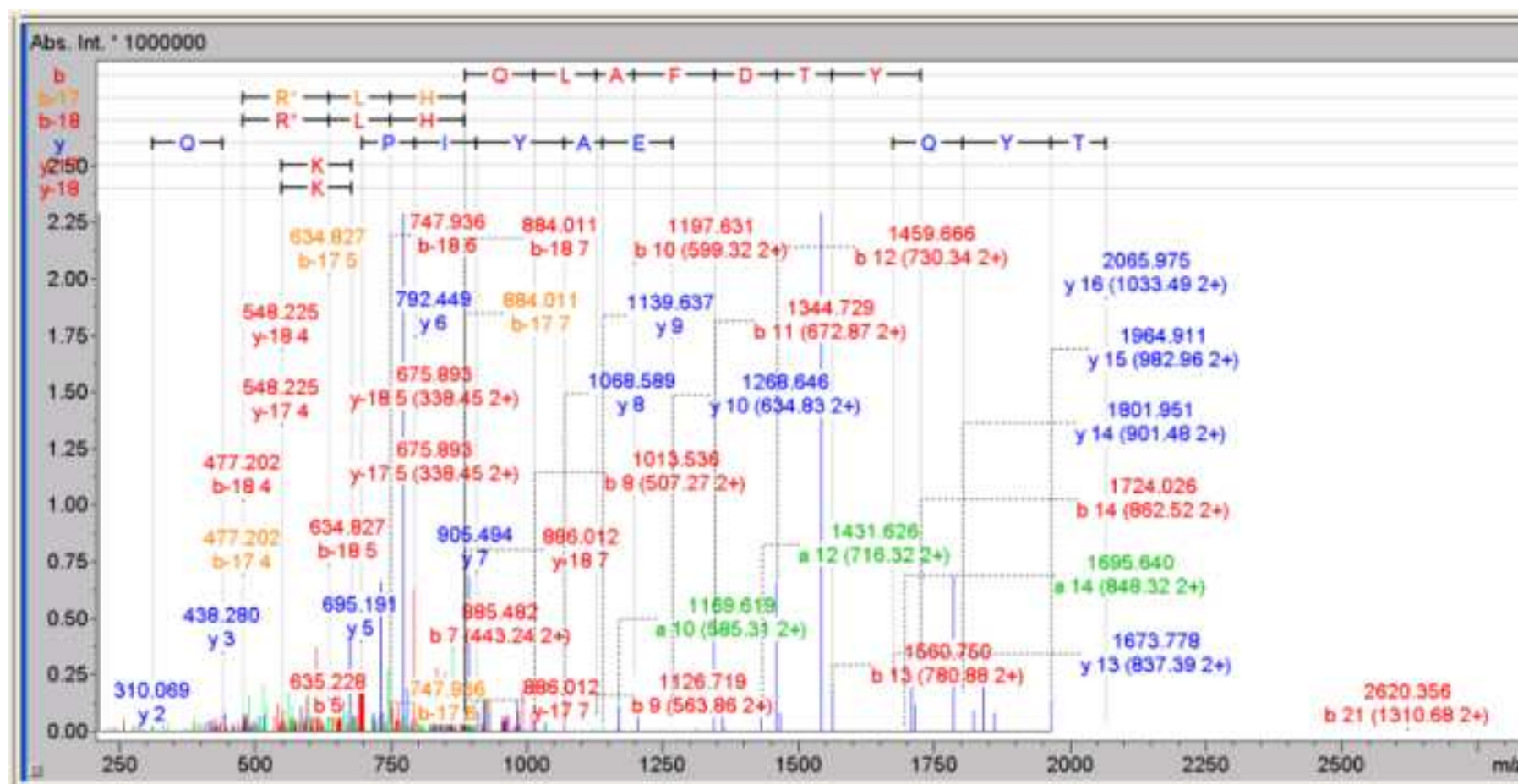
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Mascot	Carbamylation: D195	432.9113	3+
sequence (enzyme/ion score/mass error)				
195 K.D*MDKVETFLR.I Carbamylation(D) 204 (Try/44/0.0941)				



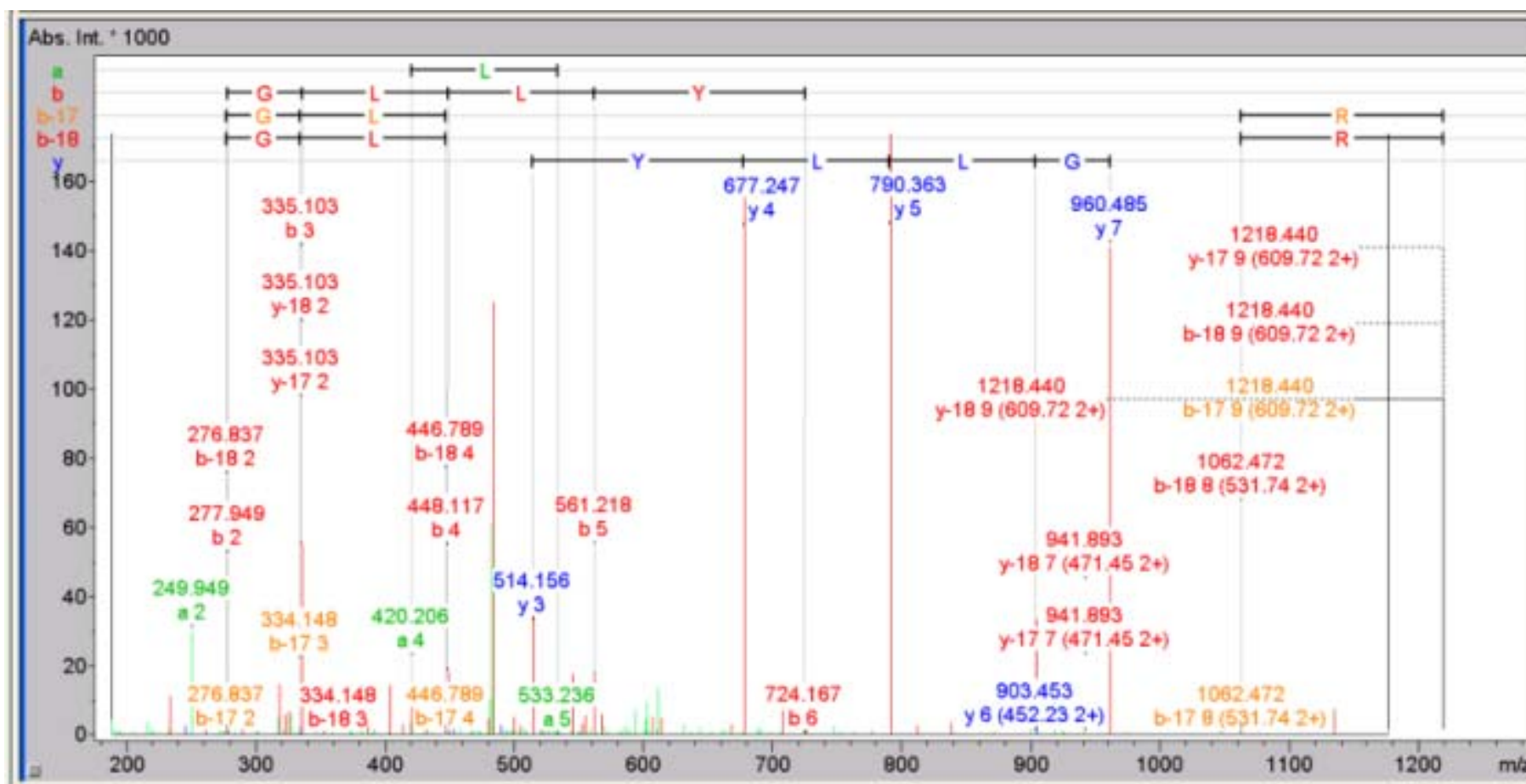
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Mascot	Deamidation: R45	705.7312	5+
sequence (enzyme/ion score/mass error)				
41 M.LRAHR*LHQLAFDTYQEFEEAYIPKEQKY.S Deamidation(R) 68 (Chy/41/-0.1328)				



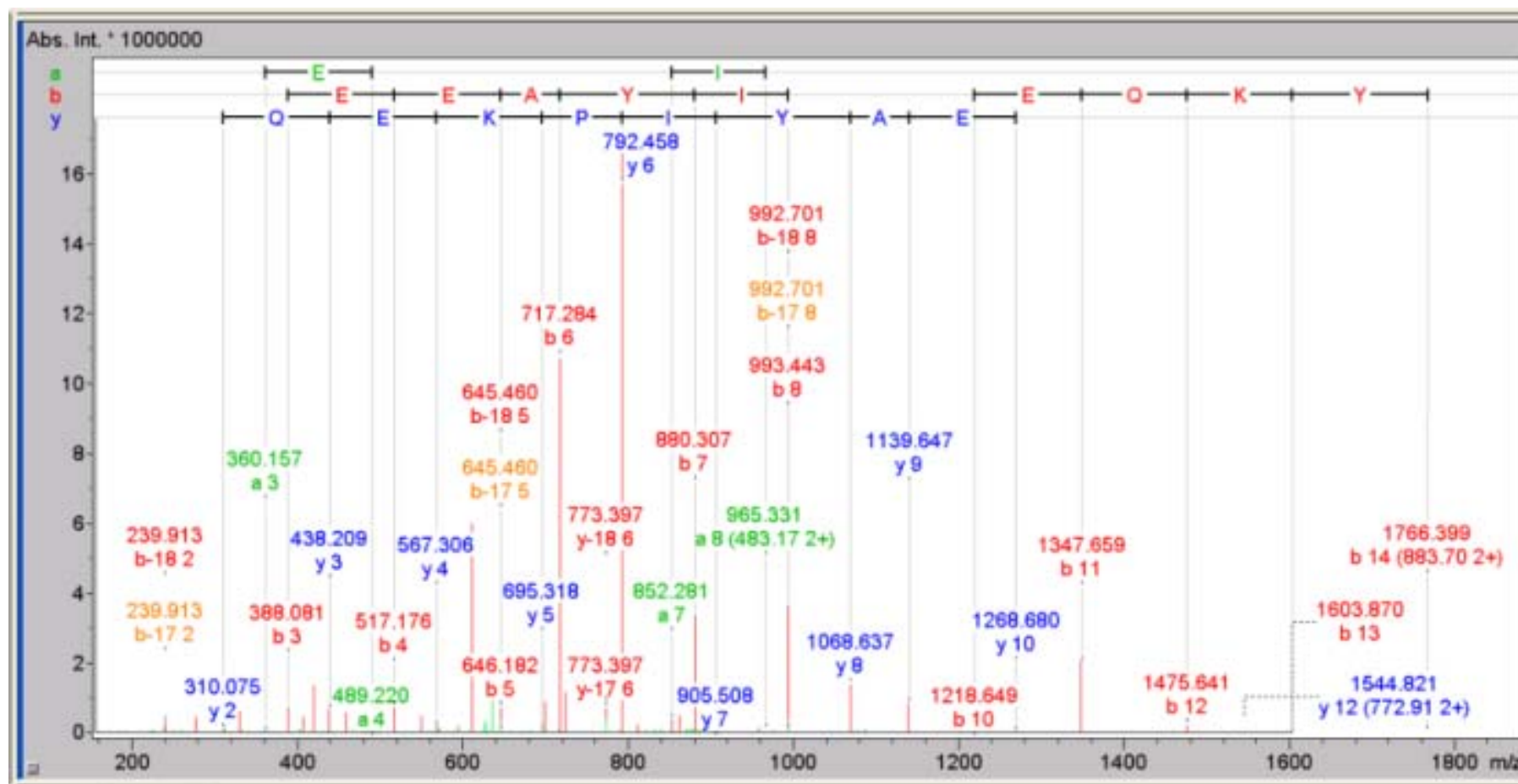
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Mascot	Dioxidation: F192	619.3197	2+
sequence (enzyme/ion score/mass error)				
185 K.NYGLLYCF*R.K Dioxidation(F) 193 (Try/30/0.0651)				



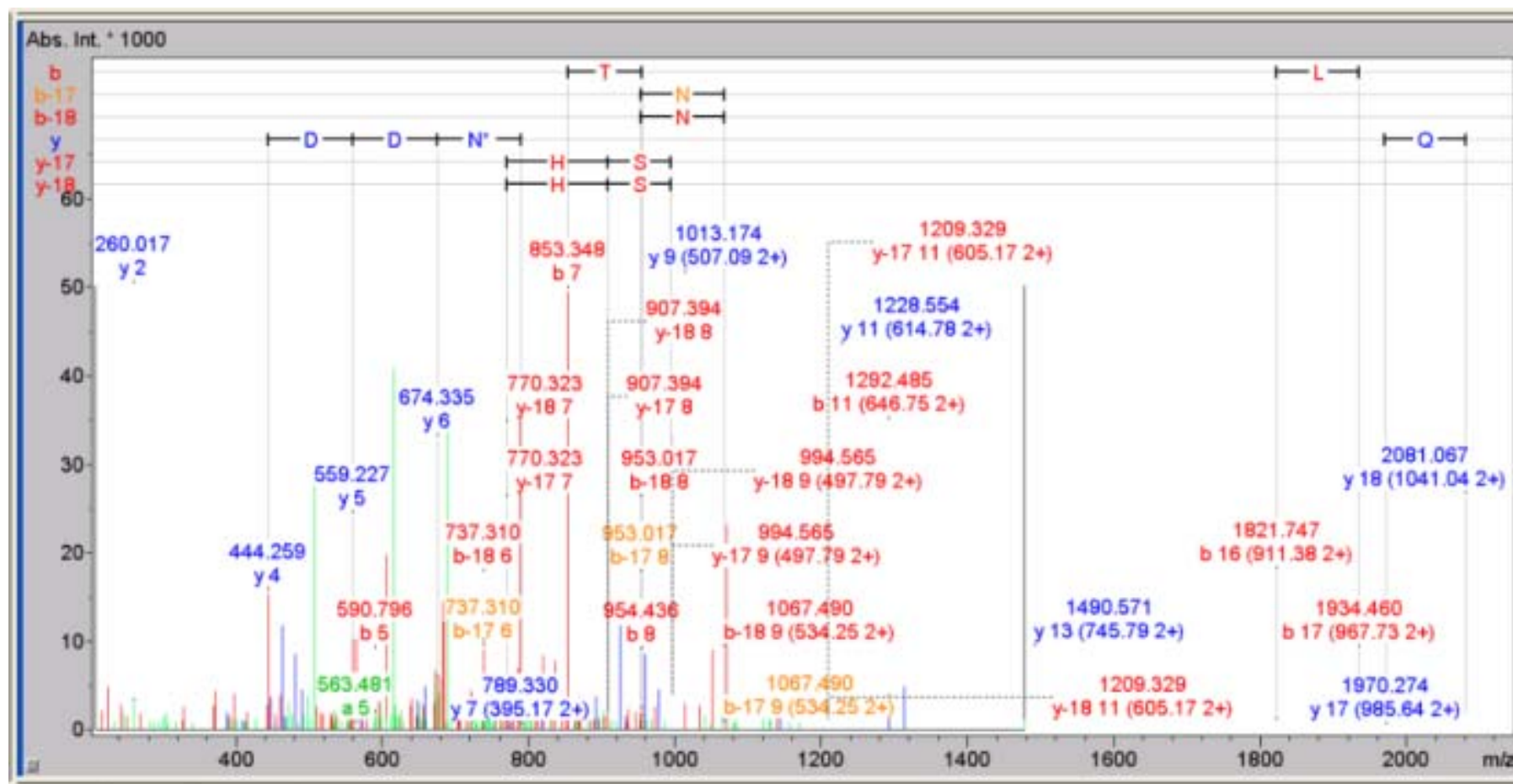
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Mascot	Gln->pyro-Glu: Q55	892.9604	2+
sequence (enzyme/ion score/mass error)				
55 Y.Q*EFEEAYIPKEQKY.S Gln->pyro-Glu(Q) 68 (Chy/63/0.0758)				



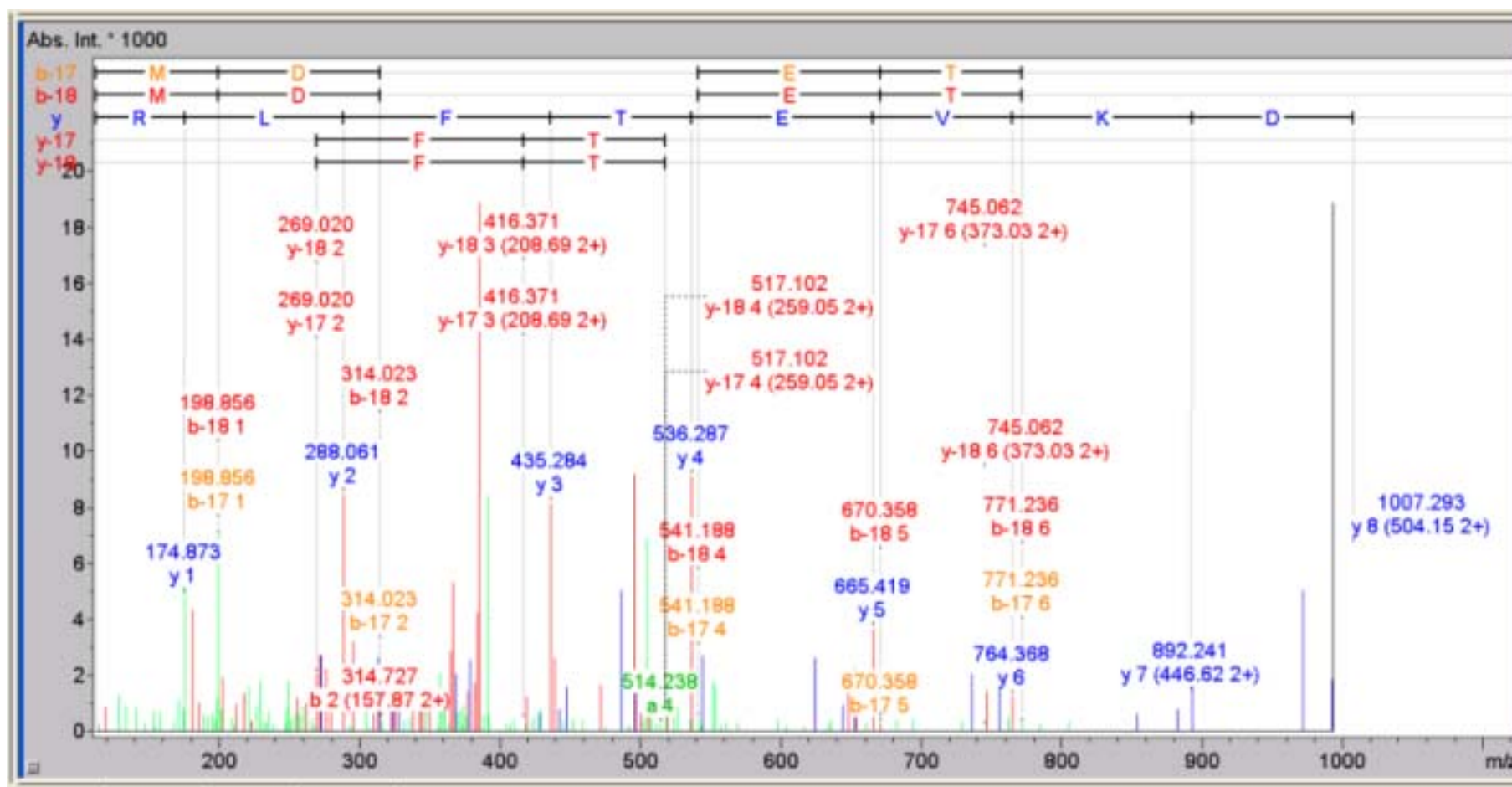
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 lower band	Mascot	Gln->pyro-Glu: Q167	694.3045	3+
sequence (enzyme/ion score/mass error)				
167 K.Q*TYSKFDTNSHN*DDALLK.N Gln->pyro-Glu(Q) Deamidation(N) 184 (Try/55/-0.0469)				



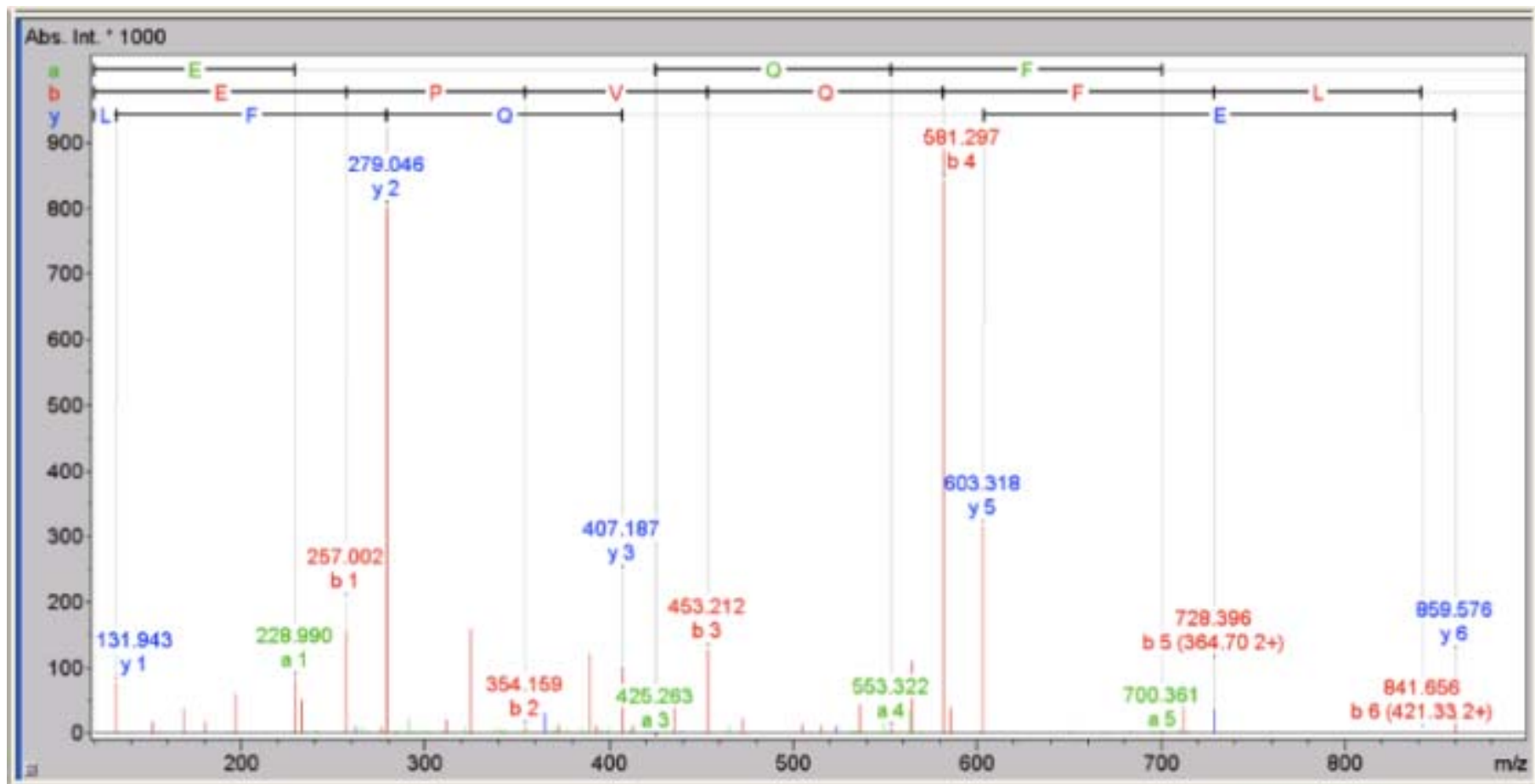
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Mascot	Piperidine: M196	402.8789	3+
sequence (enzyme/ion score/mass error)				
196 D.M*DKVETFLR.I Piperidine(M) 204 (Try/41/-0.0329)				



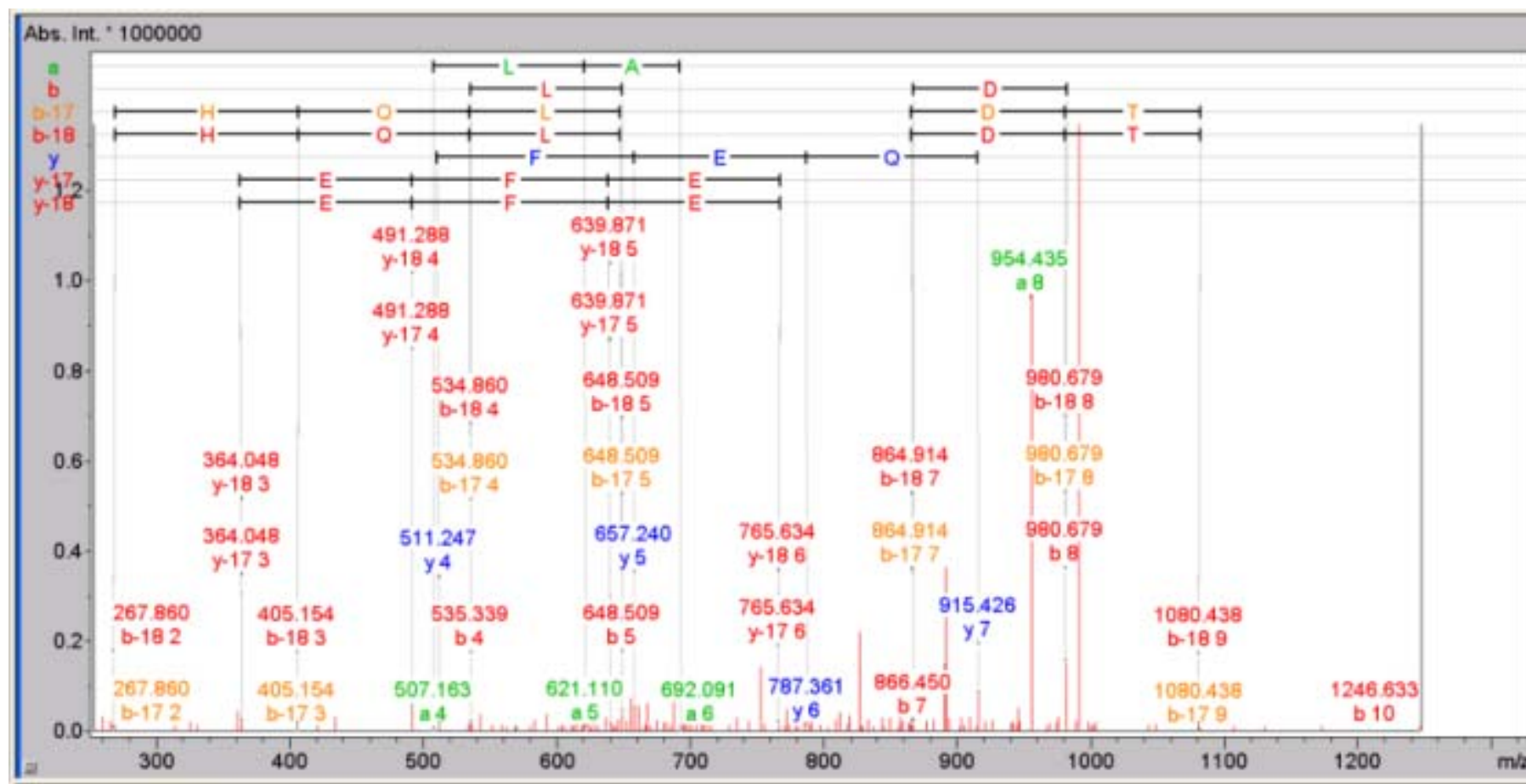
Mascot / Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Mascot	SMA: E114	430.2647	2+
sequence (enzyme/ion score/mass error)				
114 L.E*PVQFL.R SMA(E) 119 (Chy/32/0.0661)				



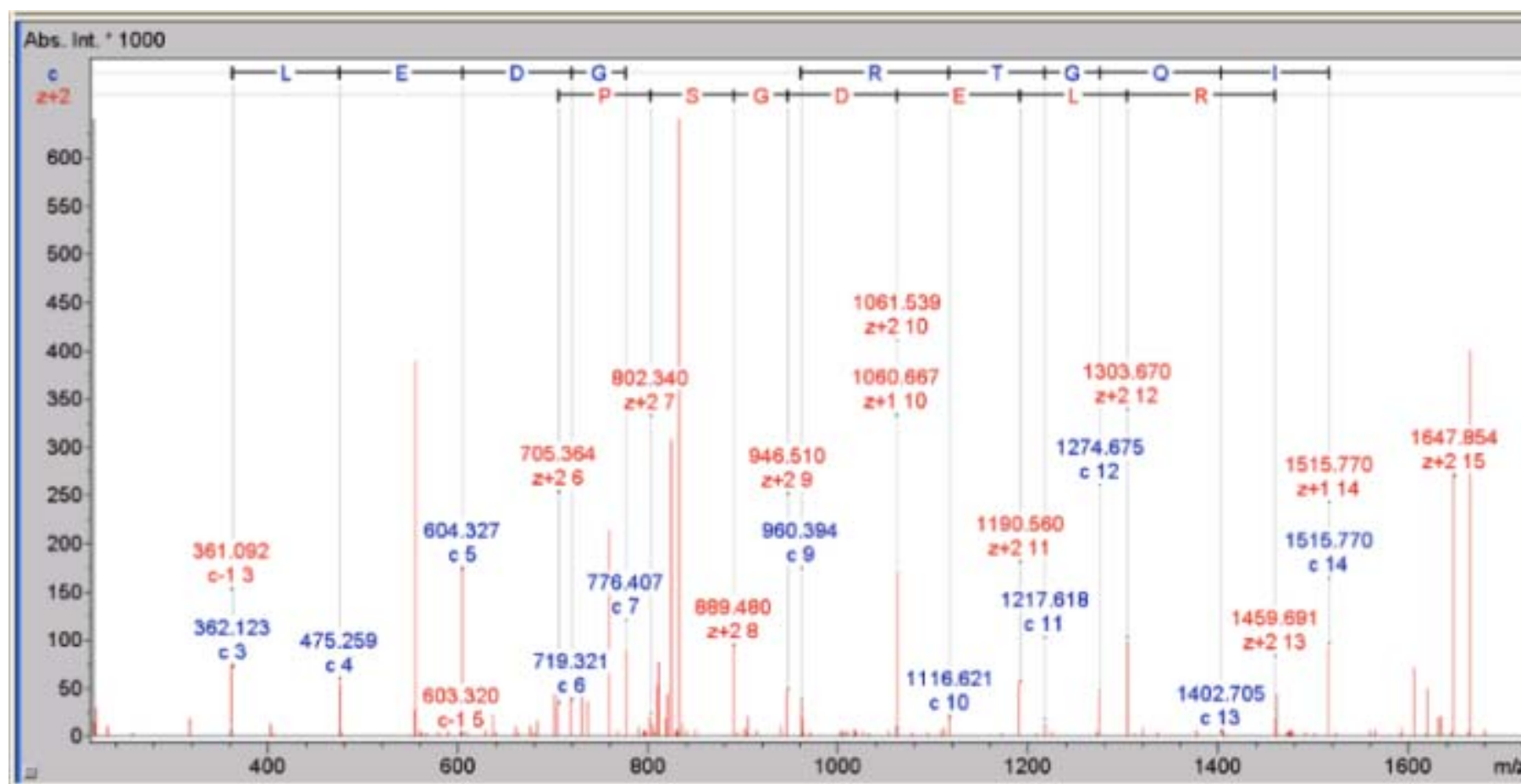
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Mascot	Amidation: Y61	720.3457	3+
sequence (enzyme/ion score/mass error)				
45 H.RLHQLAFDTYQEFEEAY*.I Amidation(Y) 61 (Chy/79/0.0033)				



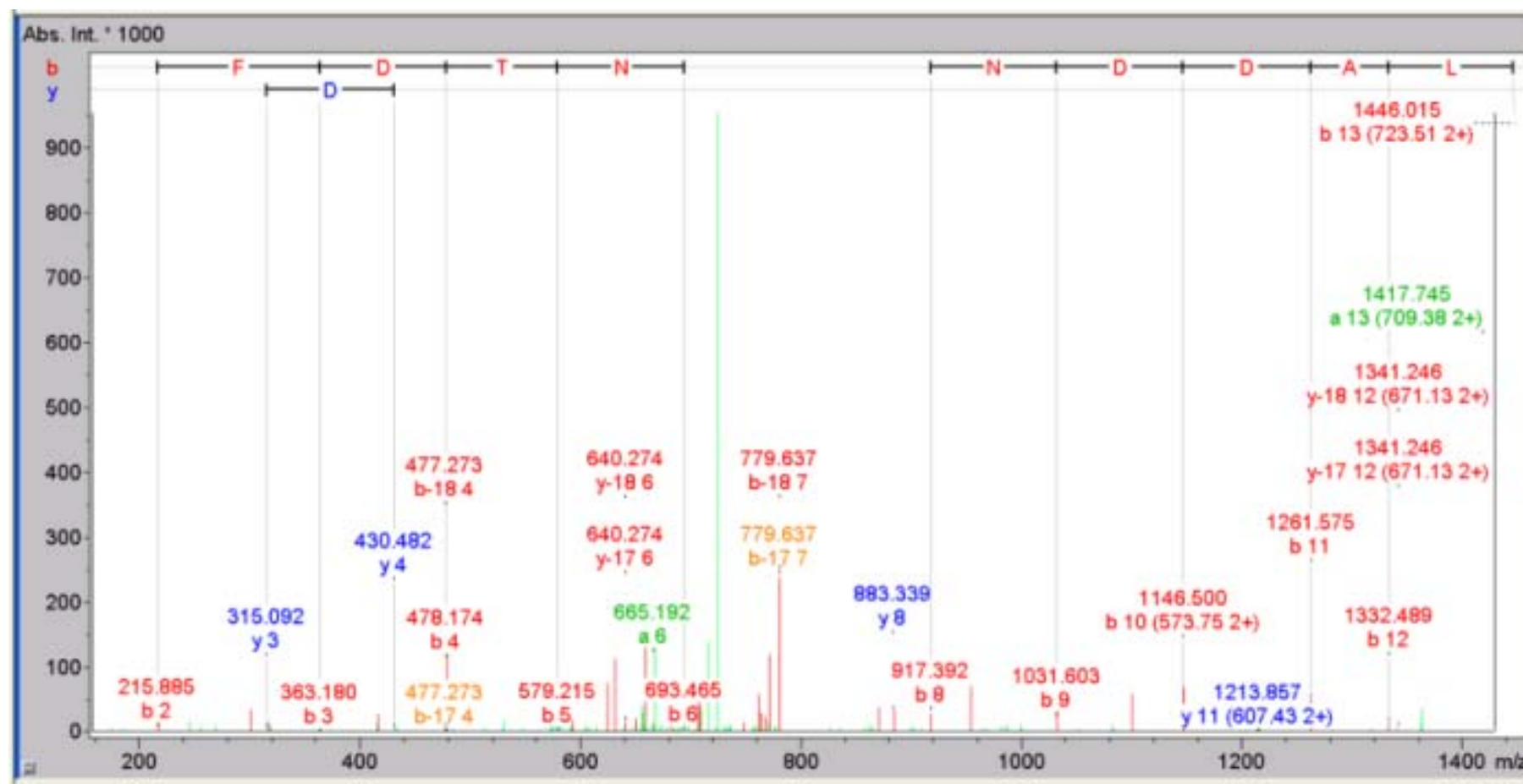
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Amidation: F165	554.9055	3+
sequence (enzyme/ion score/mass error)				
151 L.MGRLEDGSPRTGQIF*.K Amidation(F) 165 (Chy/56/-0.1361)				



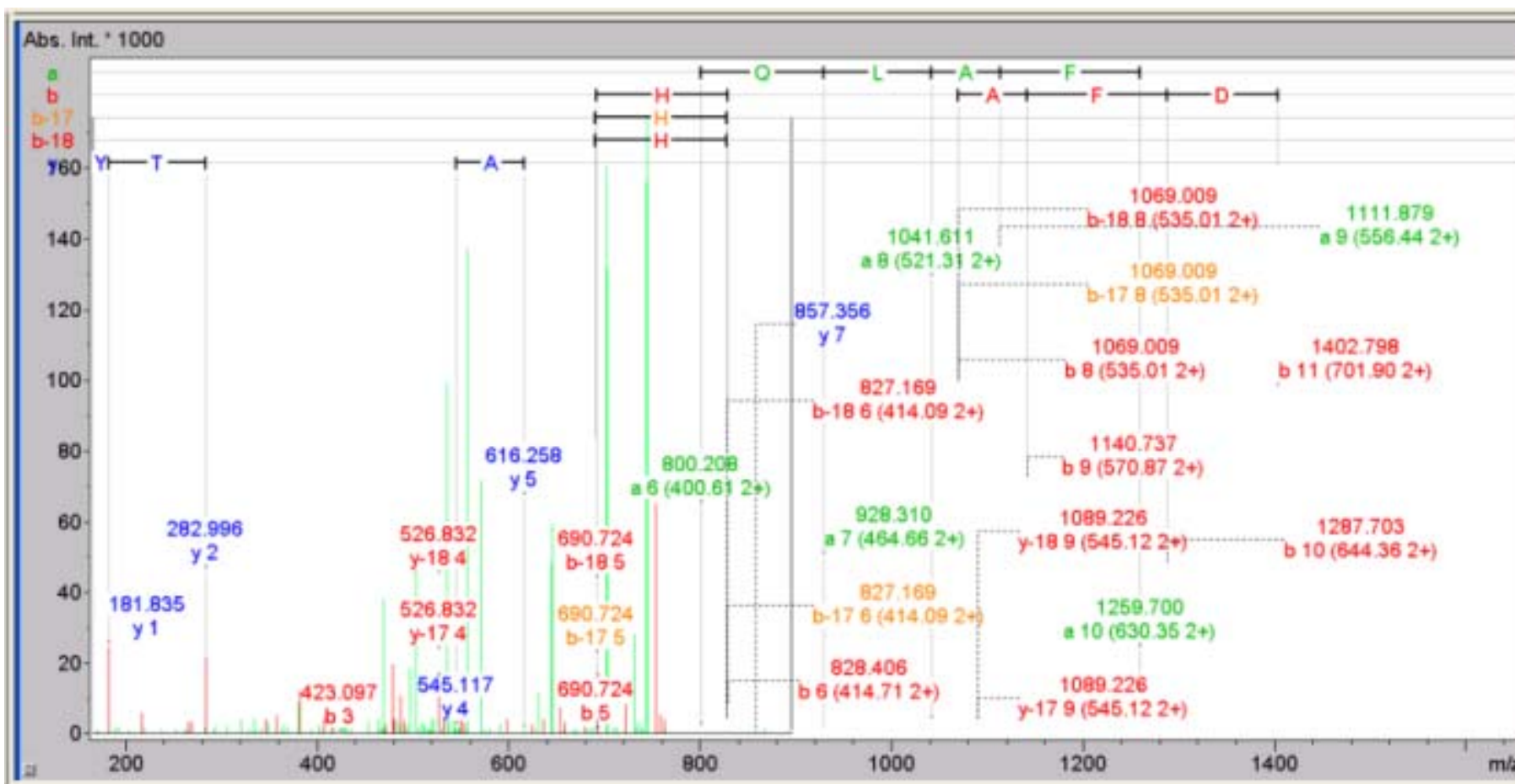
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 lower band	Mascot	Amidation: L183	788.373	2+
sequence (enzyme/ion score/mass error)				
170 Y.SKFDTNSHNDDALL*.K Amidation(L) 183 (Chy/36/-0.001)				



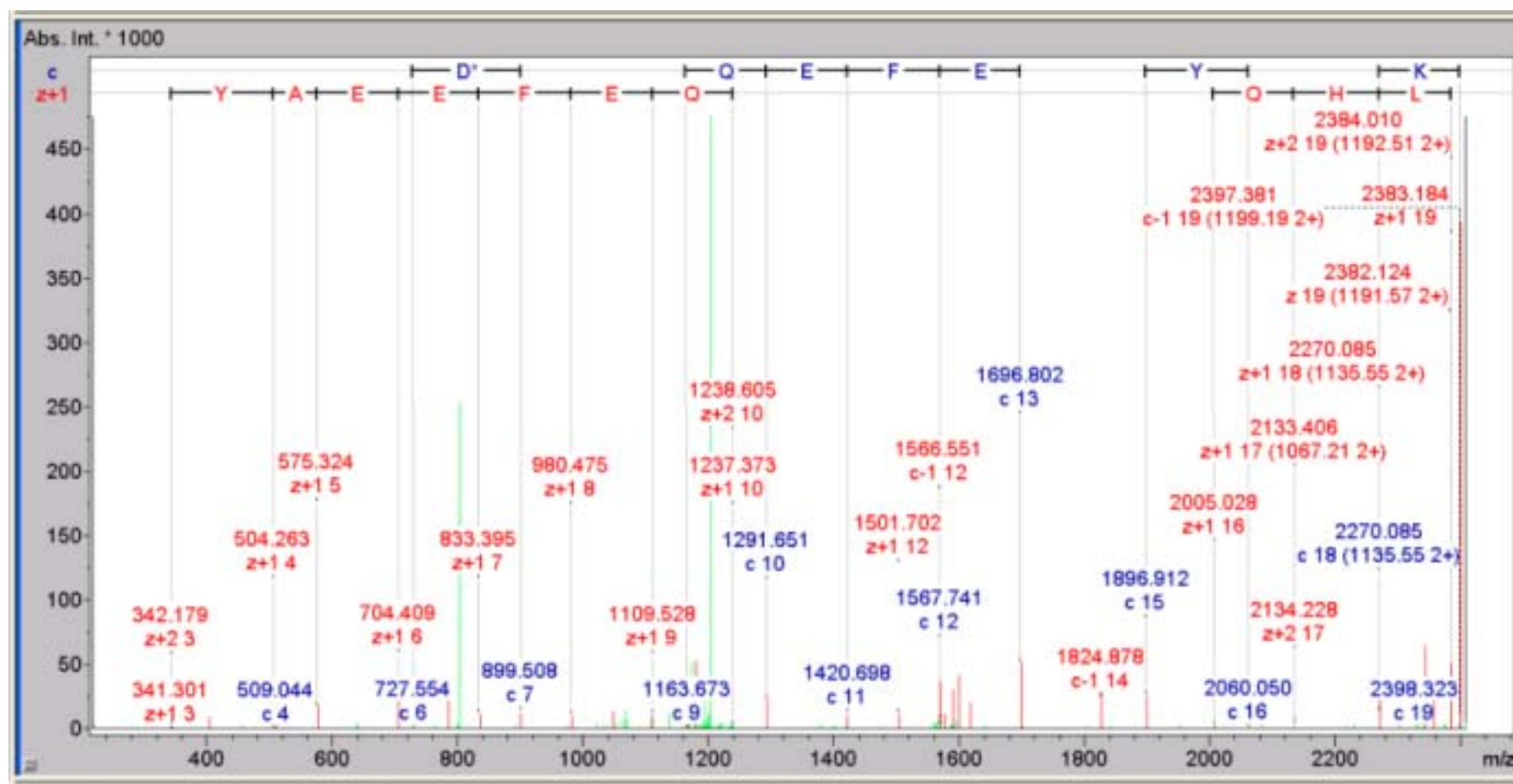
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Mascot	Carbamidomethylation: R42	562.2735	3+
sequence (enzyme/ion score/mass error)				
42 L.R*AHRLHQLAFDTY.Q Carbamidomethylation(R) 54 (Chy/41/-0.0607)				



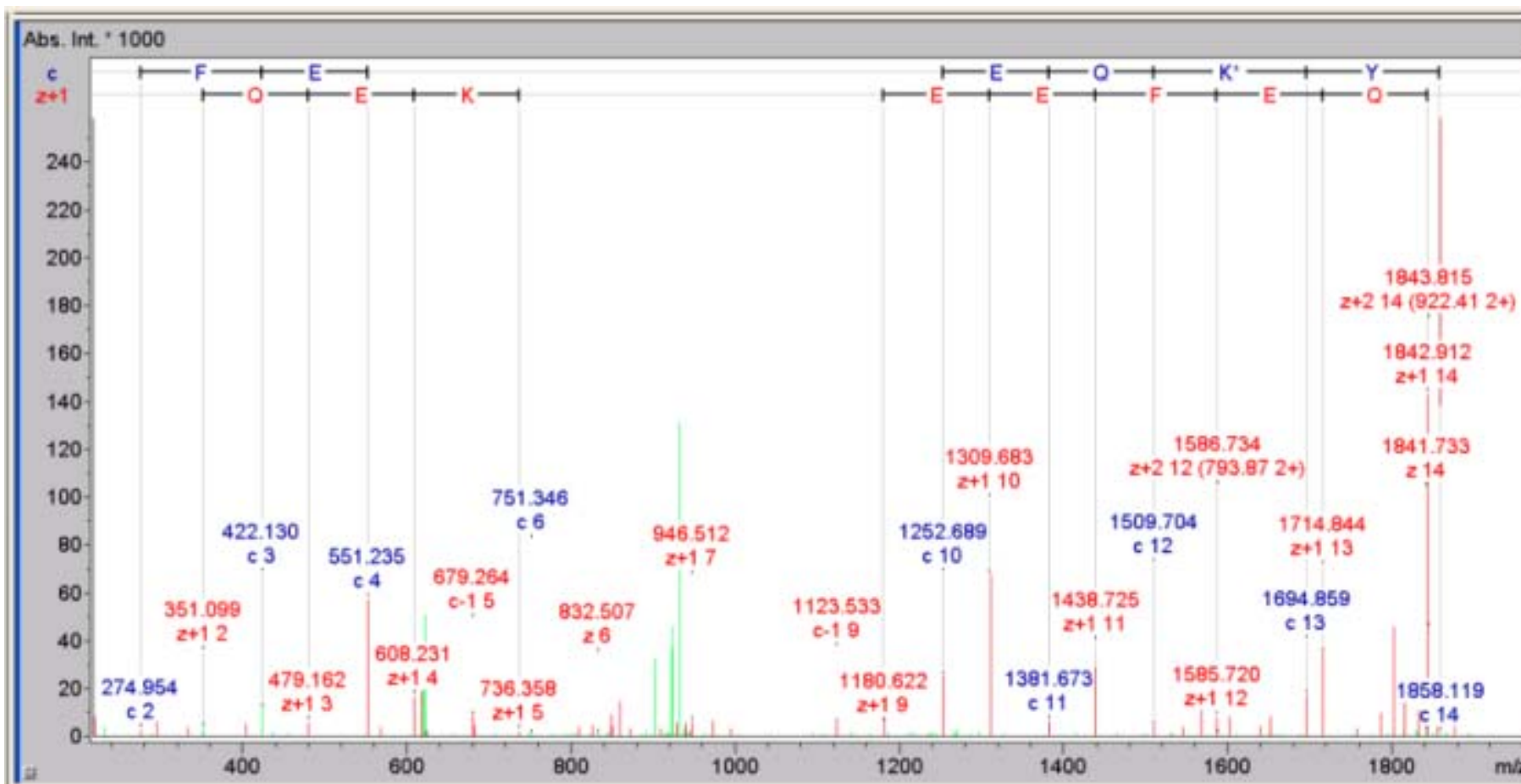
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Mascot	Carbamidomethylation: D52	800.402	3+
sequence (enzyme/ion score/mass error)				
46 R.LHQLAFD*TYQEFEEAYIPK.E Carbamidomethylation(D) 64 (Try/42/0.0361)				



Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 lower band	Mascot	Carbamidomethylation: K67	620.2764	3+
sequence (enzyme/ion score/mass error)				
55 Y.QEFEEAYIPKEQK*Y.S Carbamidomethylation(K) 68 (Chy/48/-0.0711)				



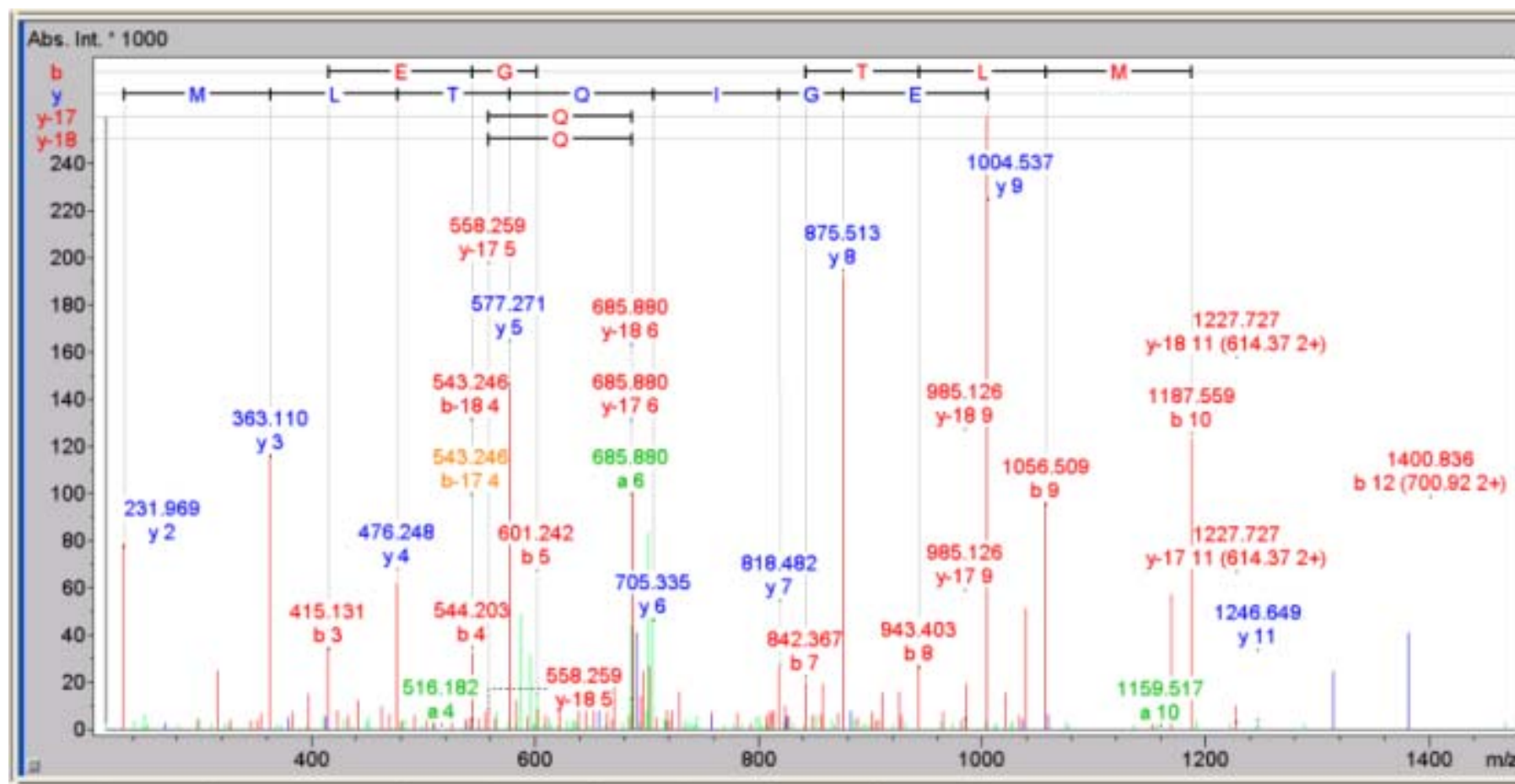
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Mascot	Carbamidomethylation: E114	451.708	2+
sequence (enzyme/ion score/mass error)				
113 W.LE*PVQFL.R Carbamidomethylation(E) 119 (Chy/30/-0.0895)				



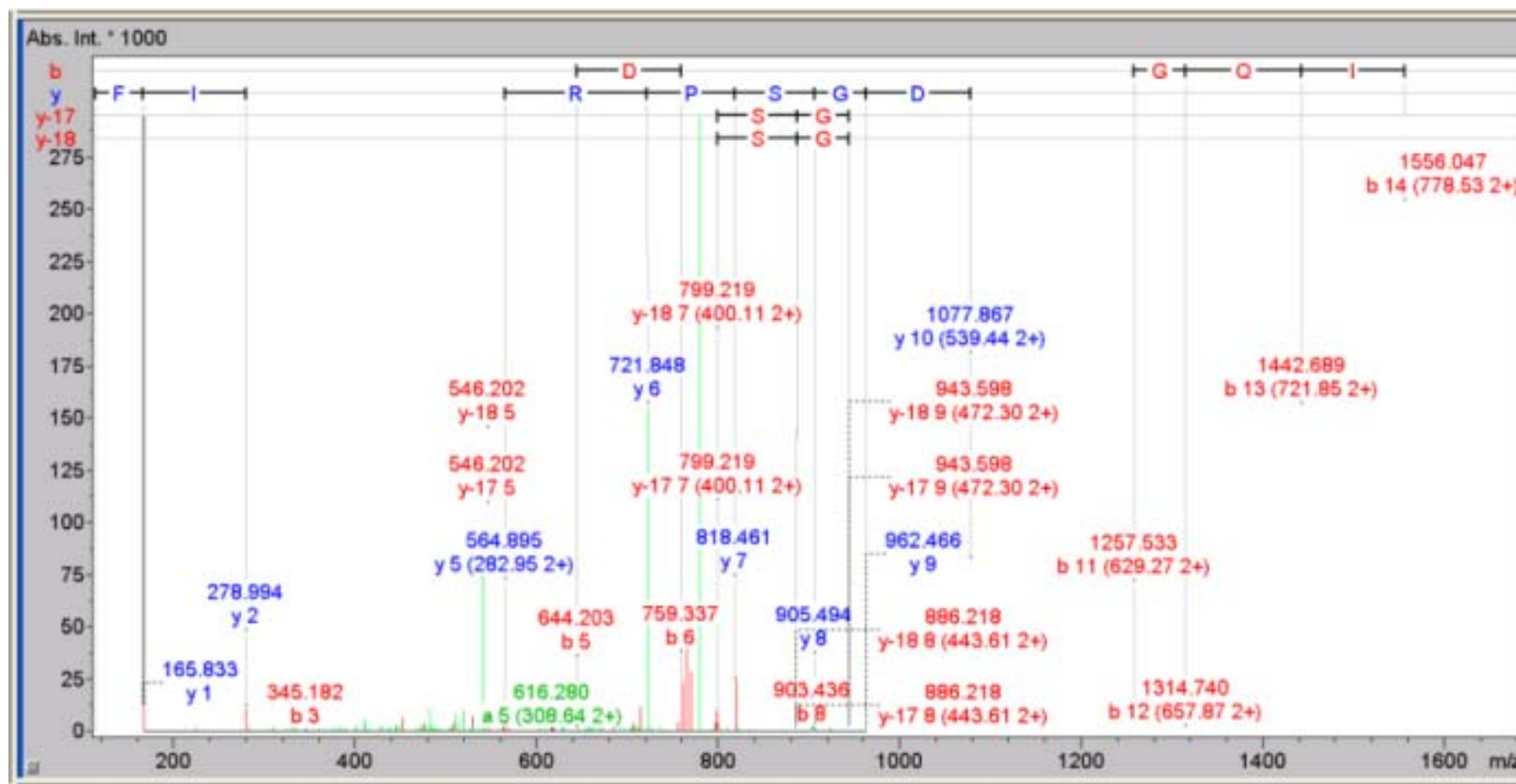
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Mascot	Carbamidomethylation: D142	709.8502	2+
sequence (enzyme/ion score/mass error)				
142 K.D*LEEGIQTLMGR.L Carbamidomethylation(D) 153 (Try/58/-0.0013)				



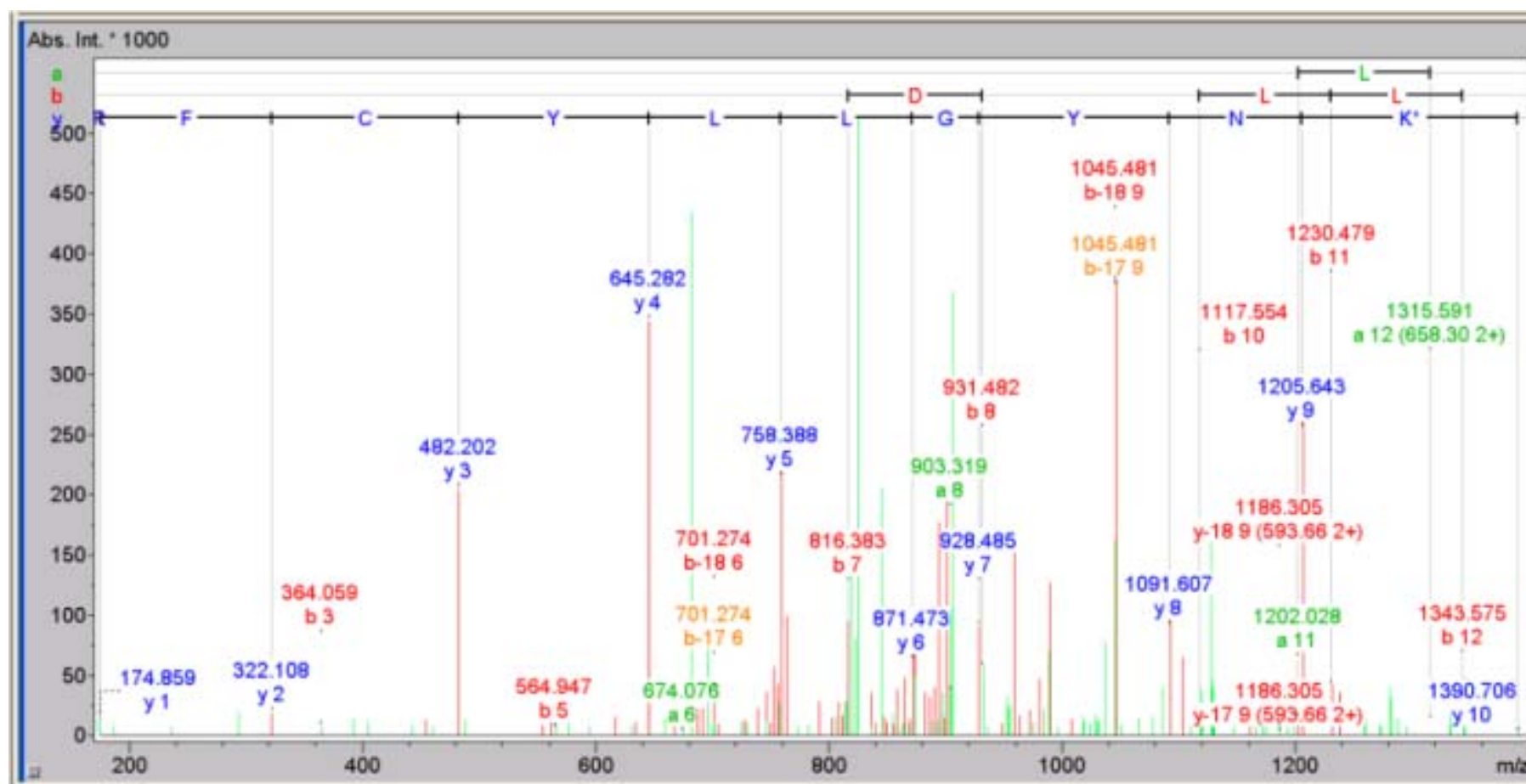
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Mascot	Carbamidomethylation: E155	574.2769	3+
sequence (enzyme/ion score/mass error)				
151 L.MGRLE*DGSPRTGQIF.K Carbamidomethylation(E) 165 (Chy/41/-0.0274)				



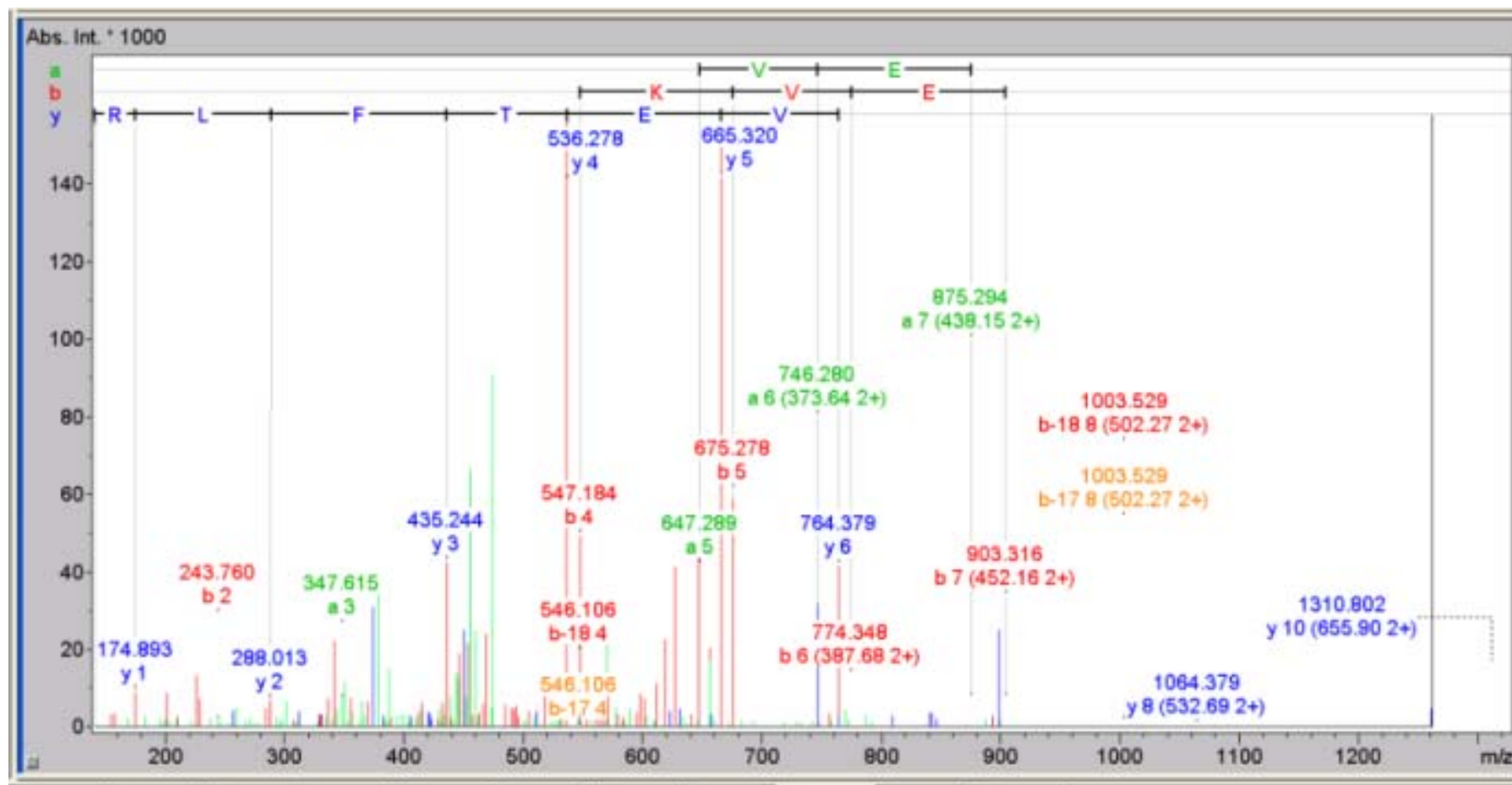
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Carbamidomethylation: K184	911.7608	3+
sequence (enzyme/ion score/mass error)				
172 K.FDTNSHNDDALLK*NYGLLYCFR.K Carbamidomethylation(K) 193 (Try/48/-0.0047)				



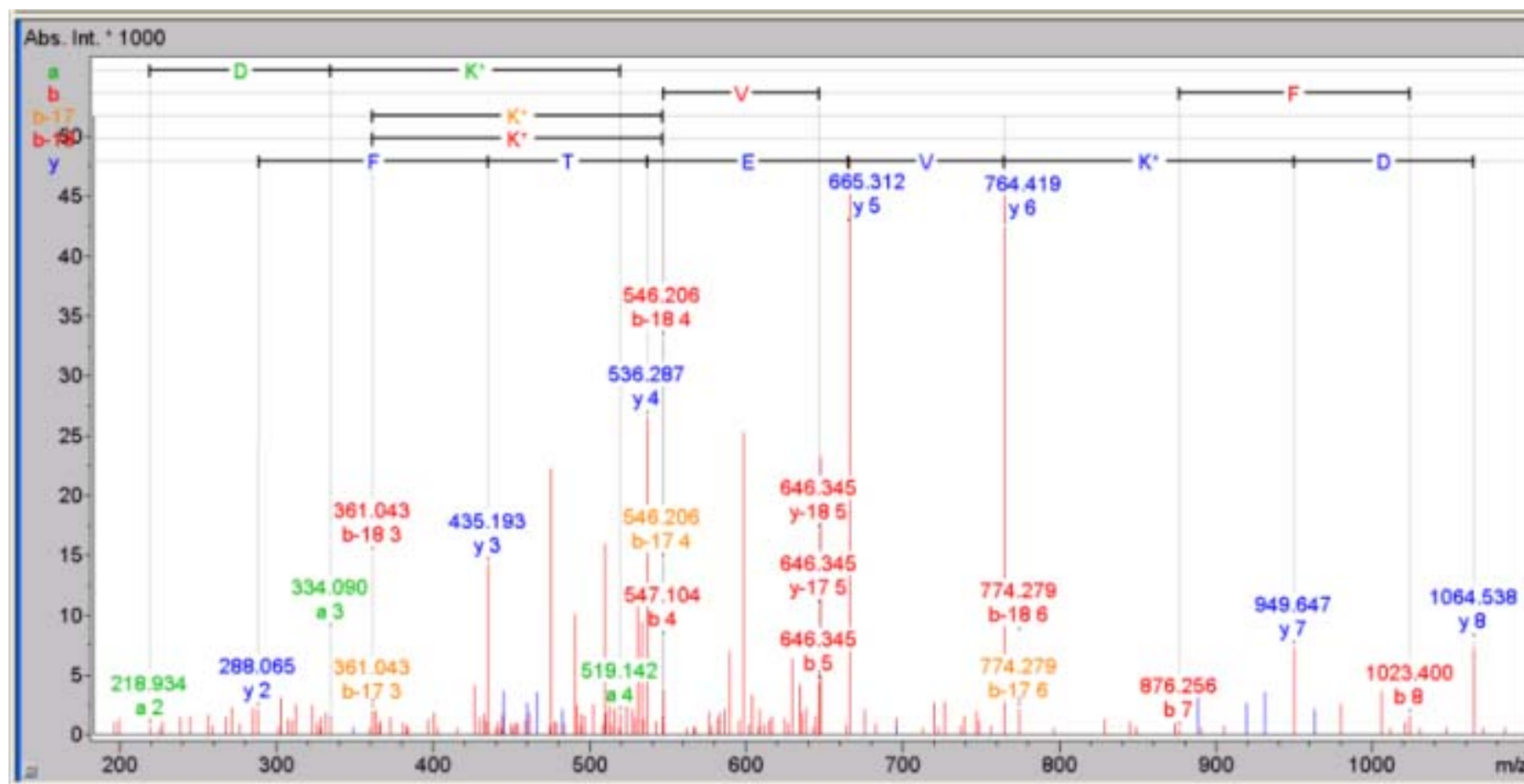
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Mascot	Carbamidomethylation: D197	480.2466	3+
sequence (enzyme/ion score/mass error)				
194 R.KDMD*KVETFLR.I Carbamidomethylation(D) 204 (Try/39/-0.0106)				



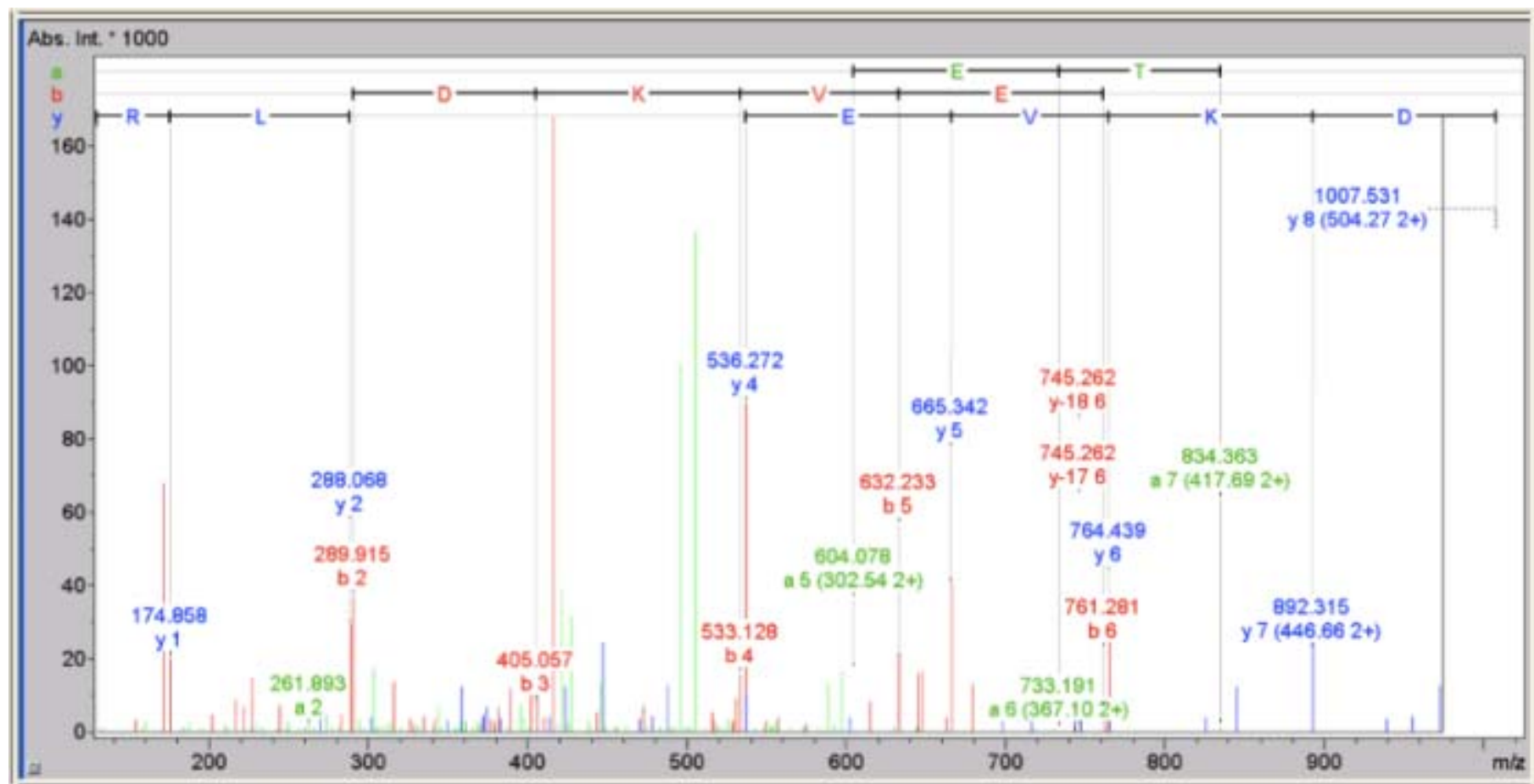
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Mascot	Carbamidomethylation: K198	655.8176	2+
sequence (enzyme/ion score/mass error)				
195 K.DMDK*VETFLR.I Carbamidomethylation(K) 204 (Try/43/-0.013)				



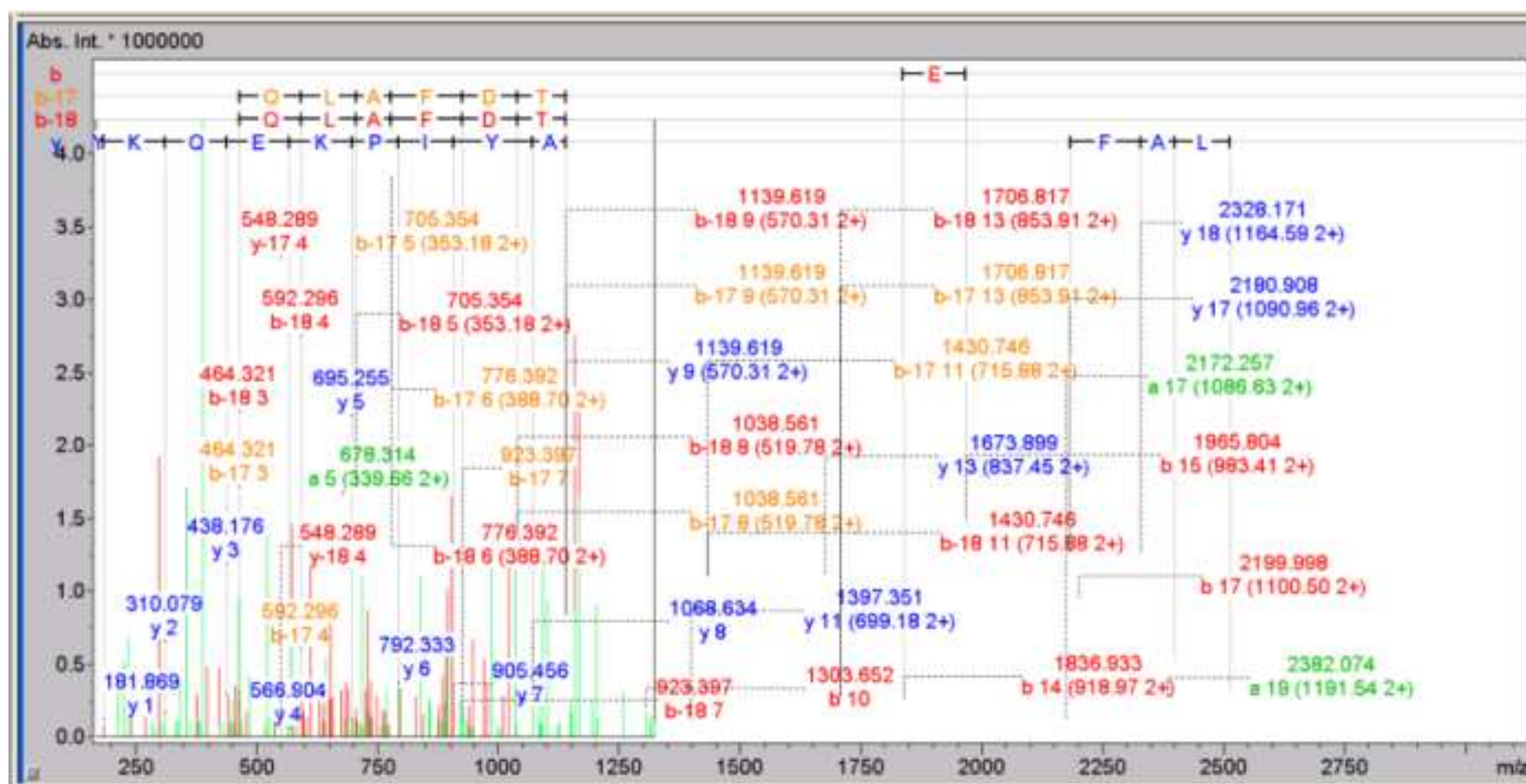
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Carbamylation: M196	432.897	3+
sequence (enzyme/ion score/mass error)				
195 K.DM*DKVETFLR.I Carbamylation(M) 204 (Try/53/0.0512)				



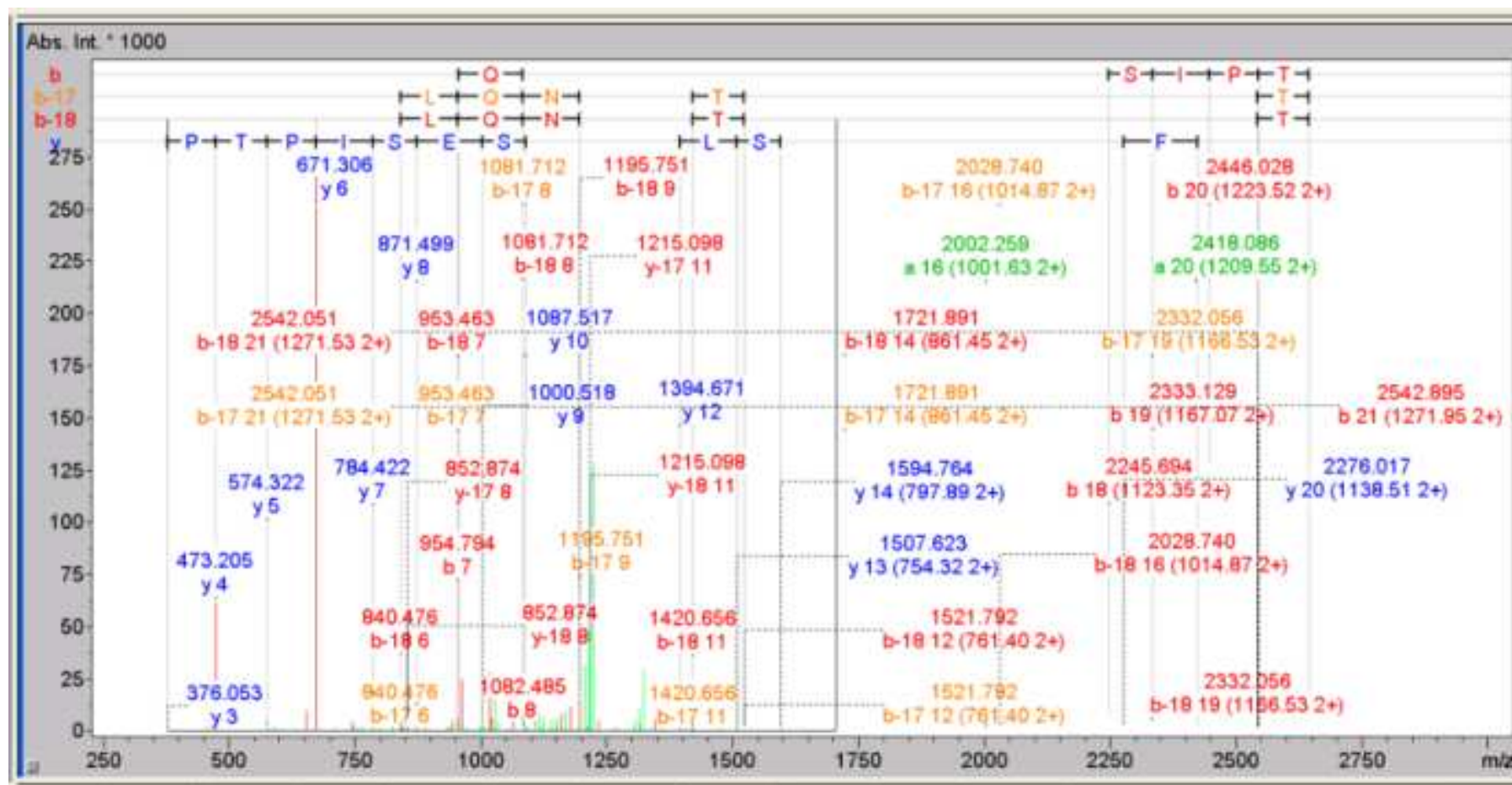
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Mascot	Carboxymethylation: R45	776.8751	4+
sequence (enzyme/ion score/mass error)				
45 H.R*LHQLAFDTYQEFEEAYIPKEQKY.S Carboxymethylation(R) 68 (Chy/40/-0.0214)				



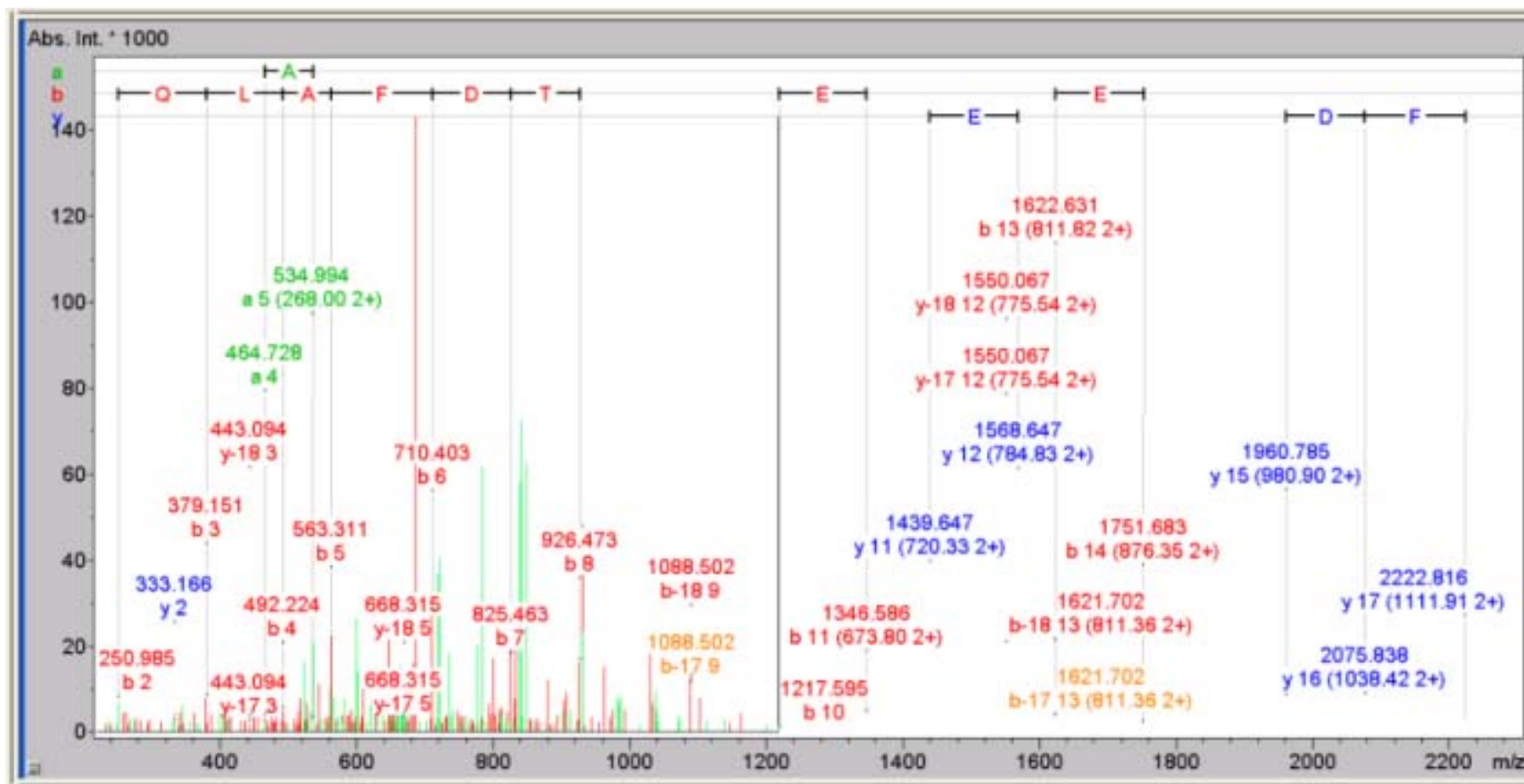
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 lower band	Mascot	Carboxymethylation: E65	1039.1646	3+
sequence (enzyme/ion score/mass error)				
65 K.E*QKYSFLQNPQTSLCFSEIPTPSNR.E Carboxymethylation(E) 90 (Try/52/0.0003)				



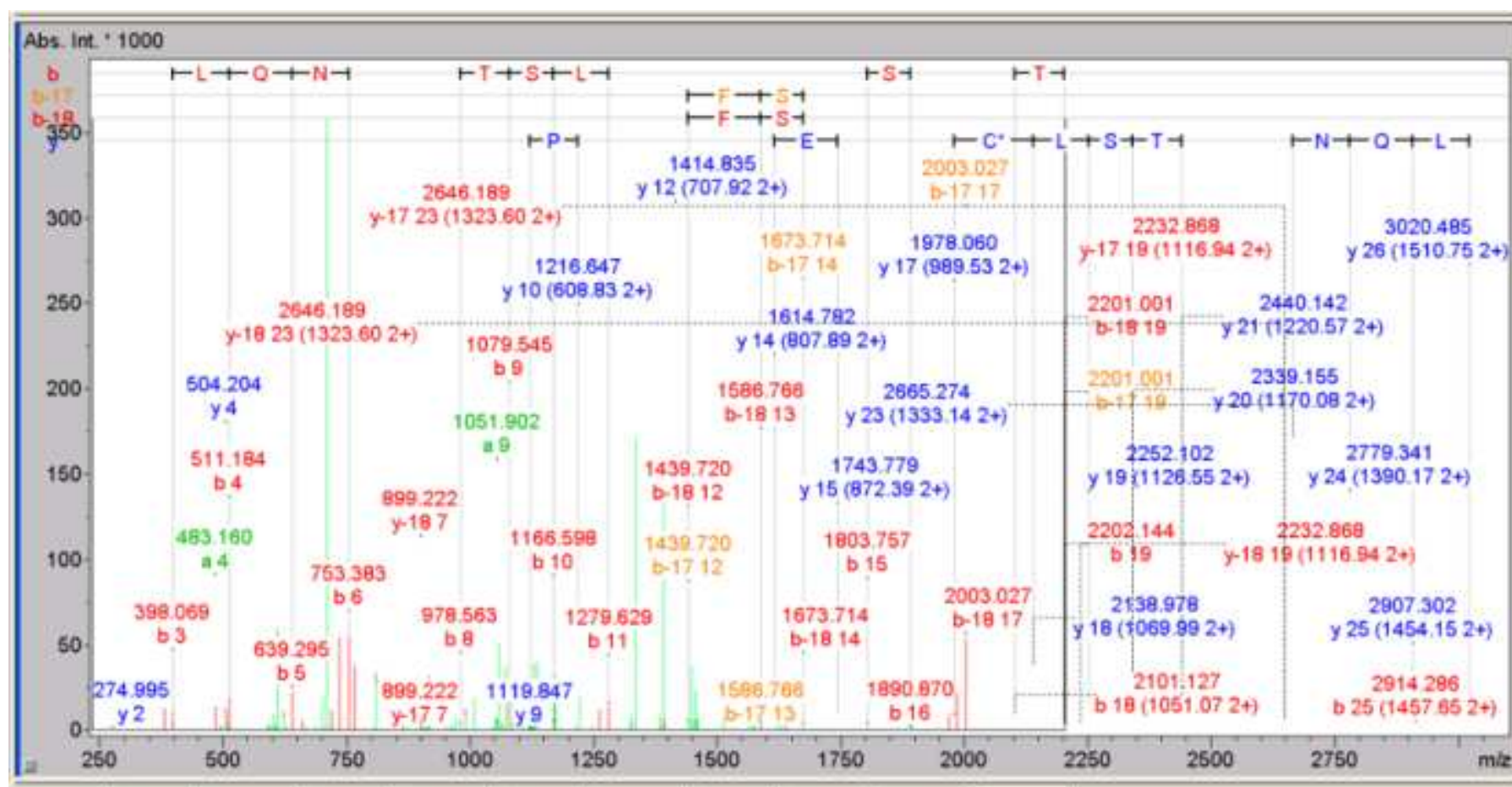
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 lower band	Mascot	Carboxymethylation: K67	697.0882	4+
sequence (enzyme/ion score/mass error)				
46 R.LHQLAFDTYQEFEEAYIPKEQK*.Y Carboxymethylation(K) 67 (Try/42/-0.0045)				



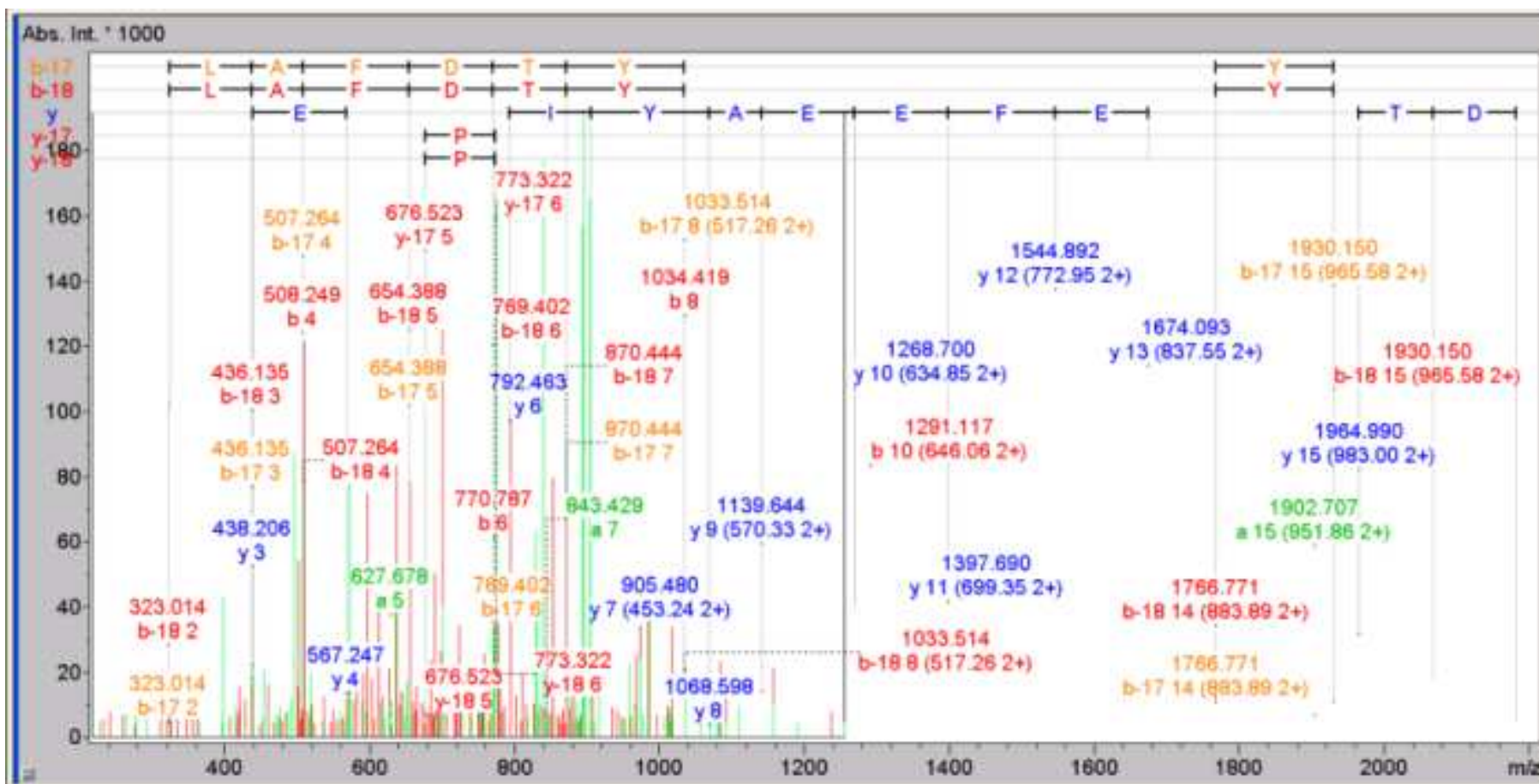
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Carboxymethylation: C79	1139.8458	3+
sequence (enzyme/ion score/mass error)				
68 K.YSFLQNPQTSLC*FSESIPTPSNREETQK.S Carboxymethylation(C) 96 (Try/78/-0.0675)				



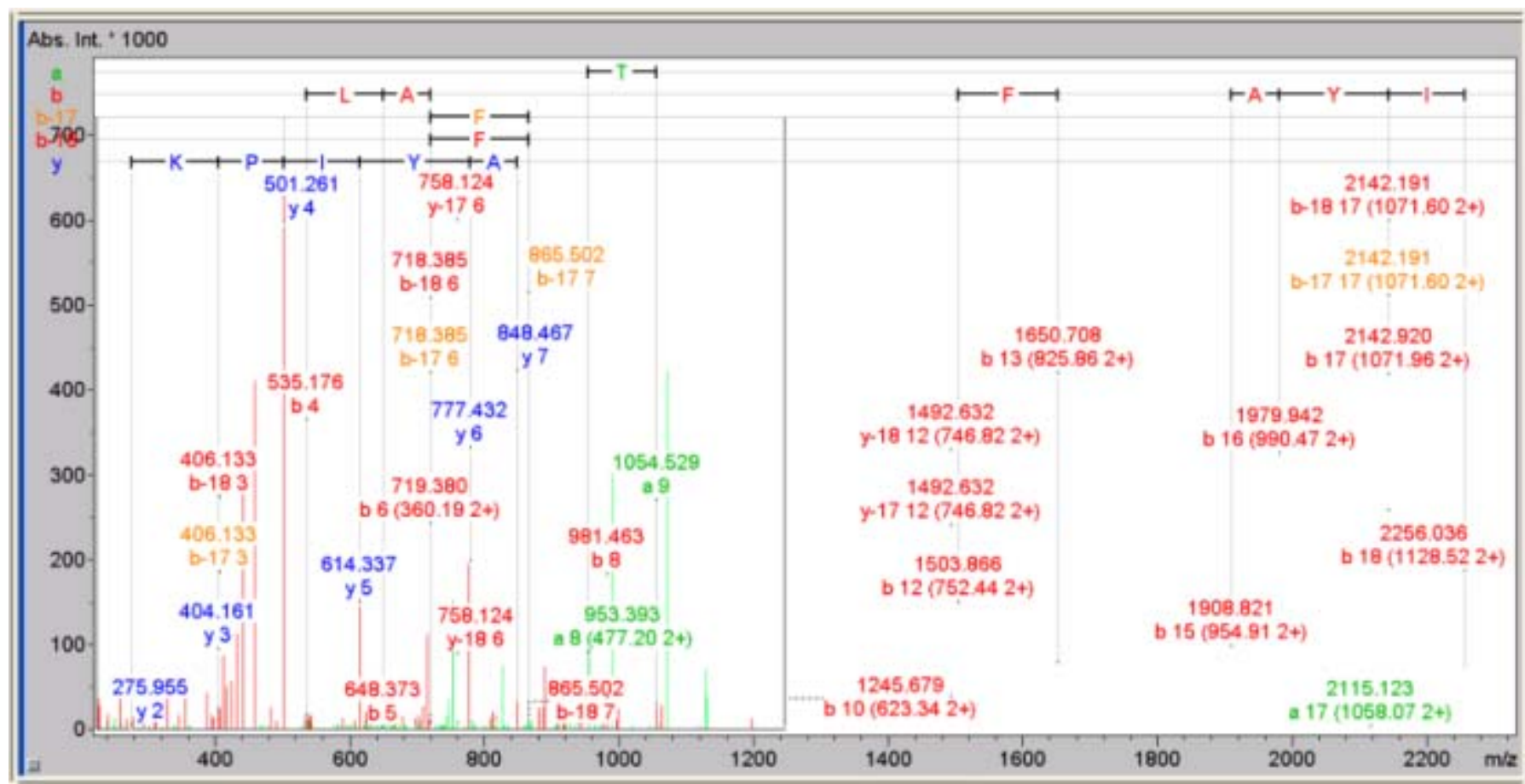
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Deamidation: Q48	709.6025	4+
sequence (enzyme/ion score/mass error)				
47 L.H*Q*LAFDTYQEFEEAYIPKEQKY.S Carbamidomethylation(H) Deamidation(Q) 68 (Chy/47/0.0734)				



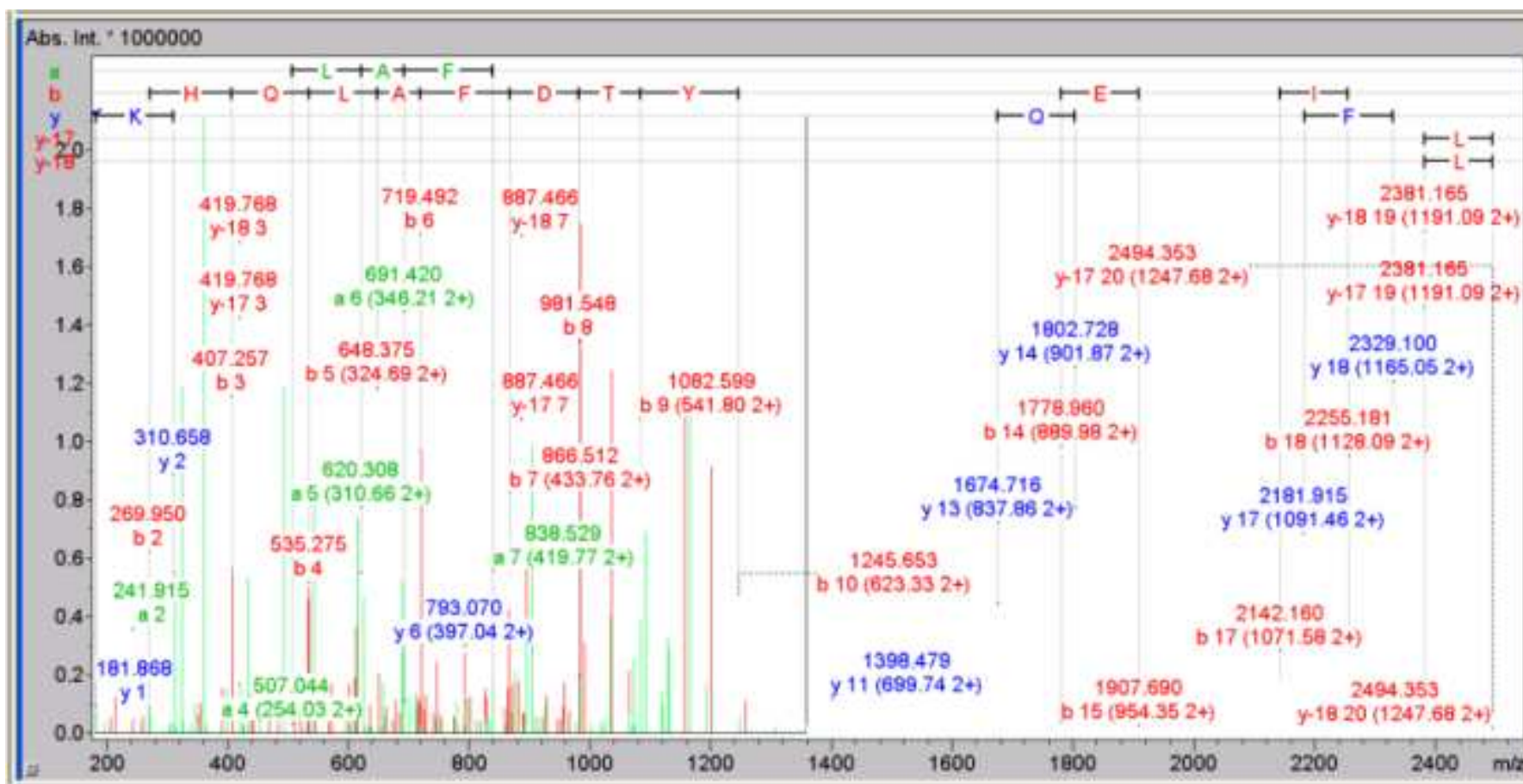
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Deamidation: Q55	689.8557	4+
sequence (enzyme/ion score/mass error)				
45 H.RLHQLAFDTYQ*EFEEAYIPKEQ.K Deamidation(Q) 66 (Chy/79/0.0808)				



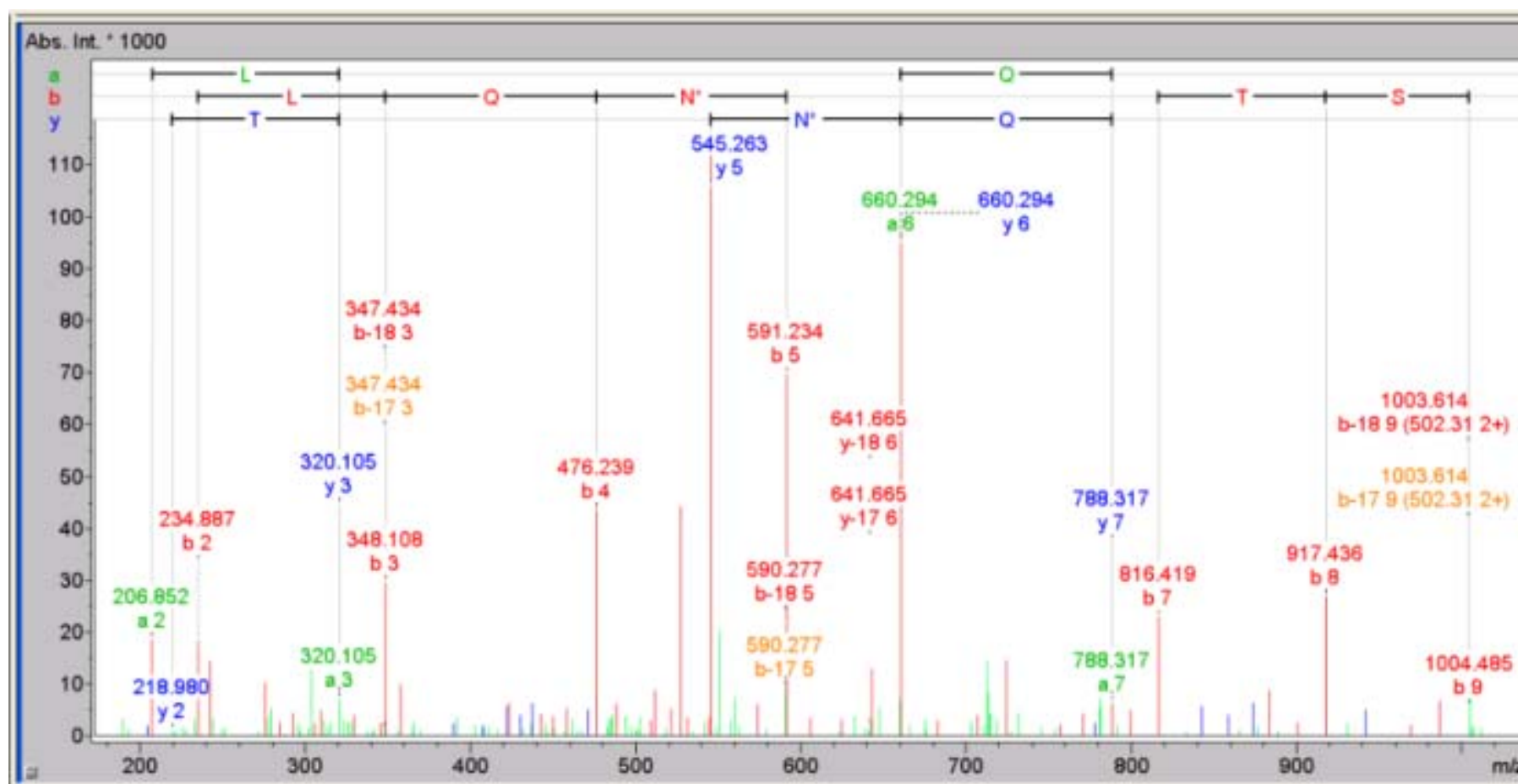
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Mascot	Deamidation: Q66	762.6142	4+
sequence (enzyme/ion score/mass error)				
45 H.RLHQLAFDTYQEFEEAYIPKEQ*KY.S Deamidation(Q) 68 (Chy/69/-0.0183)				



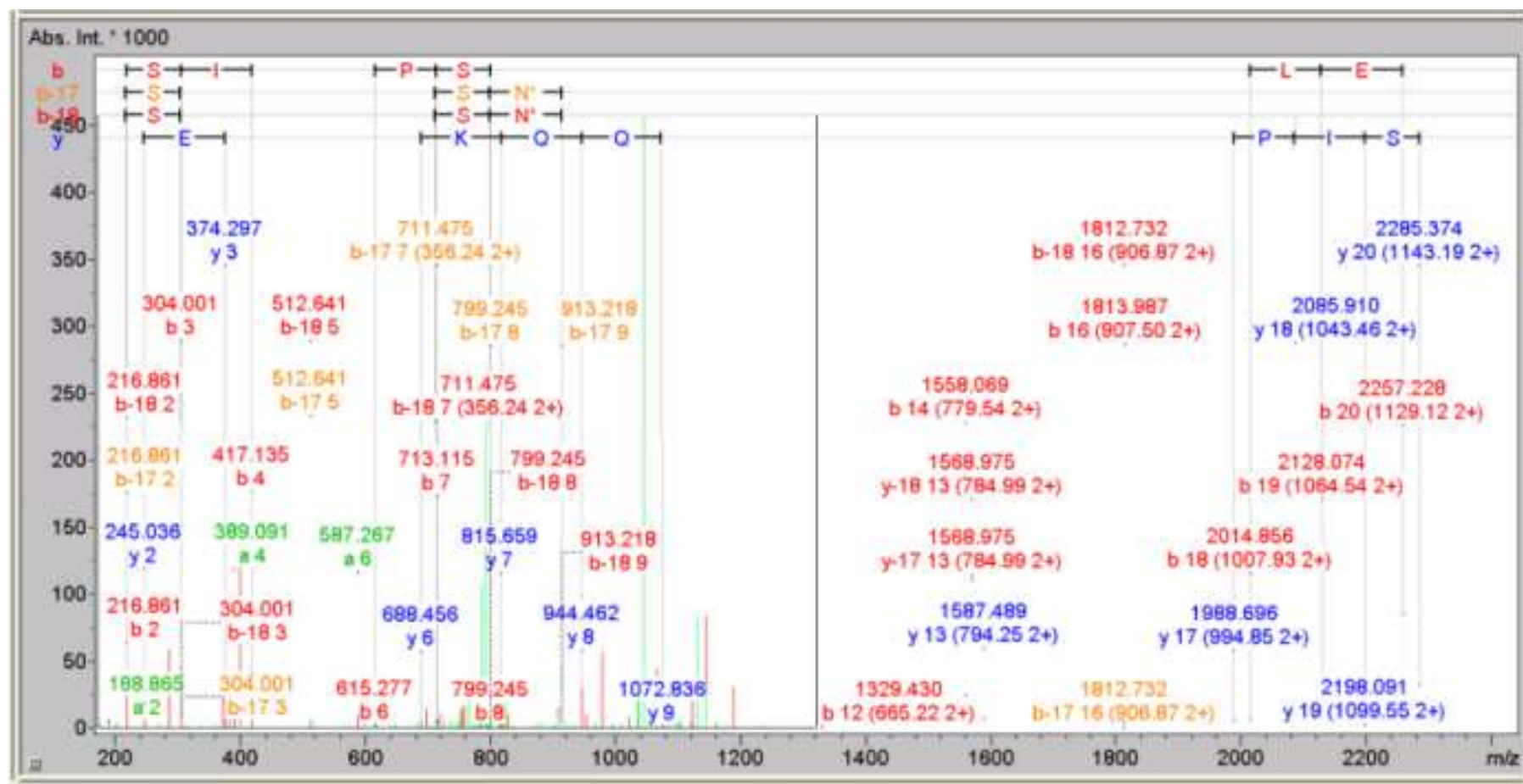
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 lower band	Mascot	Deamidation: N73	568.2881	2+
sequence (enzyme/ion score/mass error)				
69 Y.SFLQN*PQTSL.C Deamidation(N) 78 (Chy/54/0.006)				



Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 lower band	Mascot	Deamidation: N89	834.4229	3+
sequence (enzyme/ion score/mass error)				
81 F.SESIPTPSN*REETQQKSNLELL.R Deamidation(N) 102 (Chy/38/0.0176)				



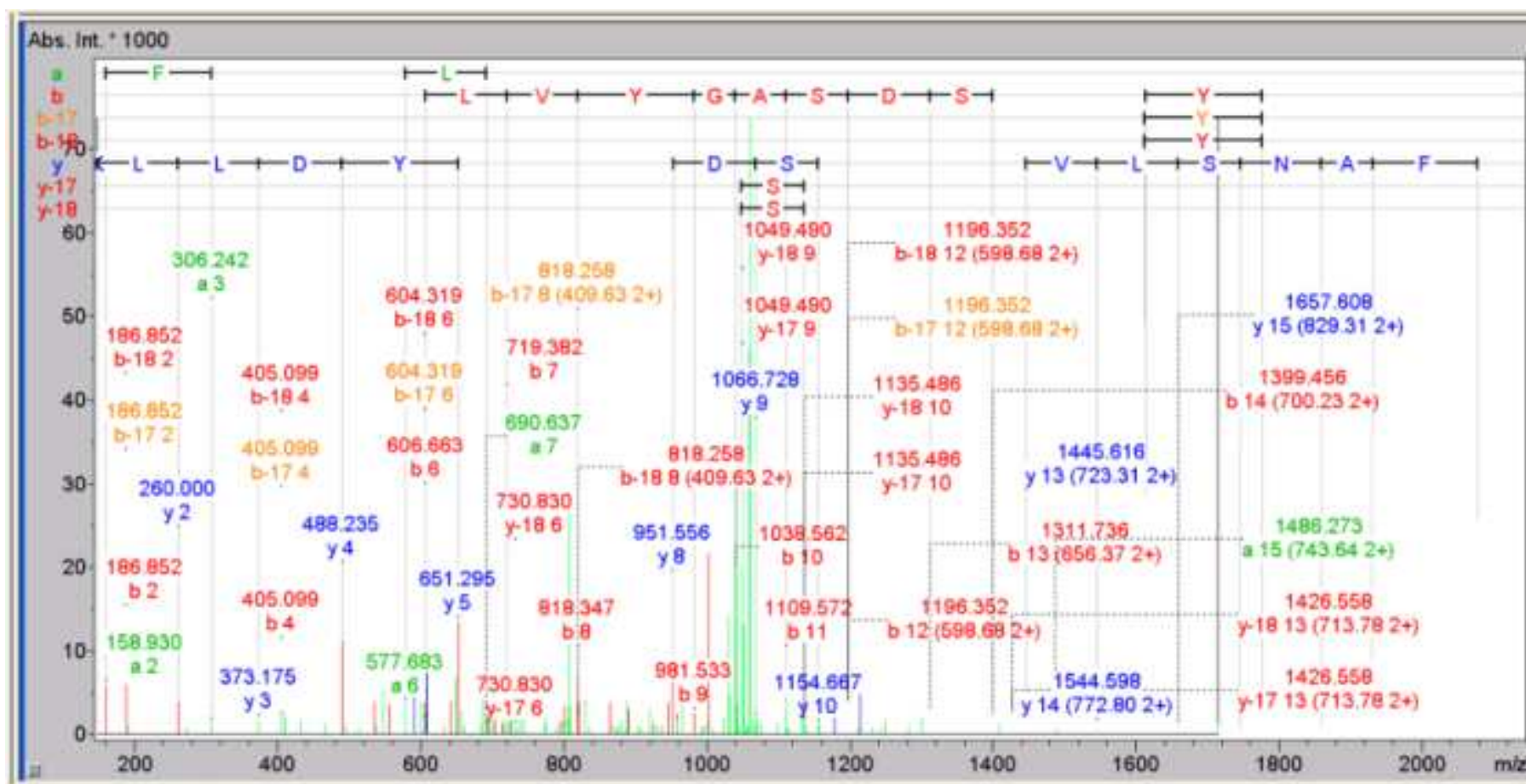
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Deamidation: N98	974.4862	3+
sequence (enzyme/ion score/mass error)				
78 S.LCFSESIPTPSNREETQQKSN*LELL.R Deamidation(N) 102 (Chy/46/0.0244)				



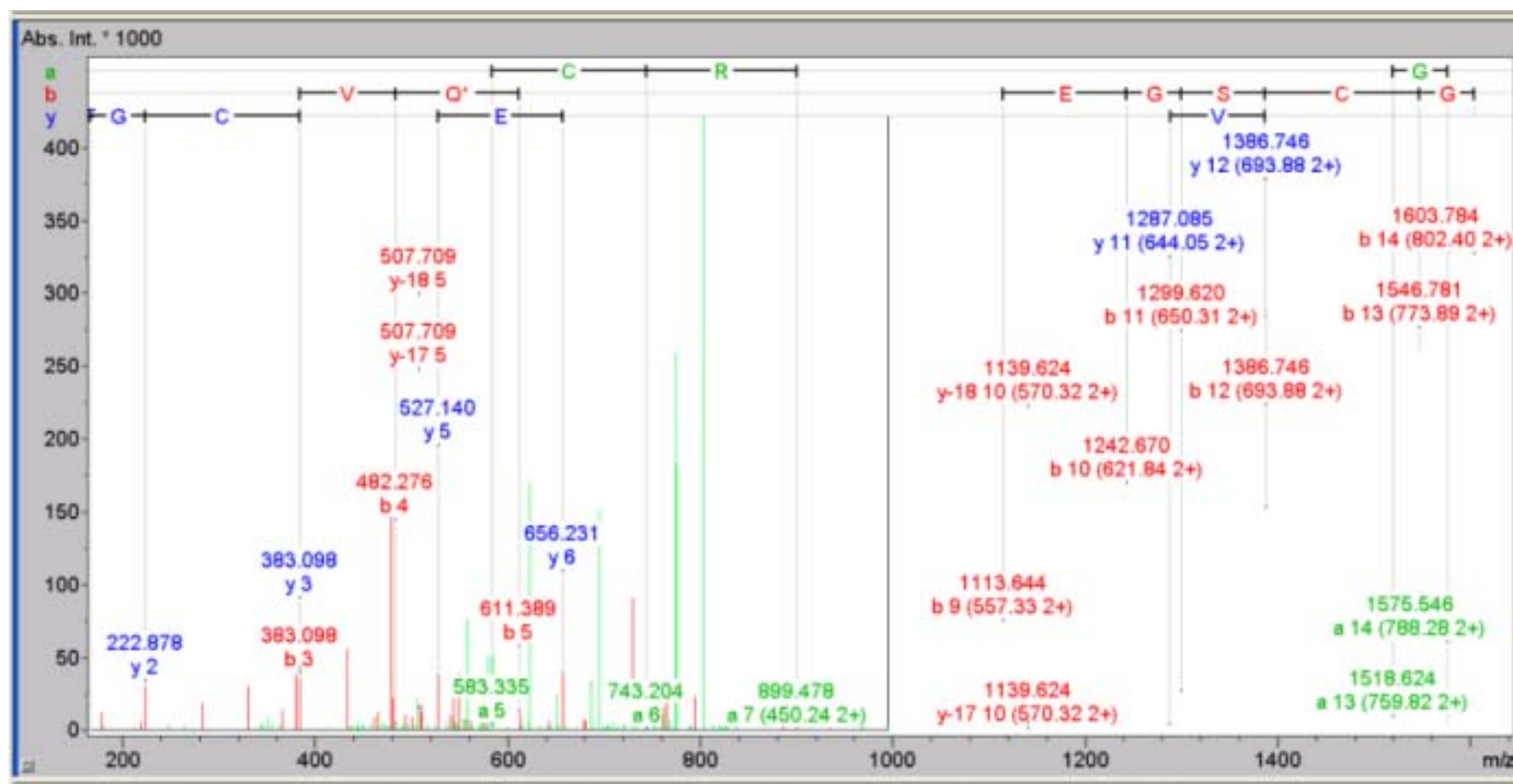
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 lower band	Mascot	Deamidation: N135	755.0445	3+
sequence (enzyme/ion score/mass error)				
121 R.SVFANSLVYGASDSN*VYDLLK.D Deamidation(N) 141 (Try/51/0.0425)				



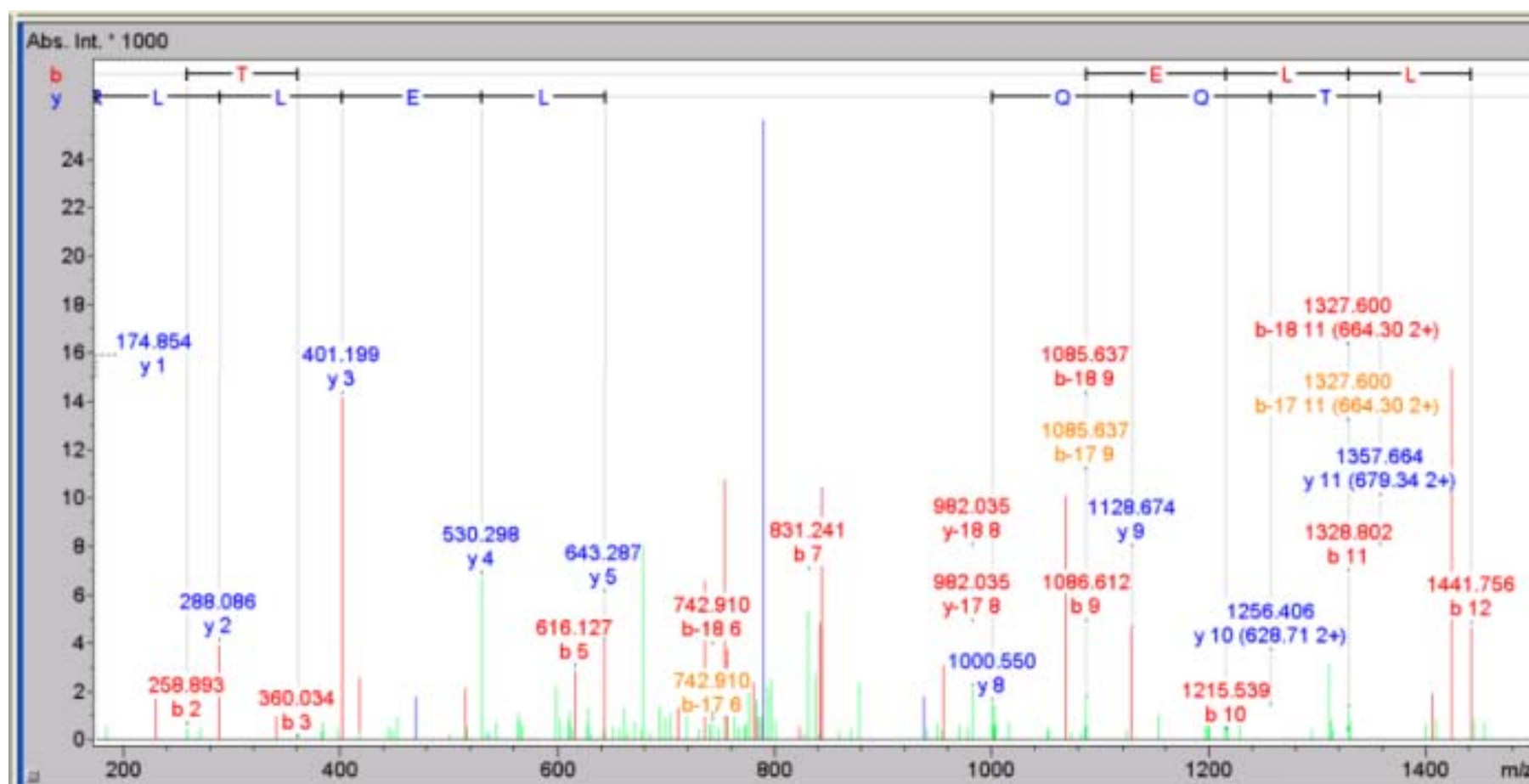
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 lower band	Mascot	Deamidation: Q207	590.2495	3+
sequence (enzyme/ion score/mass error)				
203 F.LRIVQ*CRSVEGSCGF.- Deamidation(Q) 217 (Chy/46/-0.113)				



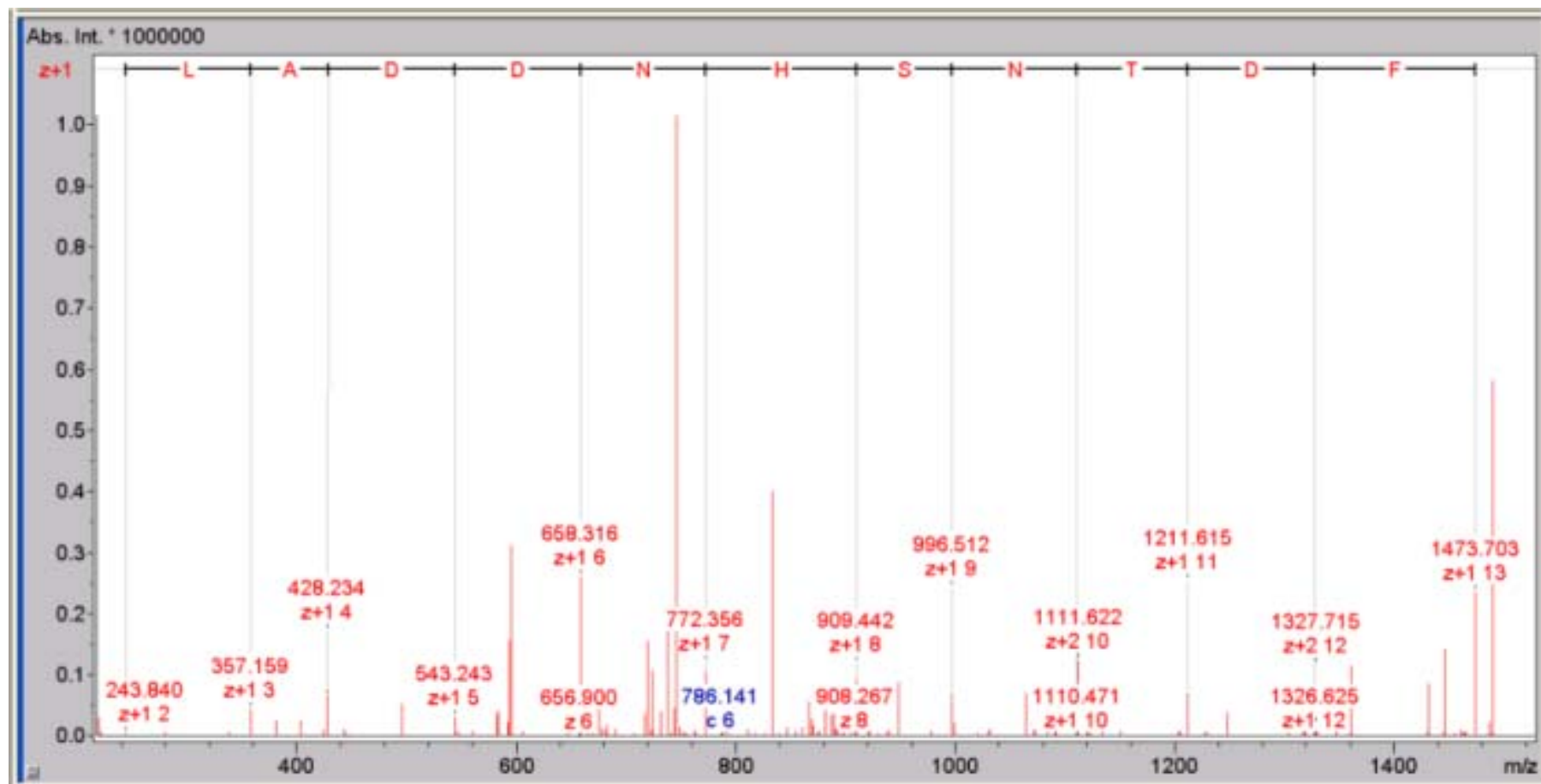
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Dimethylation: N98	808.3767	2+
sequence (enzyme/ion score/mass error)				
91 R.EETQQKSN*LELLR.I Dimethylation(N) 103 (Try/46/-0.1188)				



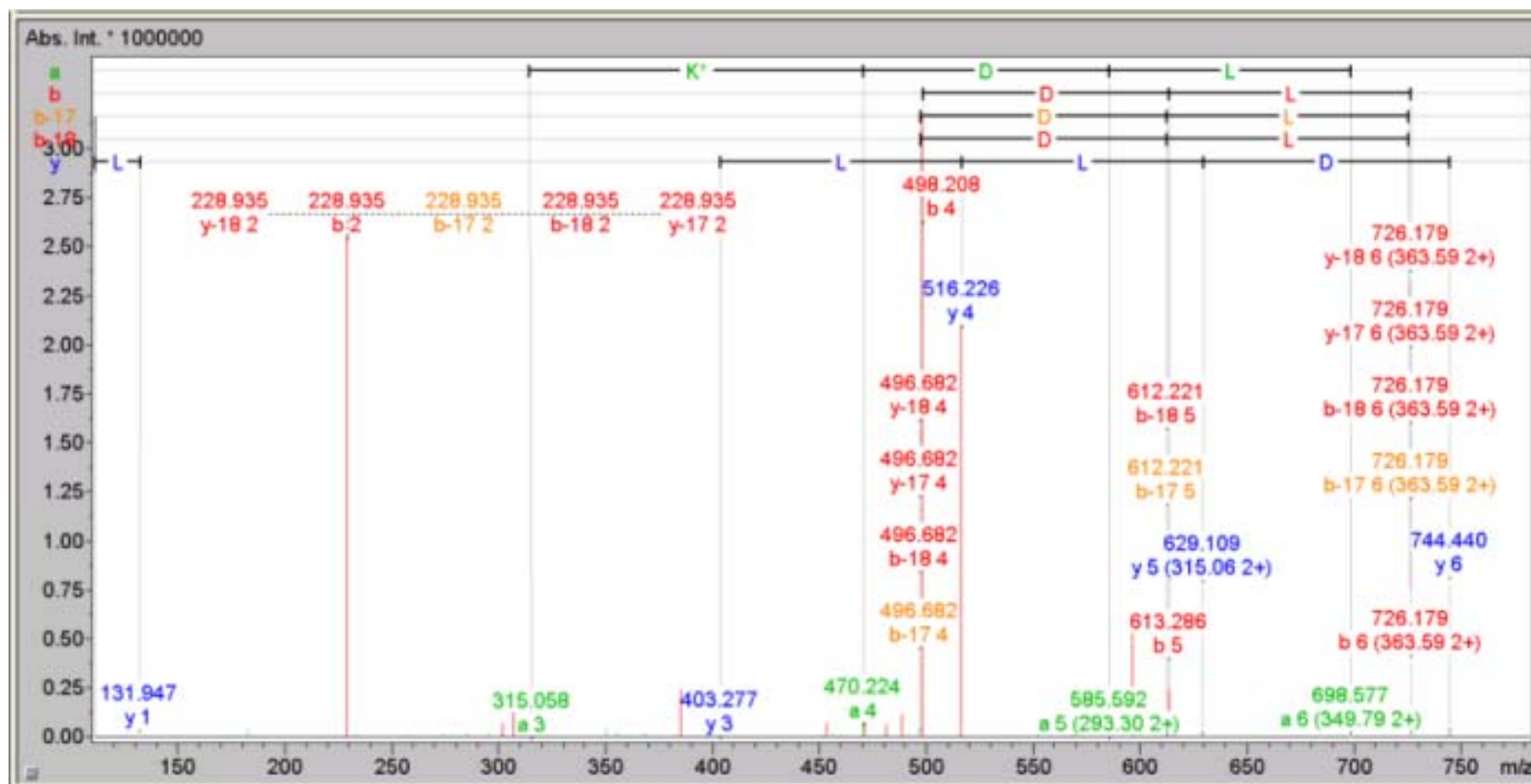
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Ethanedithiolation: S170	594.2431	3+
sequence (enzyme/ion score/mass error)				
170 Y.S*KFDTNSHNDDALLK.N Ethanedithiolation(S) 184 (Try/44/-0.0845)				



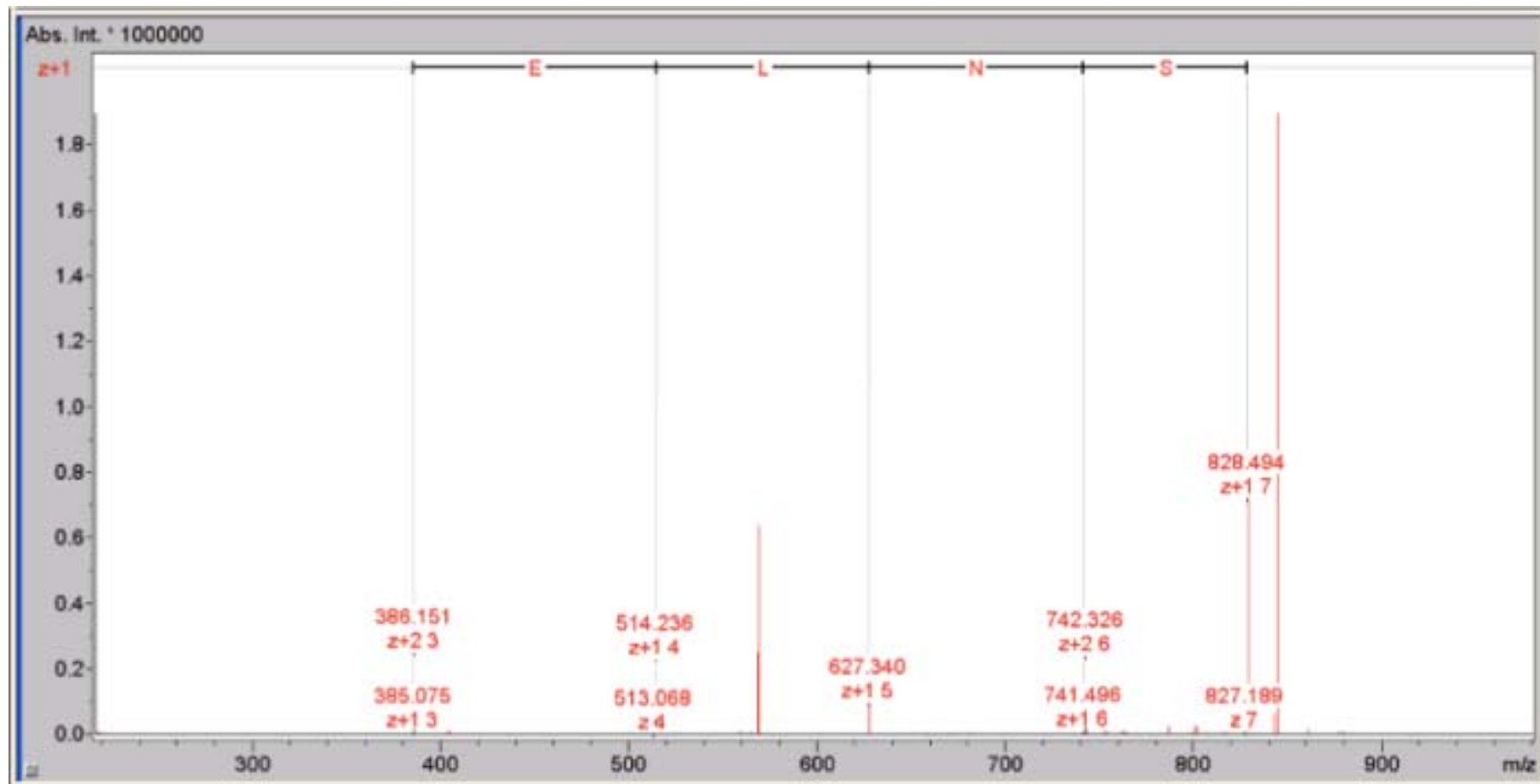
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Formylation: K141	372.7136	2+
sequence (enzyme/ion score/mass error)				
138 Y.DLLK*DL.E Formylation(K) 143 (Chy/31/0.0061)				



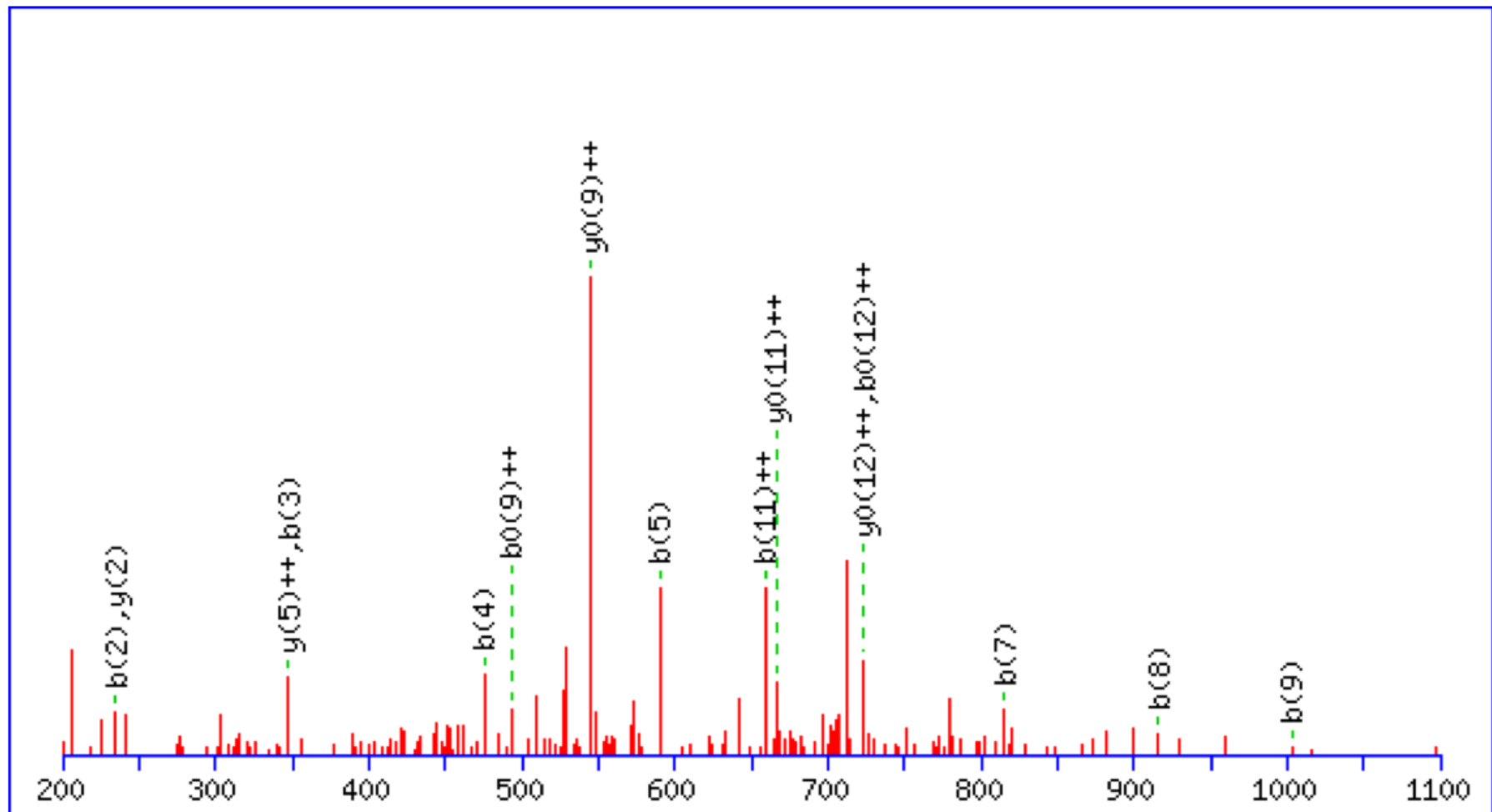
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Hexosamine: K96	567.4203	2+
sequence (enzyme/ion score/mass error)				
96 Q.K*SNLELLR.I HexN(K) 103 (Try/44/0.1809)				



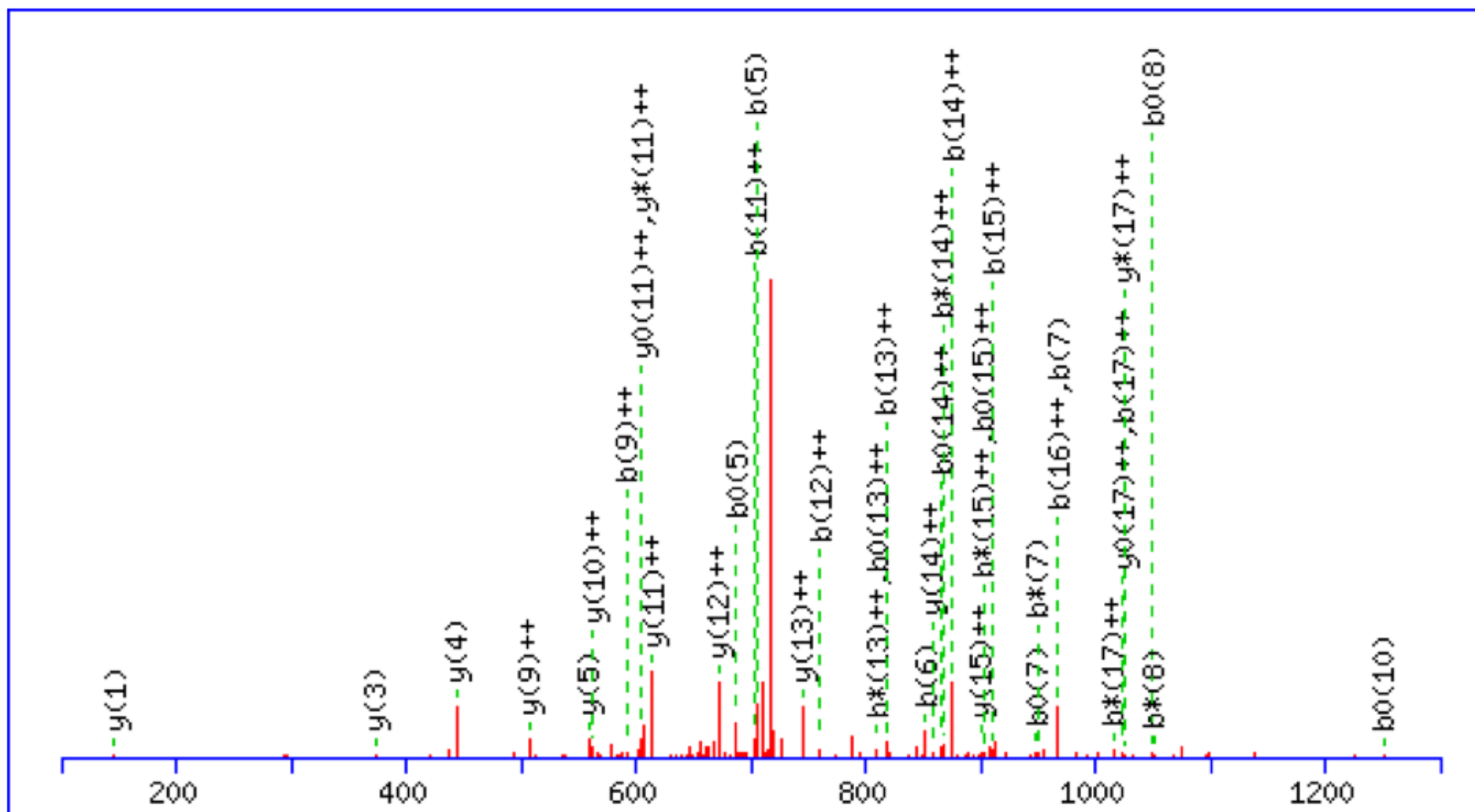
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Mascot	Maleimide: C79	566.5827	3+
sequence (enzyme/ion score/mass error)				
69 Y.SFLQNPQTSLC*FSE.S Maleimide(C) 82 (Chy/36/-0.014)				



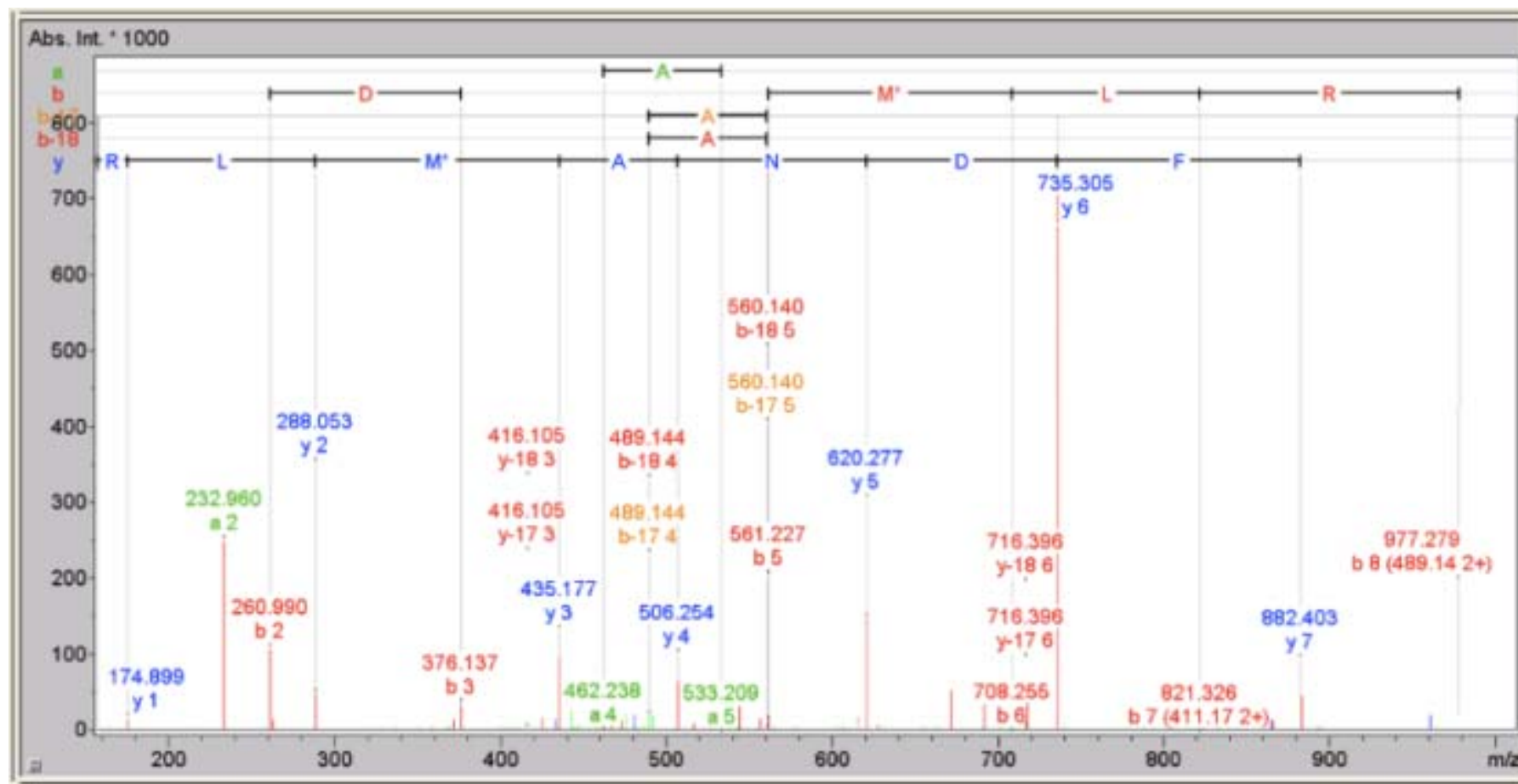
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Maleimide: K171	732.0187	3+
sequence (enzyme/ion score/mass error)				
167 K.QTYSK*FDTNSHNDDALLK.N Maleimide(K) 184 (Try/43/0.0369)				



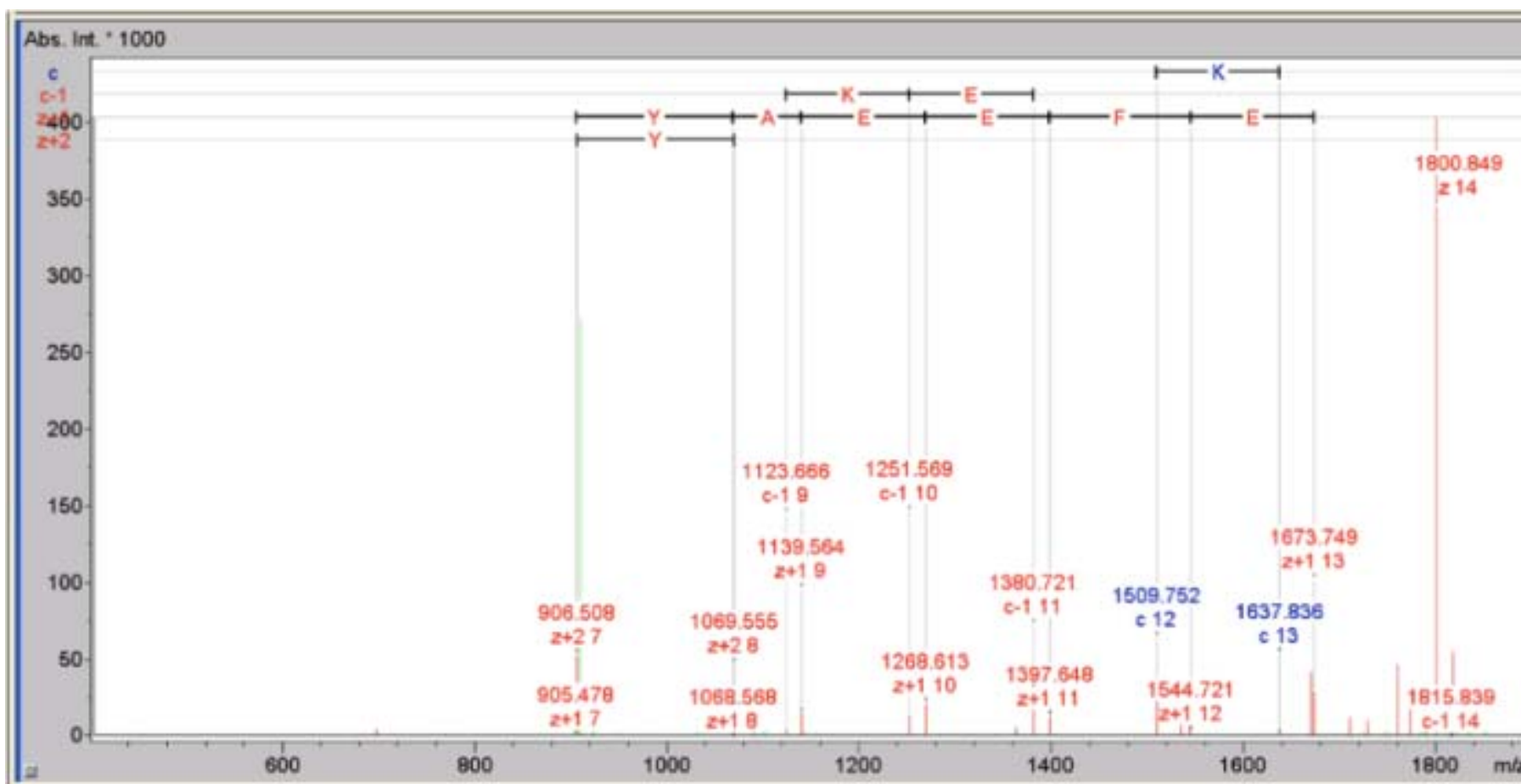
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 lower band	Mascot	Oxidation: M40	498.2315	2+
sequence (enzyme/ion score/mass error)				
35 R.LFDNAM*LR.A Oxidation(M) 42 (Try/49/-0.0421)				



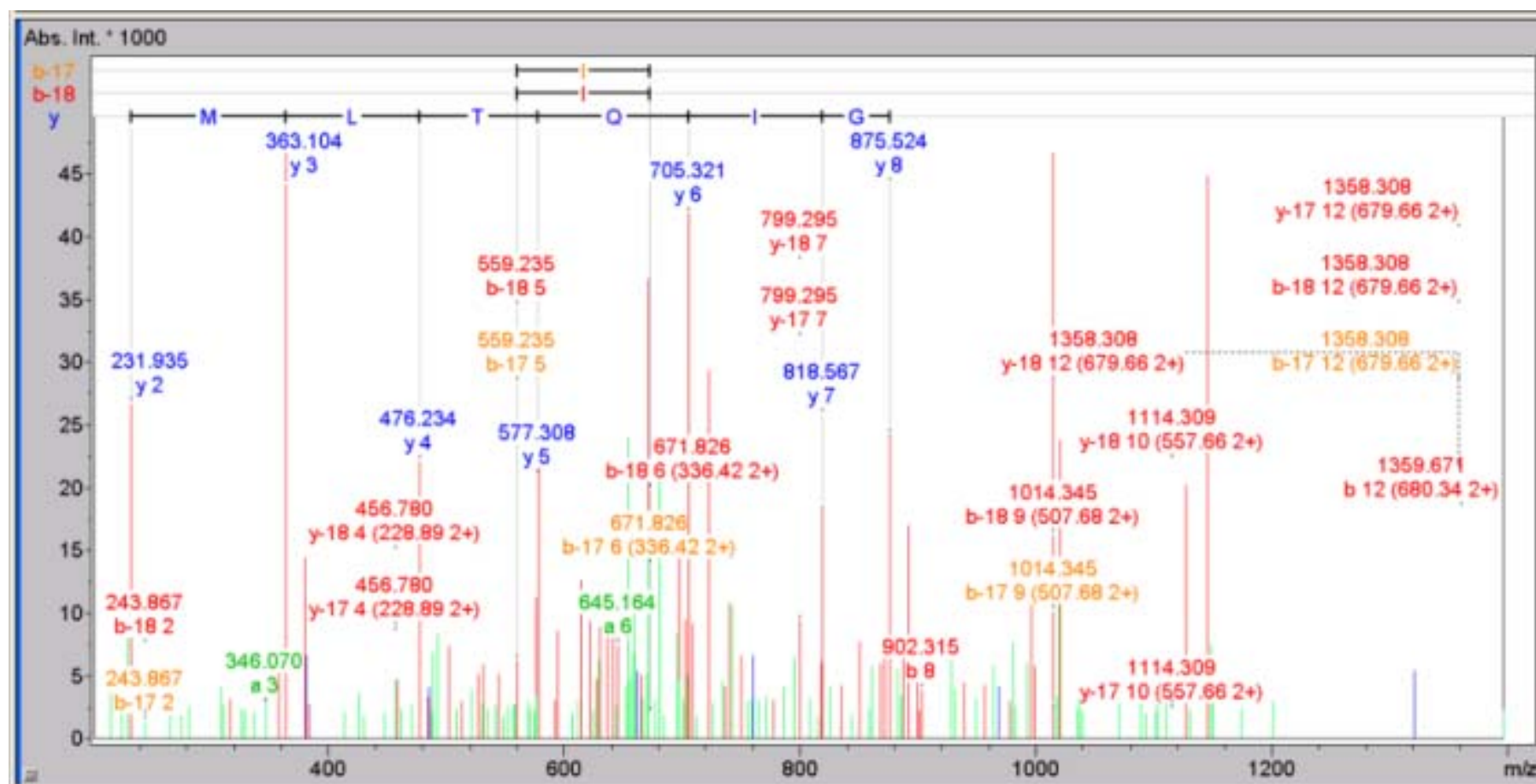
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Oxidation: Y68	909.4282	2+
sequence (enzyme/ion score/mass error)				
55 Y.QEFEEAYIPKEQKY*.S Oxidation(Y) 68 (Chy/39/-0.0101)				



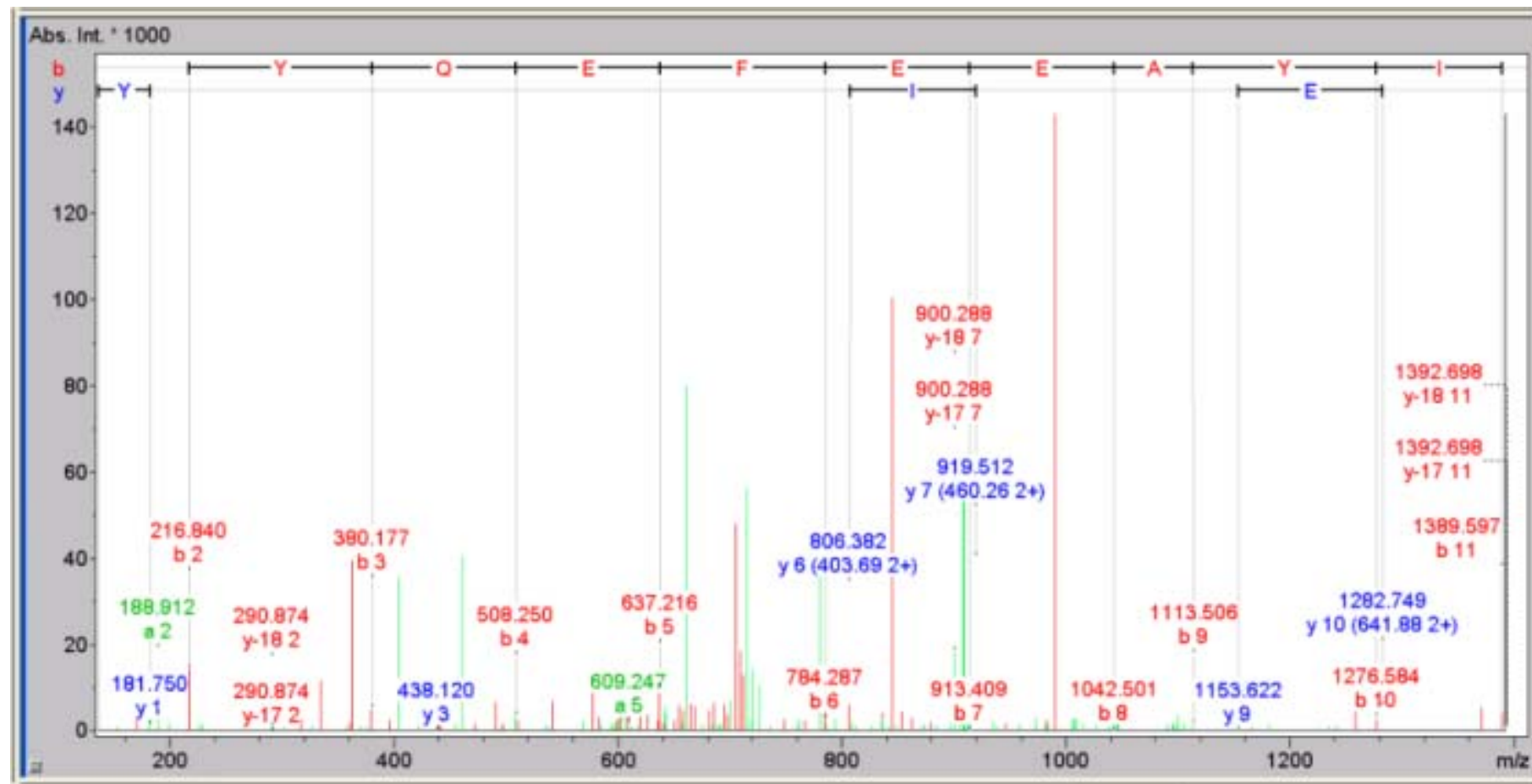
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Mascot	Oxidation: D142	689.3883	2+
sequence (enzyme/ion score/mass error)				
142 K.D*LEEGIQTLMGR.L Oxidation(D) 153 (Try/38/0.1015)				



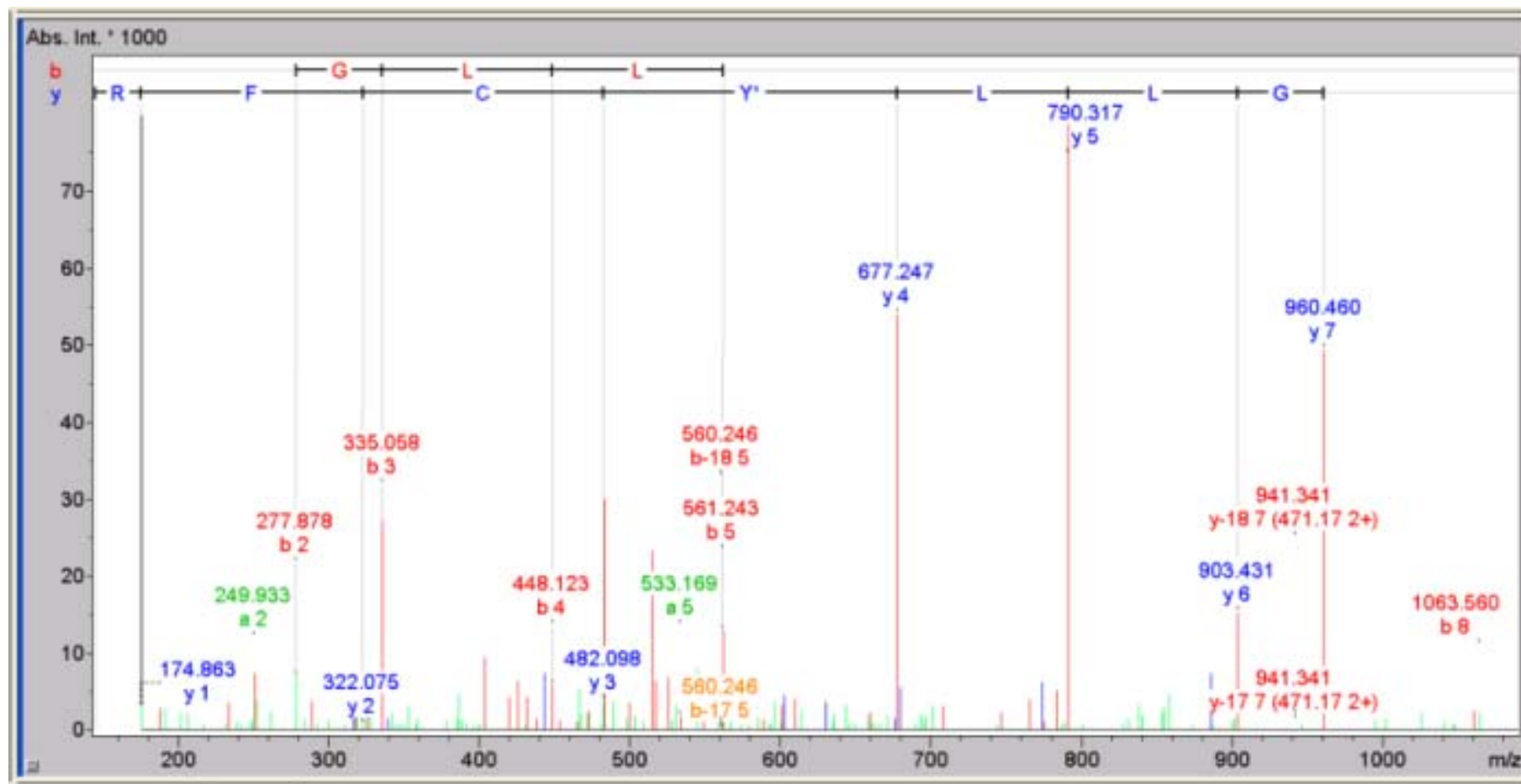
Mascot / pressurized / rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 lower band	Mascot	Pro->pyro-Glu: P63	732.3512	3+
sequence (enzyme/ion score/mass error)				
52 F.DTYQEFEAYIP*KEQKY.S Pro->pyro-Glu(P) 68 (Chy/39/0.0576)				



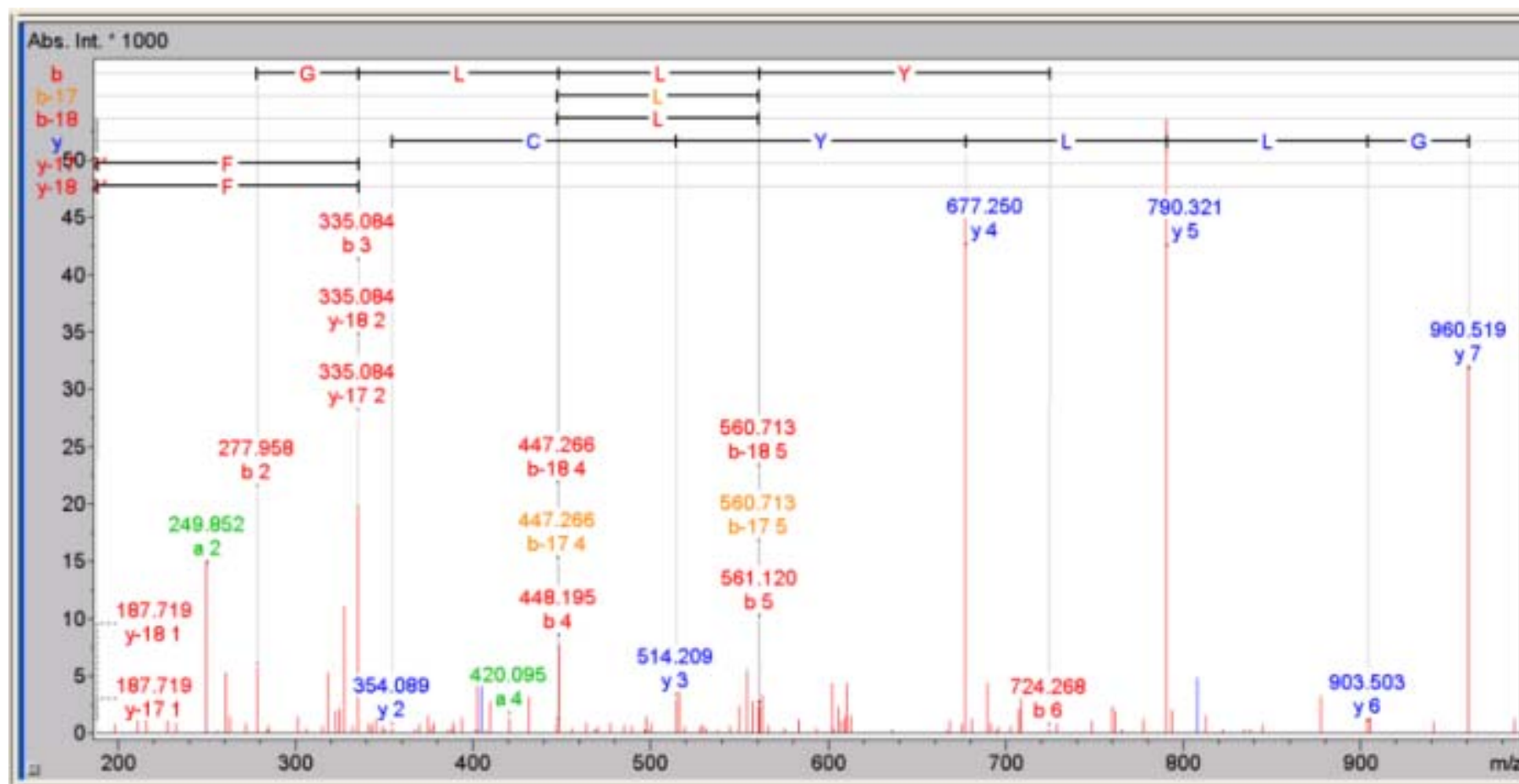
Modiro/ Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 2 upper band	Modiro	Dihydroxylation: Y190	619.30	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
185 K.NYGLLY*CFR.K Dihydroxy(Y) 193 (Try/CID/255/99.9/0.0129)				



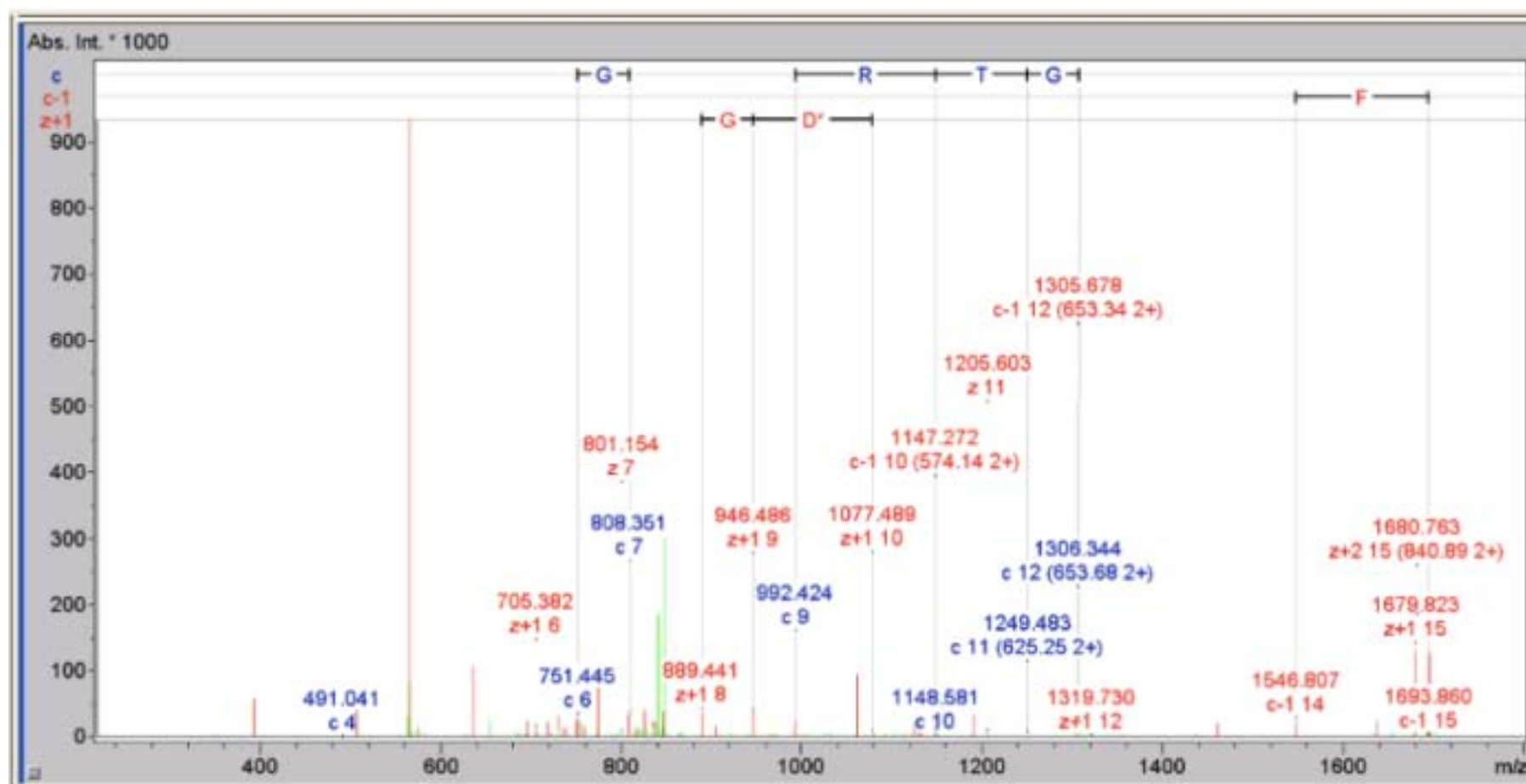
Modiro/ Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 2 lower band	Modiro	Dihydroxylation: R193	619.3	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
185 K.NYGLLYCFR*.K Dihydroxylation(R) 193 (Try/CID/308/99.8/0.0429)				



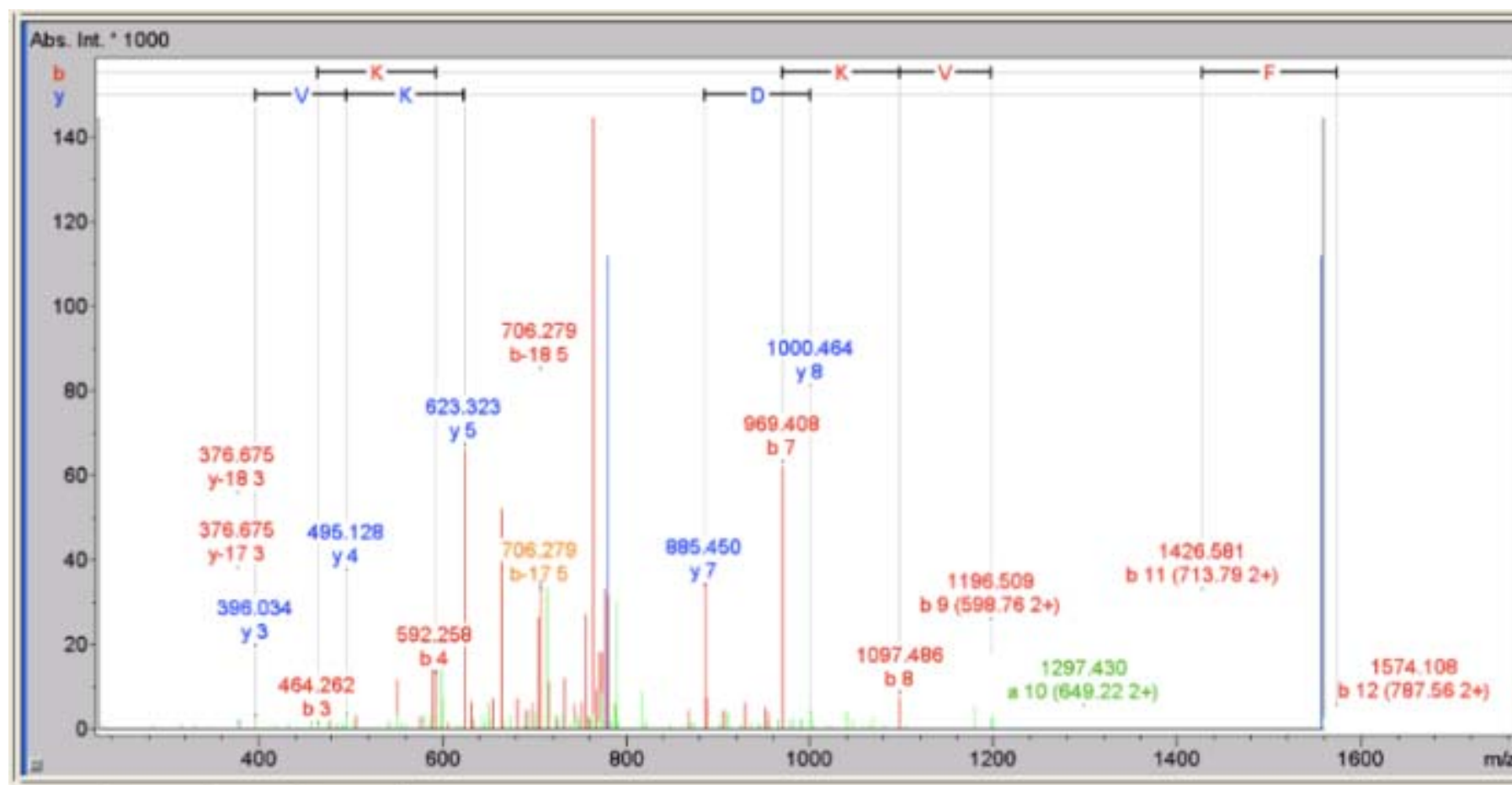
Modiro/ Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 upper band	Modiro	Hydroxylation: D156	565.94	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
151 L.M*GRLED*GSPRTGQIF.K Hydroxylation(MD) 165 (Chy/ETD/299/96.8/-0.0021)				



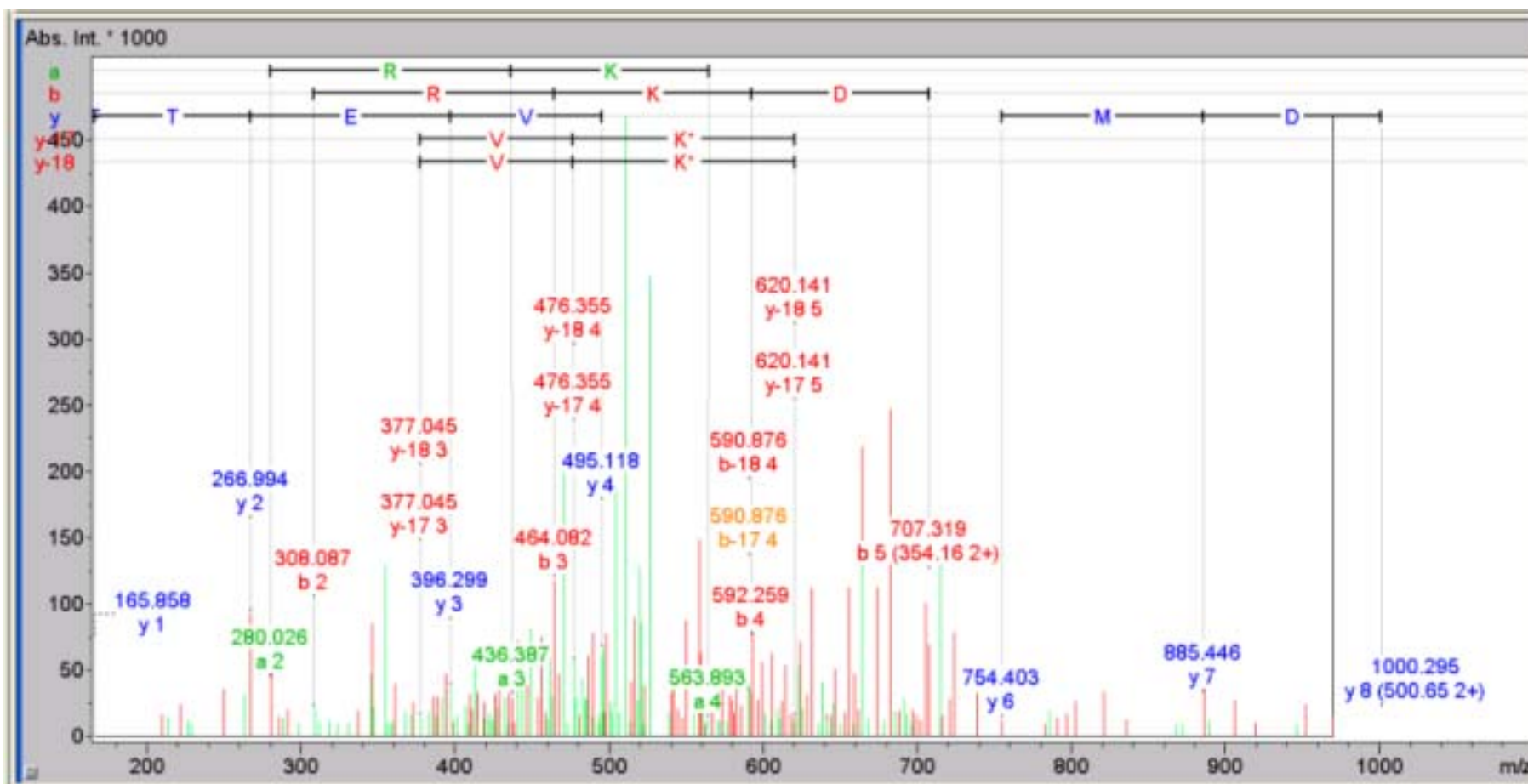
Modiro/ Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 lower band	Modiro	Hydroxylation: D197	796.35	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
191 Y.CFRKDMD*KVETF.L Hydroxylation(D) 202 (Chy/CID/237/100/-0.0158)				



Modiro/ Untreated / rhGH

Sample	Search engine	Modification	m/z	charge
Untreated rhGH sample 1 lower band	Modiro	Hydroxylation: K198	531.24	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
191 Y.CFRKDMDK*VETFL Hydroxylation(K) 202 (Chy/CID/424/91.2/-0.0063)				



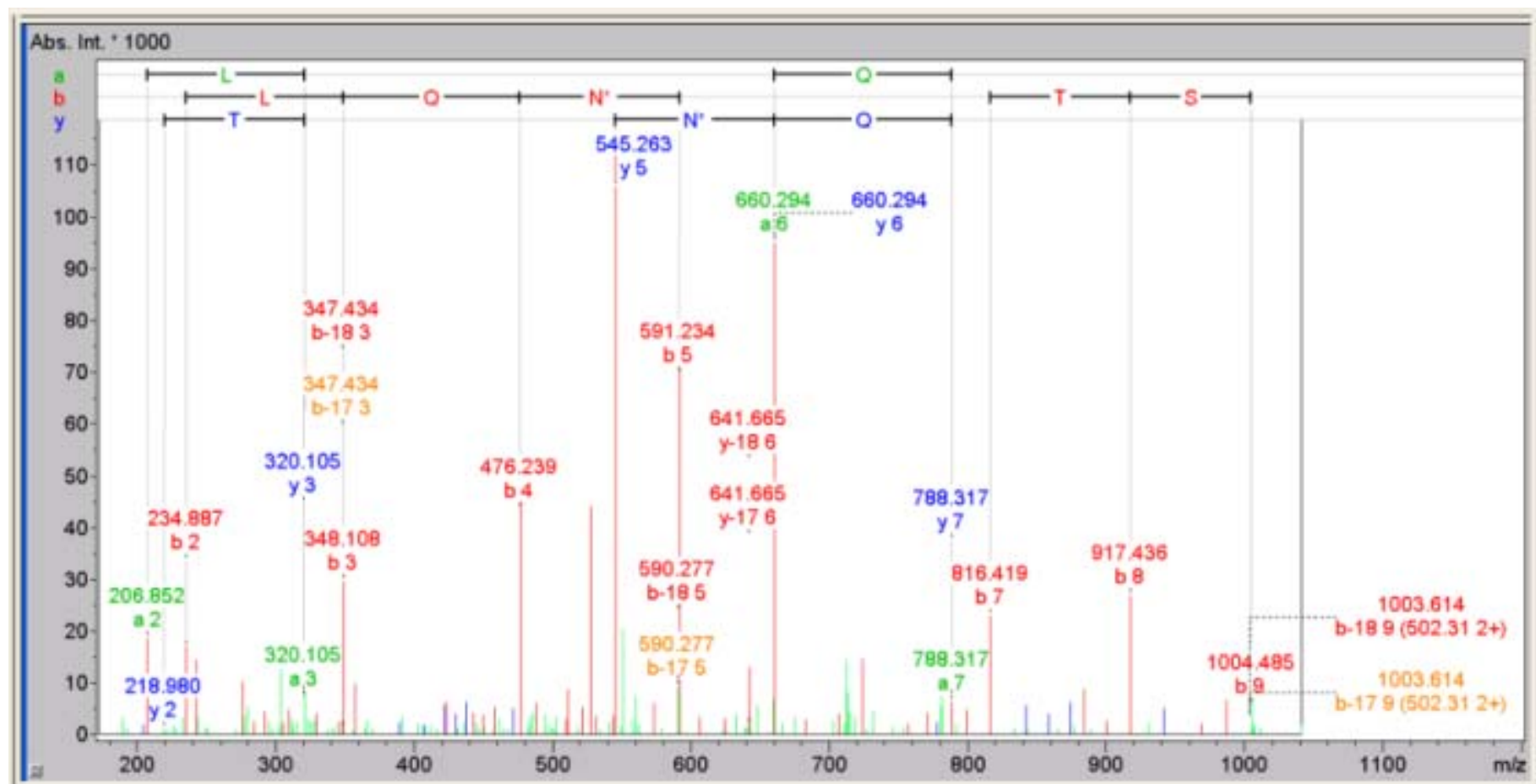
Modirol/pressurized/rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Modiro	Deamidation: R45	853.66	4+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
42 L.RAHR*LHQLAFDTYQEFEEAYIPKEQKY.S Deamidation(R) 68 (Chy/CID/549/98.5/-0.0144)				



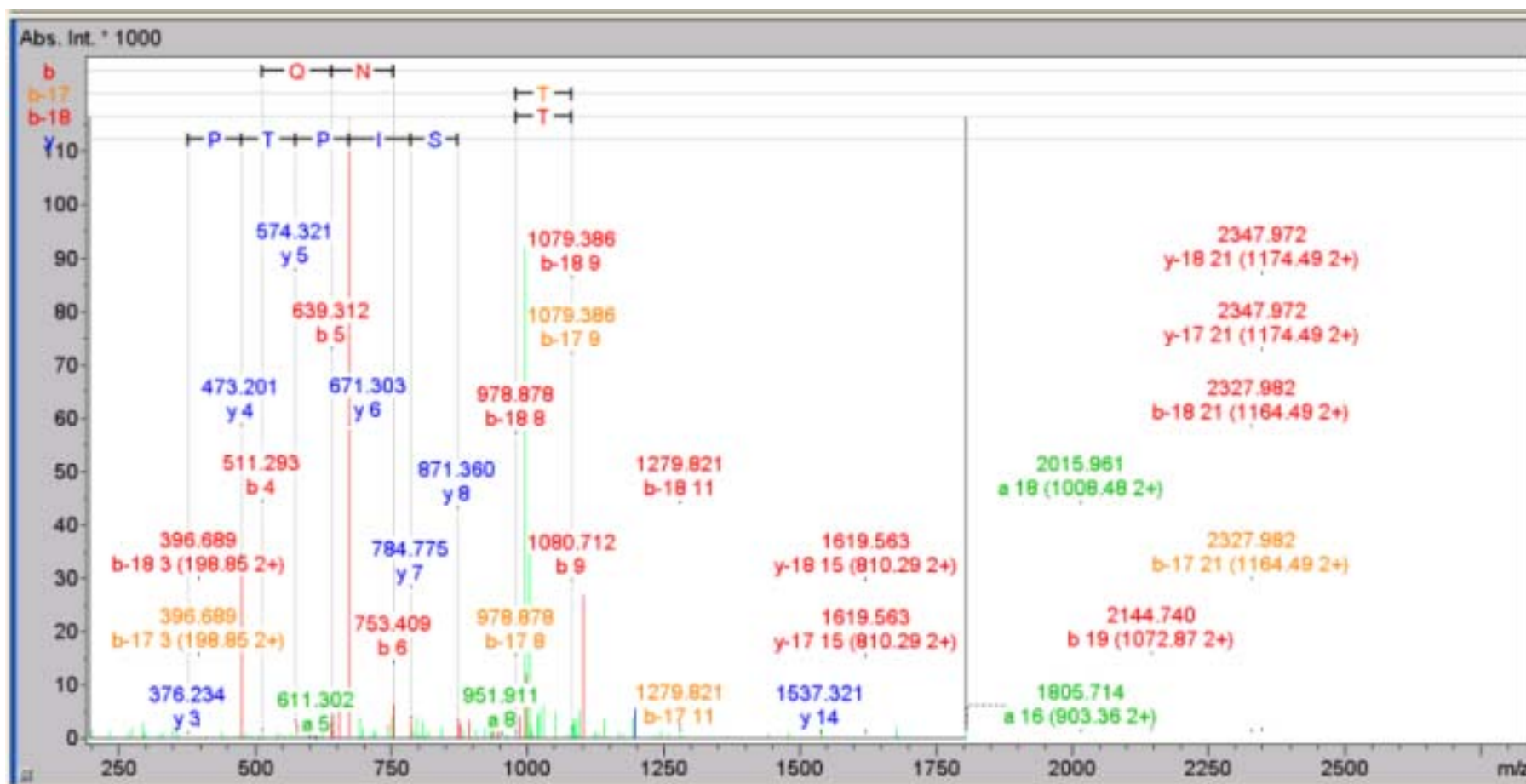
Modiro/ pressurized/ rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 lower band	Modiro	Deamidation: N73	568.29	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
69 Y.SFLQN*PQTS�.C Deamidation(N) 78 (Chy/CID/292/99.9/0.0049)				



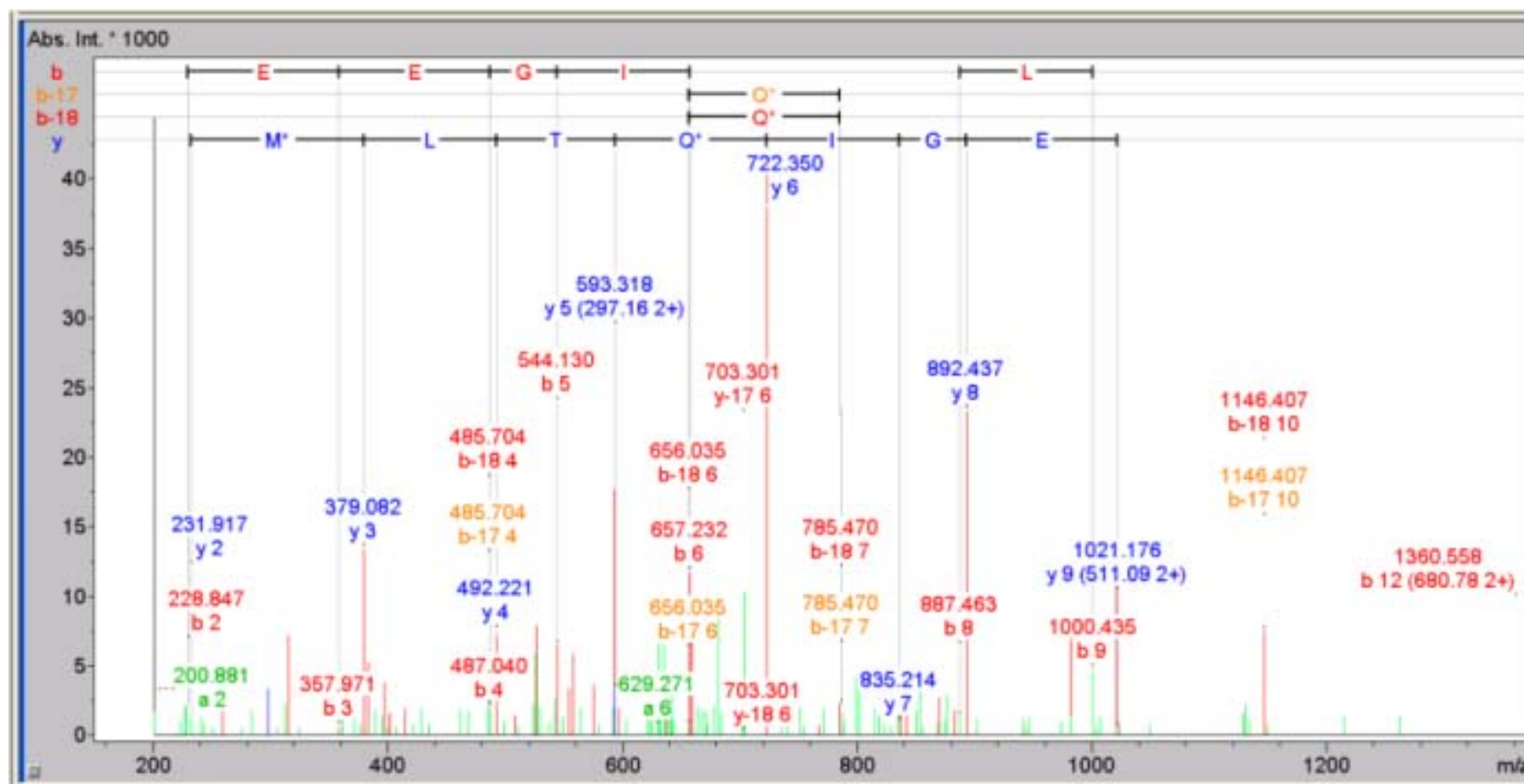
Modirol/pressurized/rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 lower band	Modiro	Deamidation: Q75	892.08	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
68 K.YSFLQNPQ*TSLCFSESIPTPSNR.E Deamidation(Q) 90 (Try/CID/318/96.4/-0.0066)				



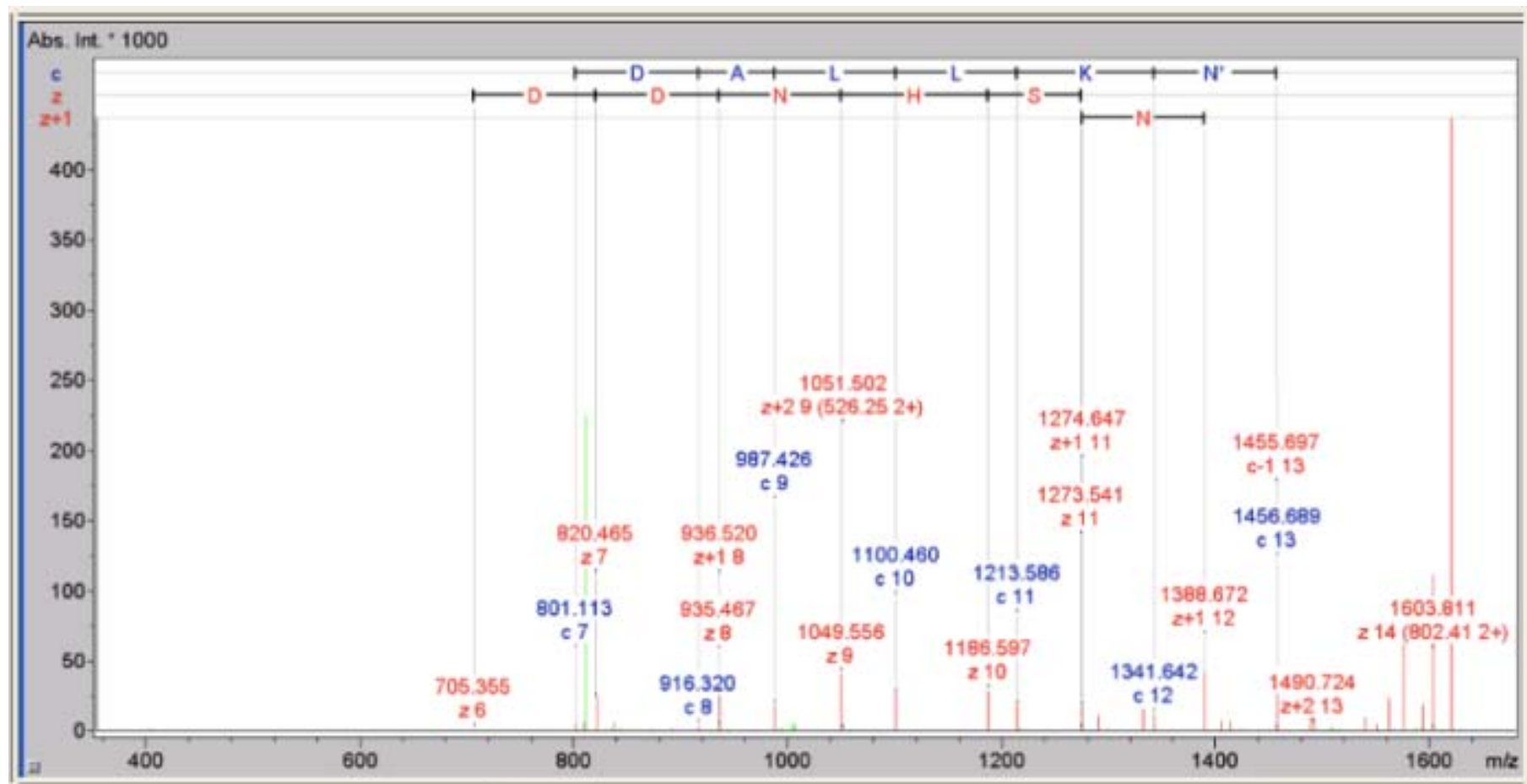
Modiro/ pressurized/ rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 lower band	Modiro	Deamidation: Q148	689.83	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
142 K.DLEEGIQ*TLM*GR.L Deamidation(Q) Oxidation(M) 153 (Try/CID/271/99.4/0.0004)				



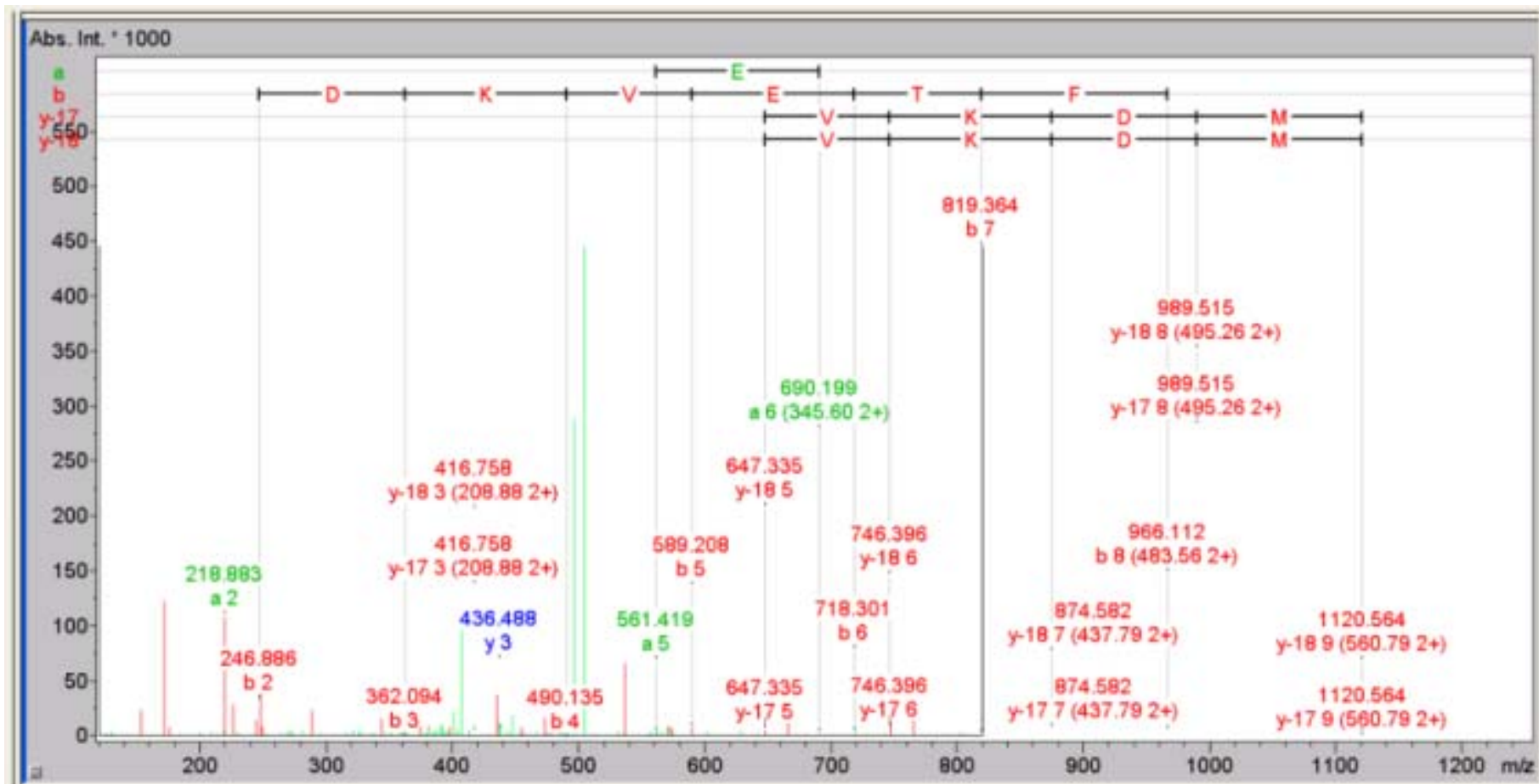
Modiro/ pressurized/ rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 lower band	Modiro	Deamidation: N185	810.86	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
173 F.DTNSHNDDALLKN*Y.G Deamidation(N) 186 (Chy/ETD/266/91.8/-0.0004)				



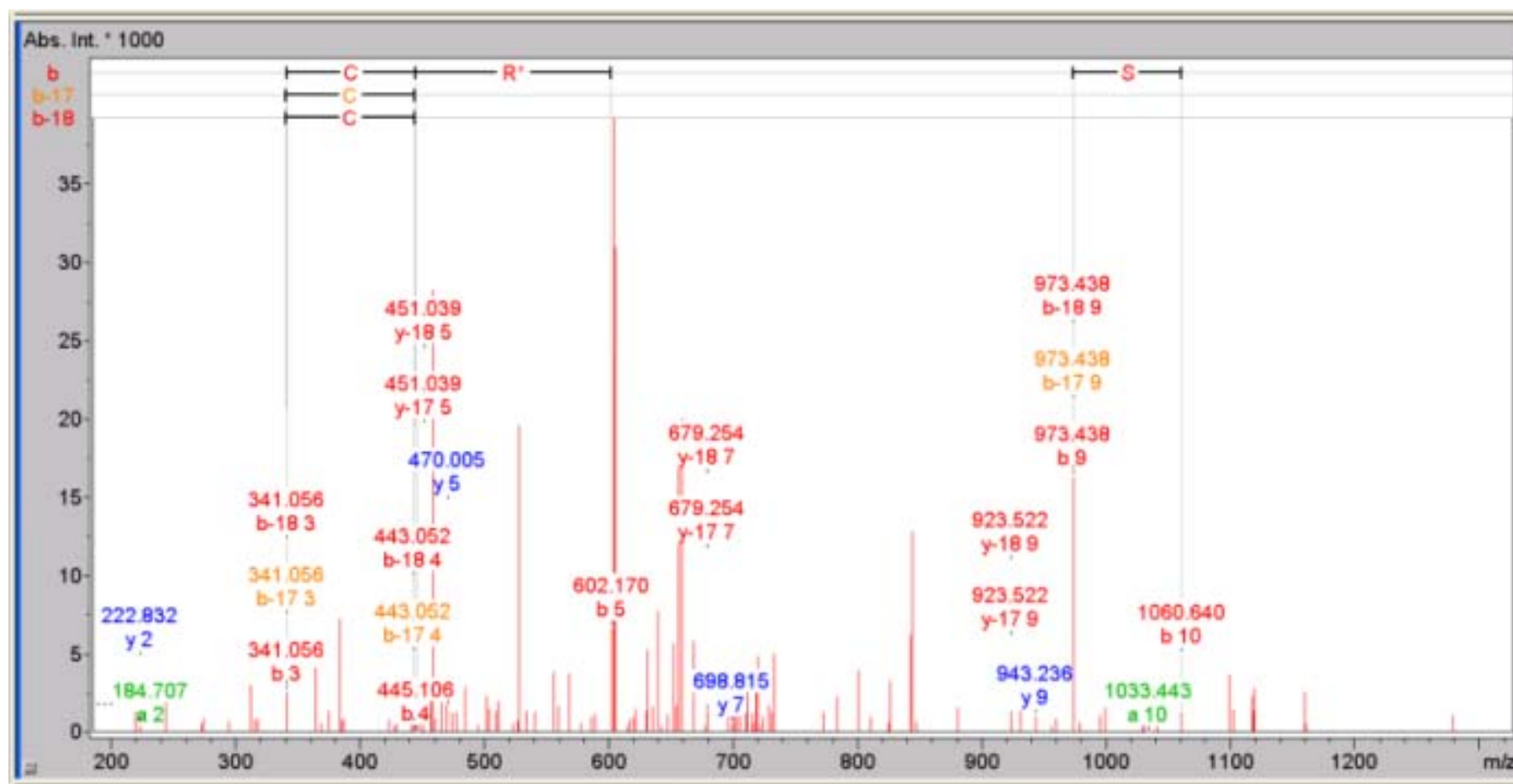
Modiro/ pressurized/ rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Modiro	Deamidation: R204	418.84	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
195 K.DMDKVETFLR*.I Deamidation(R) 204 (Try/CID/355/96.9/-0.0327)				



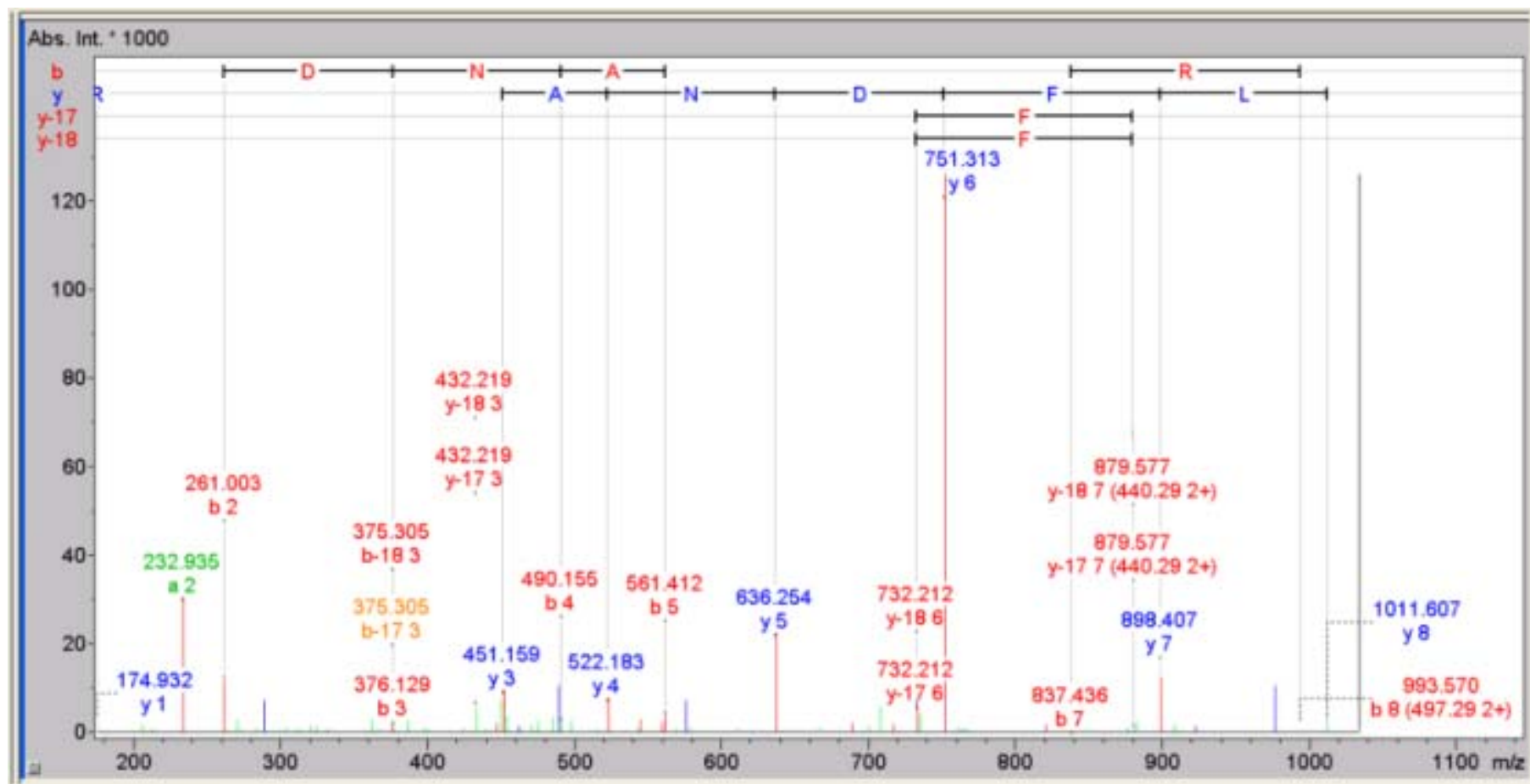
Modiro/ pressurized/ rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 lower band	Modiro	Deamidation: R209	750.29	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
205 R.IVQCR*SVEGSCGF.- Deamidation(R) 217 (Try/CID/270/99.9/-0.0445)				



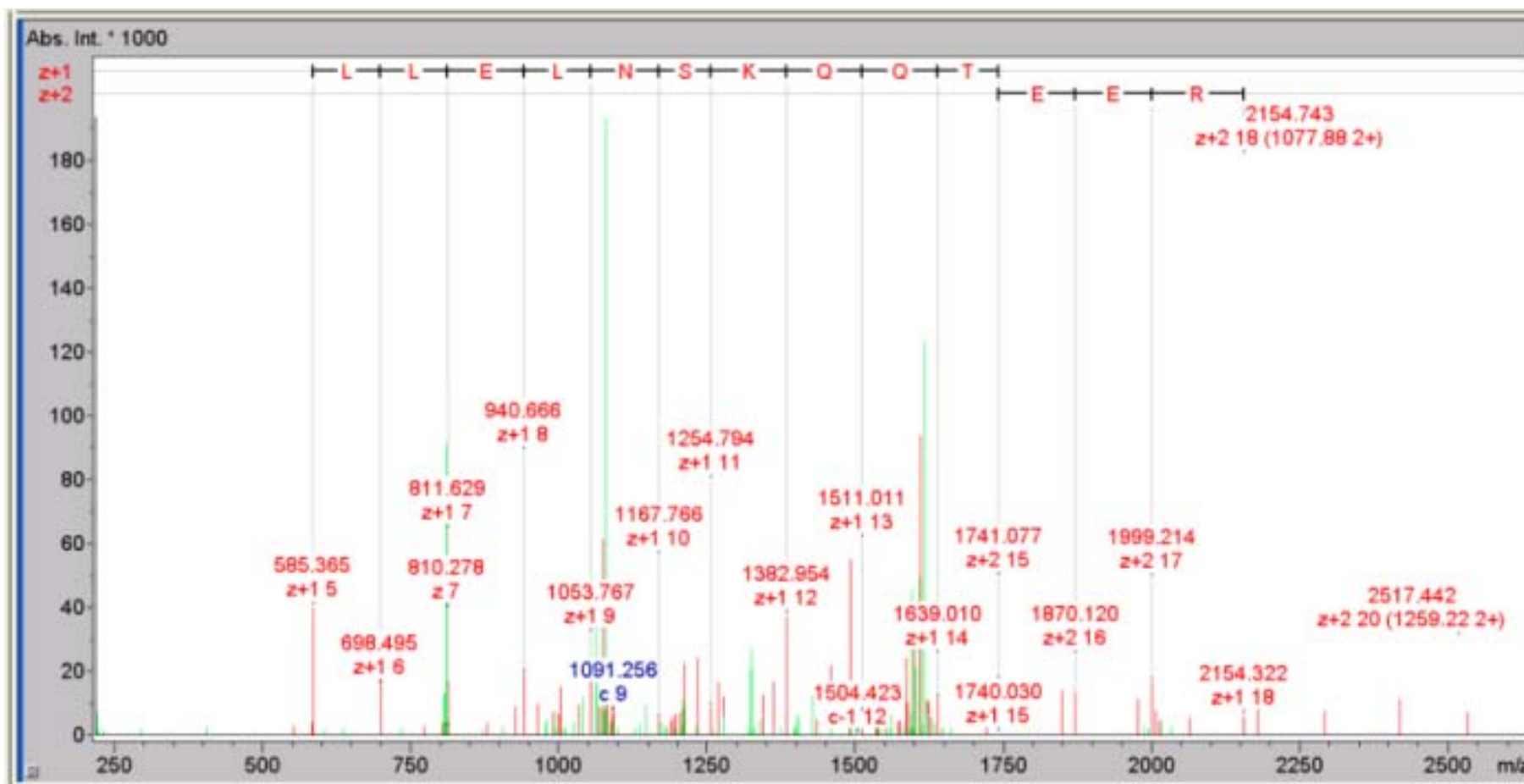
Modiro/ pressurized/ rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 upper band	Modiro	Dihydroxylation: M40	506.24	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
35 R.LFDNAM*LR.A Dihydroxylation(M) 42 (Try/CID/396/99.2/-0.01)				



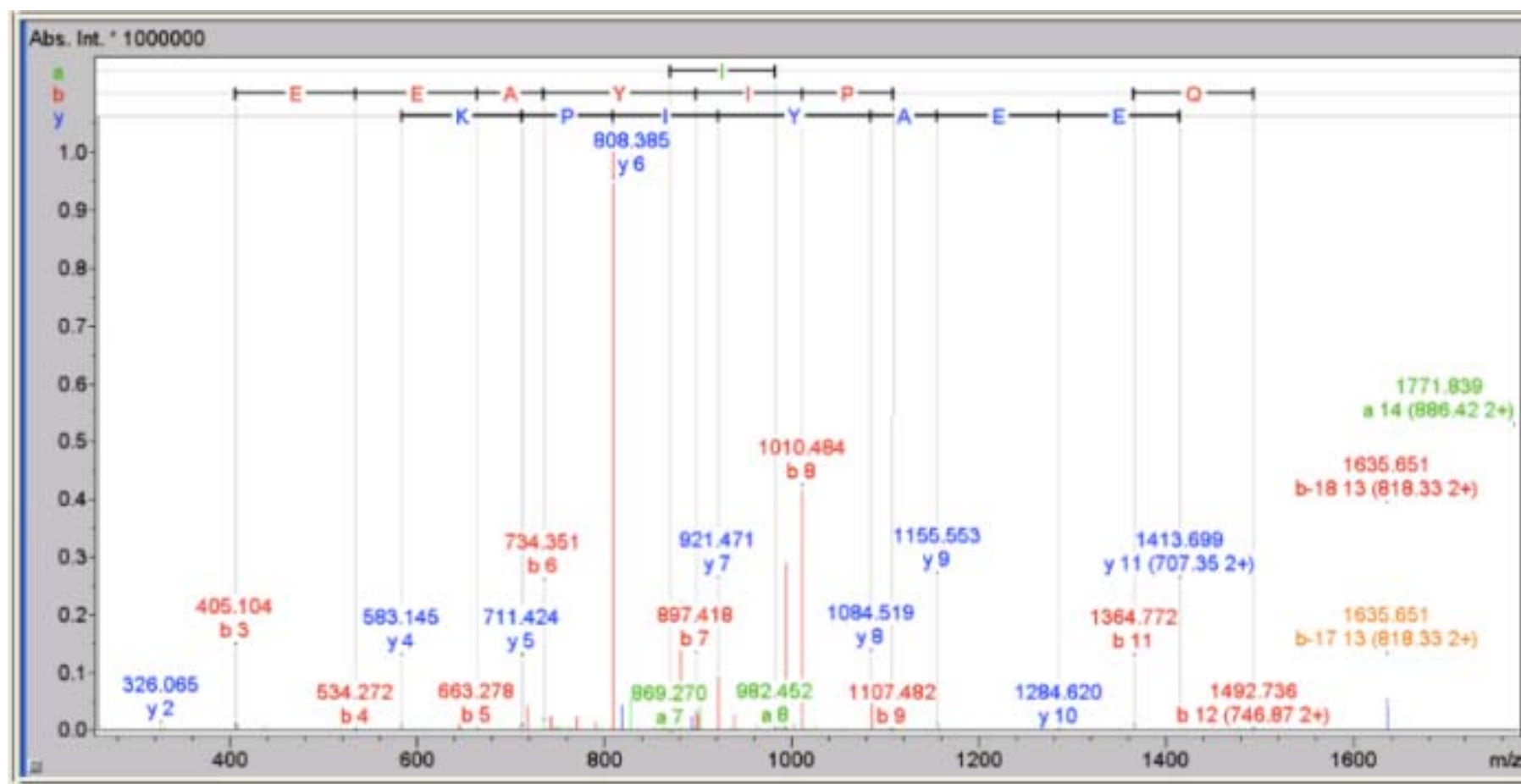
Modiro/ pressurized/ rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Modiro	Hexosamine: N89	808.22	4+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
81 F.SESIPTPSN*REETQQKSNLELLRISLL.L HexN(N) 107 (Chy/ETD/418/81.3/0.0386)				



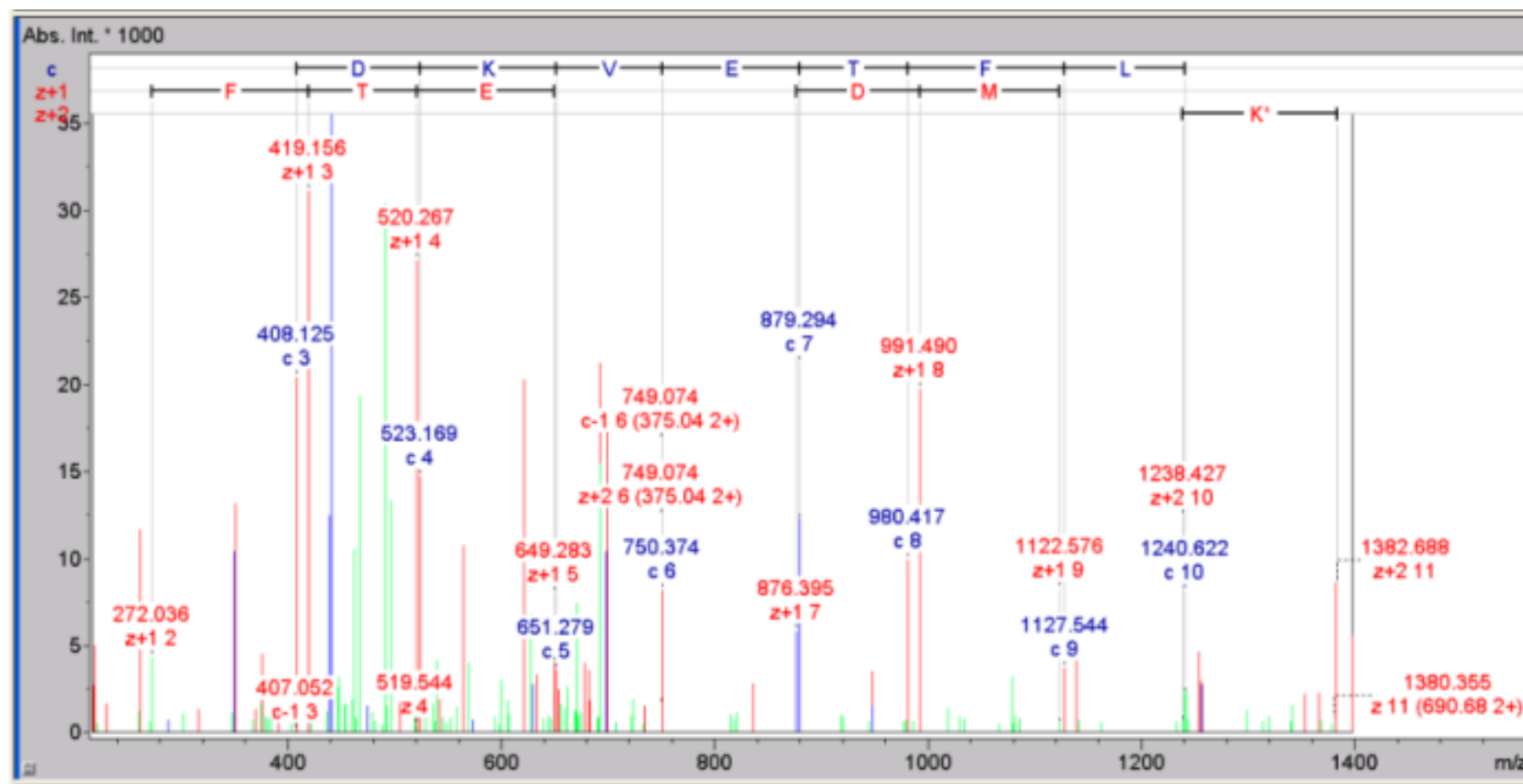
Modiro/ pressurized/ rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 1 upper band	Modiro	Hydroxylation: K67	909.43	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
55 Y.QEFEEAYIPKEQK*Y.S Hydroxylation(K) 68 (Chy/CID/380/100/-0.0032)				



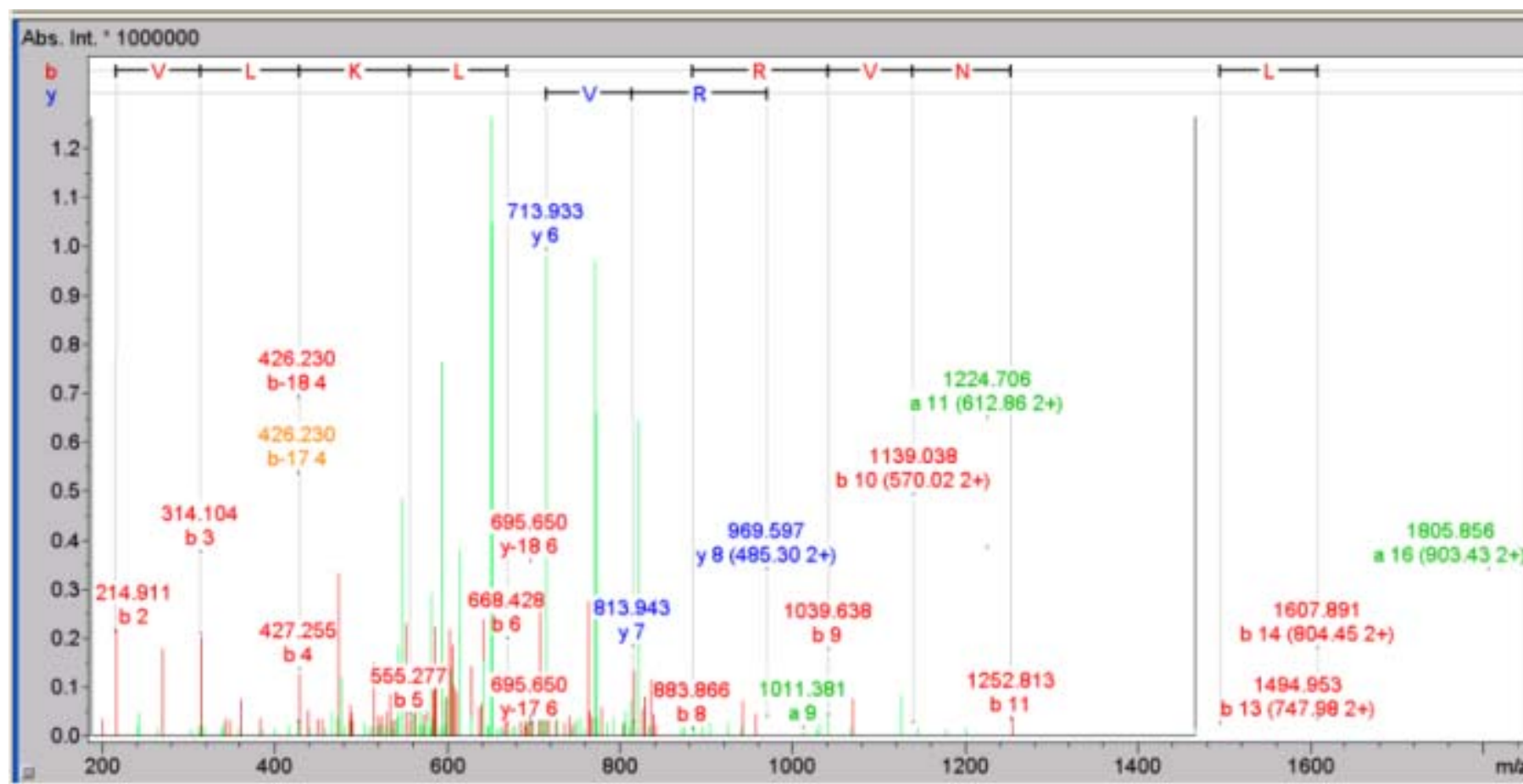
Modiro/ pressurized/ rhGH

Sample	Search engine	Modification	m/z	charge
Pressurized rhGH sample 2 lower band	Modiro	Hydroxylation: K194	350.07	4+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
194 R.K*DMDKVETFLR.I Hydroxylation(K) 204 (Try/ETD/452/96.1/-0.1128)				



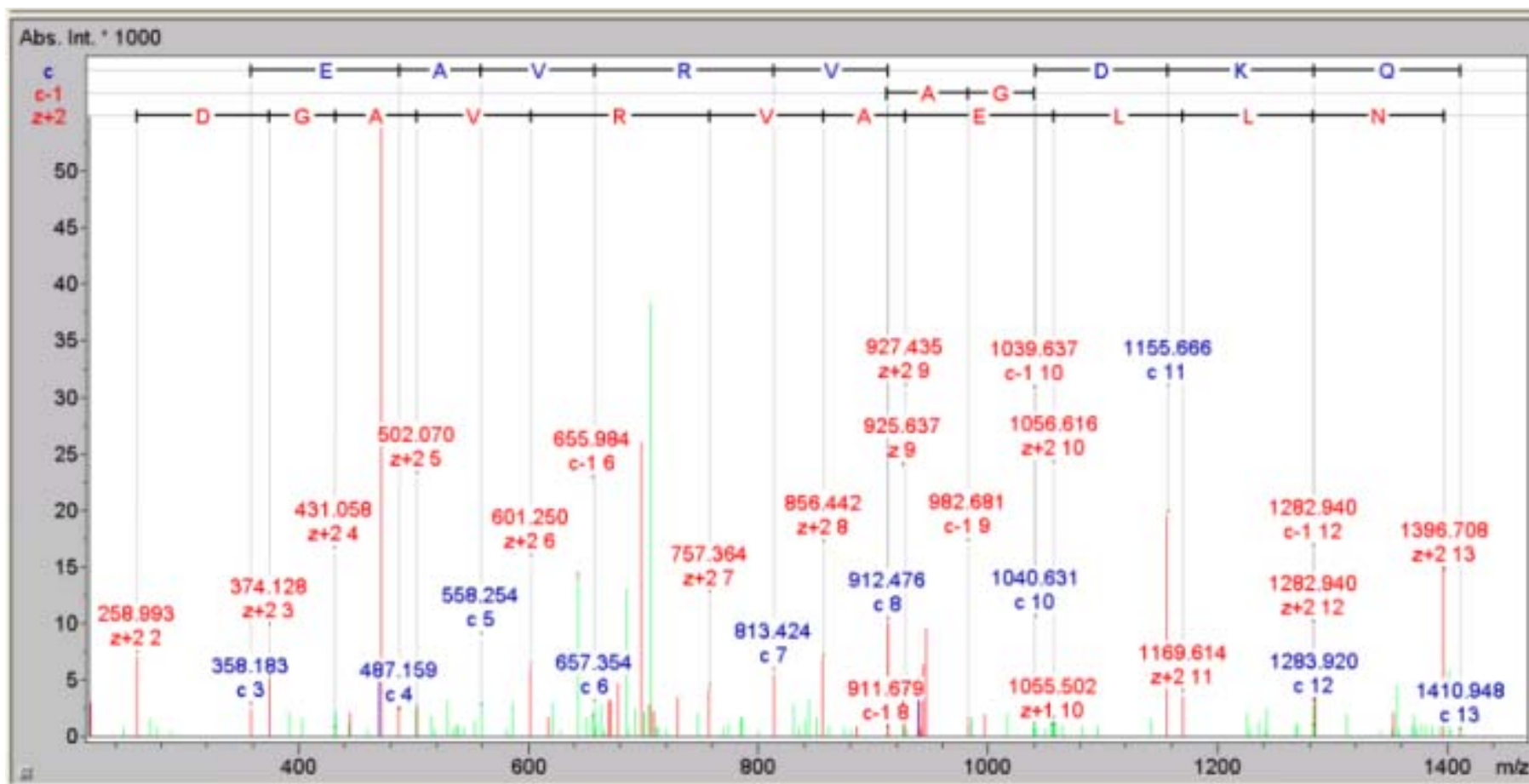
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Amidation: R104	618.0756	3+
sequence (enzyme/ ion score/ mass error)				
89 G.DVVLKLSQRVNELLAR*.D Amidation(R) 104 (AspN/36/0.0996)				



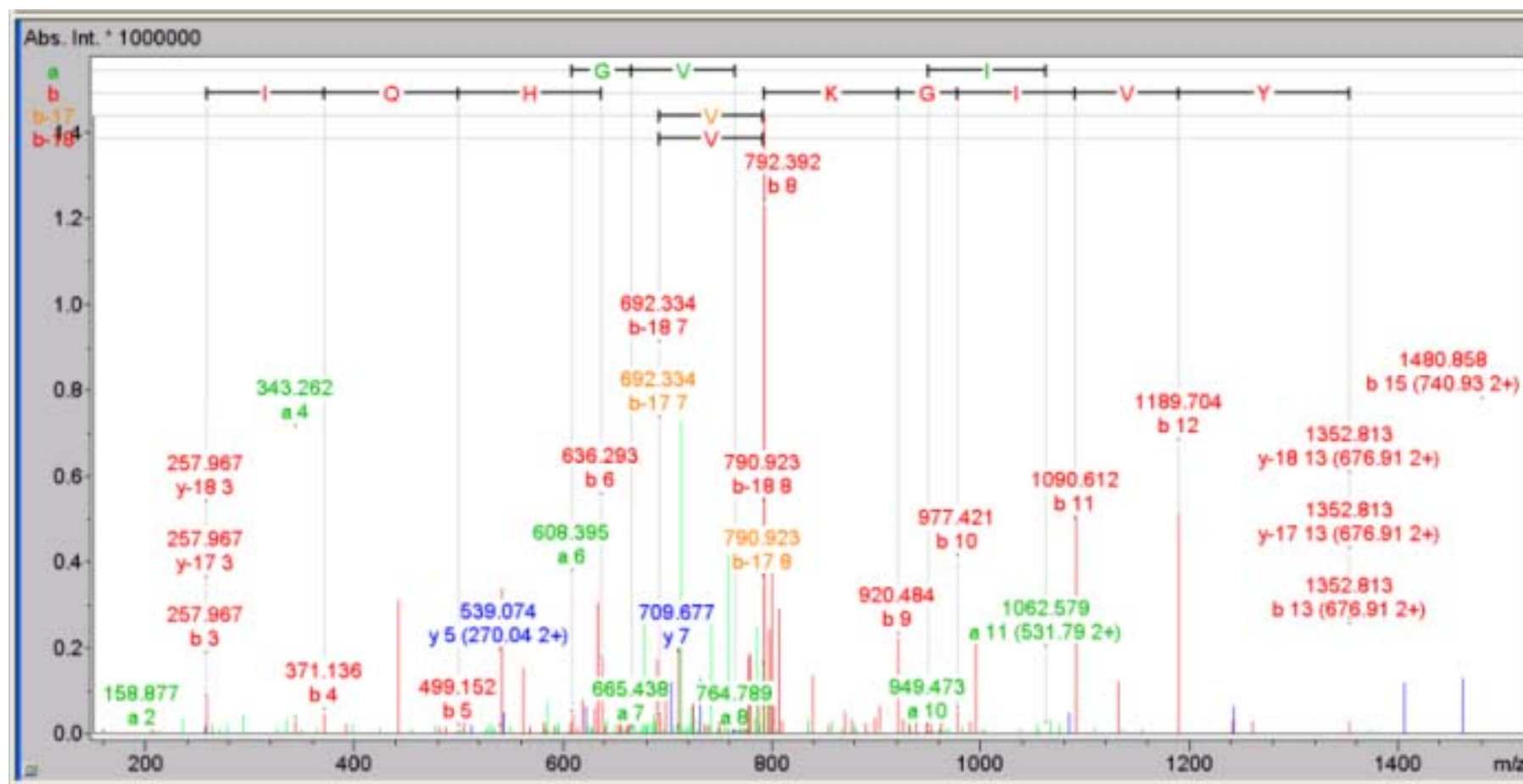
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Amidation: Q167	471.2709	3+
sequence (enzyme/ ion score/ mass error)				
155 M.NLLEAVRVAGDKQ*.S Amidation(Q) 167 (Chy/44/-0.0034)				



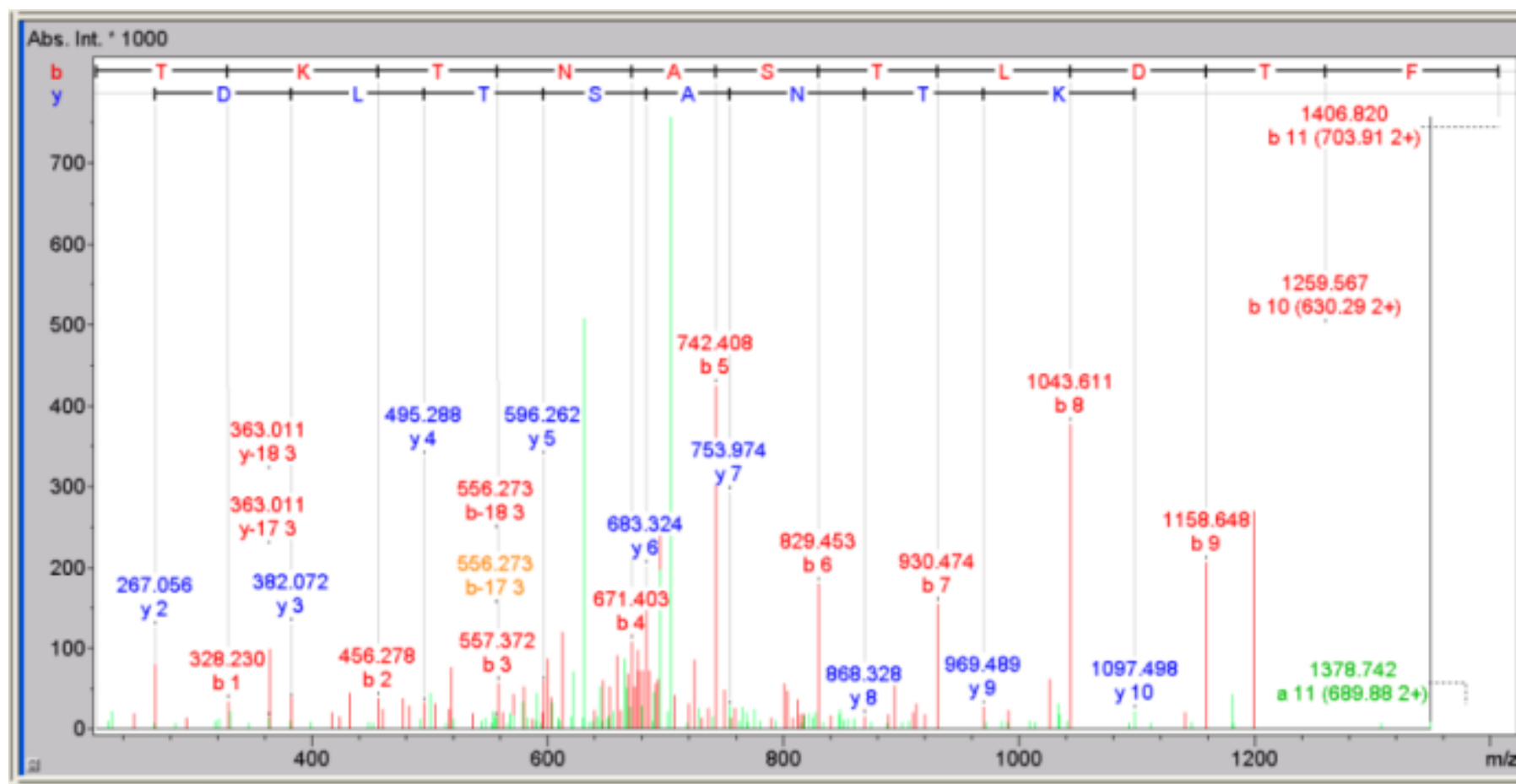
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Amidation: M271	814.8792	2+
sequence (enzyme/ ion score/ mass error)				
256 Y.DAAIQHGVKGIVYAGM*.G Amidation(M) 271 (AspN/52/-0.1066)				



Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Biotinylation: T188	712.849	2+
sequence (enzyme/ ion score/ mass error)				
188 I.T*KTNASTLDTF.K Biotinylation(T) 198 (Chy/45/0.0181)				



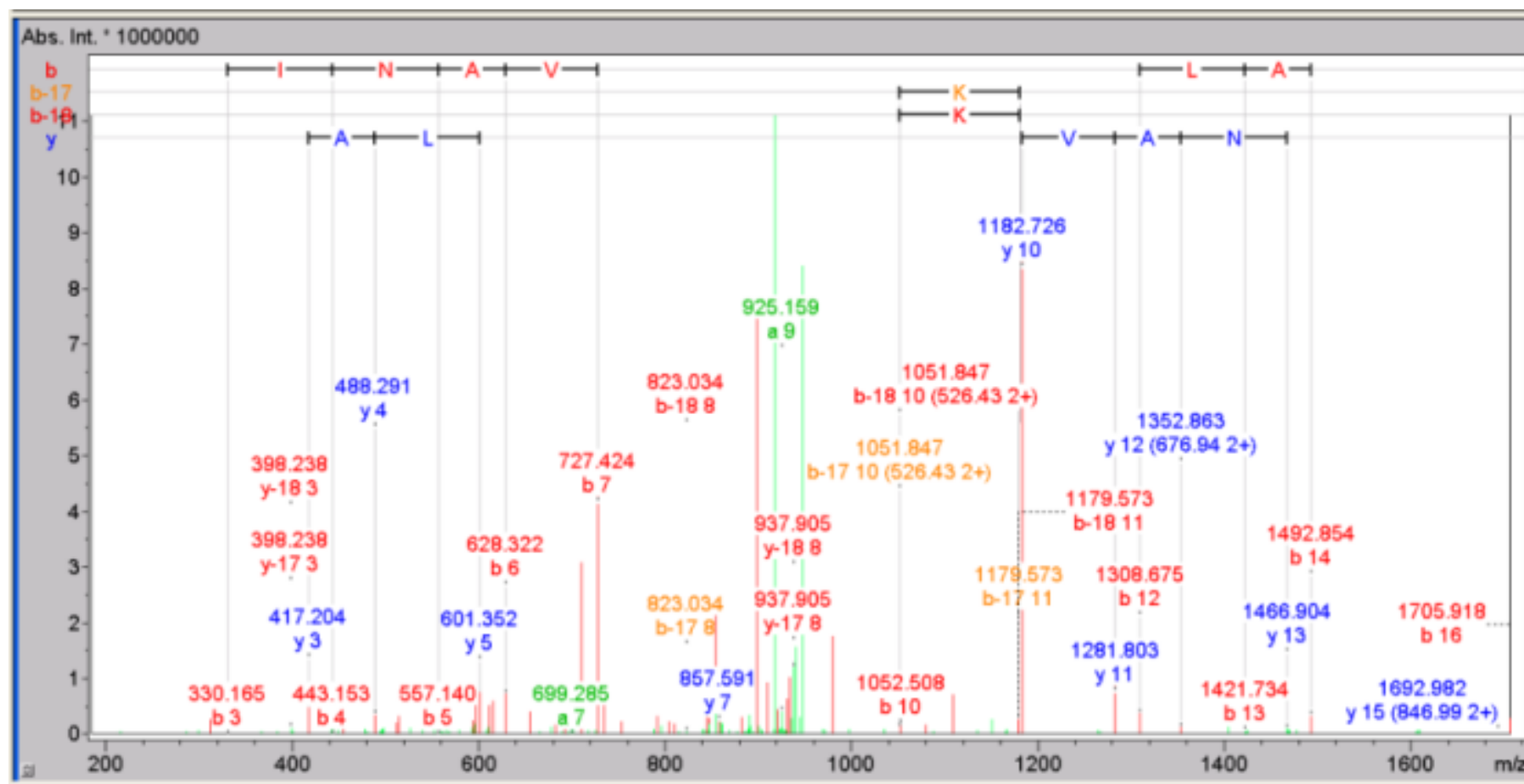
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Carbamidomethylation: K51	618.0125	3+
sequence (enzyme/ ion score/ mass error)				
51 Y.K*AGALGVDTLINAVPEVK.K Carbamidomethylation(K) 68 (Chy/78/-0.0309)				



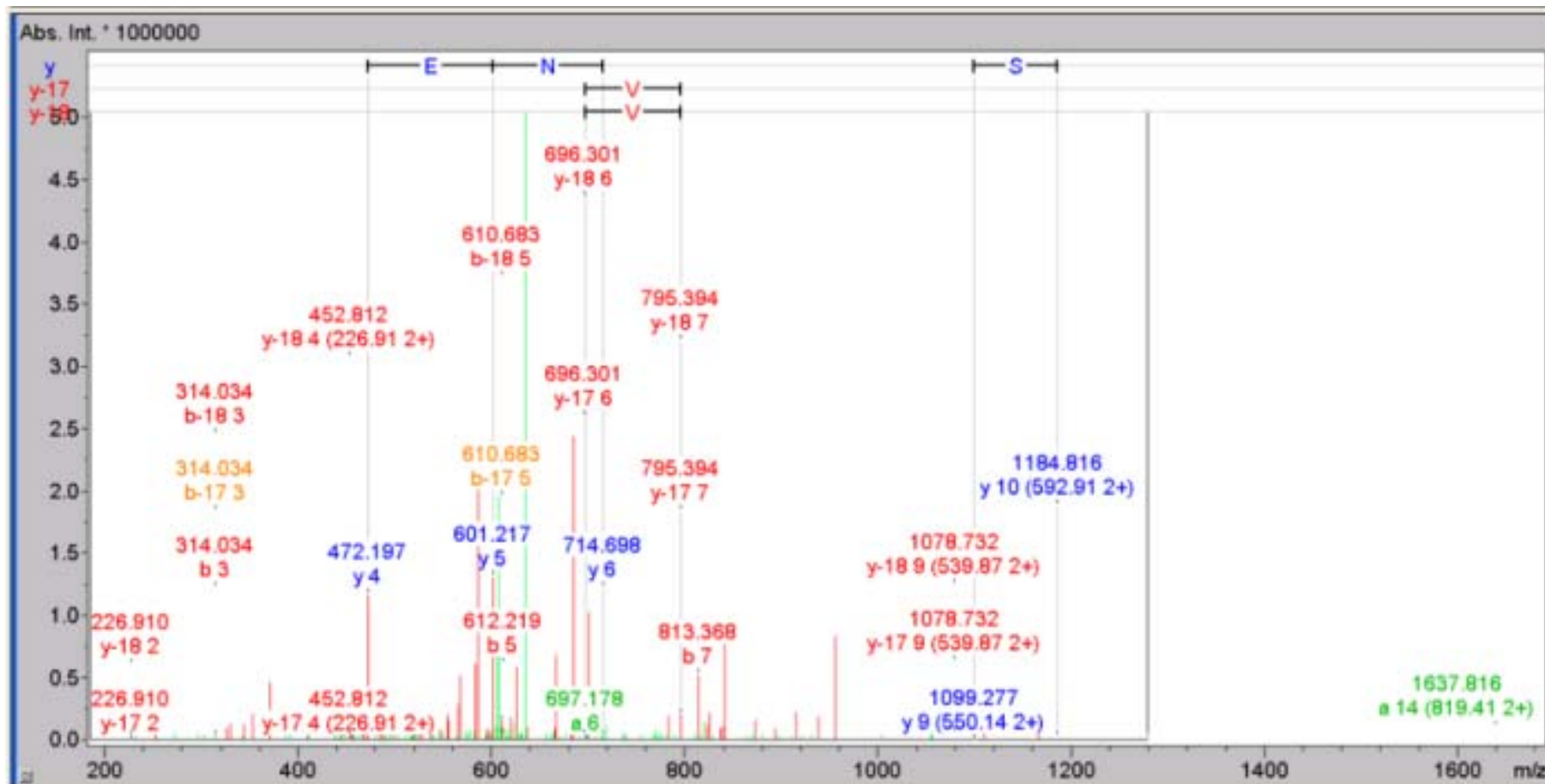
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Carbamidomethylation: K74	955.0662	2+
sequence (enzyme/ ion score/ mass error)				
58 V.DTLINAVPEVKKLANVK*.G Carbamidomethylation(K) 74 (AspN/47/0.0135)				



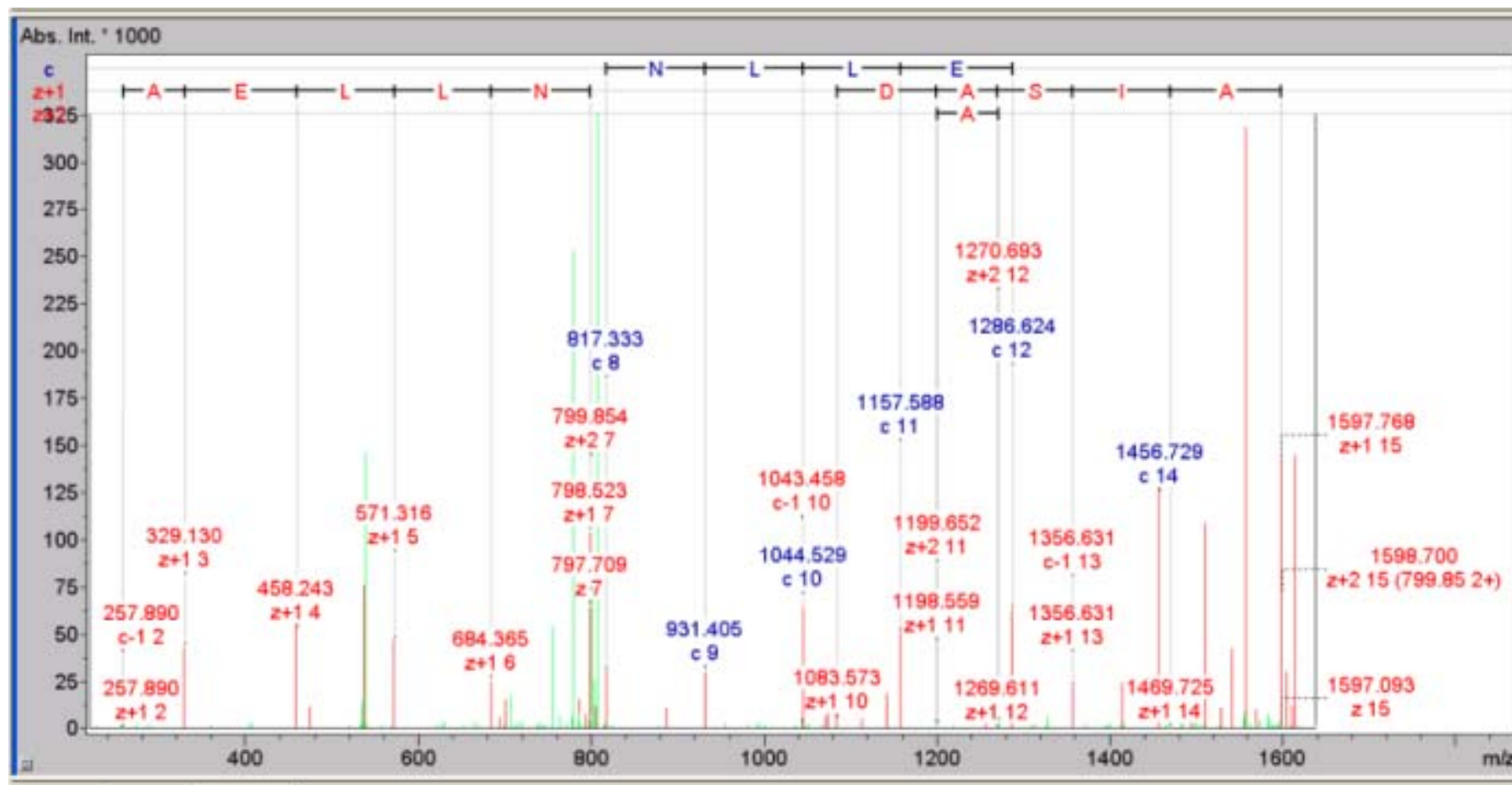
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Carbamidomethylation: K109	642.7602	2+
sequence (enzyme/ ion score/ mass error)				
105 G.DVVLK*LSQRVNELLAR.D Carbamidomethylation(K) 116 (AspN/75/-0.0936)				



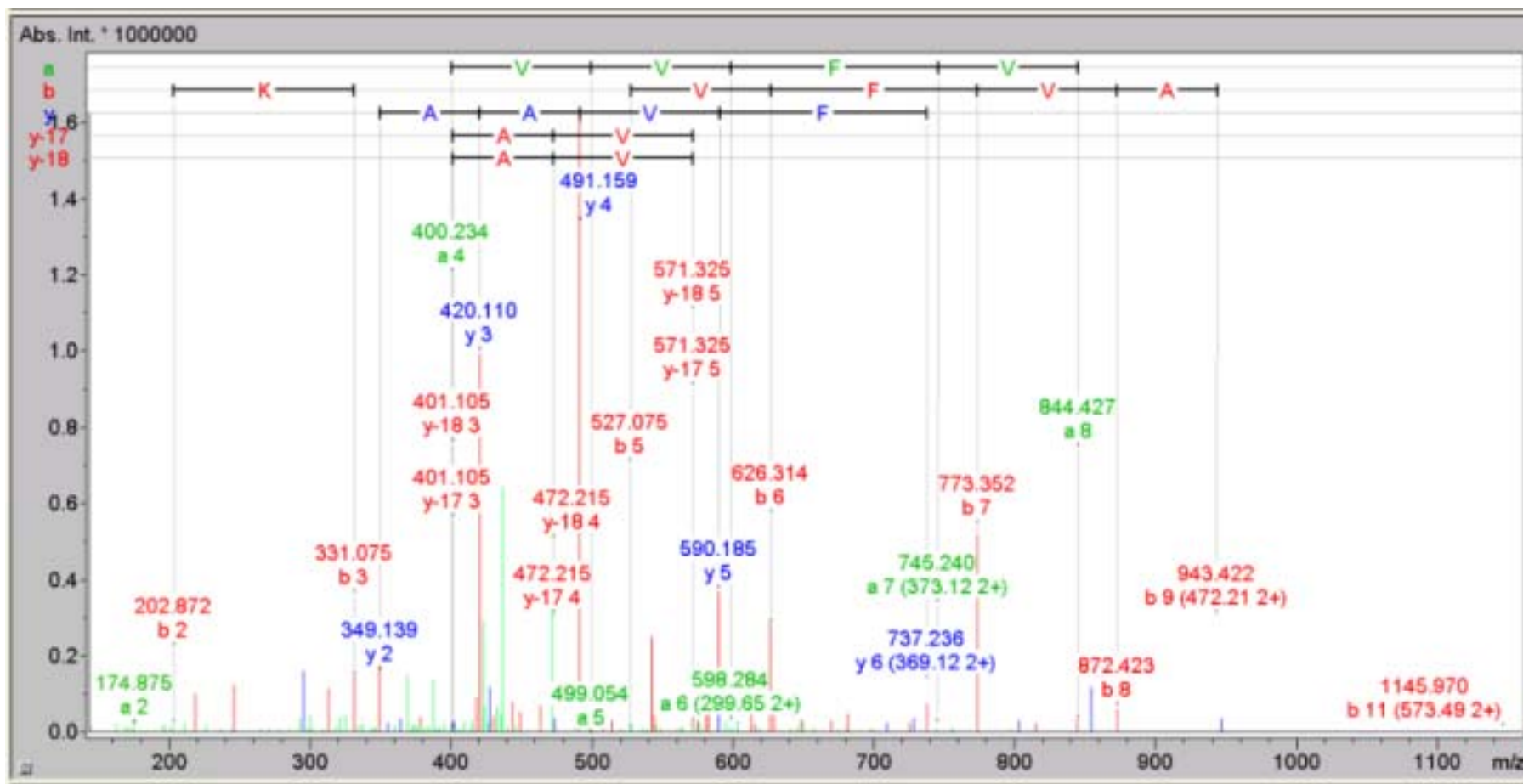
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Carbamidomethylation: A147	538.6125	3+
sequence (enzyme/ ion score/ mass error)				
147 T.A*ISADGPMNLLLEAVR.V Carbamidomethylation(A) 161 (Try/60/-0.0086)				



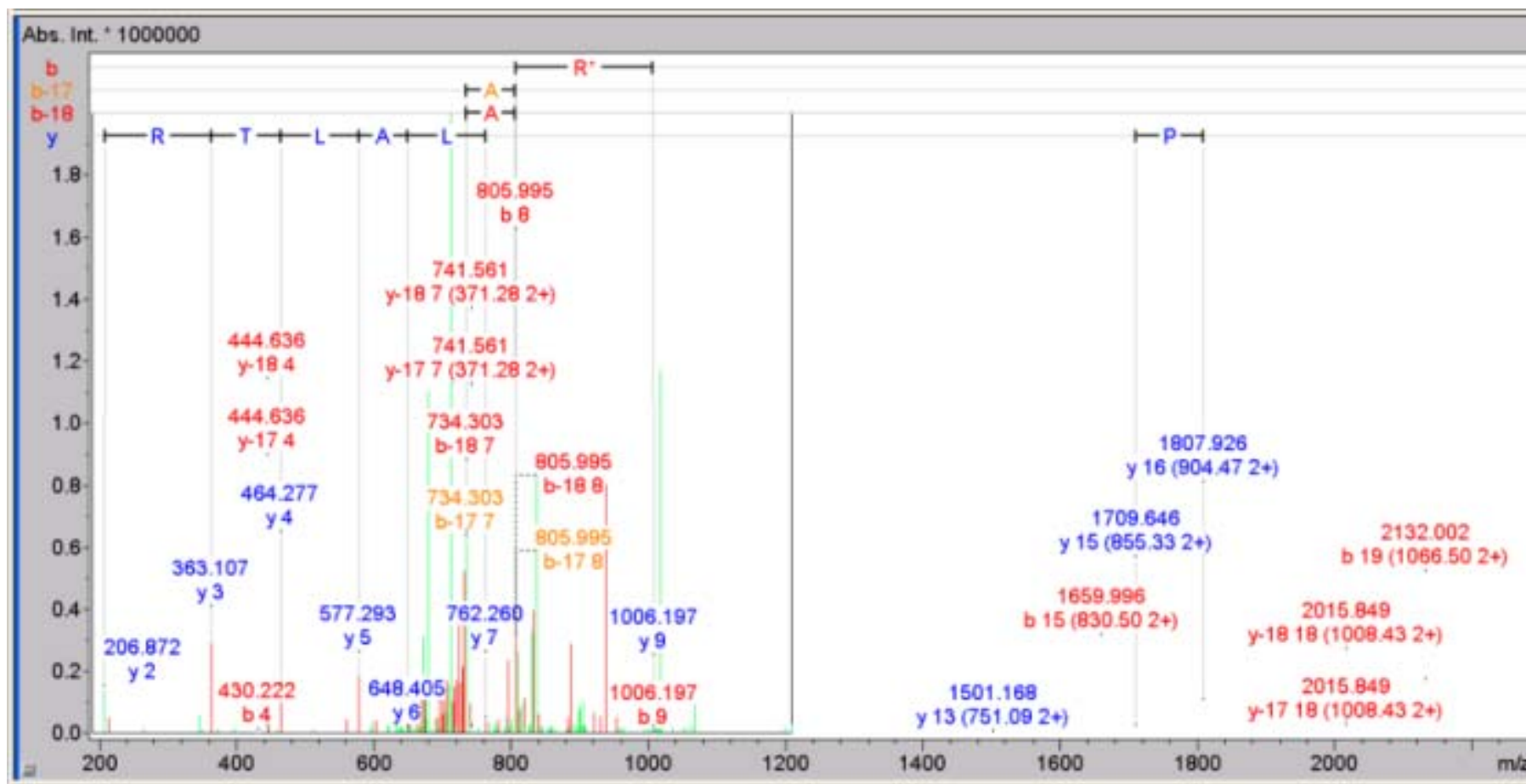
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Carbamylation: R143	454.8561	3+
sequence (enzyme/ ion score/ mass error)				
132 K.SDKPVVFVAAMR*.P Carbamylation(R) 143 (Try/52/-0.1661)				



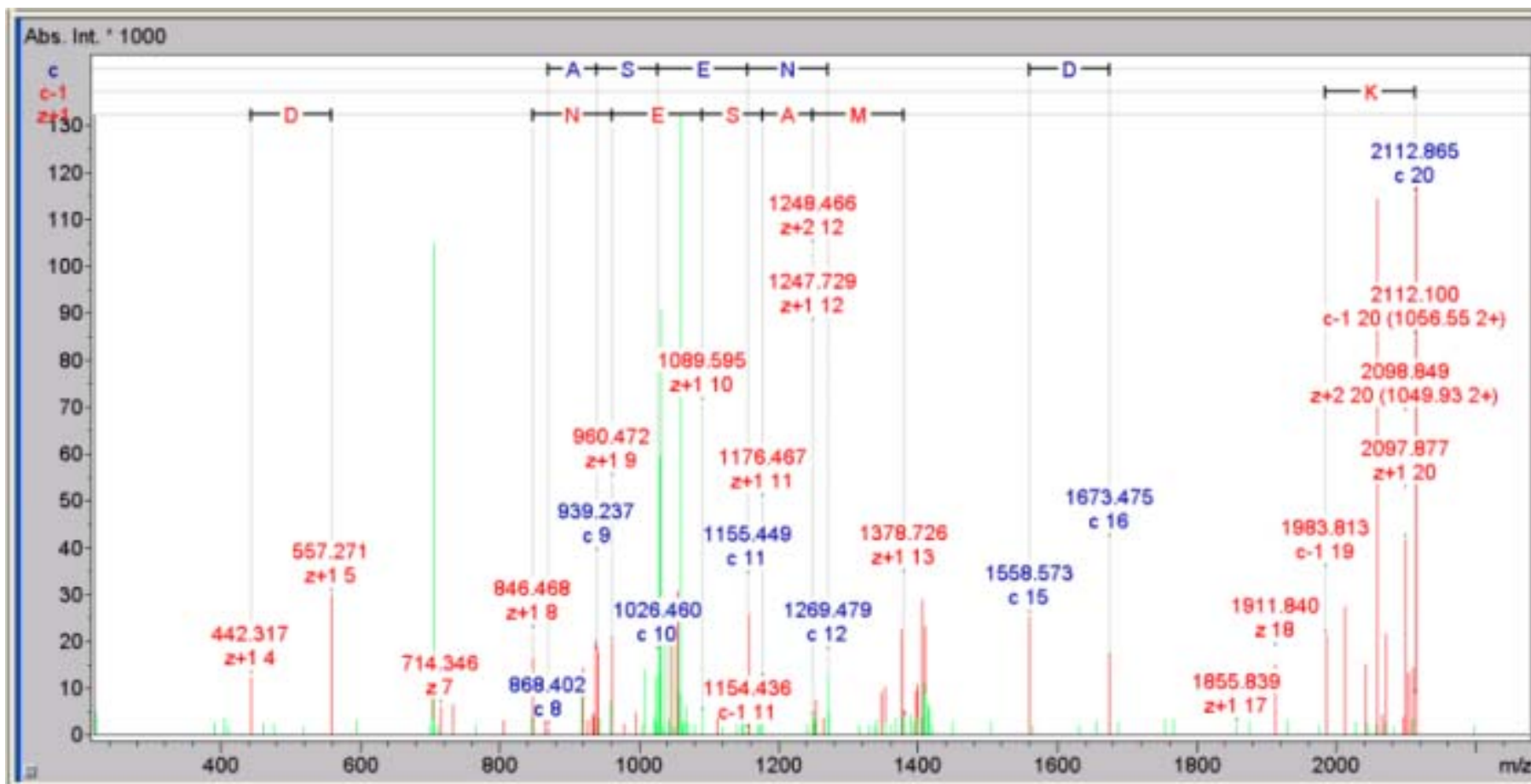
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Carbamylation: R325	746.0929	3+
sequence (enzyme/ ion score/ mass error)				
317 S.DSLNPAHAR*ILLMLALTRTS.D Carbamylation(R) 336 (AspN/42/0.0411)				



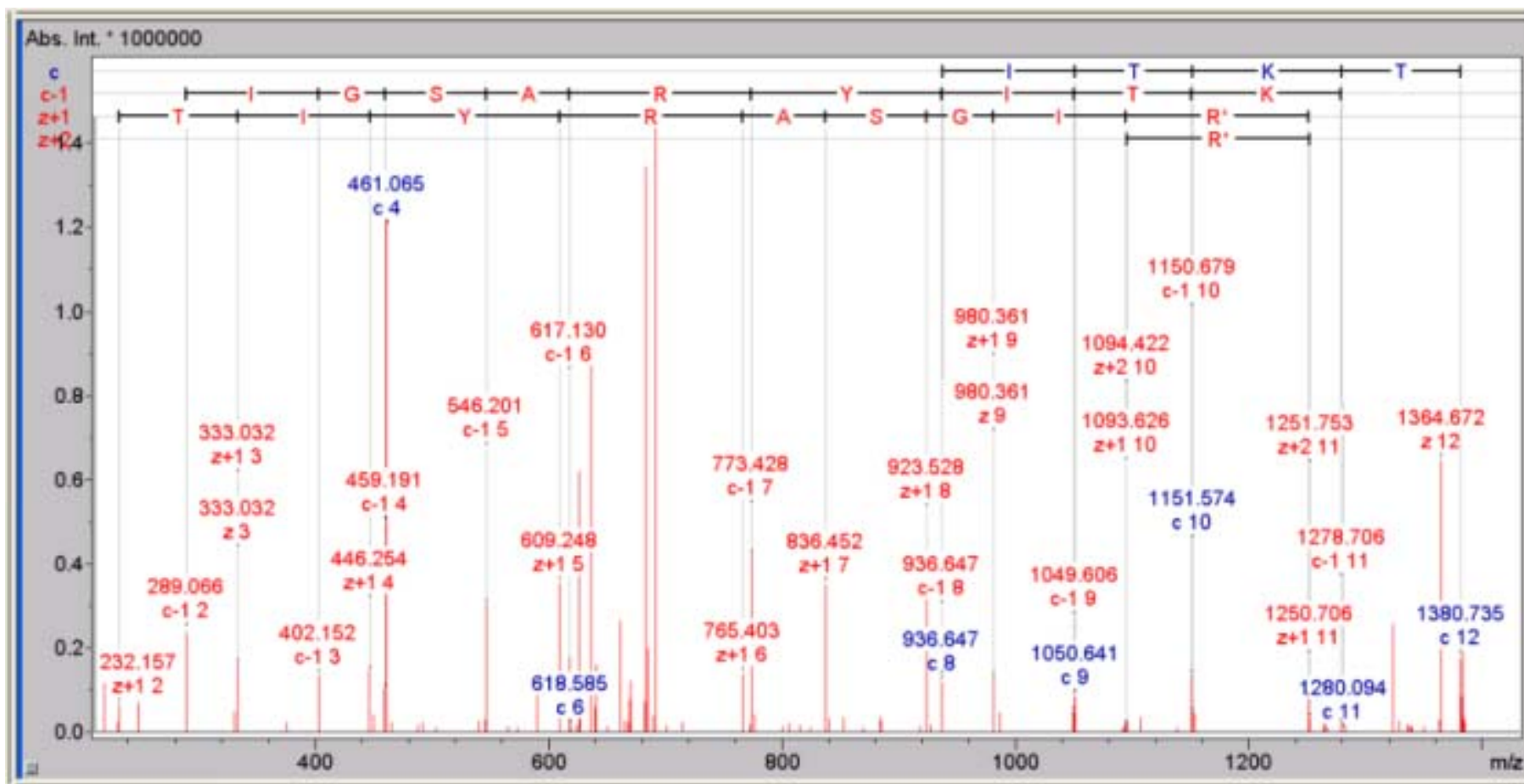
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Deamidation: N80	705.2776	3+
sequence (enzyme/ ion score/ mass error)				
74 V.KGE*QFSN*MASENMTGDVVLK.L Glu->Gly(E) Deamidation(N) 93 (Try/45/-0.171)				



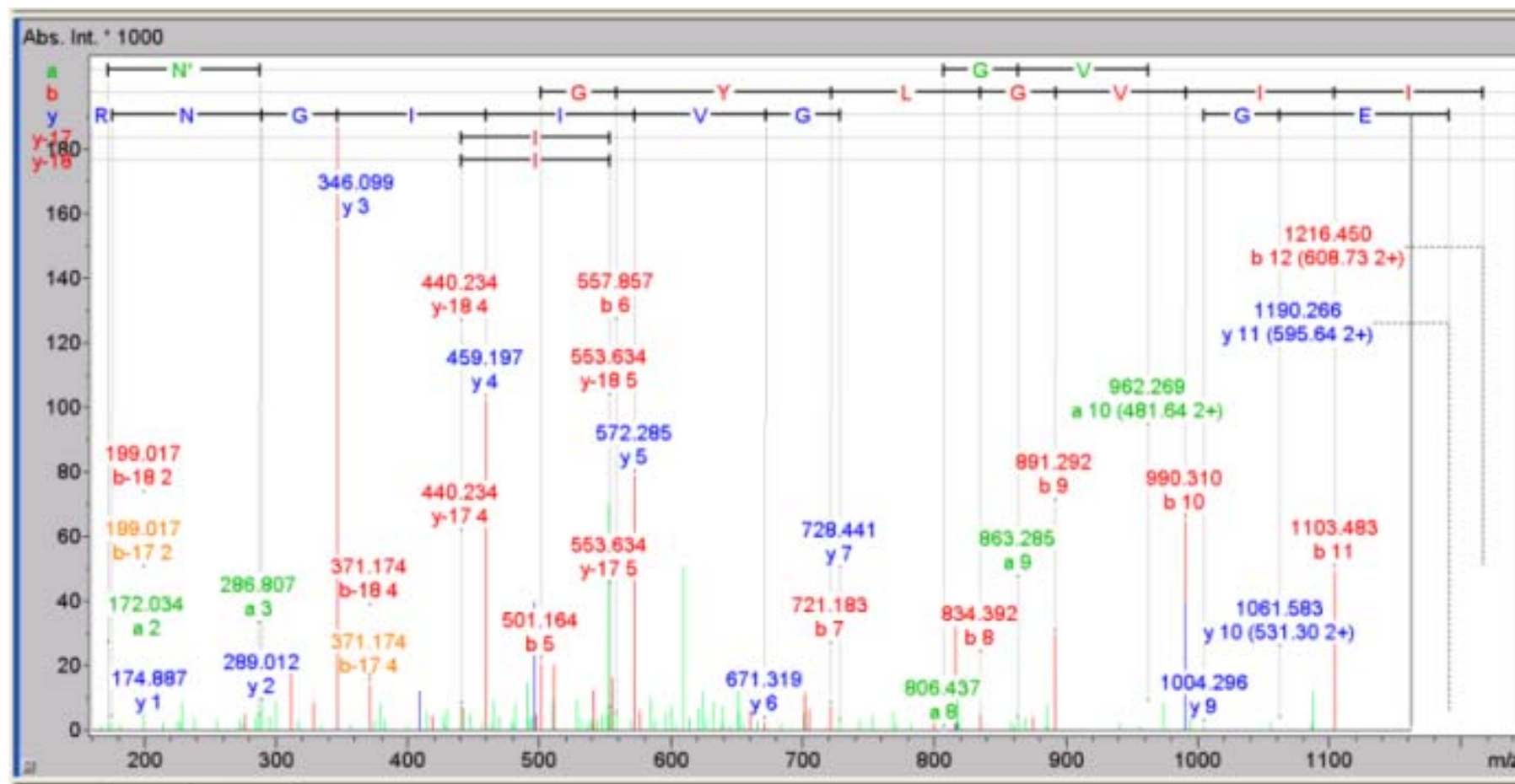
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Deamidation: R180	461.2291	3+
sequence (enzyme/ ion score/ mass error)				
179 N.DR*IGSARYITKT.N Deamidation(R) 190 (AspN/45/-0.0455)				



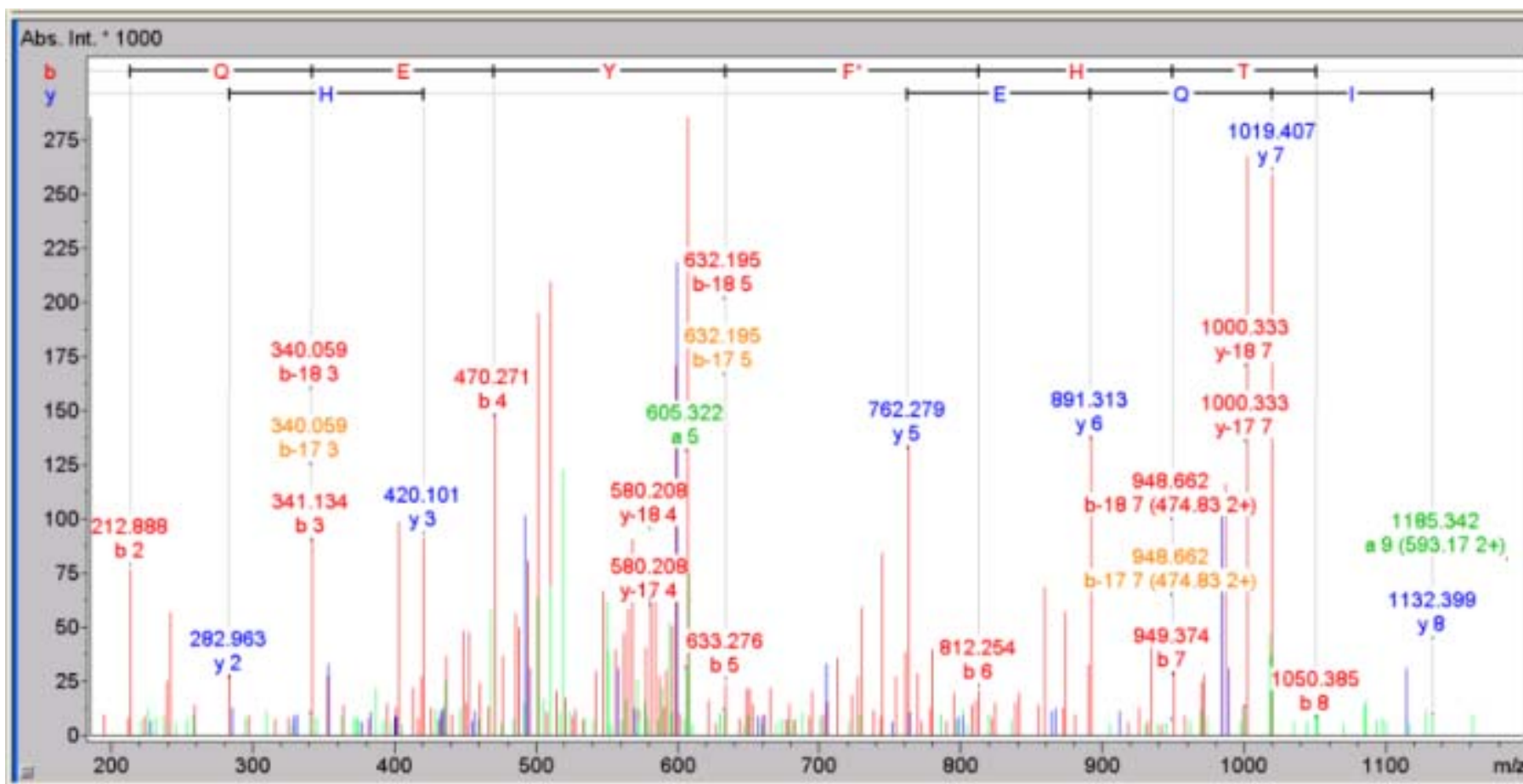
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Deamidation: N201	521.2875	3+
sequence (enzyme/ ion score/ mass error)				
199 F.KAN*E*EGYLGVIIGNR.I Deamidation(N) Glu->Gly(E) 213 (Try/48/0.0147)				



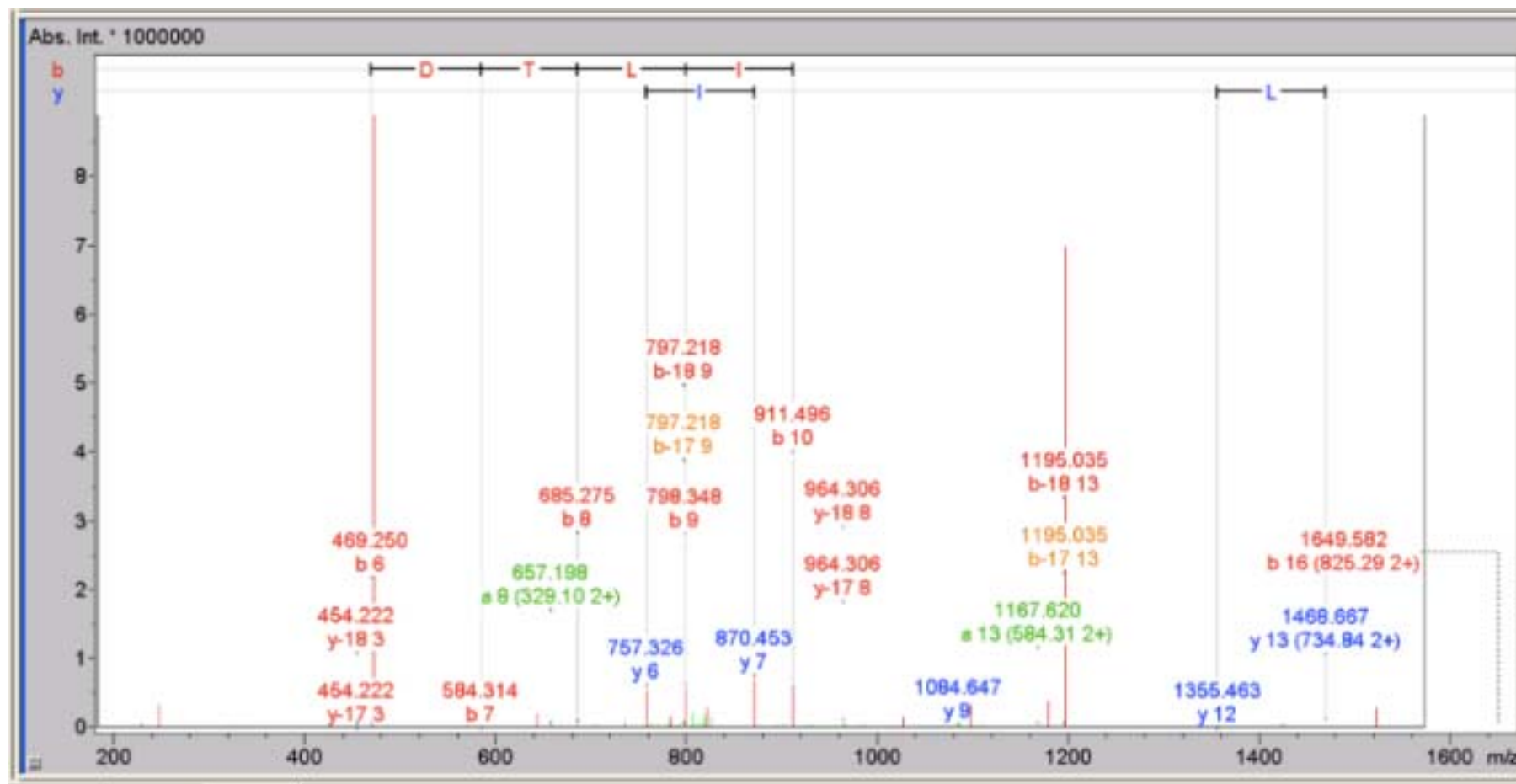
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Dioxidation: F345	616.2185	2+
sequence (enzyme/ ion score/ mass error)				
340 K.VIQEYF*HTY.- Dioxidation(F) 348 (Try/34/-0.1332)				



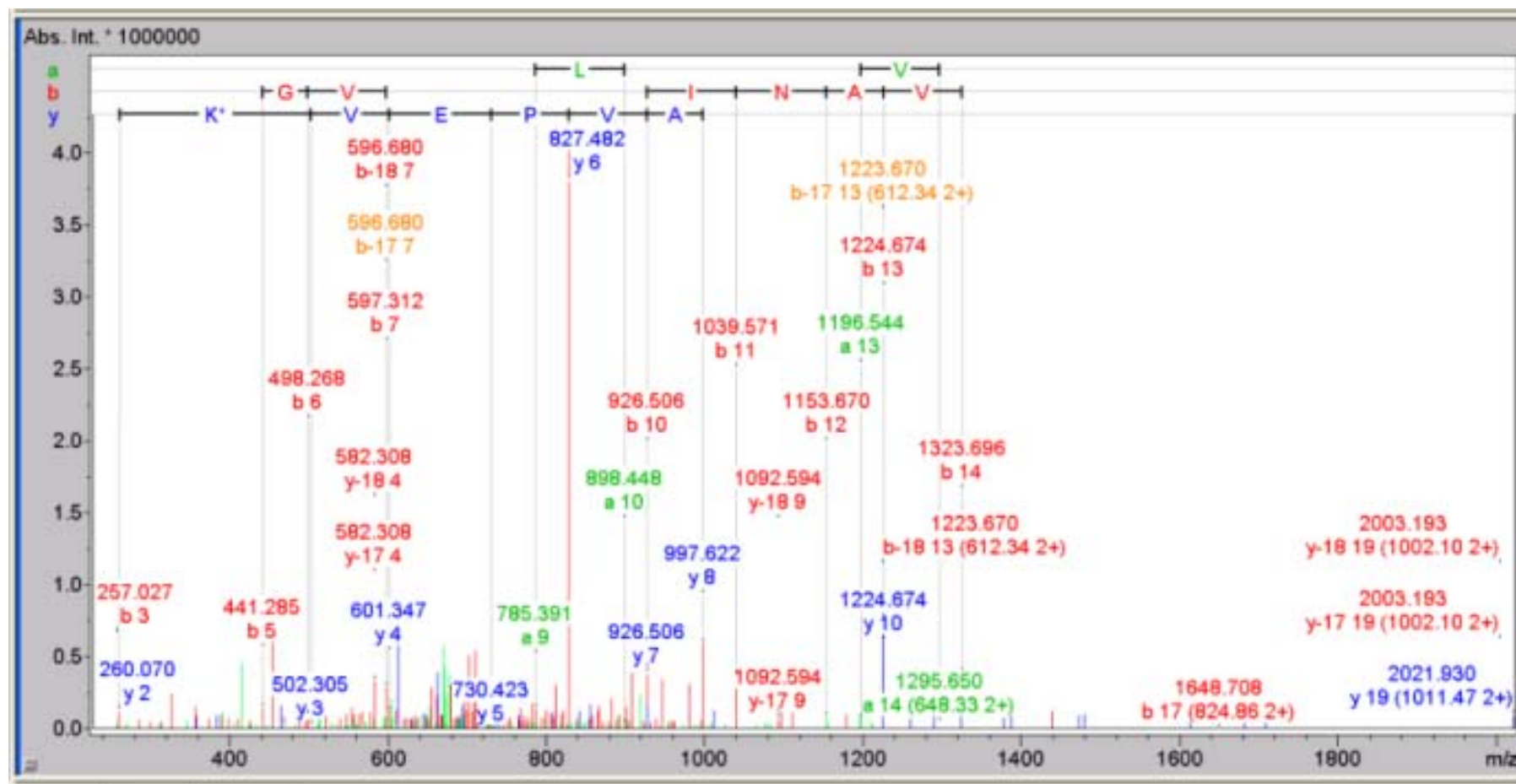
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Glu: E66	834.4456	2+
sequence (enzyme/ ion score/ mass error)				
52 K.AGALGVDTLINAVPE*V.K Glu(E) 67 (Try/47/-0.0011)				



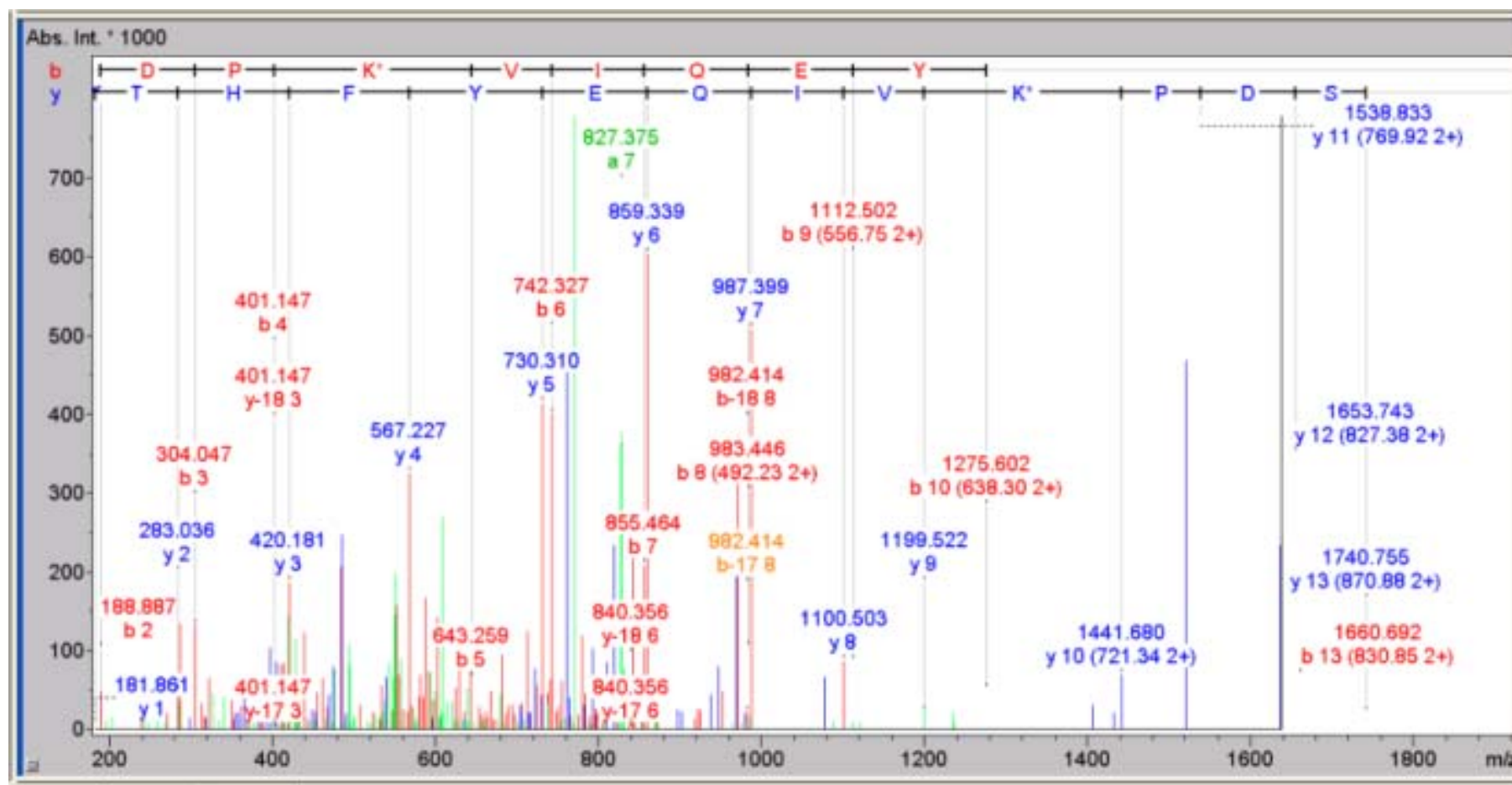
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 2	Mascot	GlyGly: K68	717.4397	3+
sequence (enzyme/ ion score/ mass error)				
51 Y.KAGALGVDTLINAVPEVK*KL.A GlyGly(K) 70 (Chy/33/0.0502)				



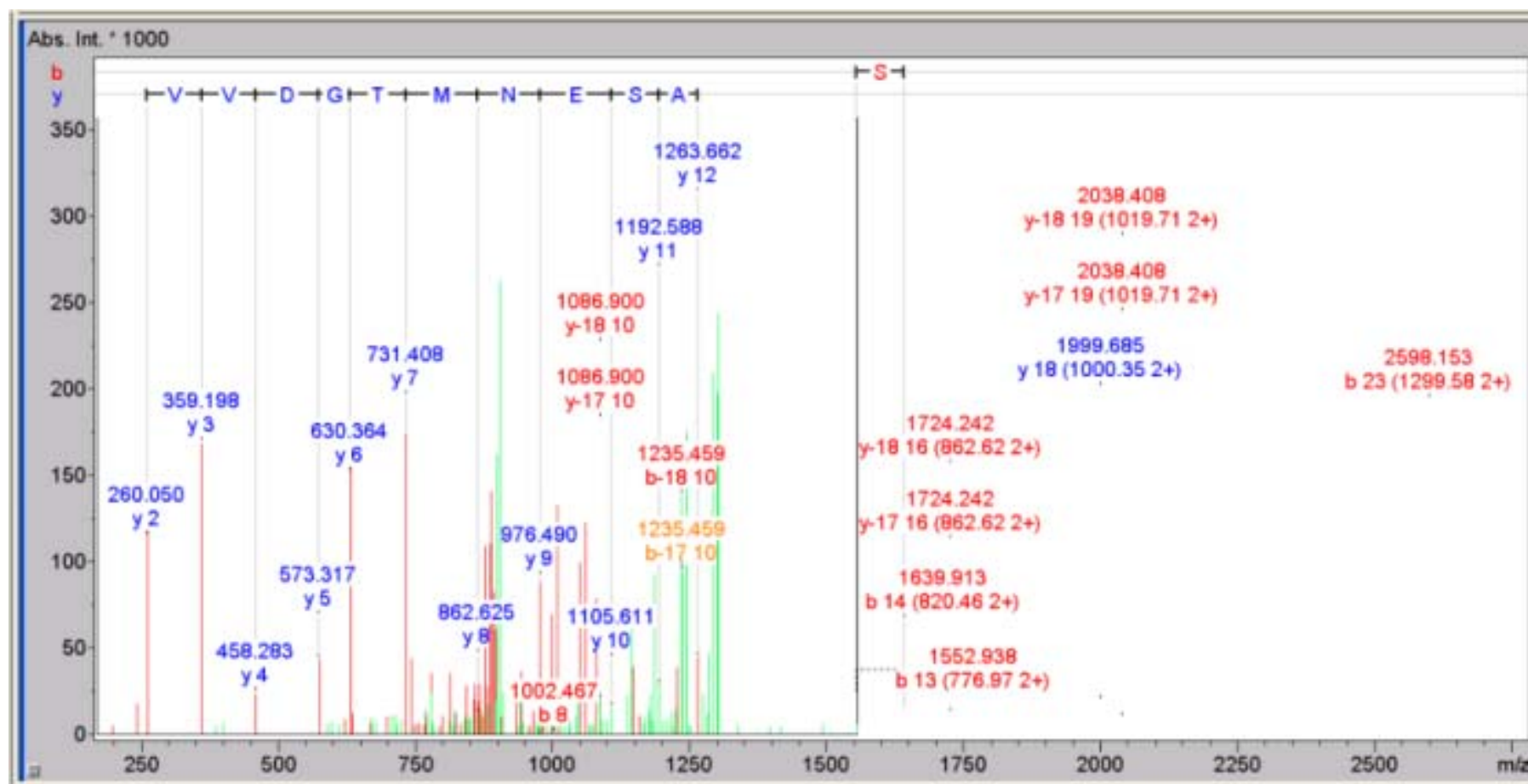
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	GlyGly: K339	614.622	3+
sequence (enzyme/ ion score/ mass error)				
335 R.TSDPK*VIQEYFHTY.- GlyGly(K) 348 (Try/49/-0.019)				



Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Hexose: L70	915.3848	3+
sequence (enzyme/ ion score/ mass error)				
70 K.L*ANVKGEQFSNMASENMTGDVVLK.L Hex(L) 93 (Try/45/-0.1719)				



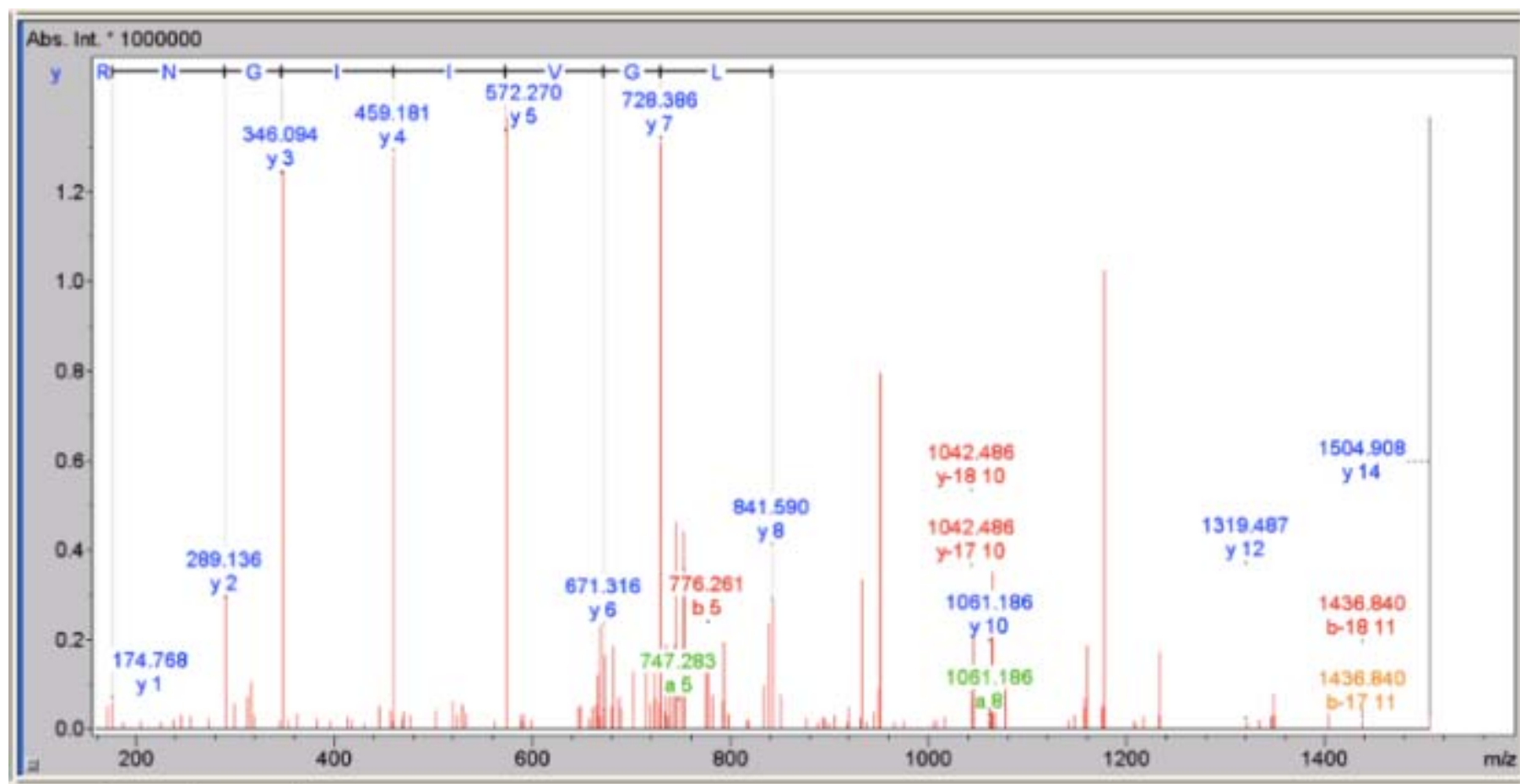
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Hexose: K198	745.3705	3+
sequence (enzyme/ ion score/ mass error)				
198 F.K*ANEEGYLGVIIGNRIYY.Q Hex(K) 216 (Try/119/-0.0158)				



Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Menodione: K199	760.3341	3+
sequence (enzyme/ ion score/ mass error)				
195 T.LDTFK*ANEEGYLGVIIGNR.I Menodione(K) 213 (Try/40/-0.1465)				



Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Oxidation: P144	957.9224	2+
sequence (enzyme/ ion score/ mass error)				
139 F.VAAMRP*ATAISADGPMNLL.E Oxidation(P) 157 (Chy/59/-0.14)				



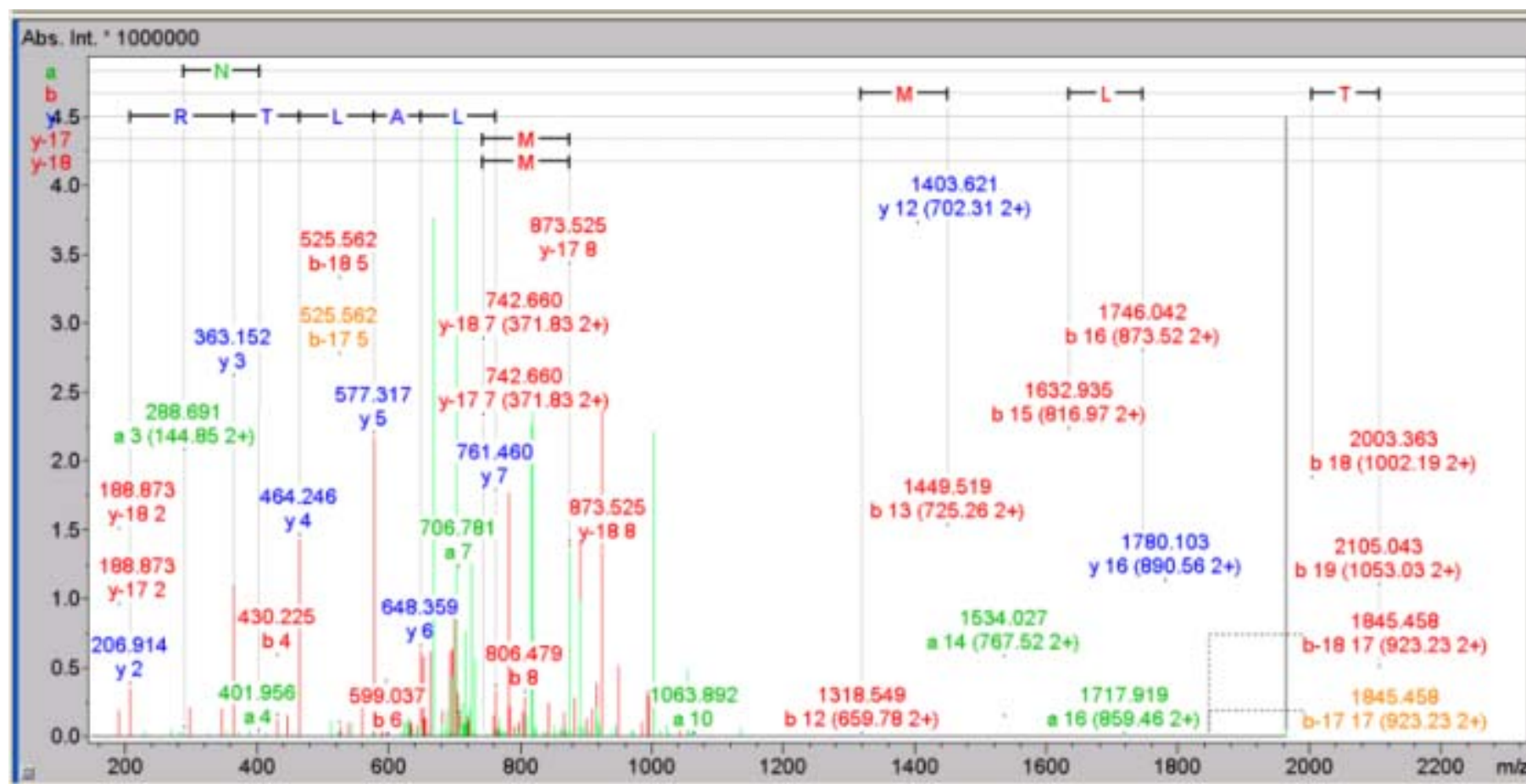
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Oxidation: Y216	648.8789	2+
sequence (enzyme/ ion score/ mass error)				
206 Y.LGVIIGNRIYY*.Q Oxidation(Y) 216 (Chy/33/0.0195)				



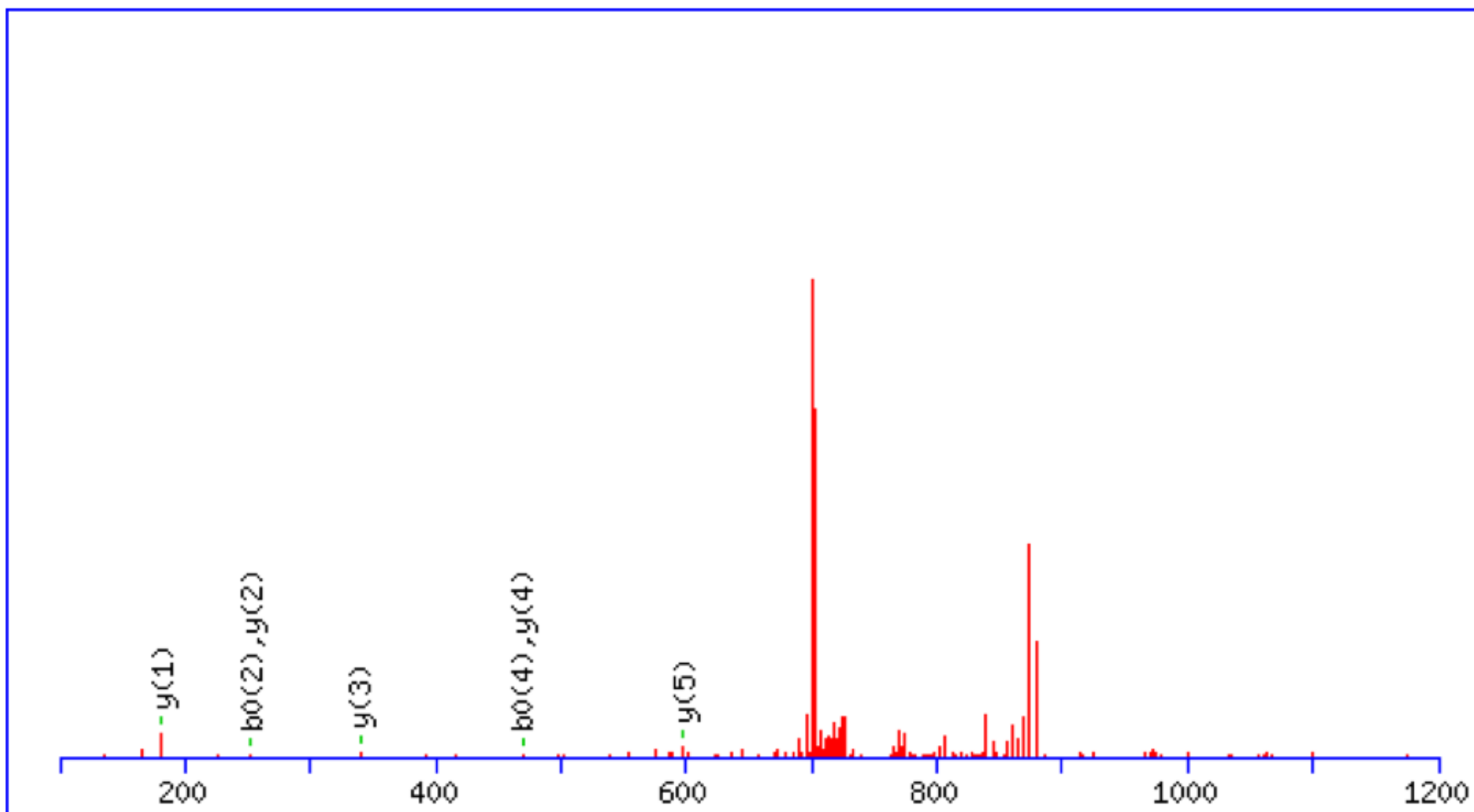
Mascot/ untreated/ L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Mascot	Oxidation: R325	737.0974	3+
sequence (enzyme/ ion score/ mass error)				
317 S.DSLNPAHAR*ILLMLALTRTS.D Oxidation(R) 336 (AspN/50/0.0655)				



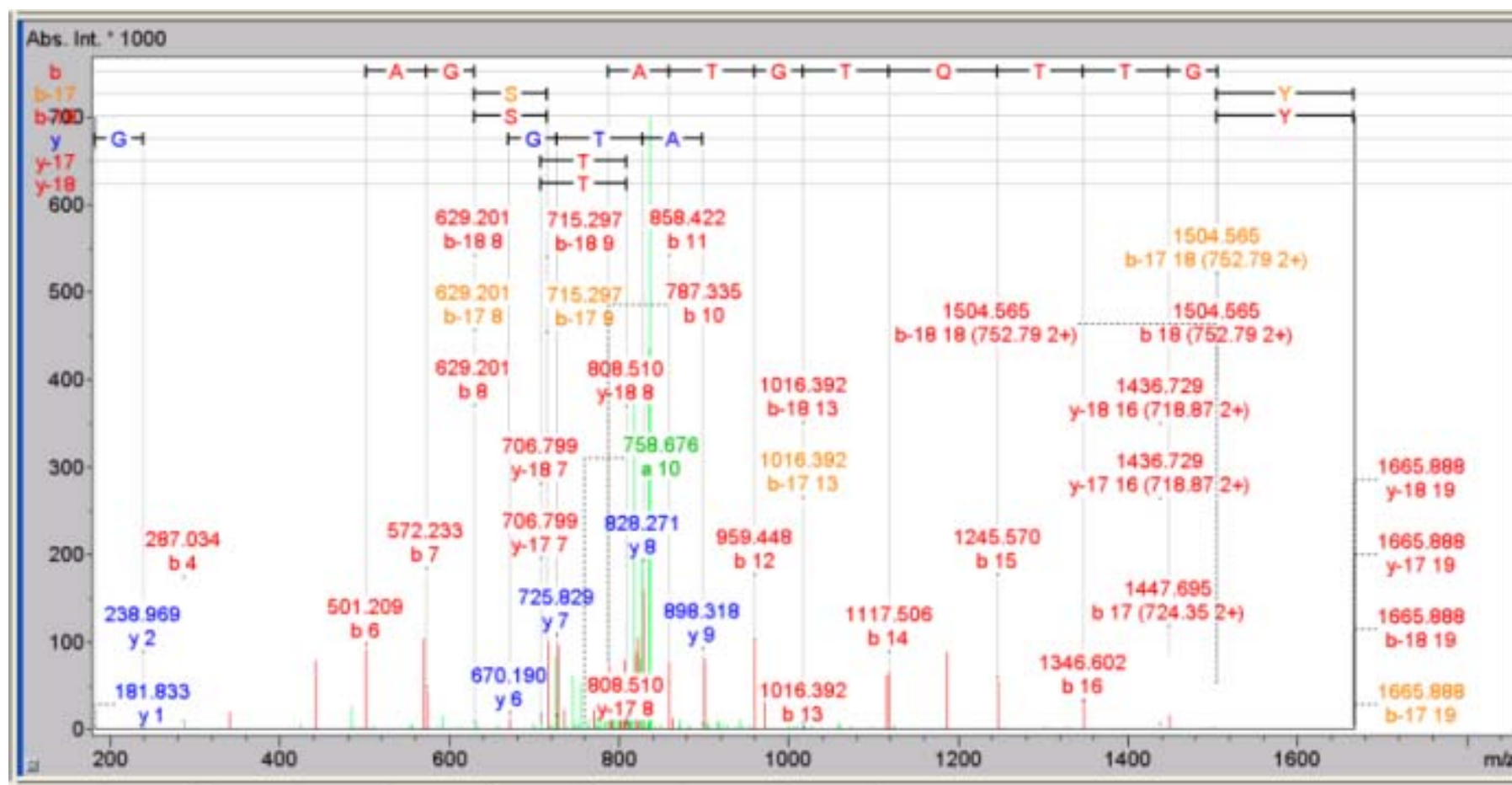
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Acetylation: V119	739.413	1+
sequence (enzyme/ ion score/ mass error)				
119 T.V*EESAY.F Acetylation(V) 124 (Chy/38/0.0985)				



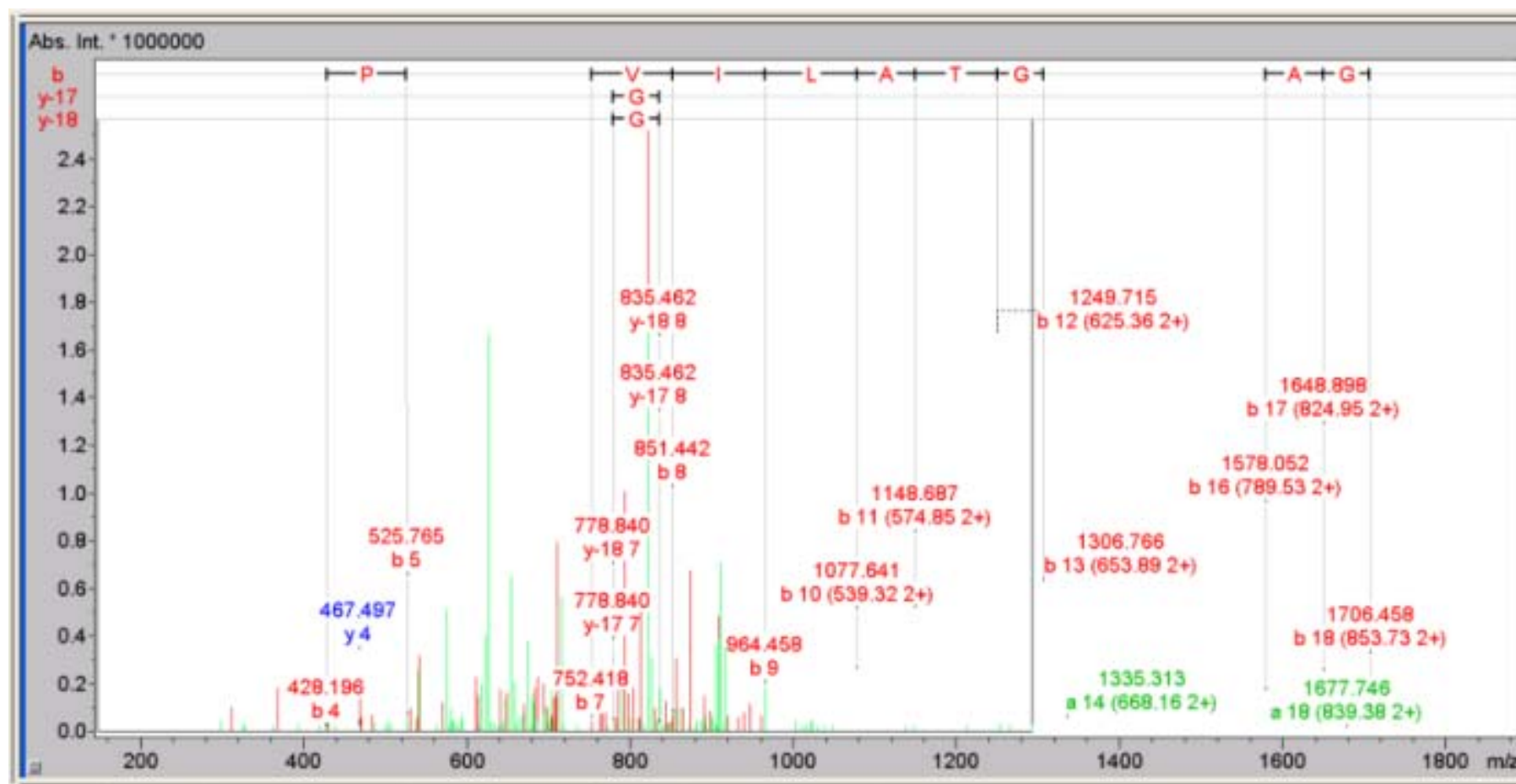
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Amidation: Y50	842.8451	2+
sequence (enzyme/ ion score/ mass error)				
32 L.ATGGTIAGSAATGTQTTGY*.K Amidation(Y) 50 (Chy/40/-0.1308)				



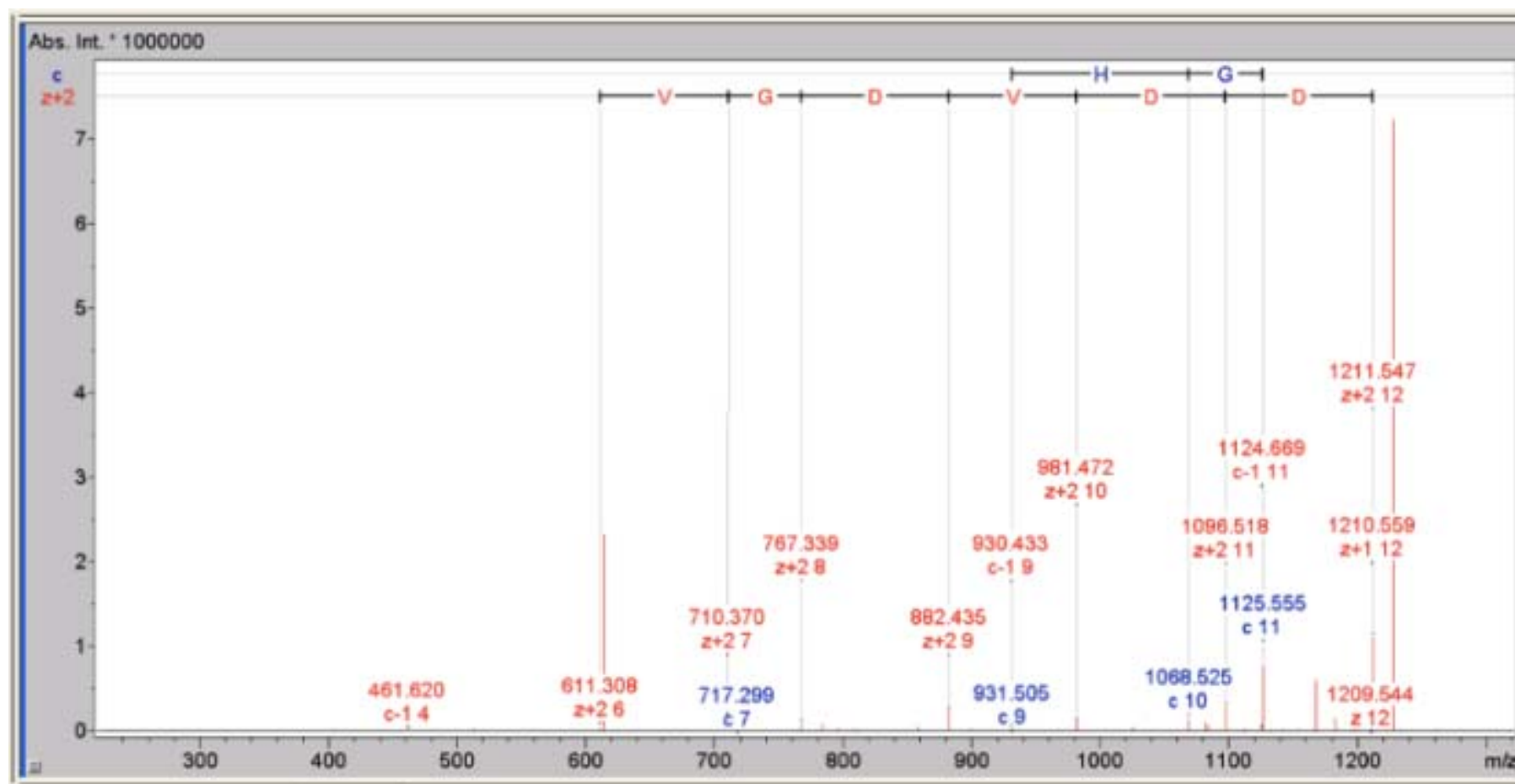
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Amidation: K51	723.1173	4+
sequence (enzyme/ ion score/ mass error)				
22 A.ADKLPNIVILATGGTIAGSAATGTQTTGYK*.A Amidation(K) 51 (Try/68/-0.1206)				



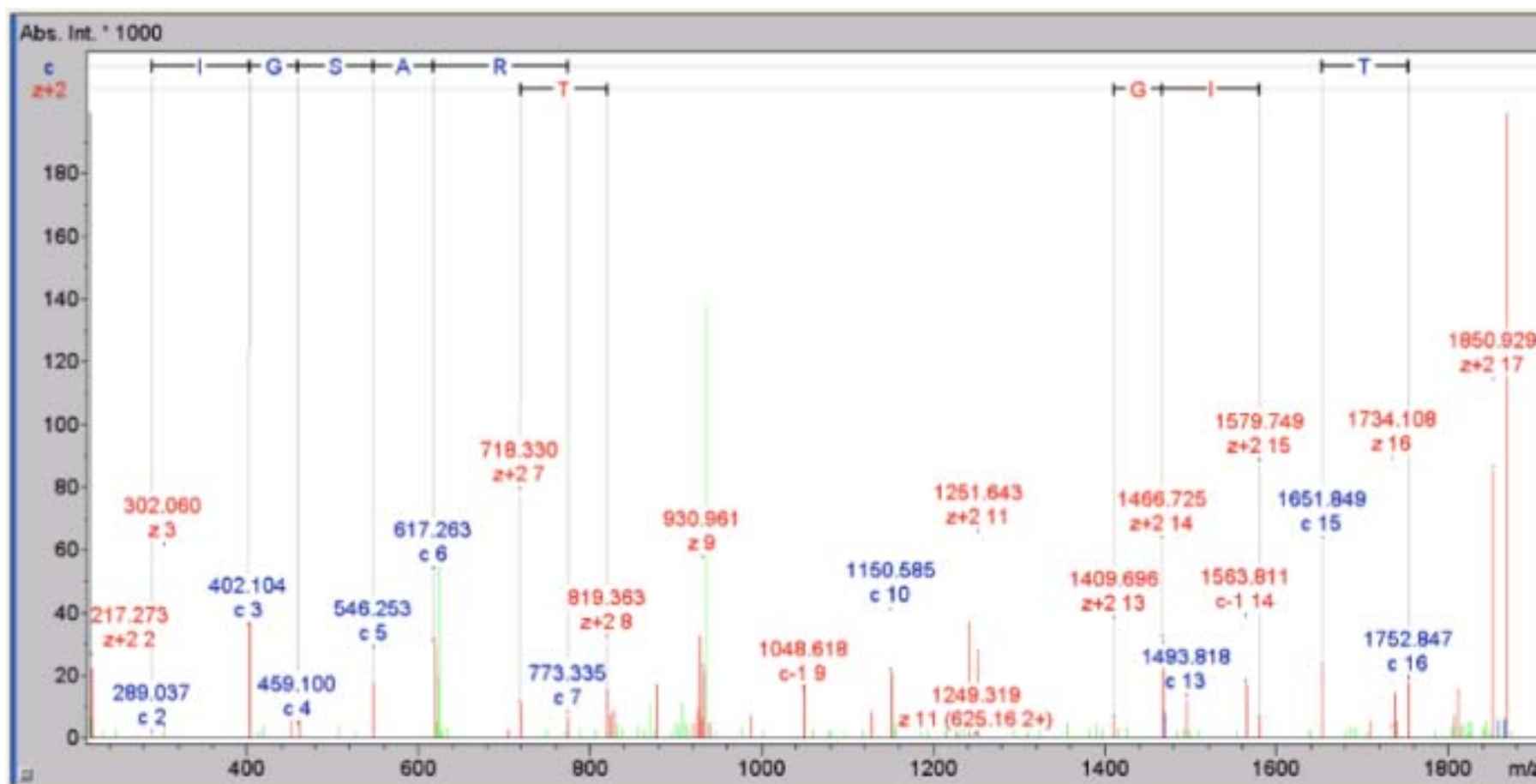
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Amidation: T116	613.7721	2+
sequence (enzyme/ ion score/ mass error)				
105 R.DDVDGVVITHGT*.D Amidation(T) 116 (AspN/48/-0.0643)				



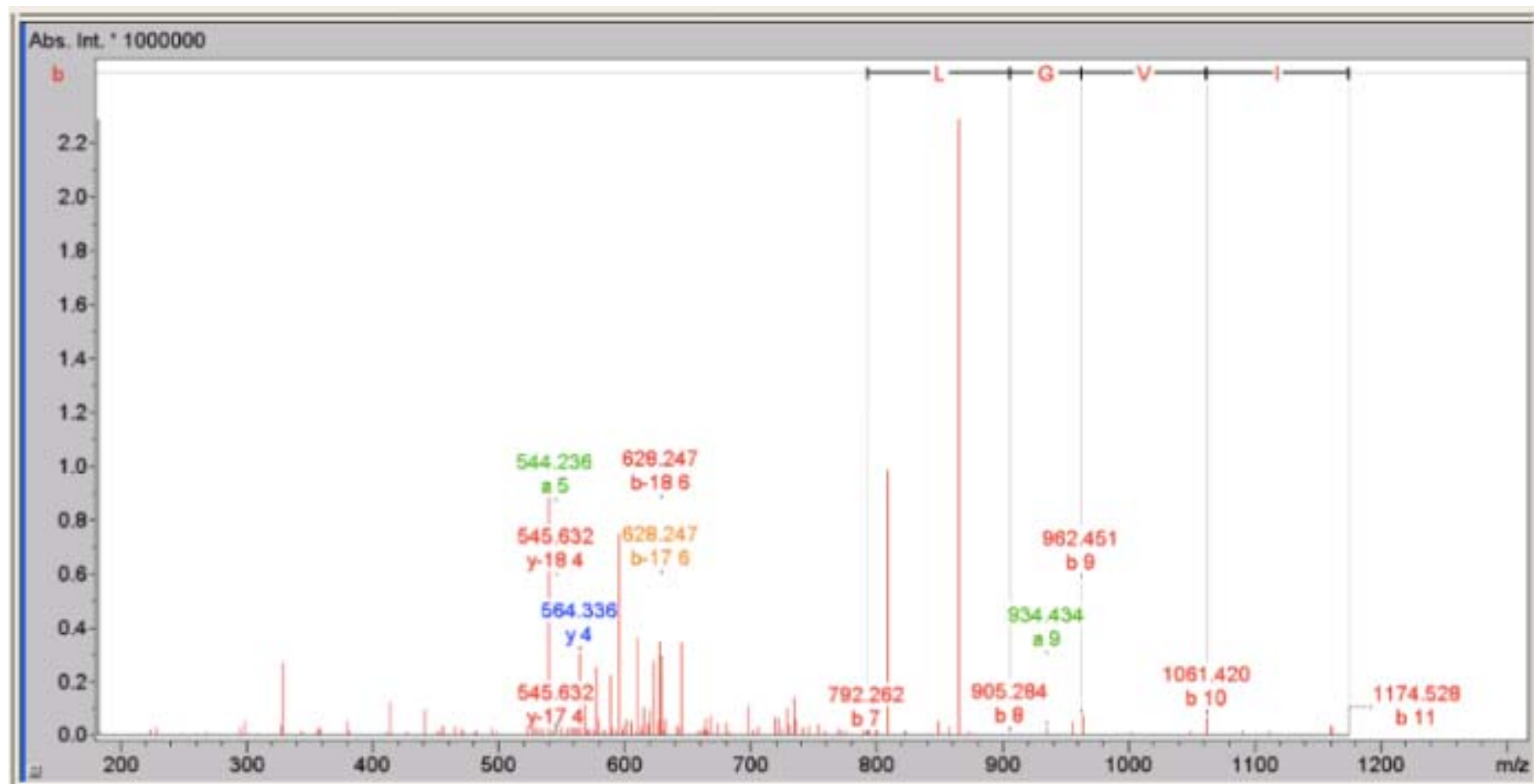
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Amidation: L195	622.6712	3+
sequence (enzyme/ ion score/ mass error)				
179 N.DRIGSARYITKTNASTL*.D Amidation(L) 195 (AspN/51/-0.0201)				



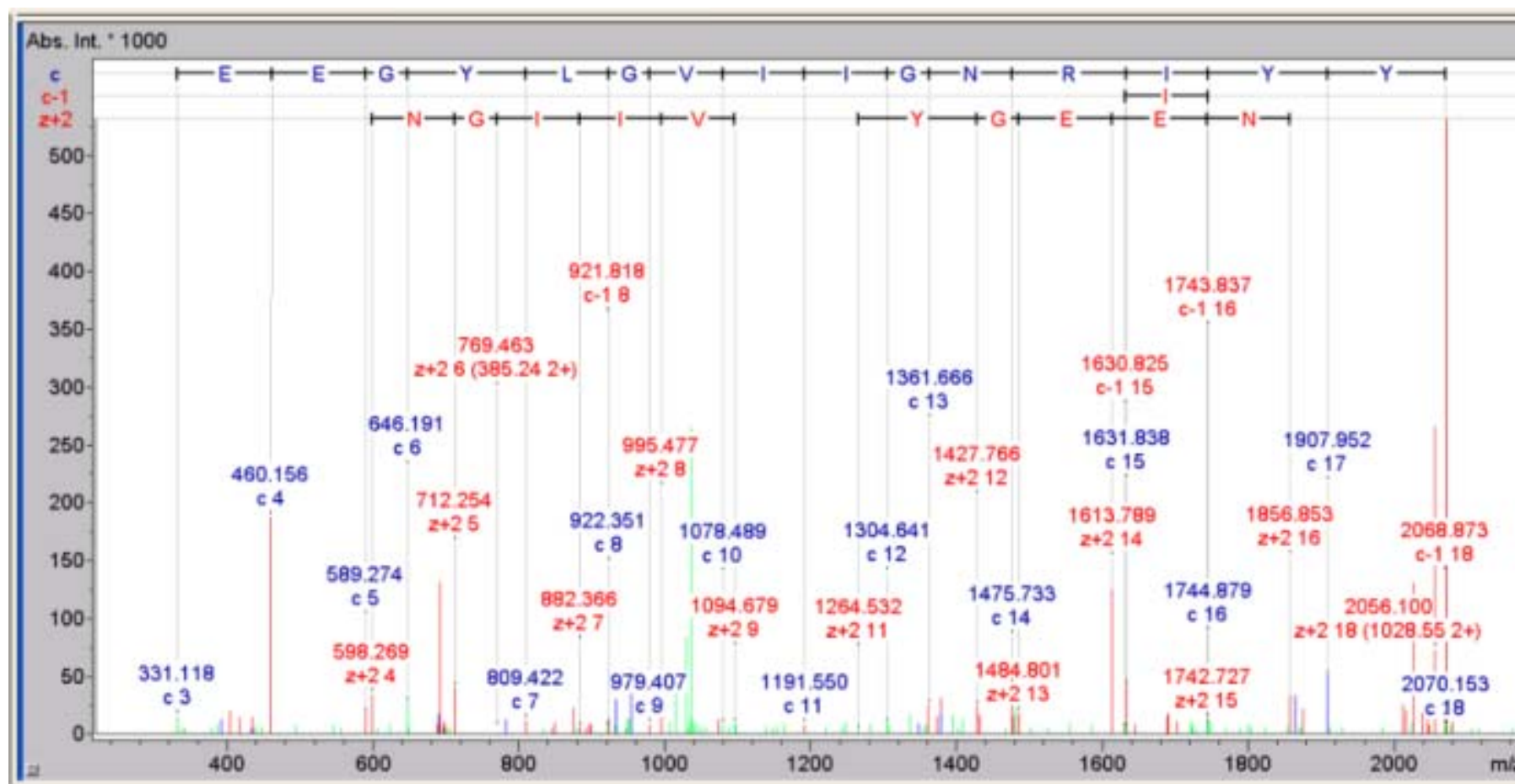
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Amidation: Y215	636.6371	3+
sequence (enzyme/ ion score/ mass error)				
199 F.KANEEGYLGVIIGNRIY*.Y Amidation(Y) 215 (Chy/50/-0.137)				



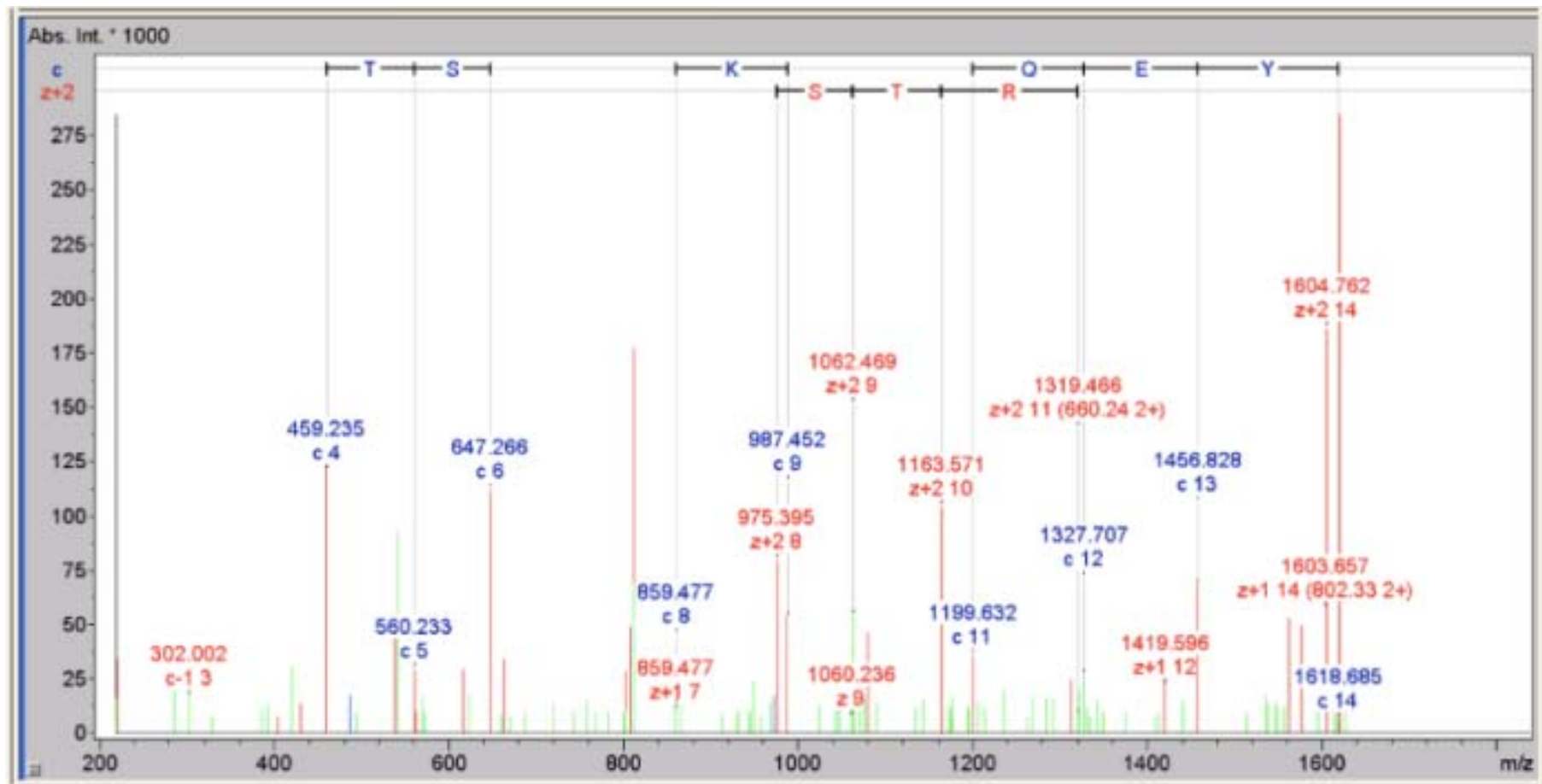
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Amidation: Y216	691.0786	3+
sequence (enzyme/ ion score/ mass error)				
199 F.KANEEGYLGVIIGNRIYY*.Q Amidation(Y) 216 (Chy/85/0.1242)				



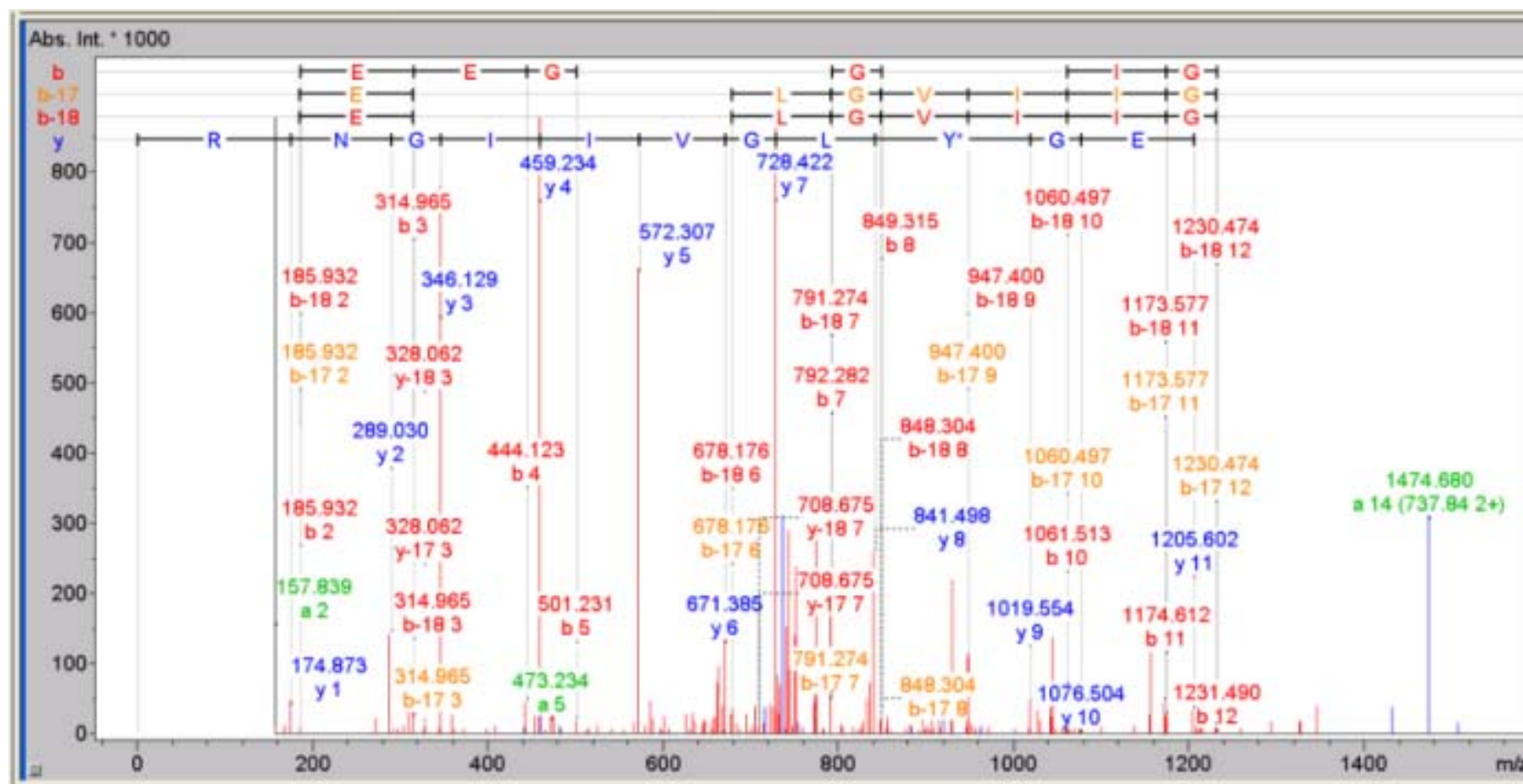
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Amidation: Y344	540.6681	3+
sequence (enzyme/ ion score/ mass error)				
331 L.ALTRTSDPKVIEY*.F Amidation(Y) 344 (Chy/42/0.1146)				



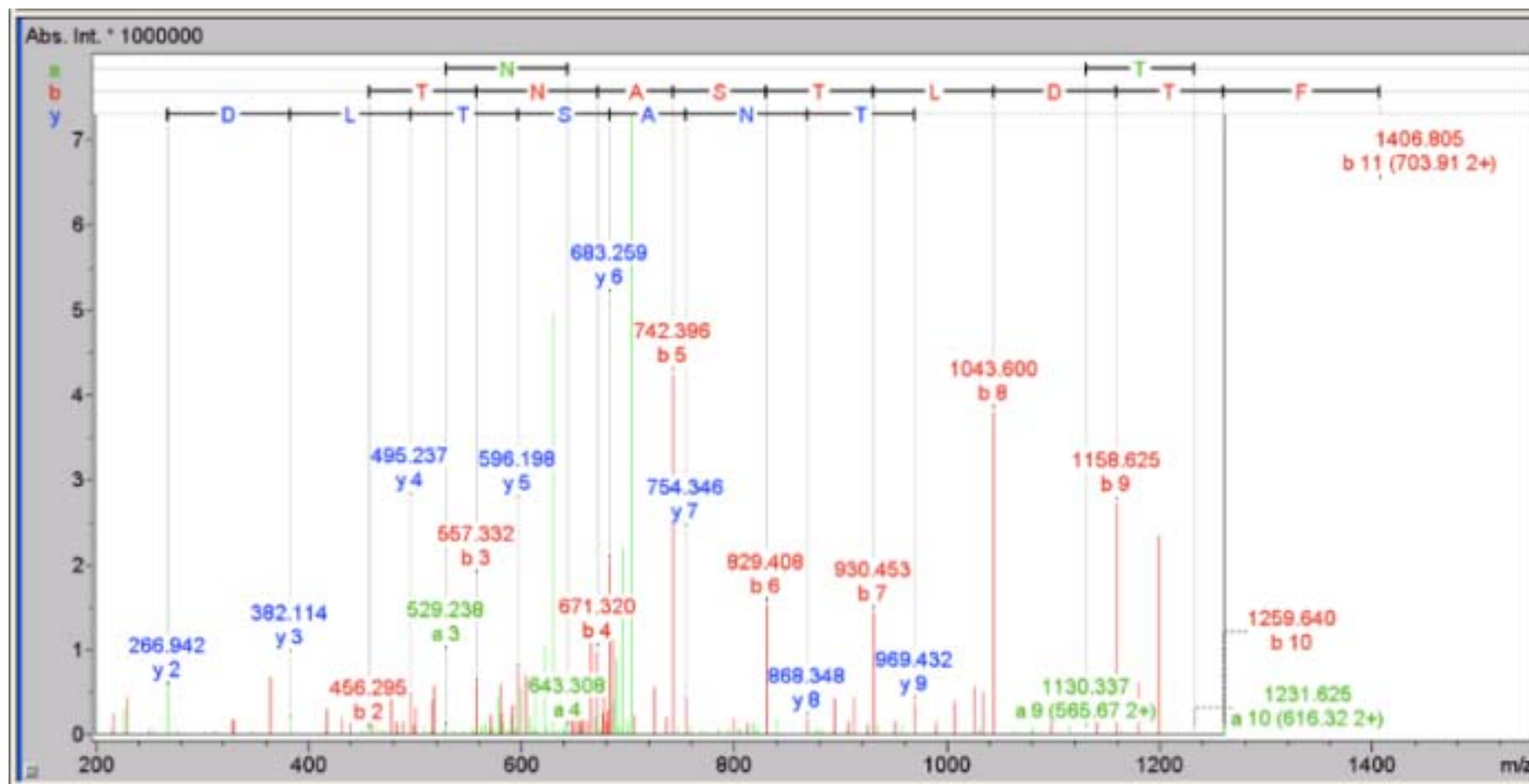
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Amino: Y205	760.3659	2+
sequence (enzyme/ ion score/ mass error)				
200 K.ANEEGY*LGVIIGNR.I Amino(Y) 213 (Try/59/-0.0618)				



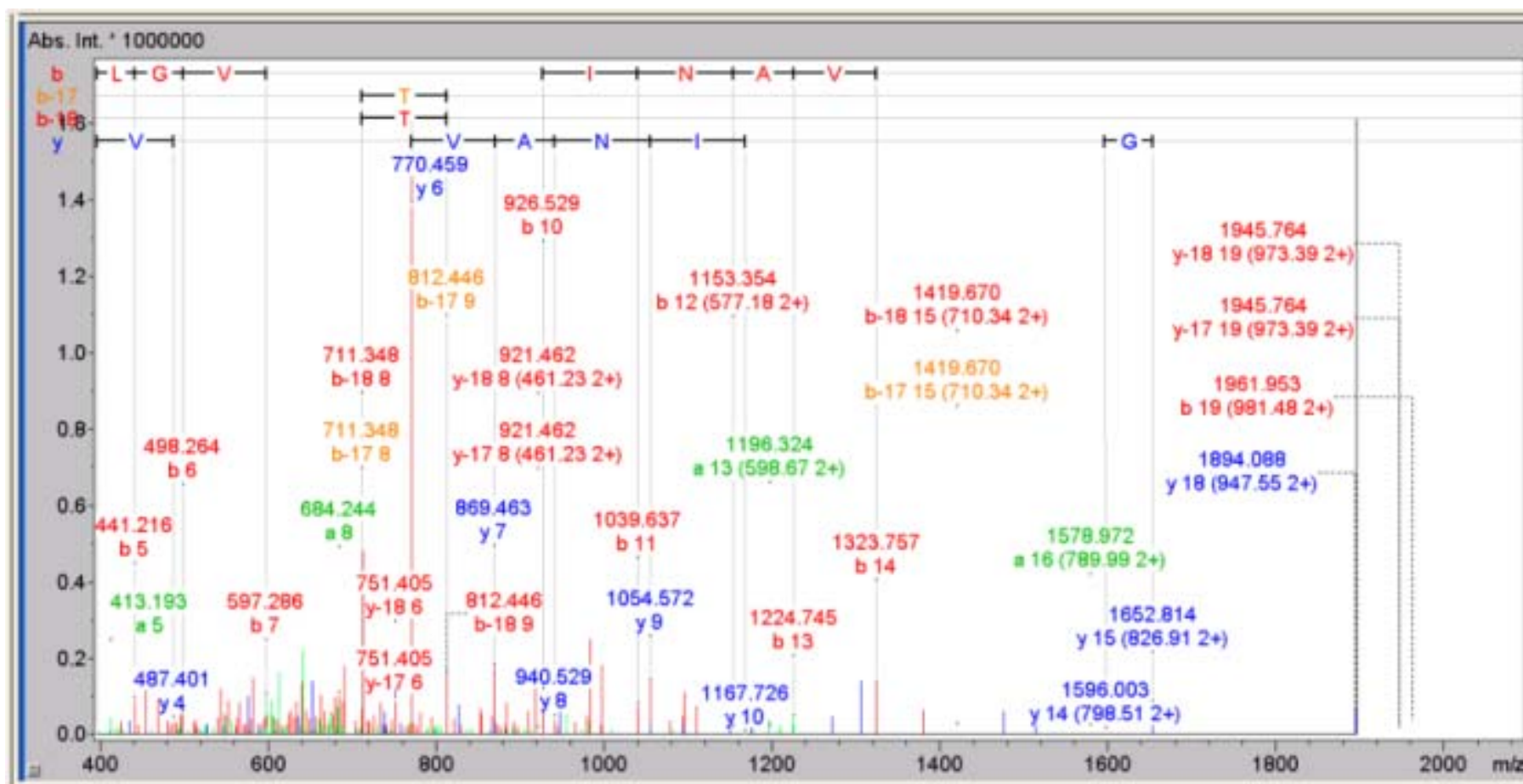
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Biotinylation: K189	712.8635	2+
sequence (enzyme/ ion score/ mass error)				
188 I.TK*TNASTLDTF.K Biotinylation(K) 198 (Chy/69/0.0471)				



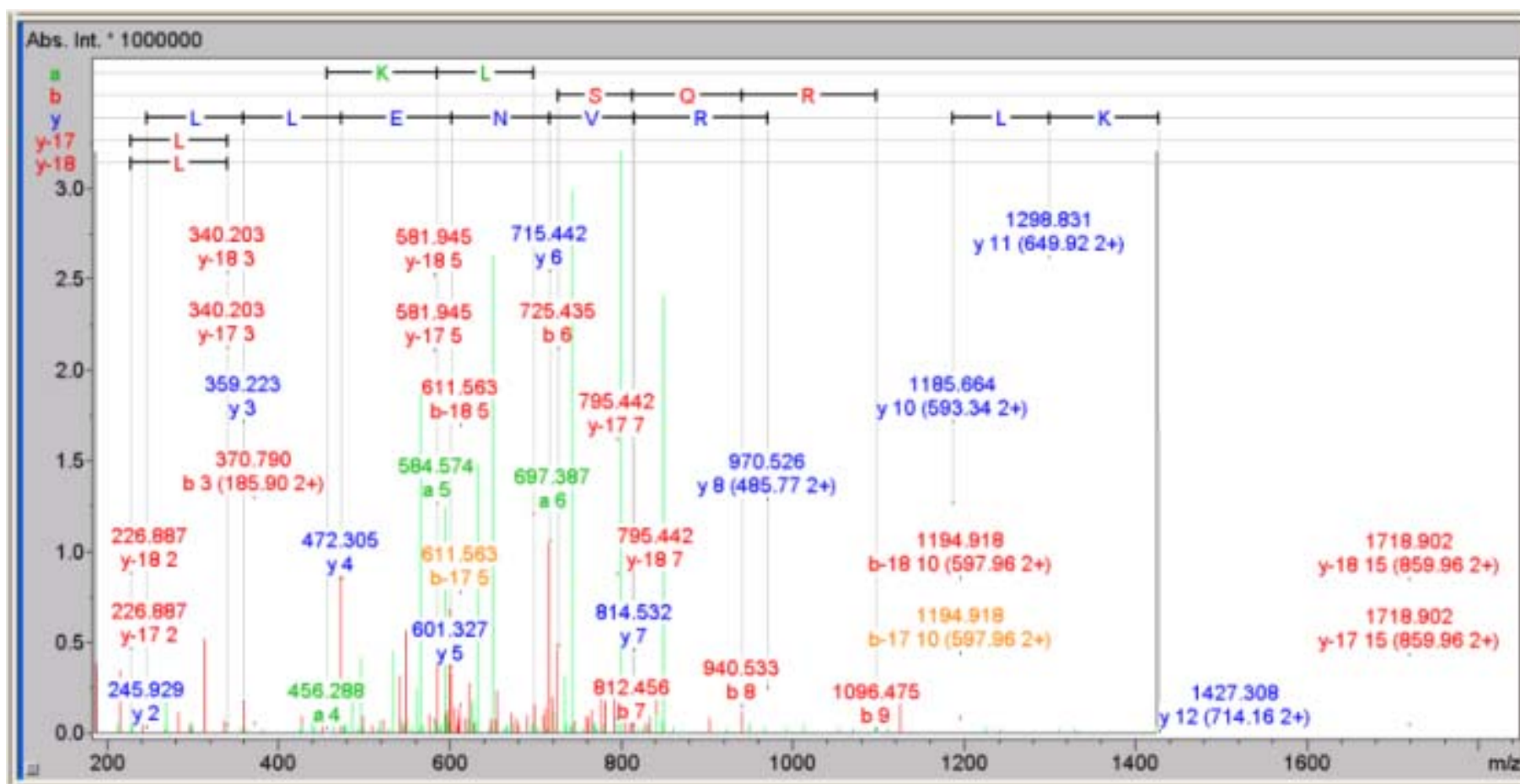
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Carbamidomethylation: E66	698.3758	3+
sequence (enzyme/ ion score/ mass error)				
51 Y.KAGALGVDTLINAVPE*VKKL.A Carbamidomethylation(E) 70 (Chy/42/-0.12)				



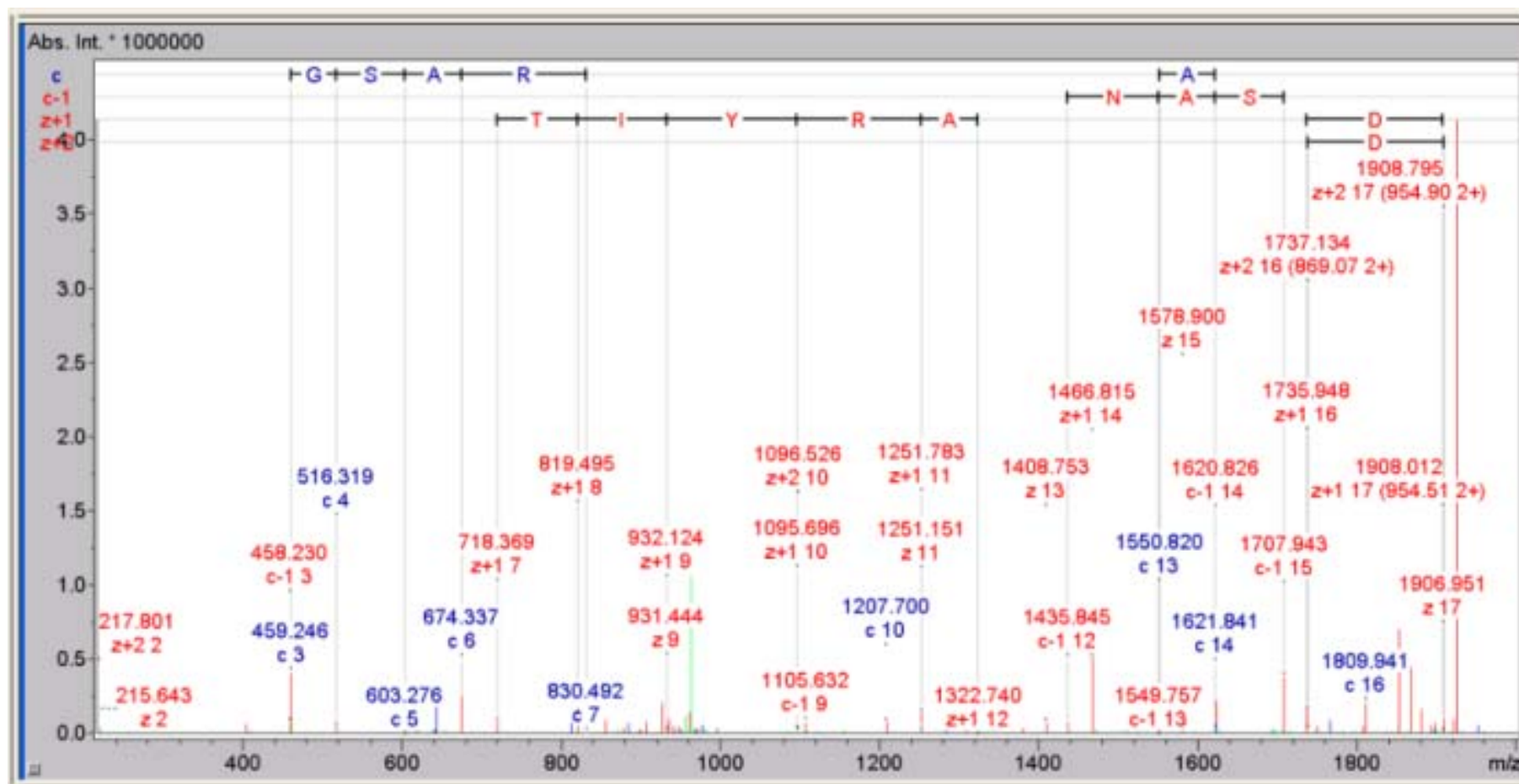
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Carbamidomethylation: D89	637.3756	3+
sequence (enzyme/ ion score/ mass error)				
89 G.D*VVLKLSQRVNELLAR.D Carbamidomethylation(D) 104 (AspN/50/-0.0059)				



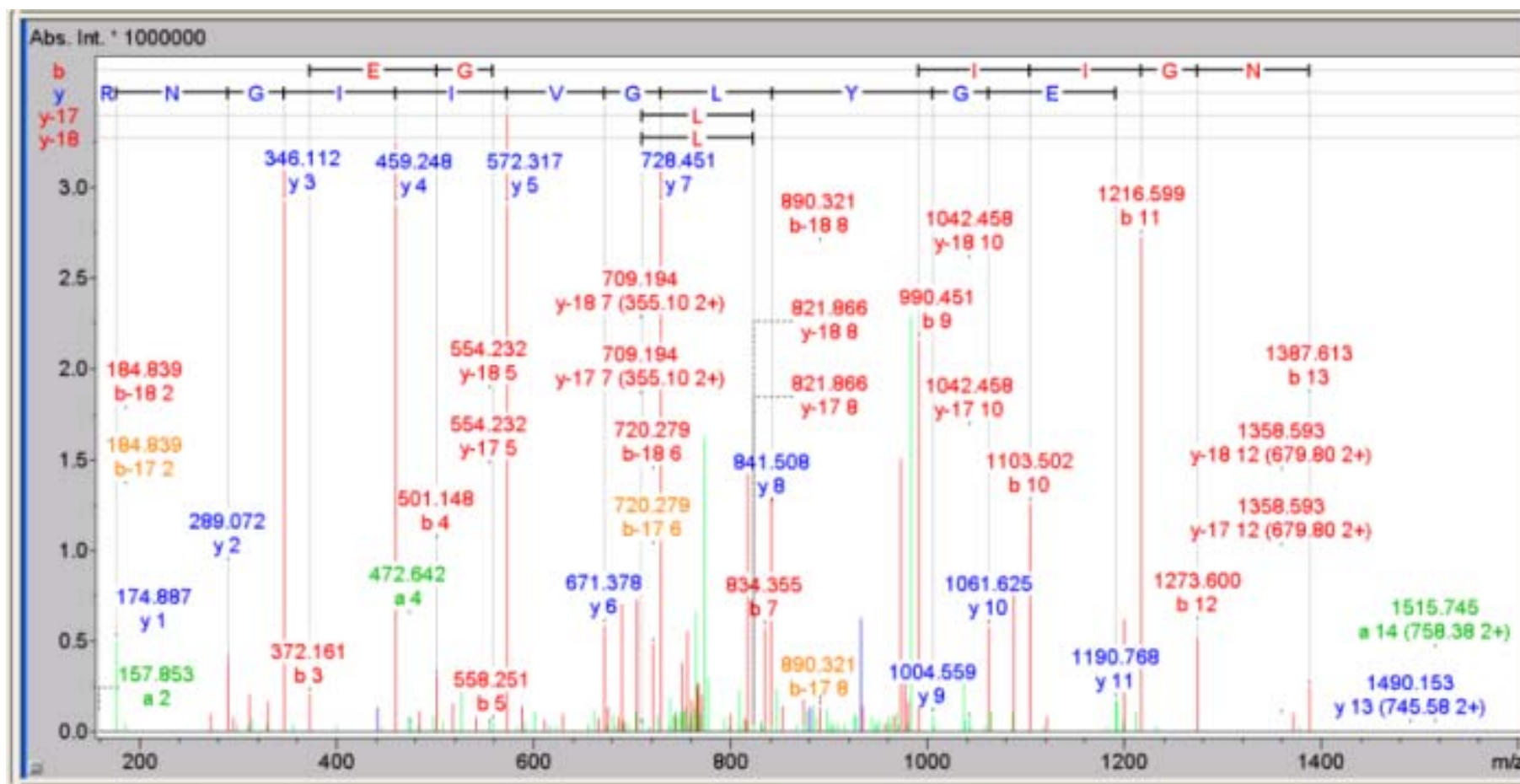
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Carbamidomethylation: D179	641.9953	3+
sequence (enzyme/ ion score/ mass error)				
179 N.D*RIGSARYITKTNASTL.D Carbamidomethylation(D) 195 (AspN/42/-0.0533)				



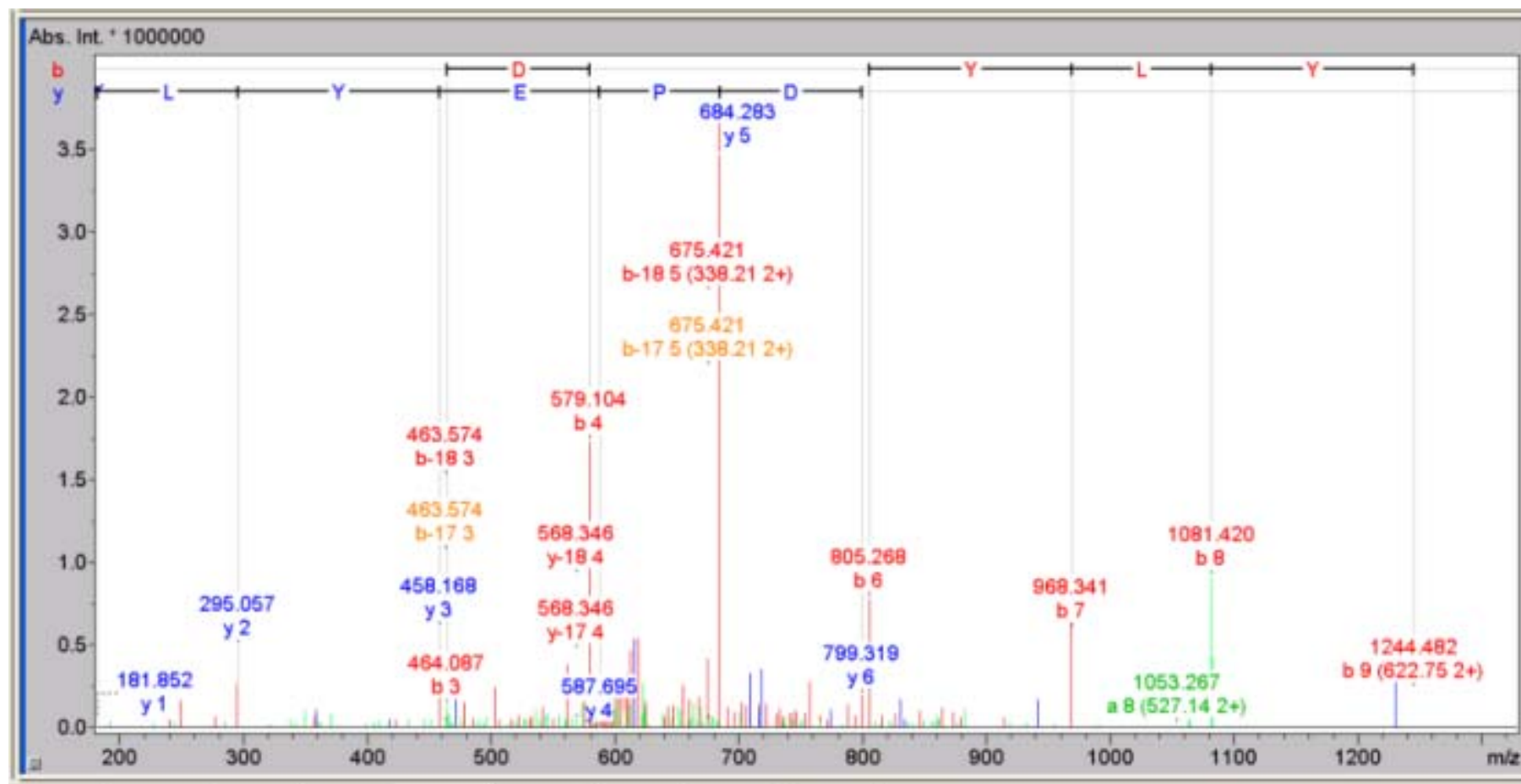
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Carbamidomethylation: E202	781.4115	2+
sequence (enzyme/ ion score/ mass error)				
200 K.ANE*EGYLGVIIGNR.I Carbamidomethylation(E) 213 (Try/69/0.0189)				



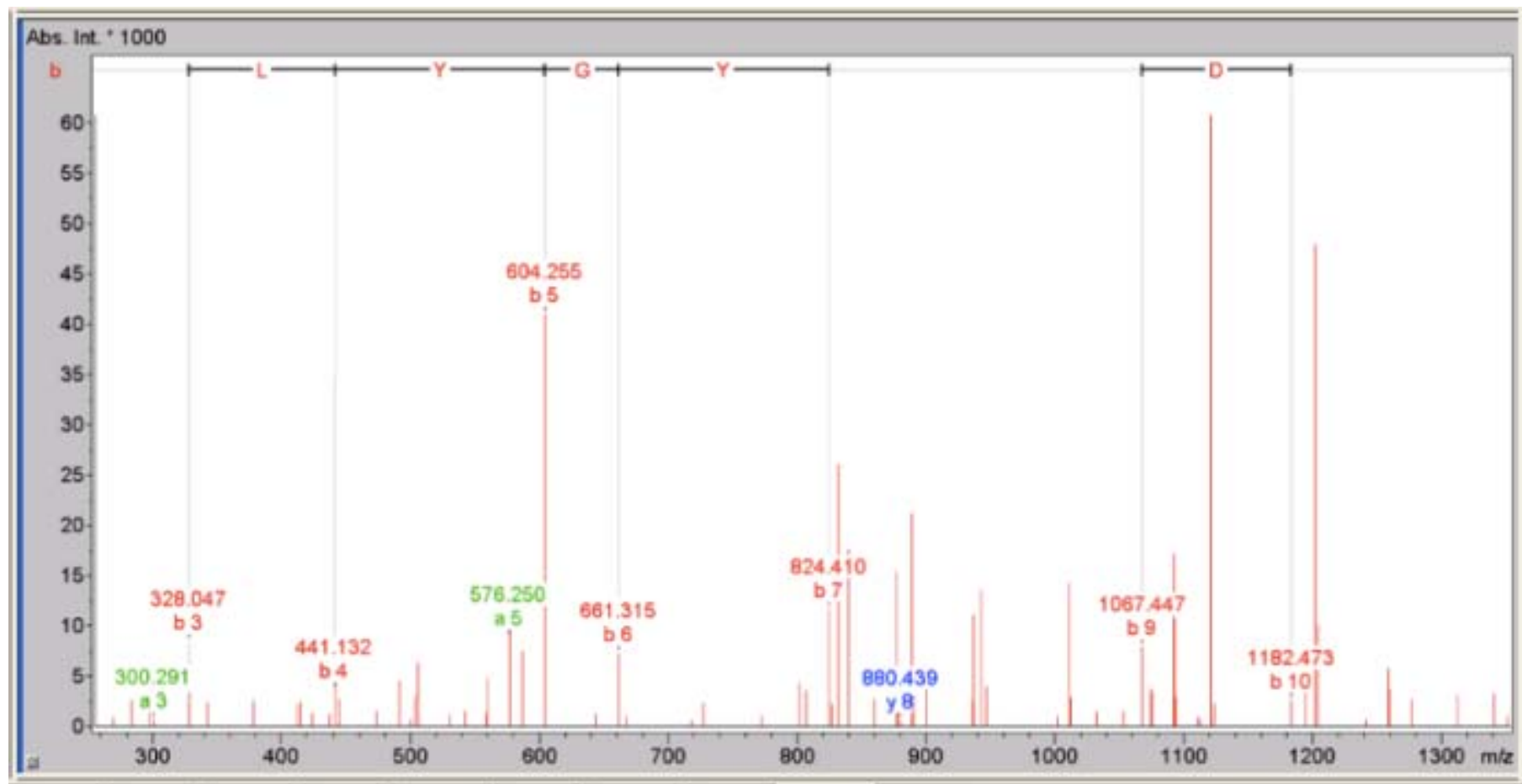
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Carbamidomethylation: D249	631.759	2+
sequence (enzyme/ ion score/ mass error)				
247 G.YQD*DPEYLY.D Carbamidomethylation(D) 255 (Chy/33/-0.0104)				



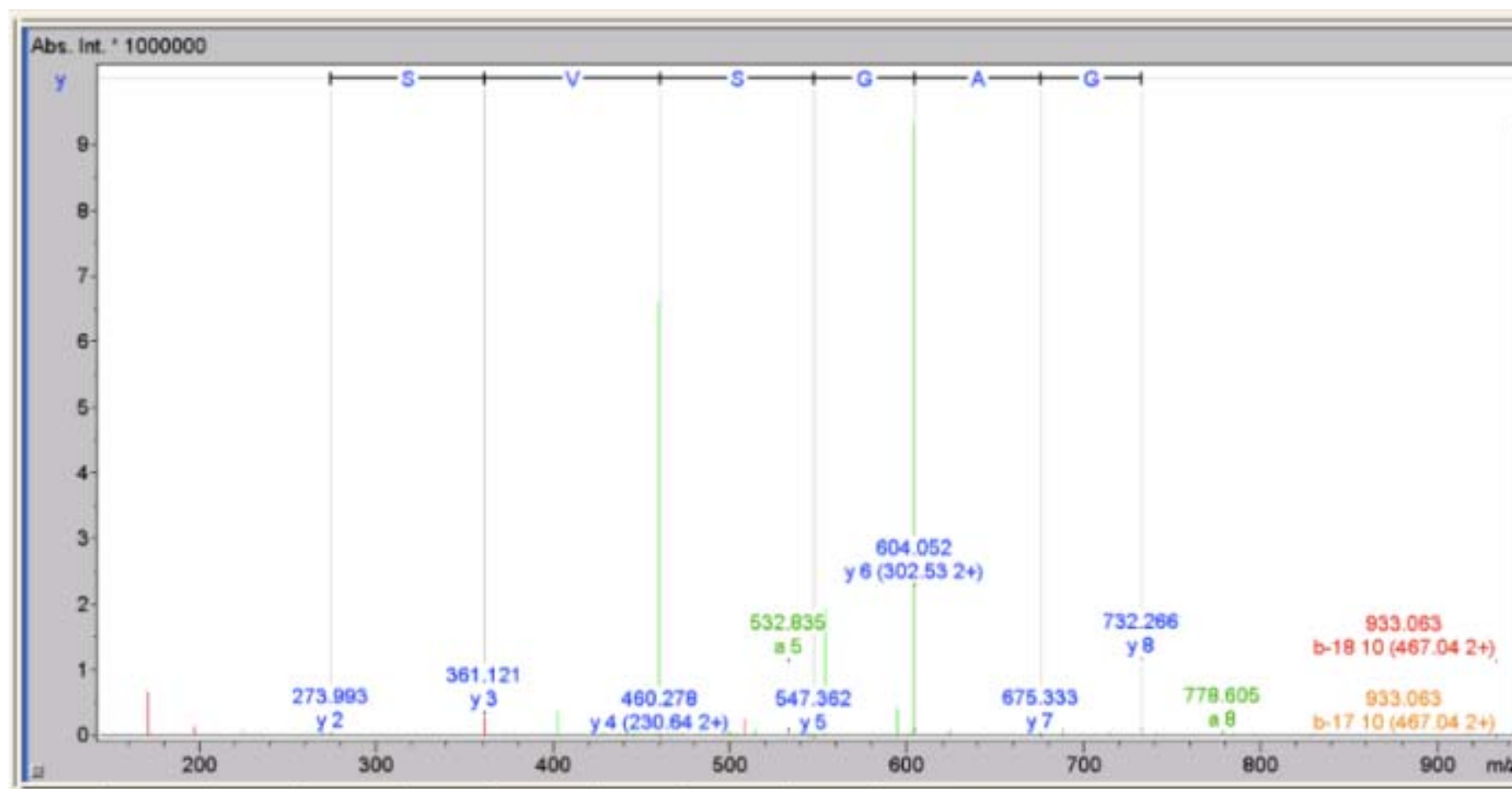
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Carbamidomethylation: K264	948.1598	3+
sequence (enzyme/ ion score/ mass error)				
241 K.VDILYGYQDDPEYLYDAAIQHGVK*.G Carbamidomethylation(K) 264 (Try/39/0.1078)				



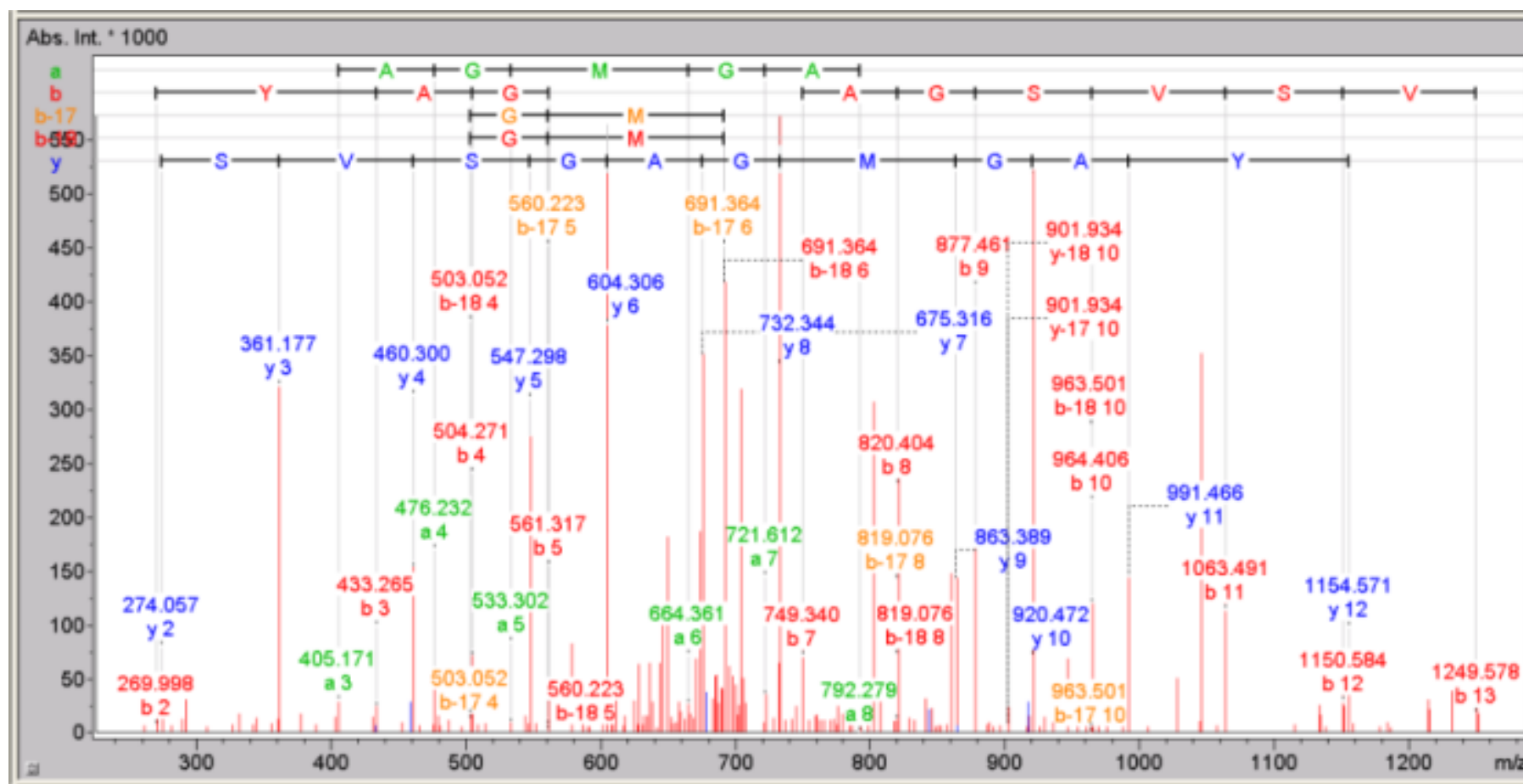
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Carbamidomethylation: G265	494.2286	3+
sequence (enzyme/ ion score/ mass error)				
265 K.G*IVYAGMGAGSVSVR.G Carbamidomethylation(G) 279 (Try/43/-0.0864)				



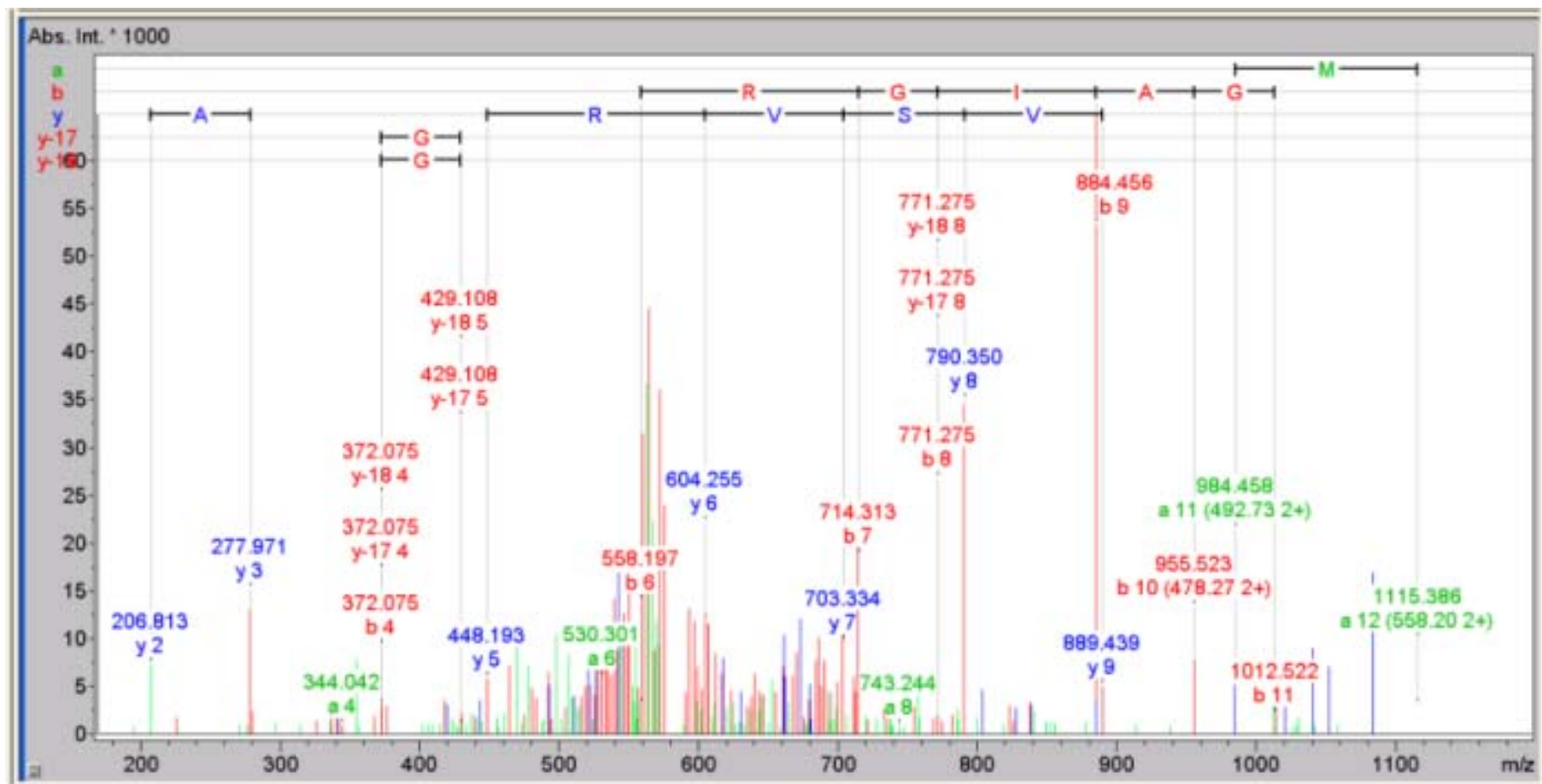
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Carbamidomethylation: I266	712.3335	2+
sequence (enzyme/ ion score/ mass error)				
266 G.I*VYAGMGAGSVSVR.G Carbamidomethylation(I) 279 (Try/113/-0.0765)				



Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Carbamidomethylation: A273	581.2812	2+
sequence (enzyme/ ion score/ mass error)				
273 G.A*GSVSVRGIAGM.R Carbamidomethylation(A) 284 (Chy/34/-0.0493)				



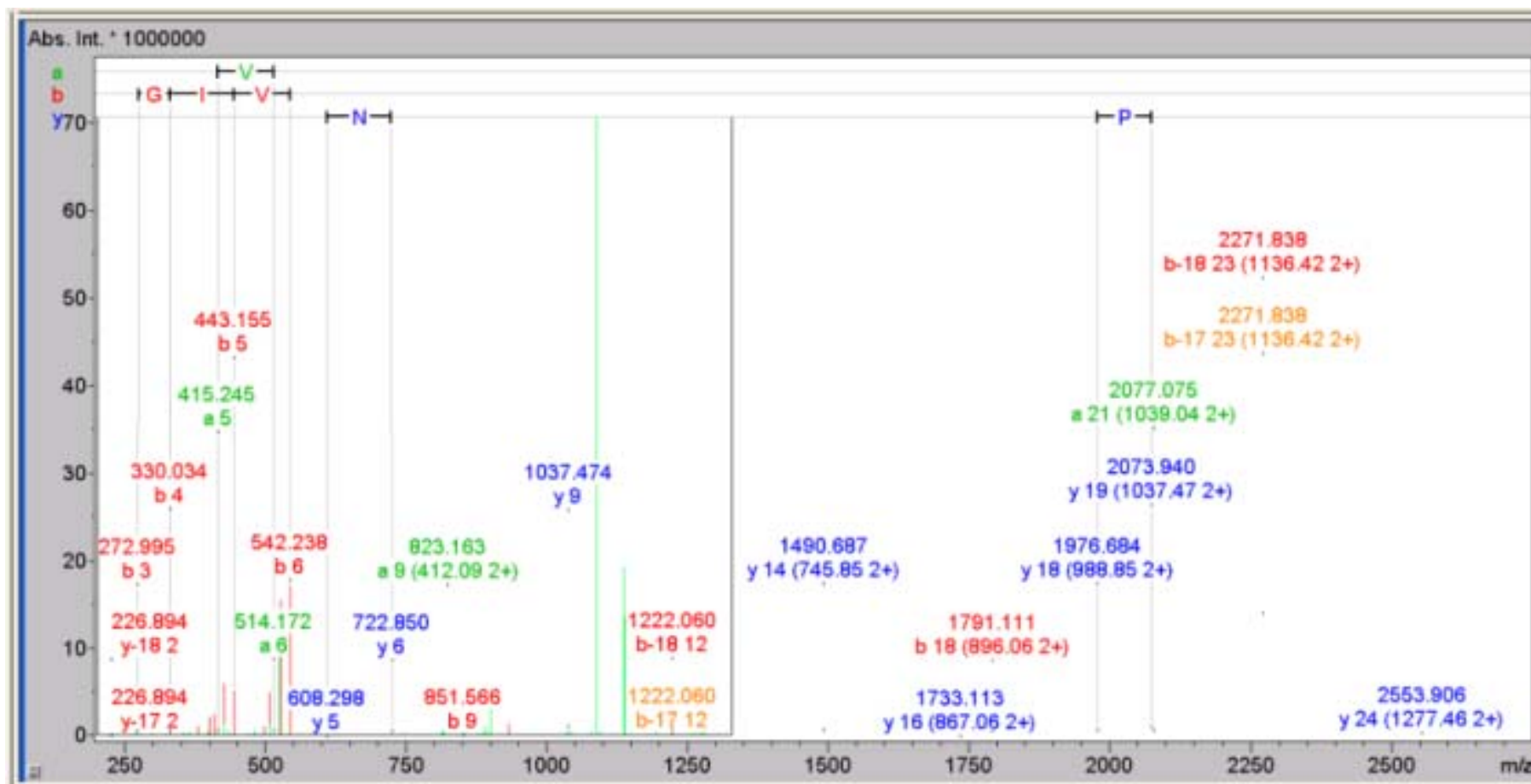
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Carbamidomethylation: D317	750.7871	3+
sequence (enzyme/ ion score/ mass error)				
317 S.D*SLNPAHARILLMLALTRTS.D Carbamidomethylation(D) 336 (AspN/40/0.1081)				



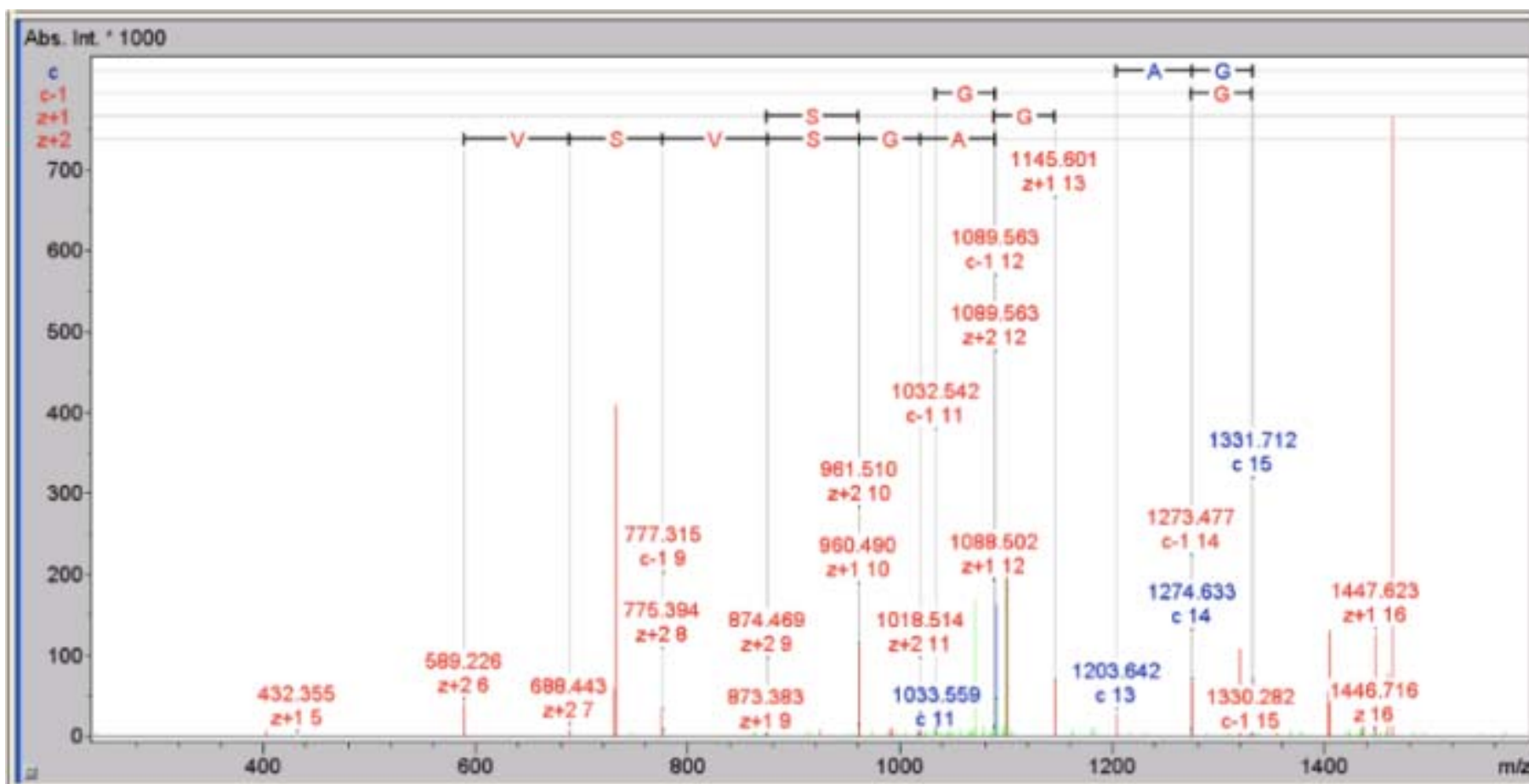
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Carbamidomethylation: H323	904.7752	3+
sequence (enzyme/ ion score/ mass error)				
300 R.TGNGIVPPDEELPGLVSDSLNPAH*AR.I Carbamidomethylation(H) 325 (Try/43/-0.0477)				



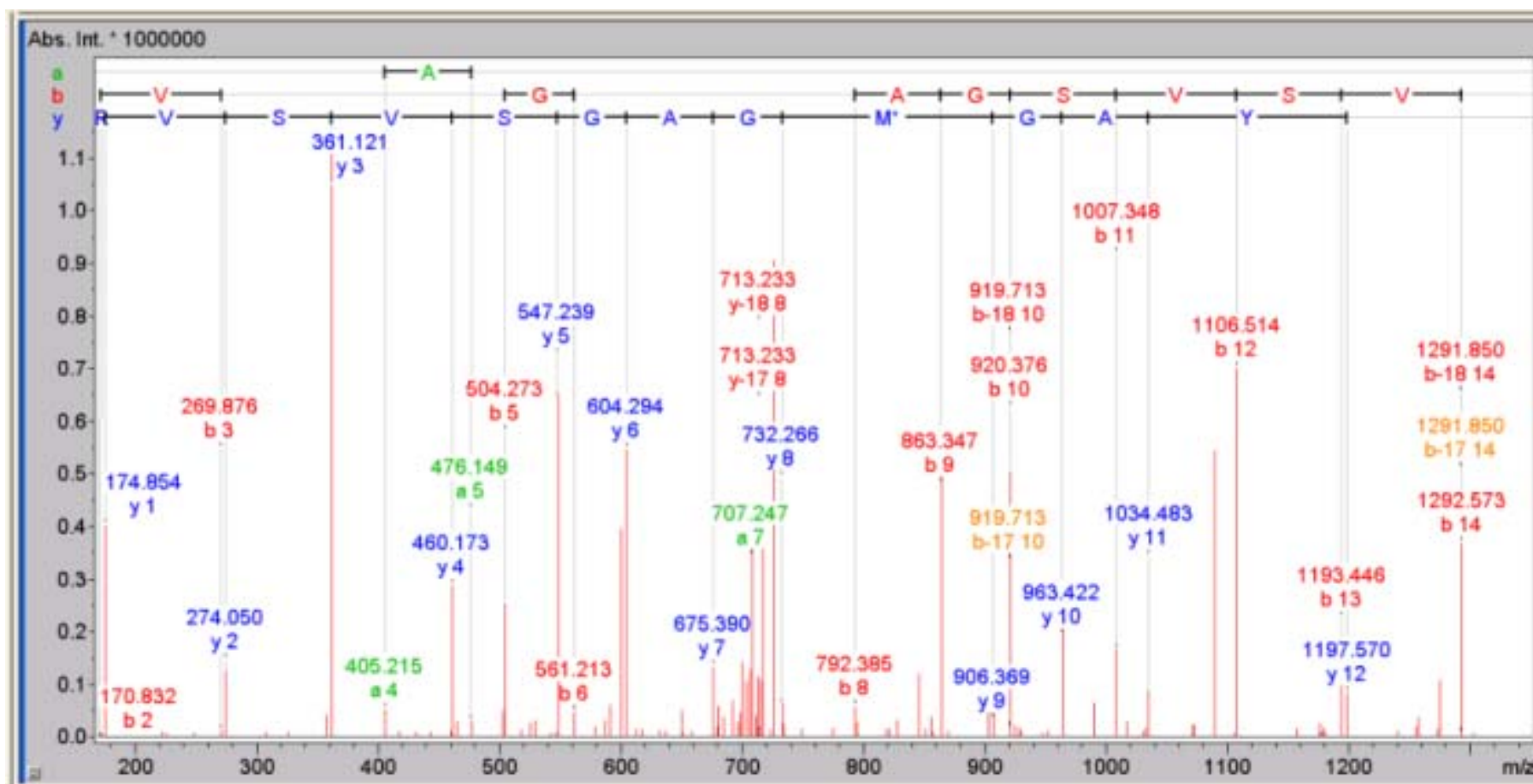
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Carbamylation: A269	732.3166	2+
sequence (enzyme/ ion score/ mass error)				
269 Y.A*GMGAGSVSVRGIAGM.R Carbamylation(A) 284 (Chy/72/-0.0834)				



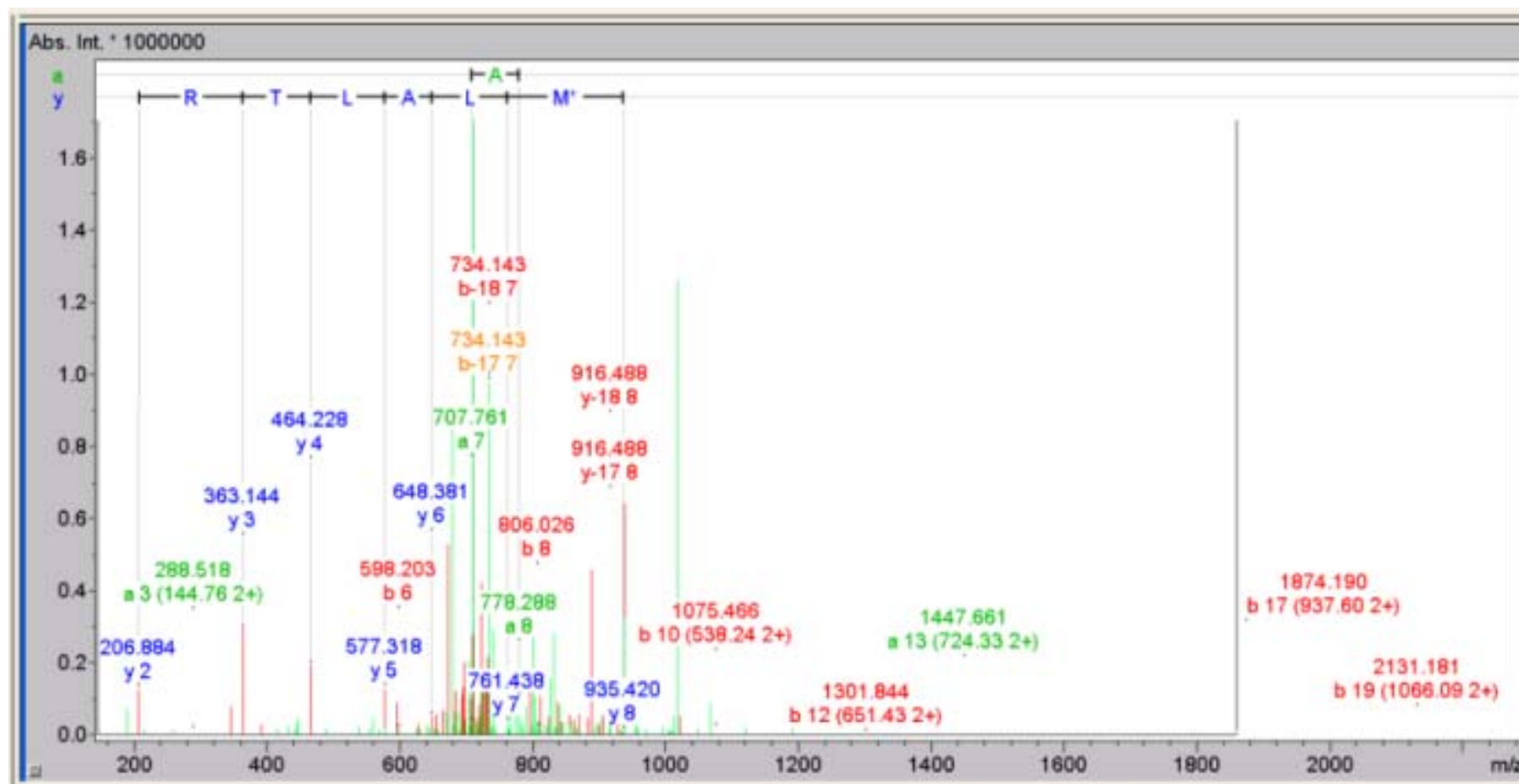
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Carbamylation: M271	733.8145	2+
sequence (enzyme/ ion score/ mass error)				
265 K.GIVYAGM*GAGSVSVR.G Carbamylation(M) 279 (Try/92/-0.1203)				



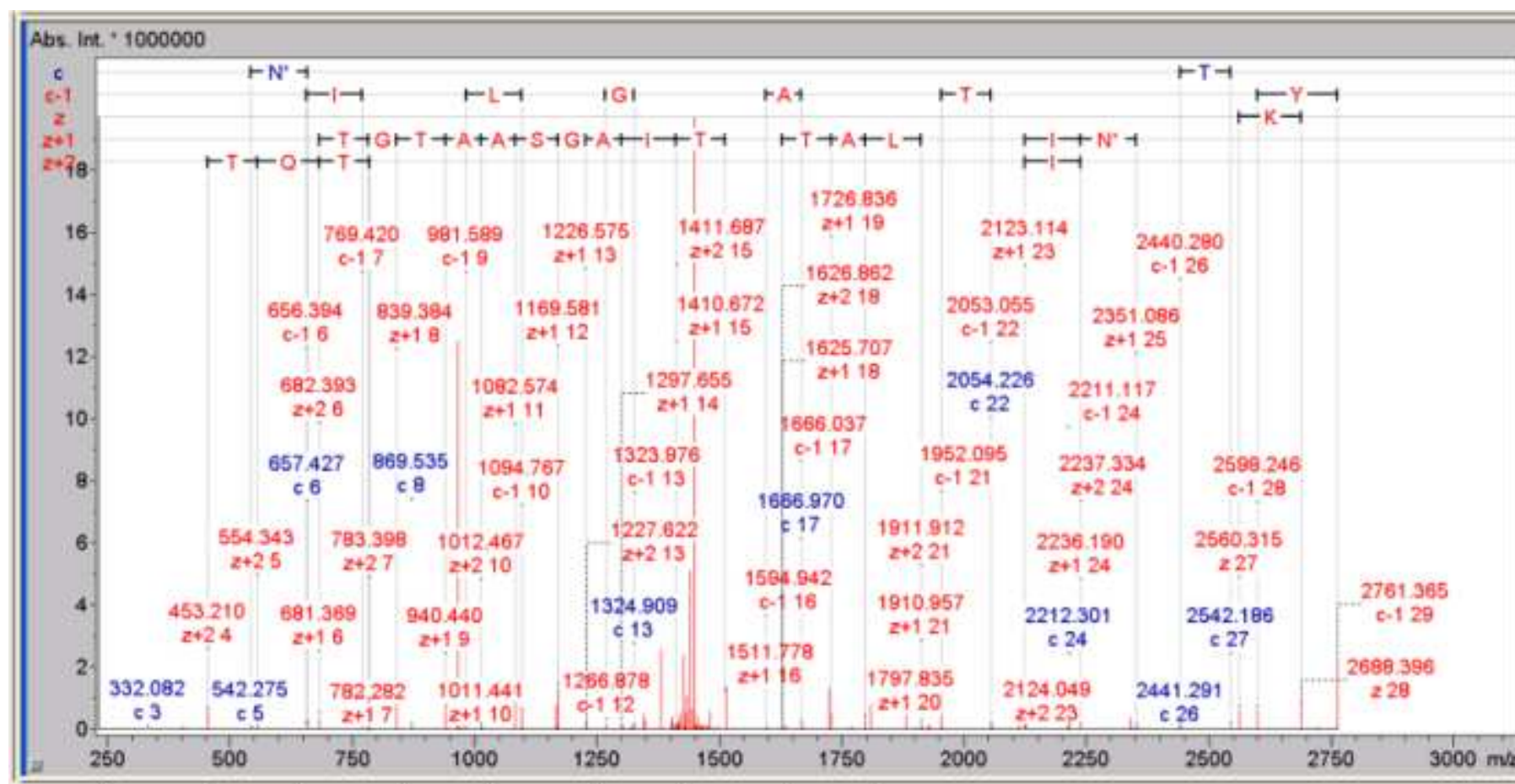
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Carbamylation: M329	746.0744	3+
sequence (enzyme/ ion score/ mass error)				
317 S.DSLNPAHARILLM*LALTRTS.D Carbamylation(M) 336 (AspN/40/-0.0144)				



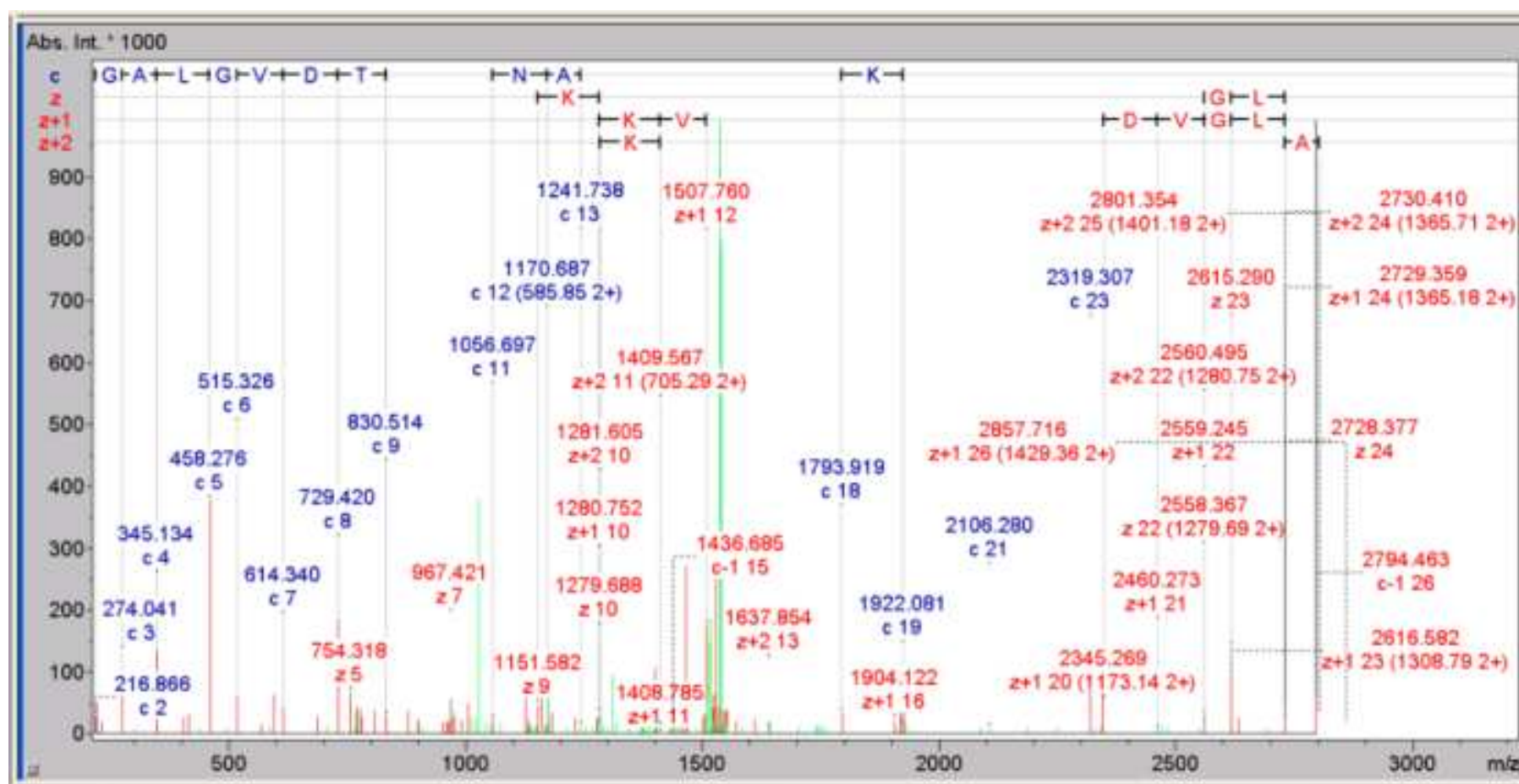
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Deamidation: N27	964.5759	3+
sequence (enzyme/ ion score/ mass error)				
22 A.ADKLPN*IVILATGGTIAGSAATGTQTTGYK.A Deamidation(N) 51 (Try/72/0.1771)				



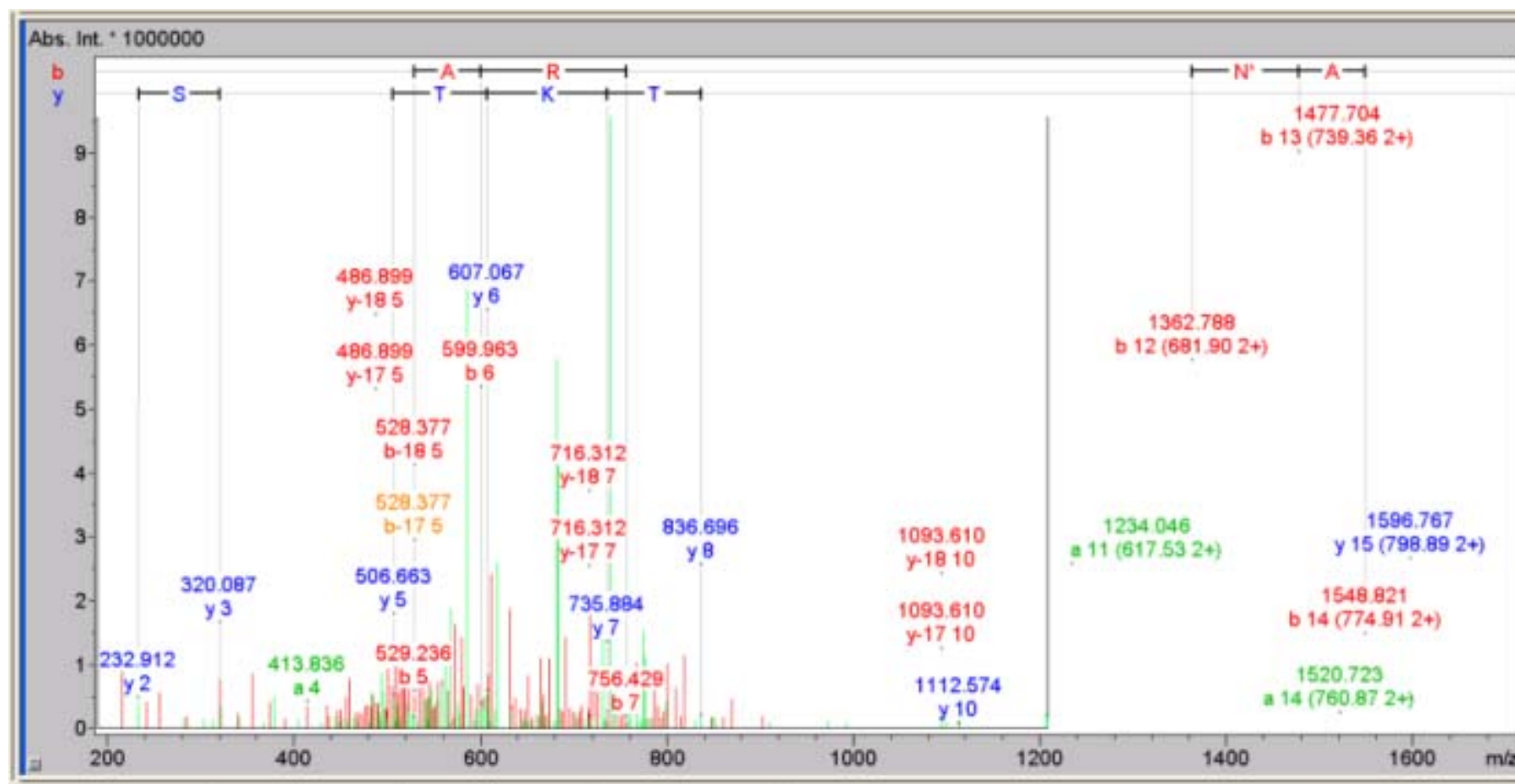
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Deamidation: Q77	768.9491	4+
sequence (enzyme/ ion score/ mass error)				
51 Y.KAGALGVDTLINAVPEVKKLANVK*GEQ*F.S Hex(K) Deamidation(Q) 78 (Chy/50/0.0919)				



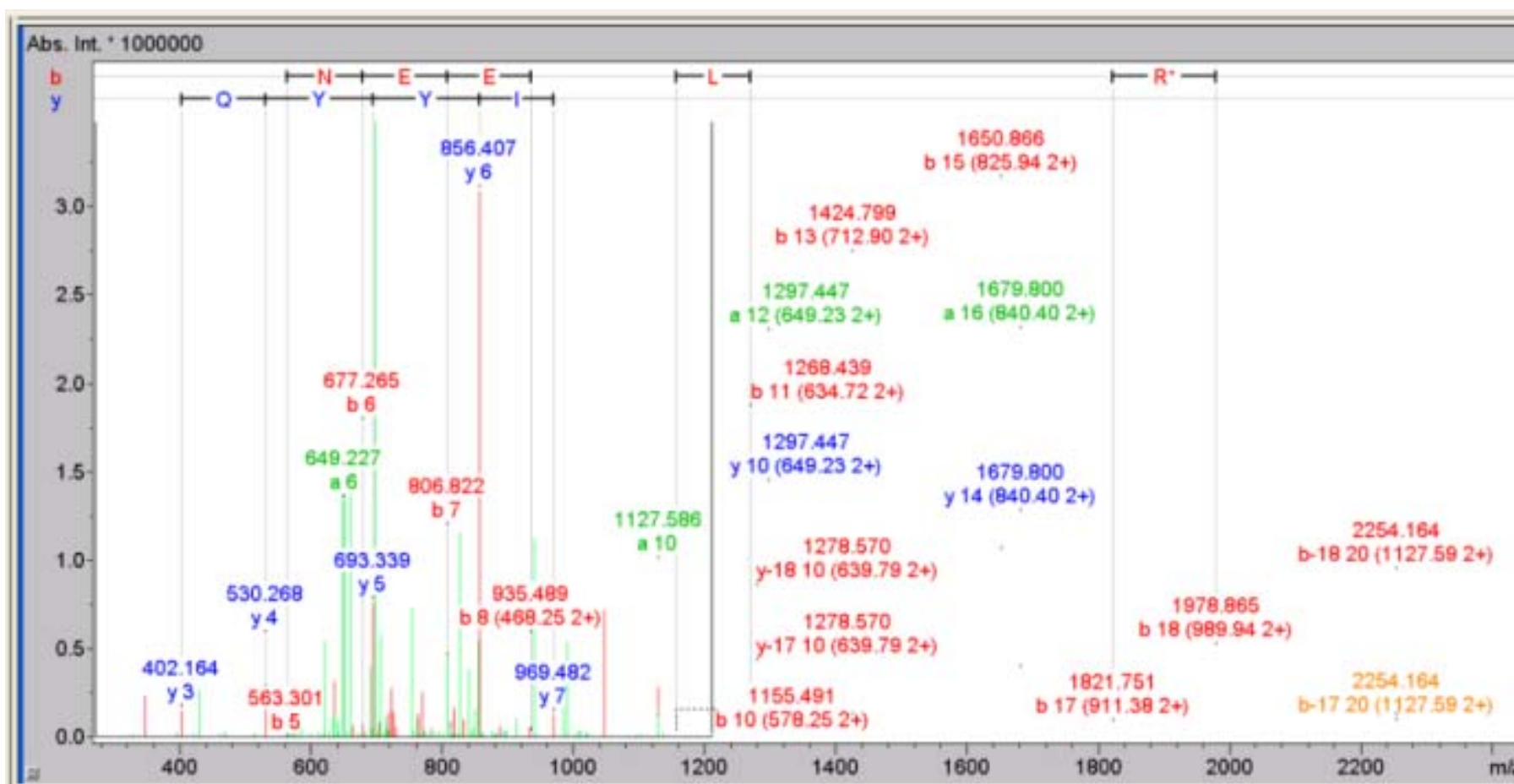
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Deamidation: N191	623.3406	3+
sequence (enzyme/ ion score/ mass error)				
179 N.DRIGSARYITKTN*ASTL.D Deamidation(N) 195 (AspN/42/0.0201)				



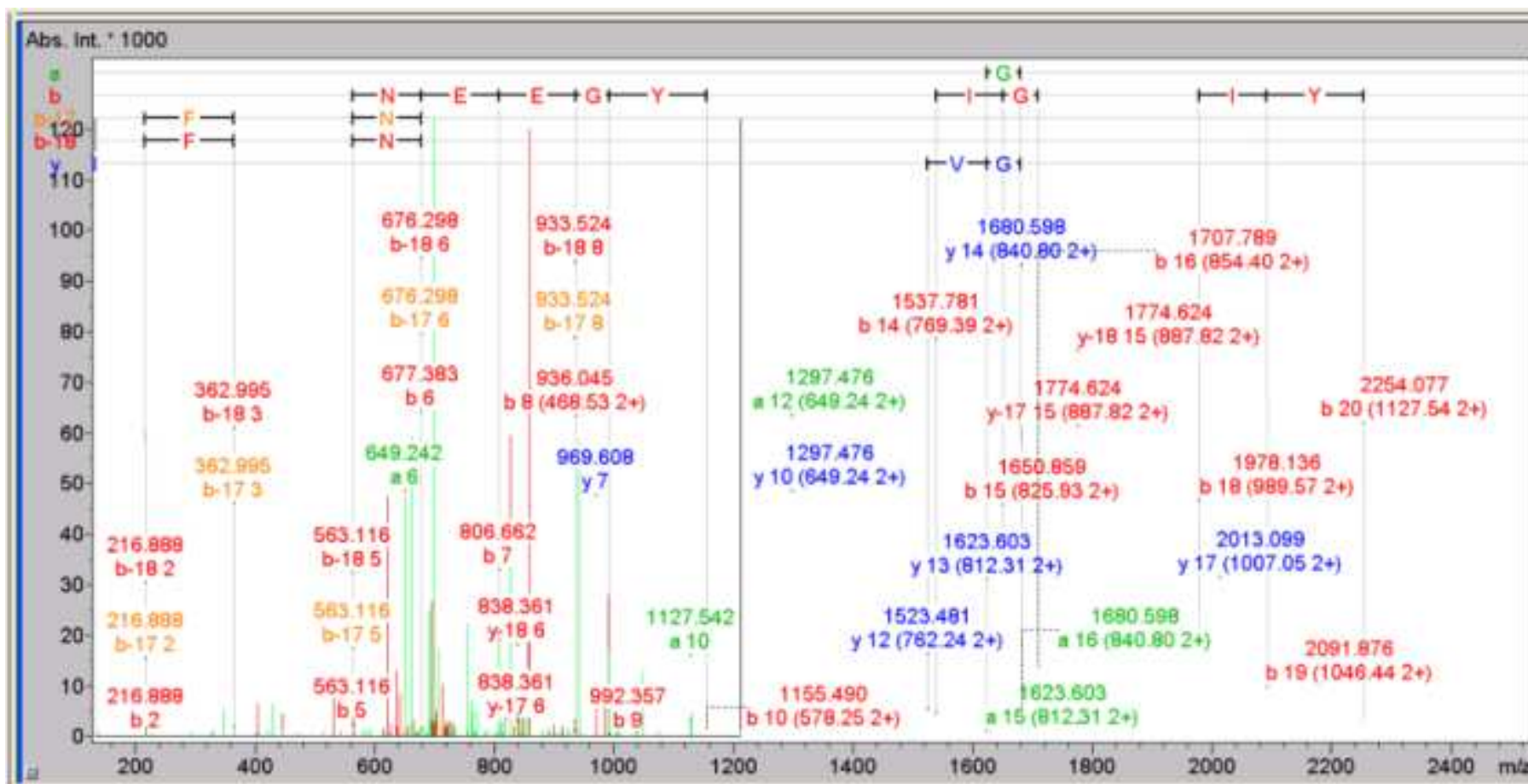
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Deamidation: R213	737.6476	4+
sequence (enzyme/ ion score/ mass error)				
196 L.DTFKANEEGYLGVIIGNR*IYYQNRI.D Deamidation(R) 220 (AspN/60/0.0738)				



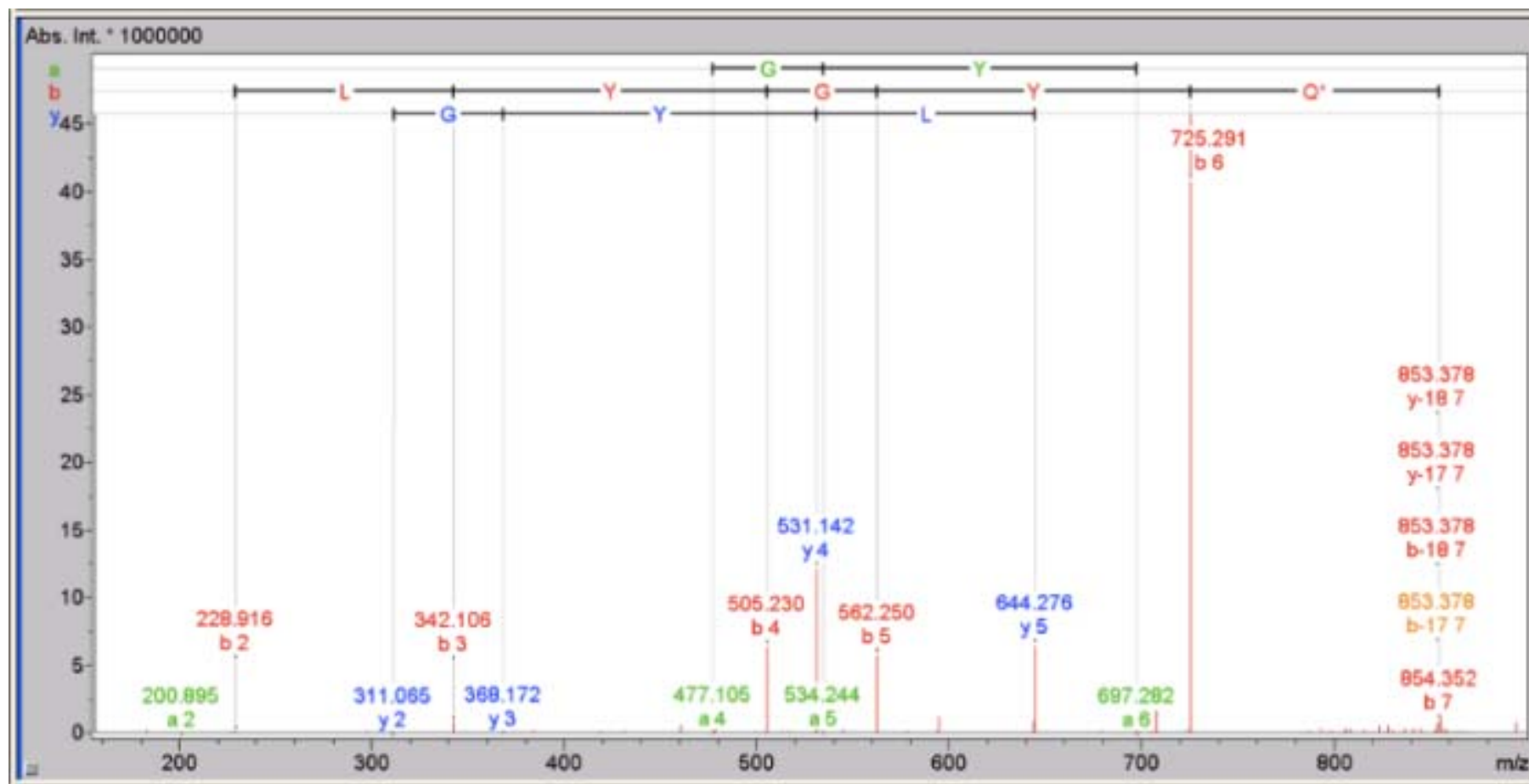
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Deamidation: N218	737.6185	4+
sequence (enzyme/ ion score/ mass error)				
196 L.DTFKANEEGYLGVIIGNRIYYQN*RI.D Deamidation(N) 220 (AspN/62/-0.0426)				



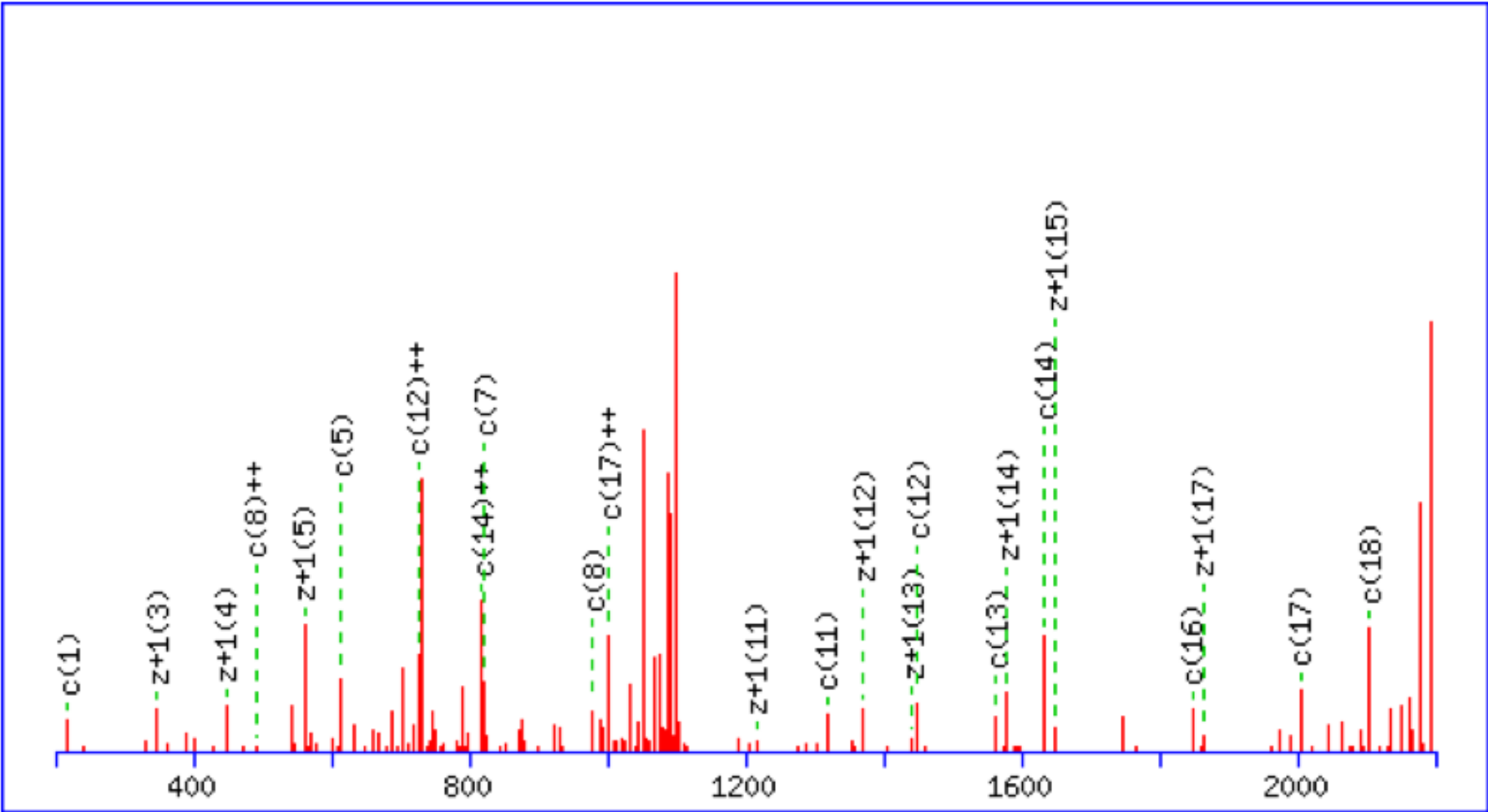
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Deamidation: Q248	872.4342	1+
sequence (enzyme/ ion score/ mass error)				
242 V.DILYGYQ*.D Deamidation(Q) 248 (AspN/38/0.0306)				



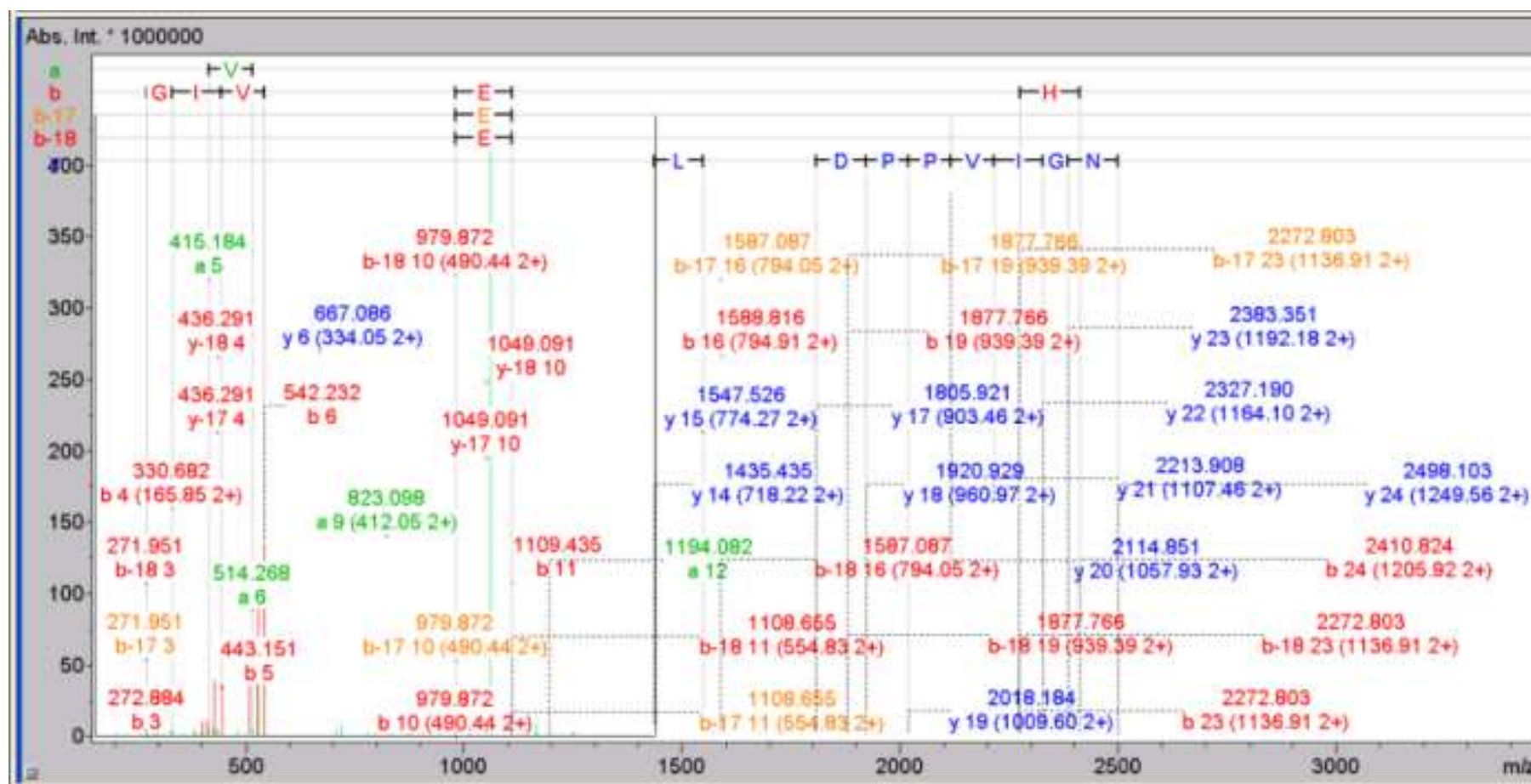
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Deamidation: N320	549.0492	4+
sequence (enzyme/ ion score/ mass error)				
318 D.S*LN*PAHARILLMLALTRTS.D GlyGly(S) Deamidation(N) 336 (AspN/79/-0.0422)				



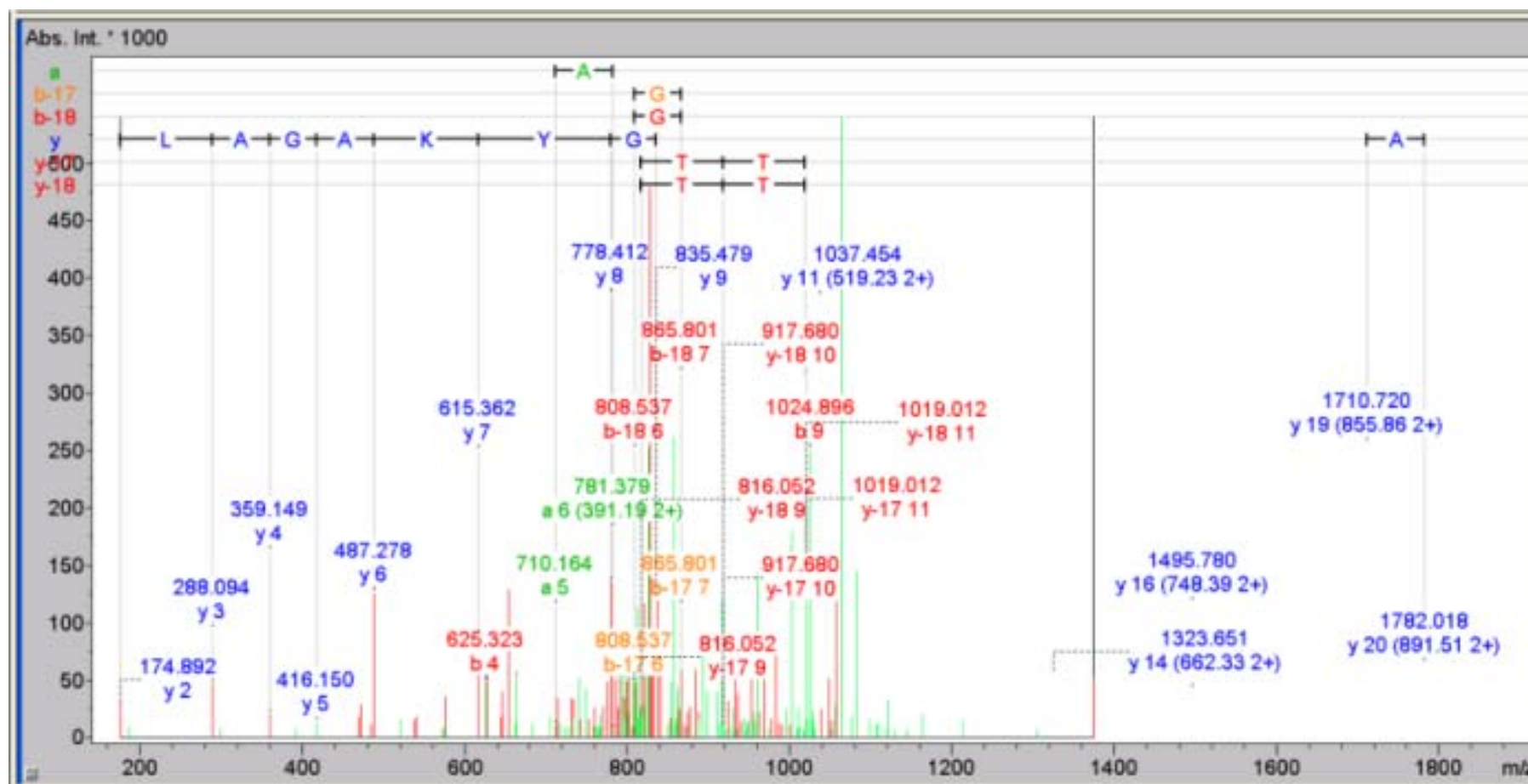
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Deamidation: R325	886.0455	3+
sequence (enzyme/ ion score/ mass error)				
300 R.TGNGIVPPDEELPGLVSDSLNPAHAR*.I Deamidation(R) 325 (Try/37/-0.1993)				



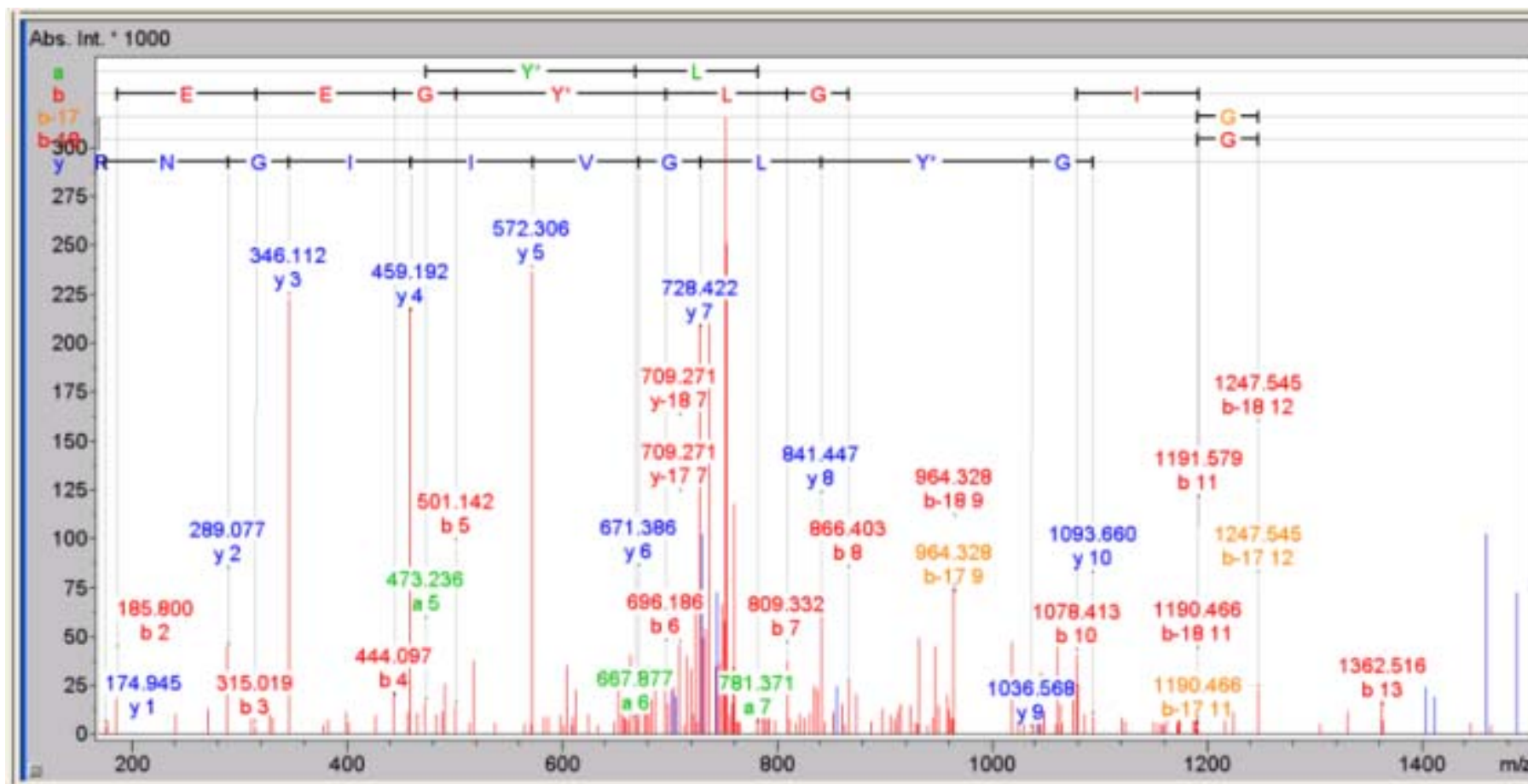
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Decanoyl: T33, T36	840.484	3+
sequence (enzyme/ ion score/ mass error)				
33 A.T*GGT*IAGSAATGTQTTGYKAGALGV.D 2 Decanoyl(T) 57 (AspN/47/0.0407)				



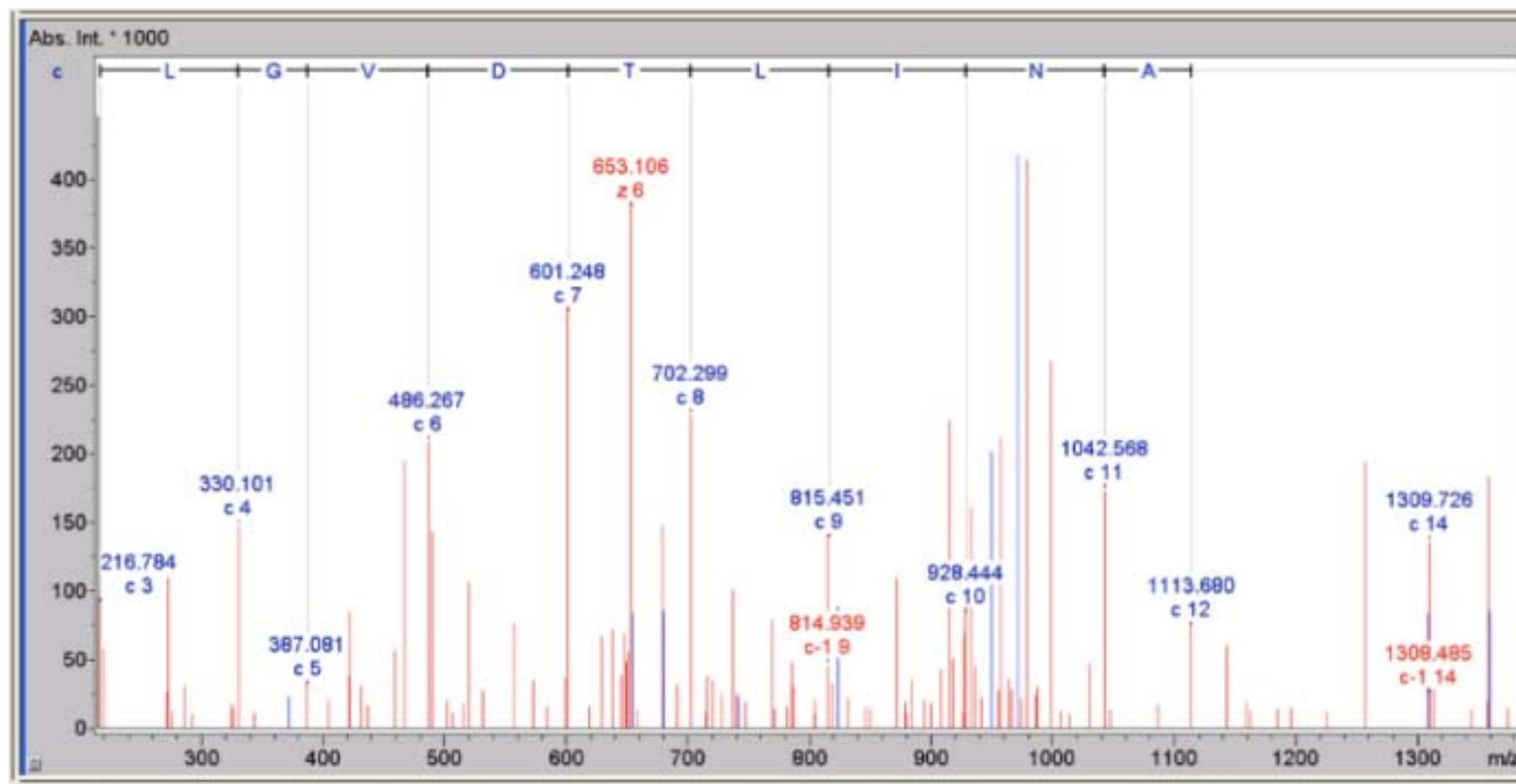
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Dioxidation: Y205	768.8961	2+
sequence (enzyme/ ion score/ mass error)				
200 K.ANEEGY*LGVIIGNR.I Dioxidation(Y) 213 (Try/38/0.0197)				



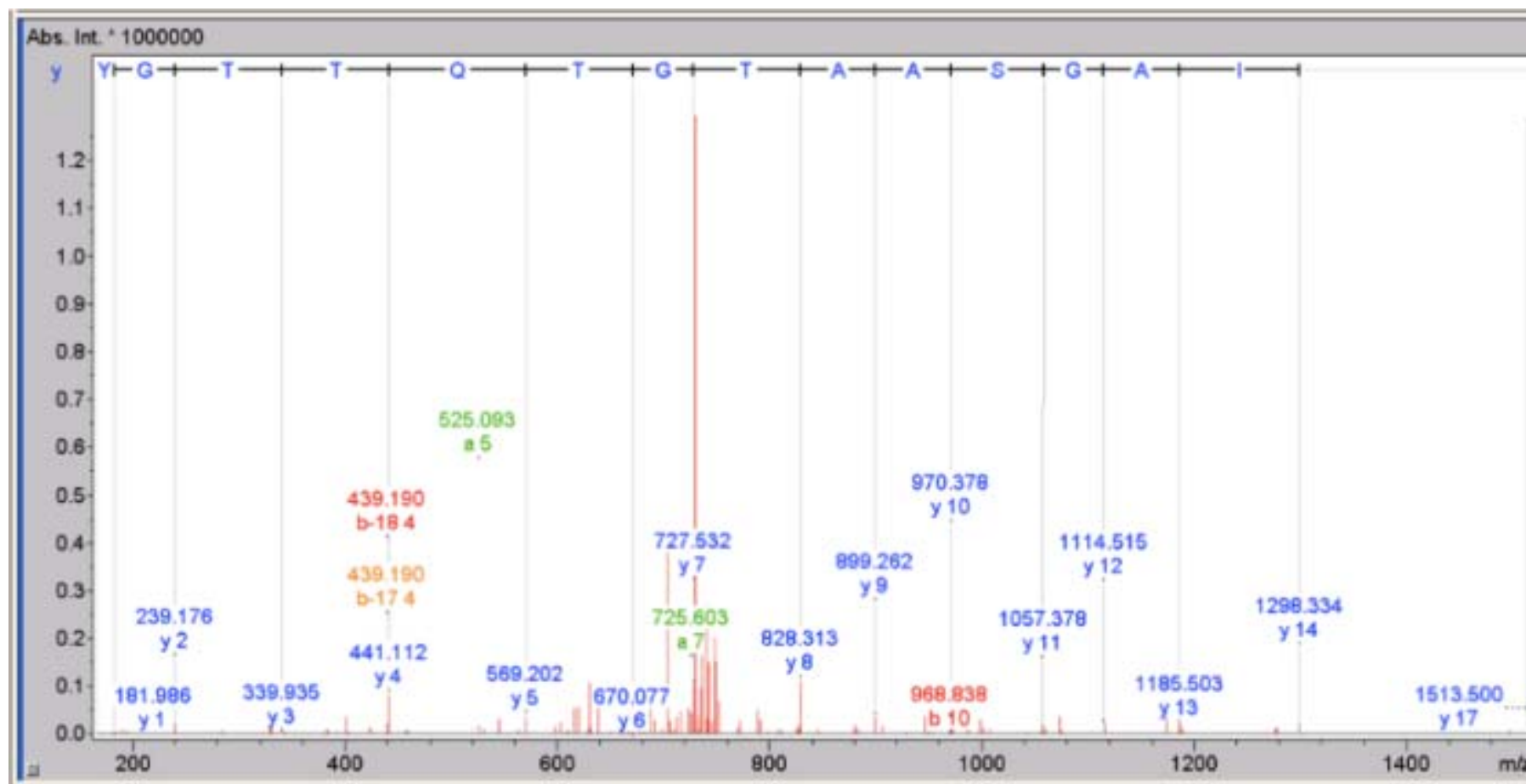
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Ethylation: E66	489.9593	3+
sequence (enzyme/ ion score/ mass error)				
52 K.AGALGVDTLINAVPE*.V Ethylation(E) 66 (Try/54/0.058)				



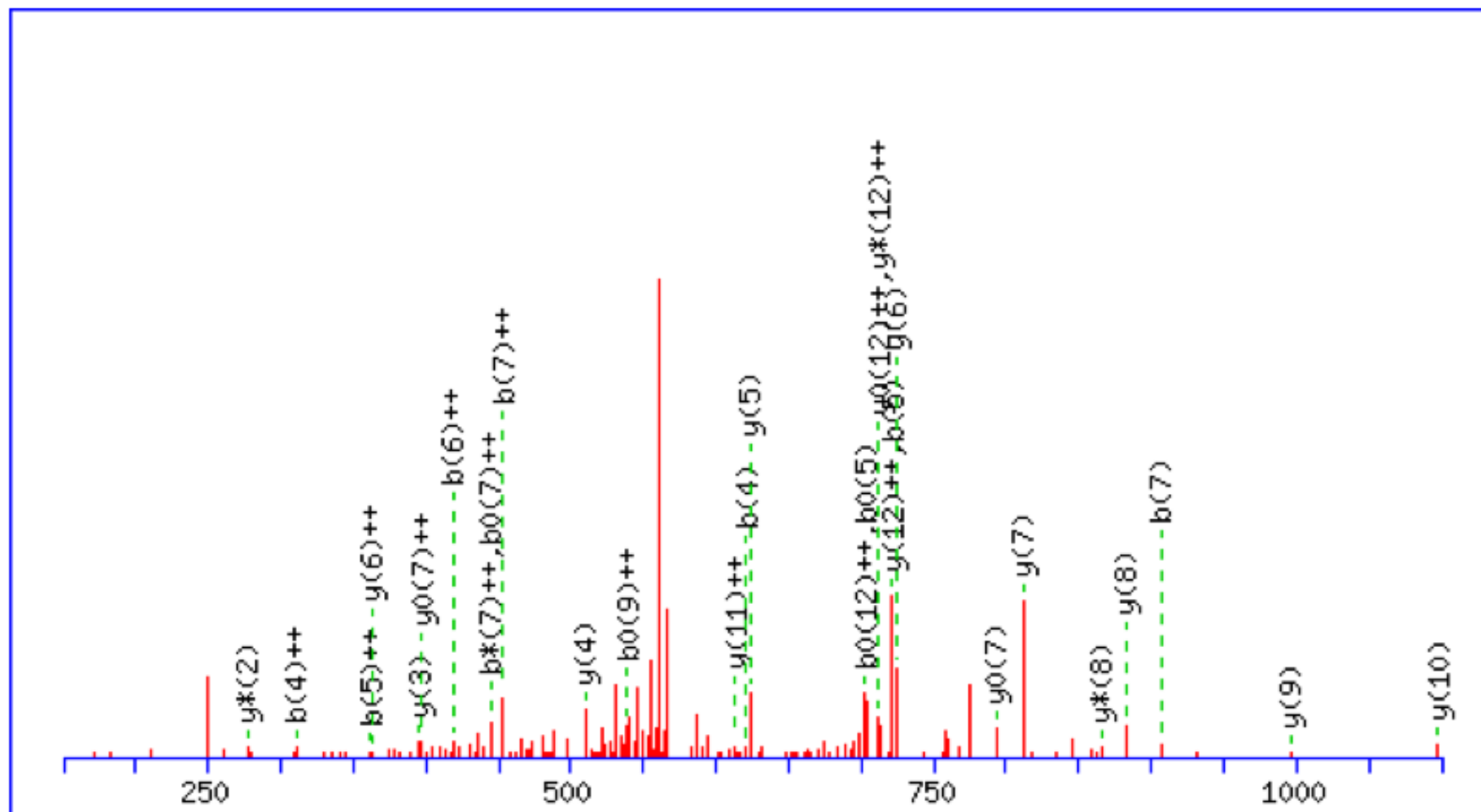
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Formylation: T33	756.0759	3+
sequence (enzyme/ ion score/ mass error)				
27 P.NIVILAT*GGTIAGSAATGTQTTGY.K Formylation(T) 50 (Chy/46/0.057)				



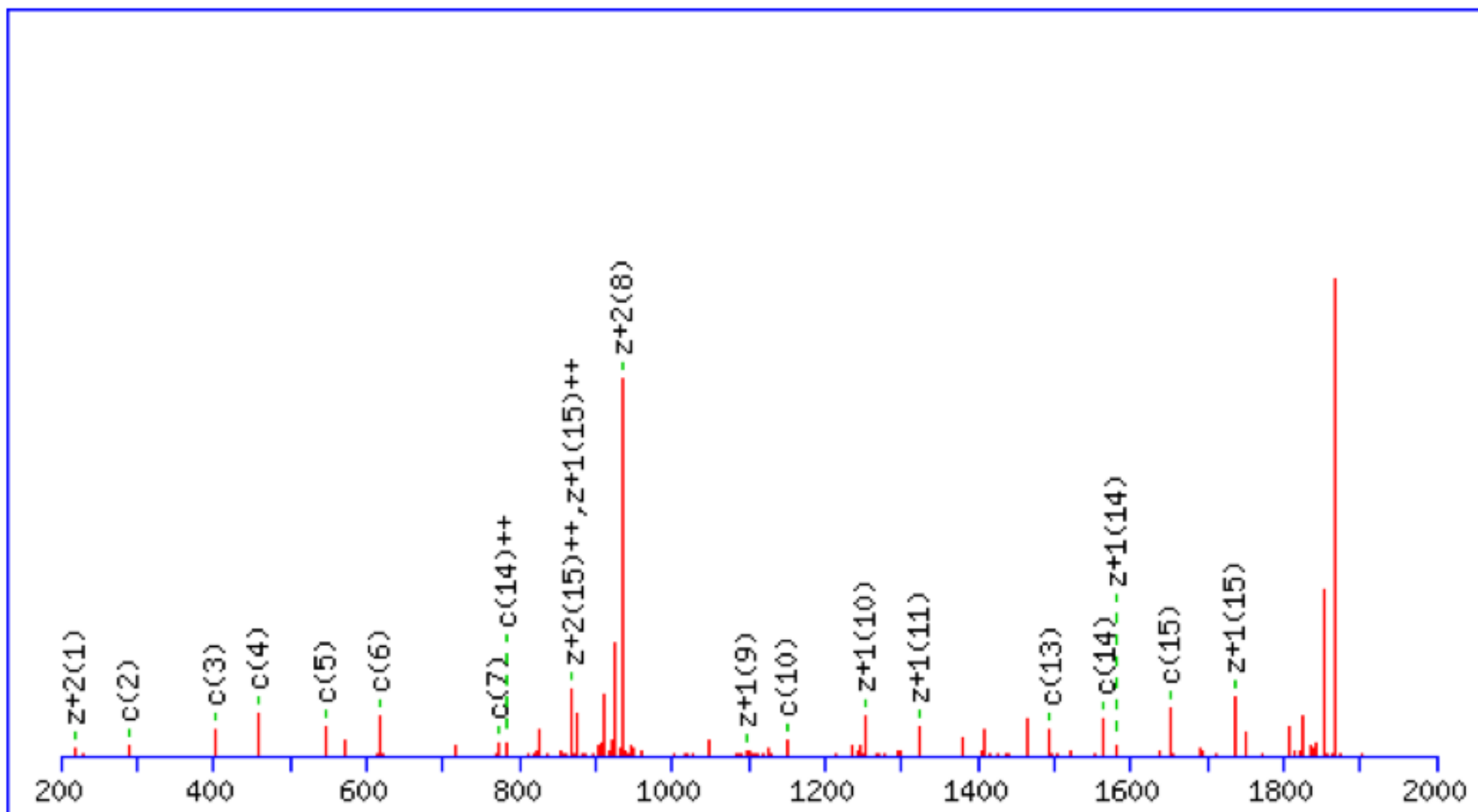
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	GlyGly: T188	572.936	3+
sequence (enzyme/ ion score/ mass error)				
186 R.YIT*KTNASTLDTFK.A GlyGly(T) 199 (Try/35/-0.0868)				



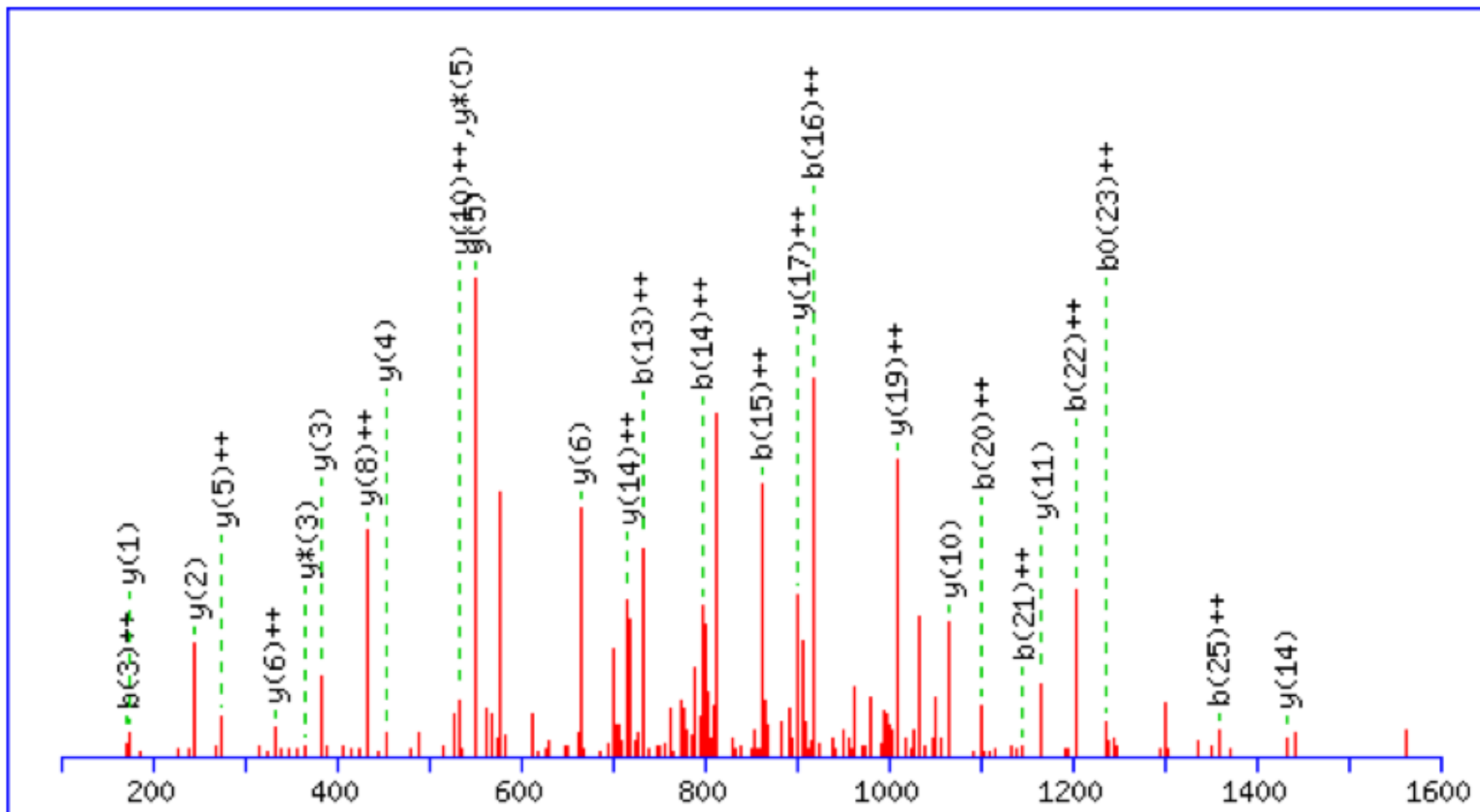
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	GlyGly: T194	623.3178	3+
sequence (enzyme/ ion score/ mass error)				
179 N.DRIGSARYITKTNAST*.L GlyGly(T) 194 (AspN/63/-0.0232)				



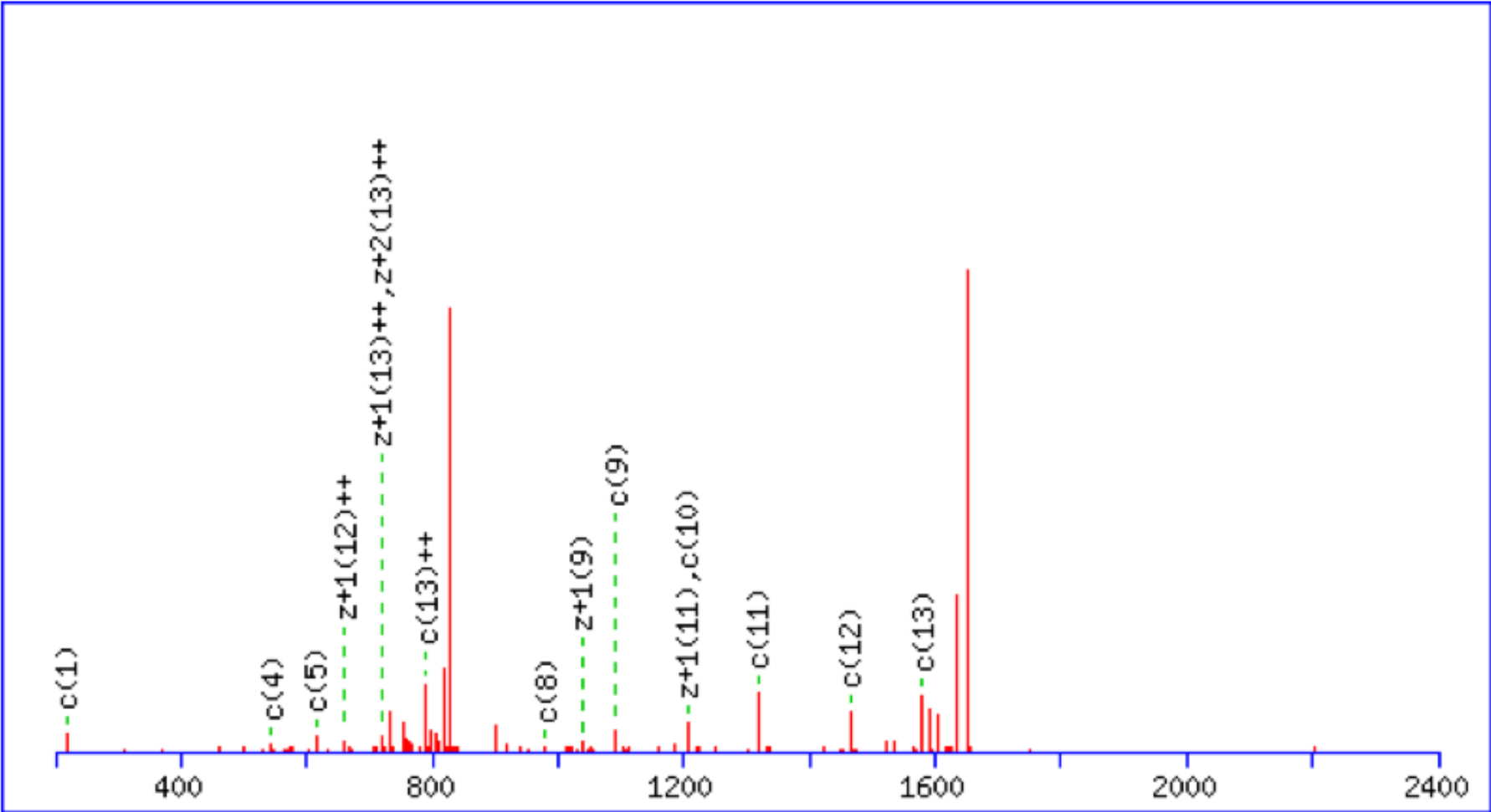
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	GlyGly: T300	818.1625	4+
sequence (enzyme/ ion score/ mass error)				
296 I.RSTRT*GNGIVPPDEELPGLVSDSLNPAHAR.I GlyGly(T) 325 (Chy/76/-0.034)				



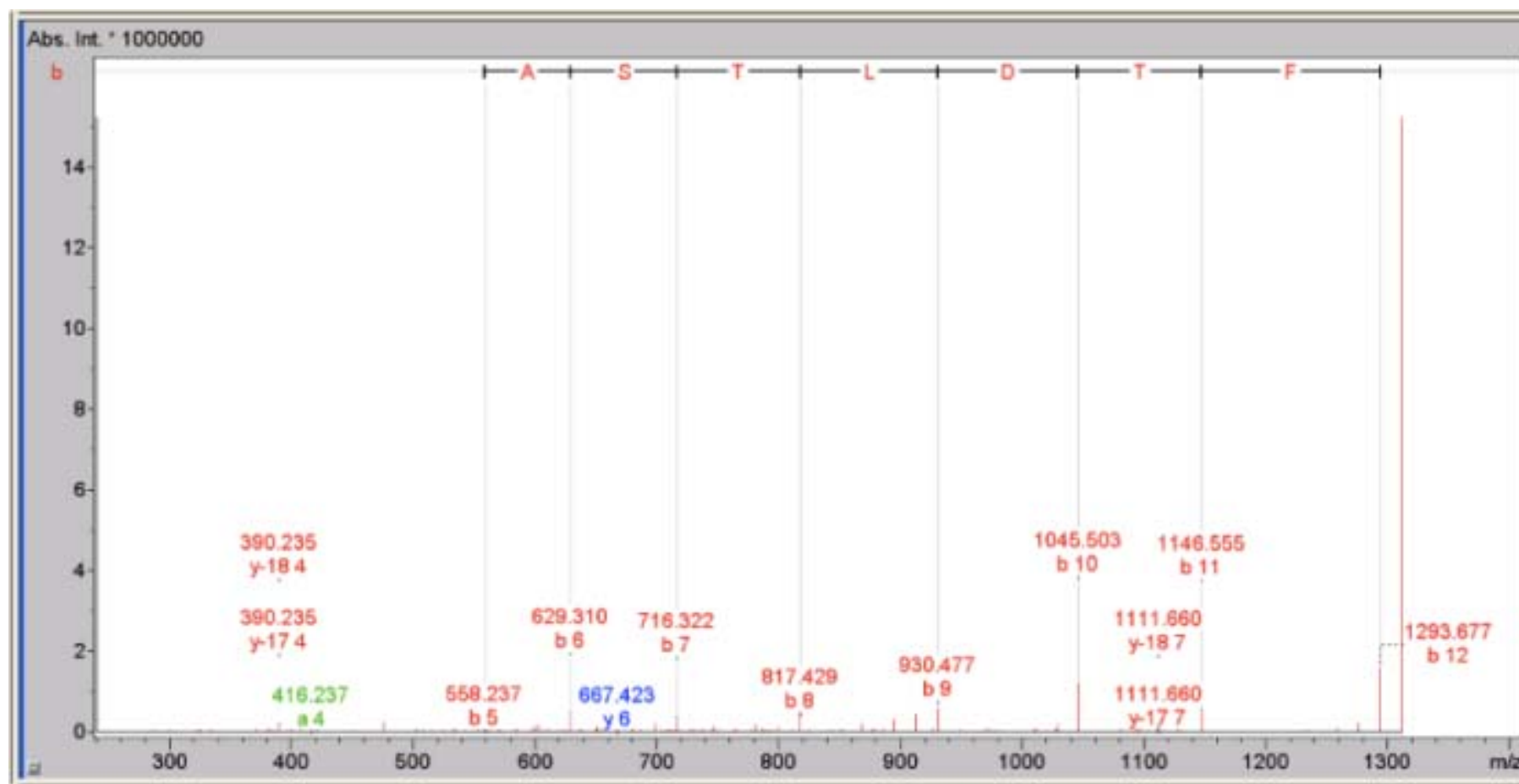
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	GlyGly: S318	550.9958	3+
sequence (enzyme/ ion score/ mass error)				
318 D.S*LN*PAHARILLM*LA.L GlyGly(S) Deamidation(N) Oxidation(M) 331 (AspN/51/0.0733)				



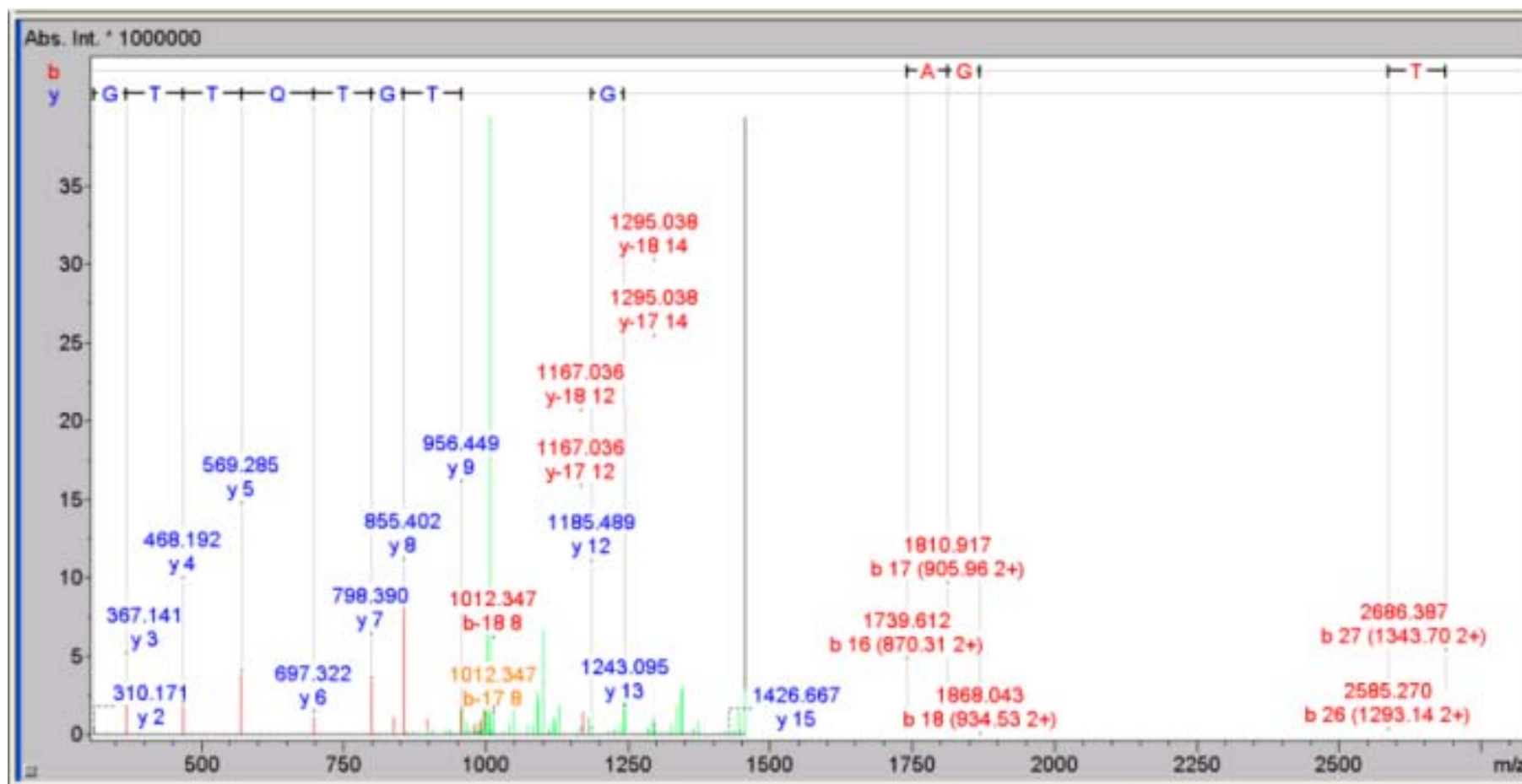
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	HexNAc(1)dHex(1): N201	1311.6093	2+
sequence (enzyme/ ion score/ mass error)				
187 Y.ITKTNASTLDTFKAN*EEGYLG.V HexNAc(1)dHex(1)(N) 207 (Chy/47/-0.0555)				



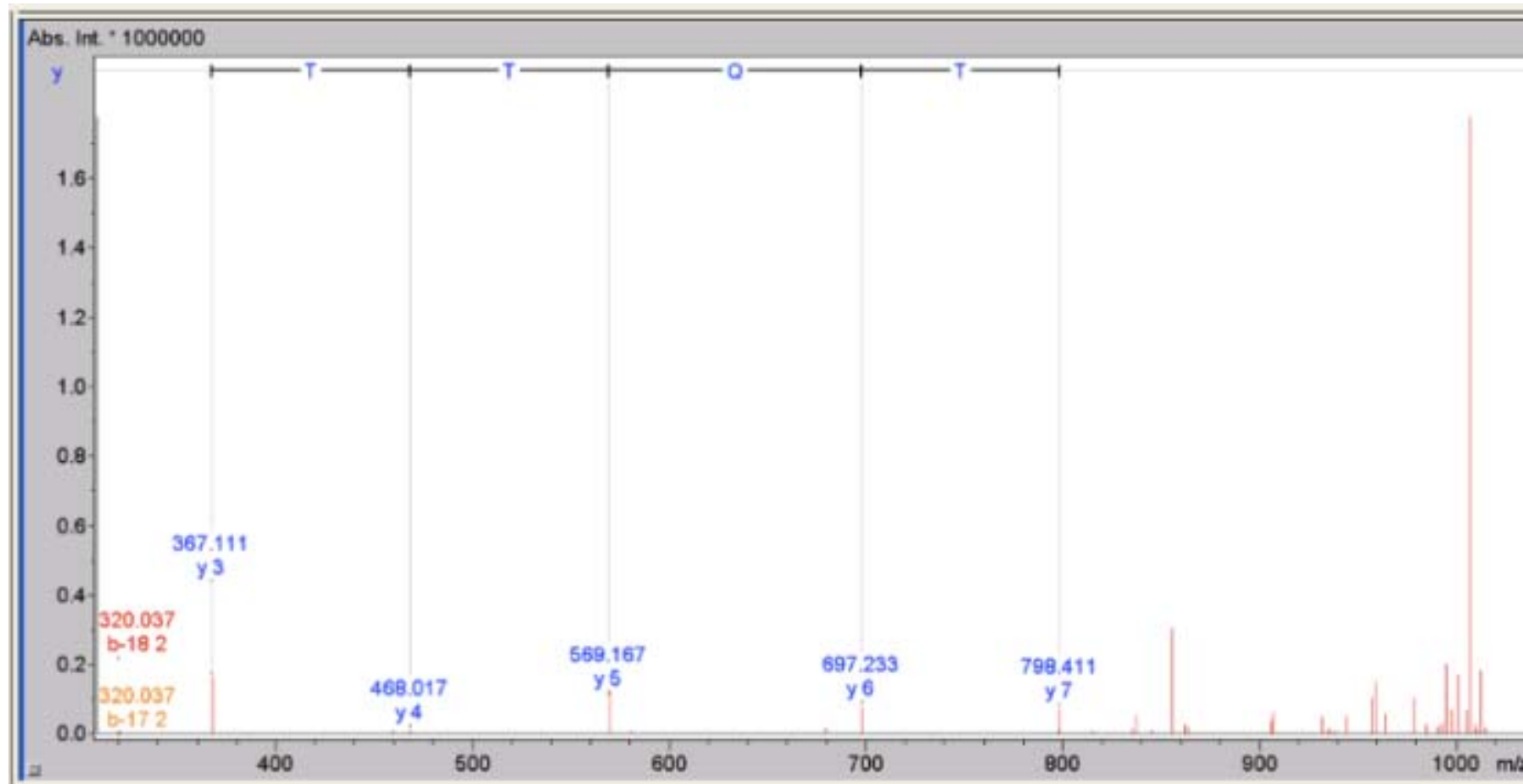
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Hexose: K24	1018.1654	3+
sequence (enzyme/ ion score/ mass error)				
22 A.ADK*LPNIVILATGGTIAGSAATGTQTTGYK.A Hex(K) 51 (Try/75/-0.1232)				



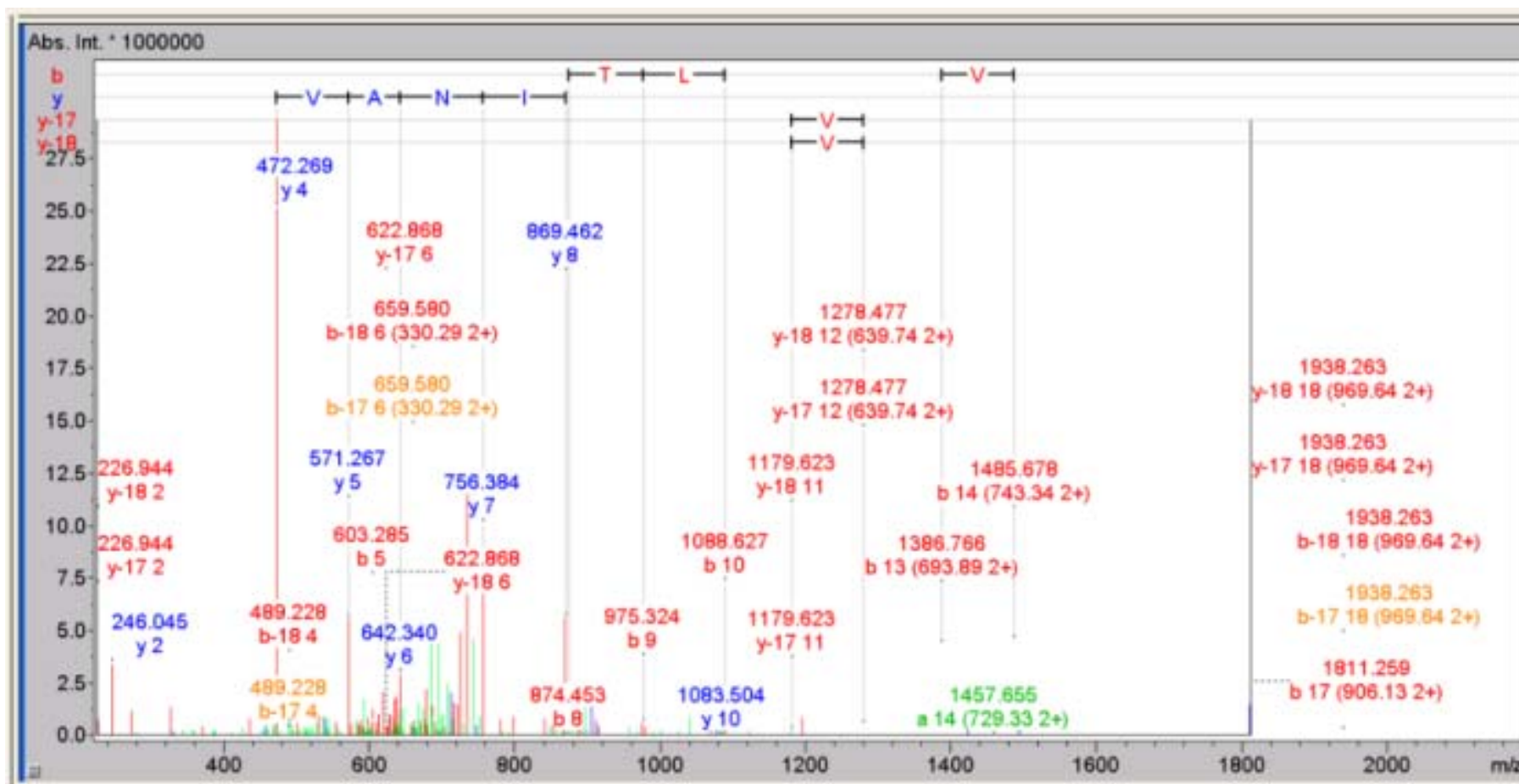
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Hexose: G44	1017.6568	1+
sequence (enzyme/ ion score/ mass error)				
44 T.G*TQTTGYK.A Hex(G) 51 (Try/37/0.1833)				



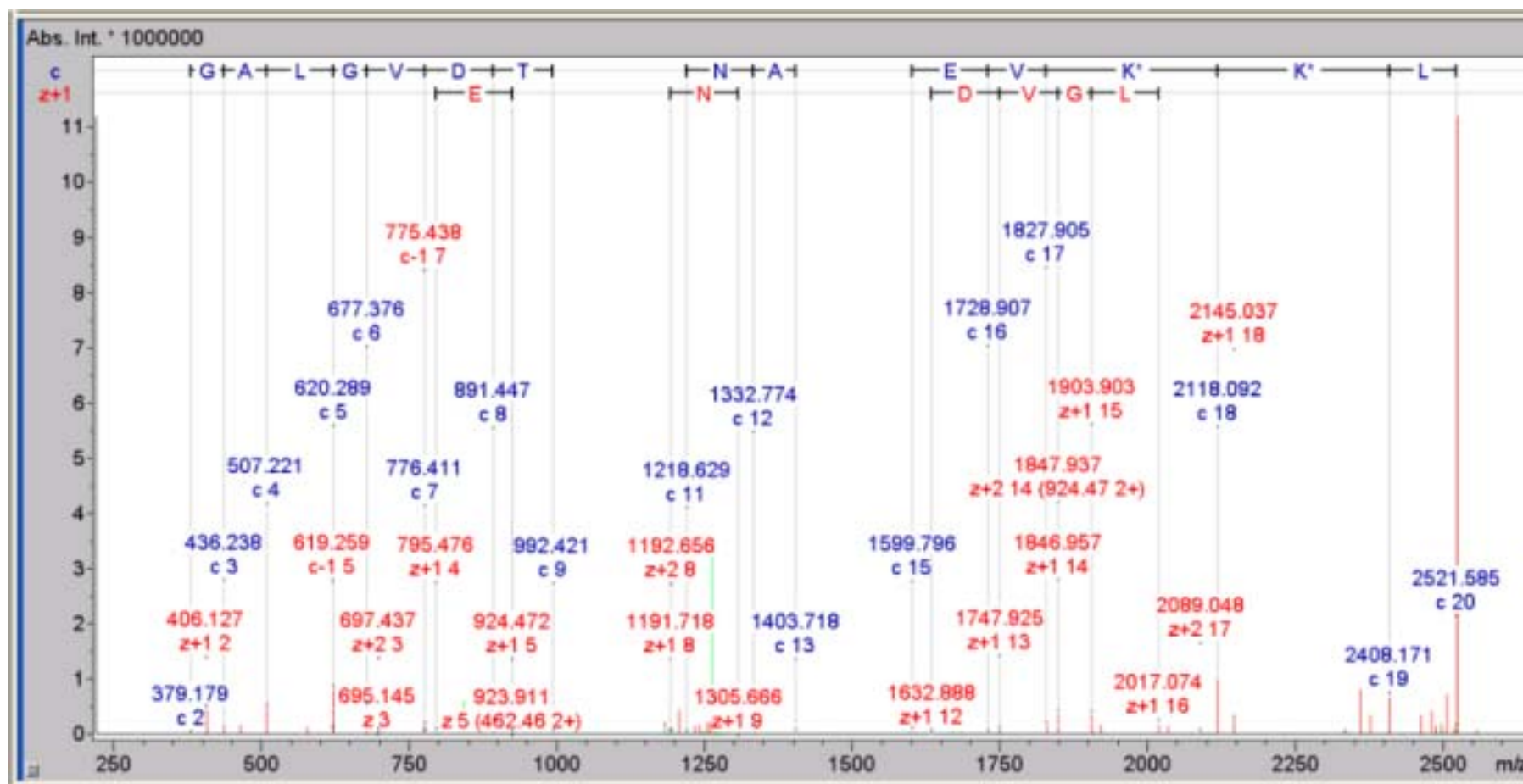
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Hexose: K51	653.0298	3+
sequence (enzyme/ ion score/ mass error)				
51 Y.K*AGALGVDTLINAVPEVK.K Hex(K) 68 (Chy/107/-0.0103)				



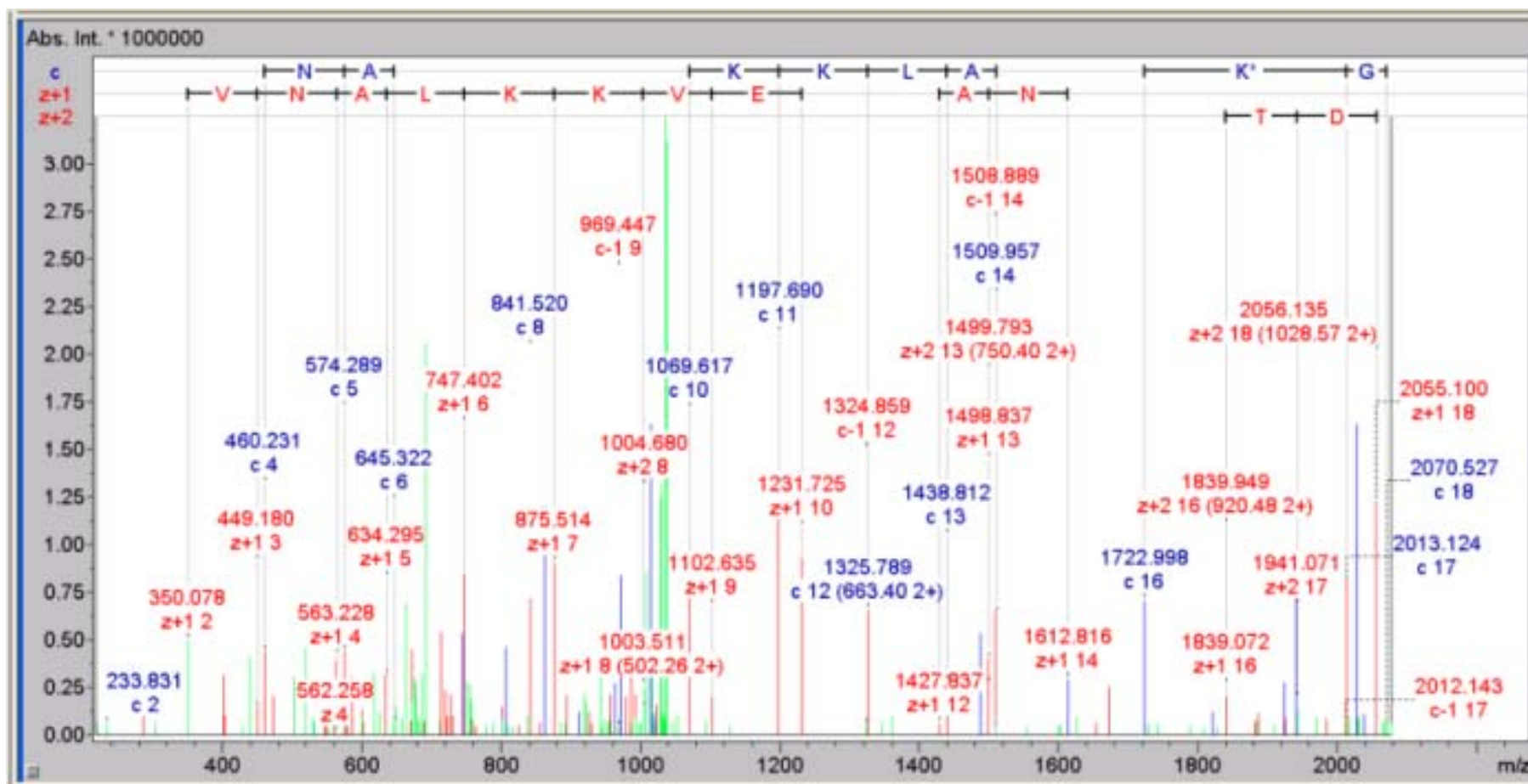
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Hexose: K68	841.4119	3+
sequence (enzyme/ ion score/ mass error)				
51 Y.K*AGALGVDTLINAVPEVK*K*L.A 3 Hex(K) 70 (Chy/77/-0.1487)				



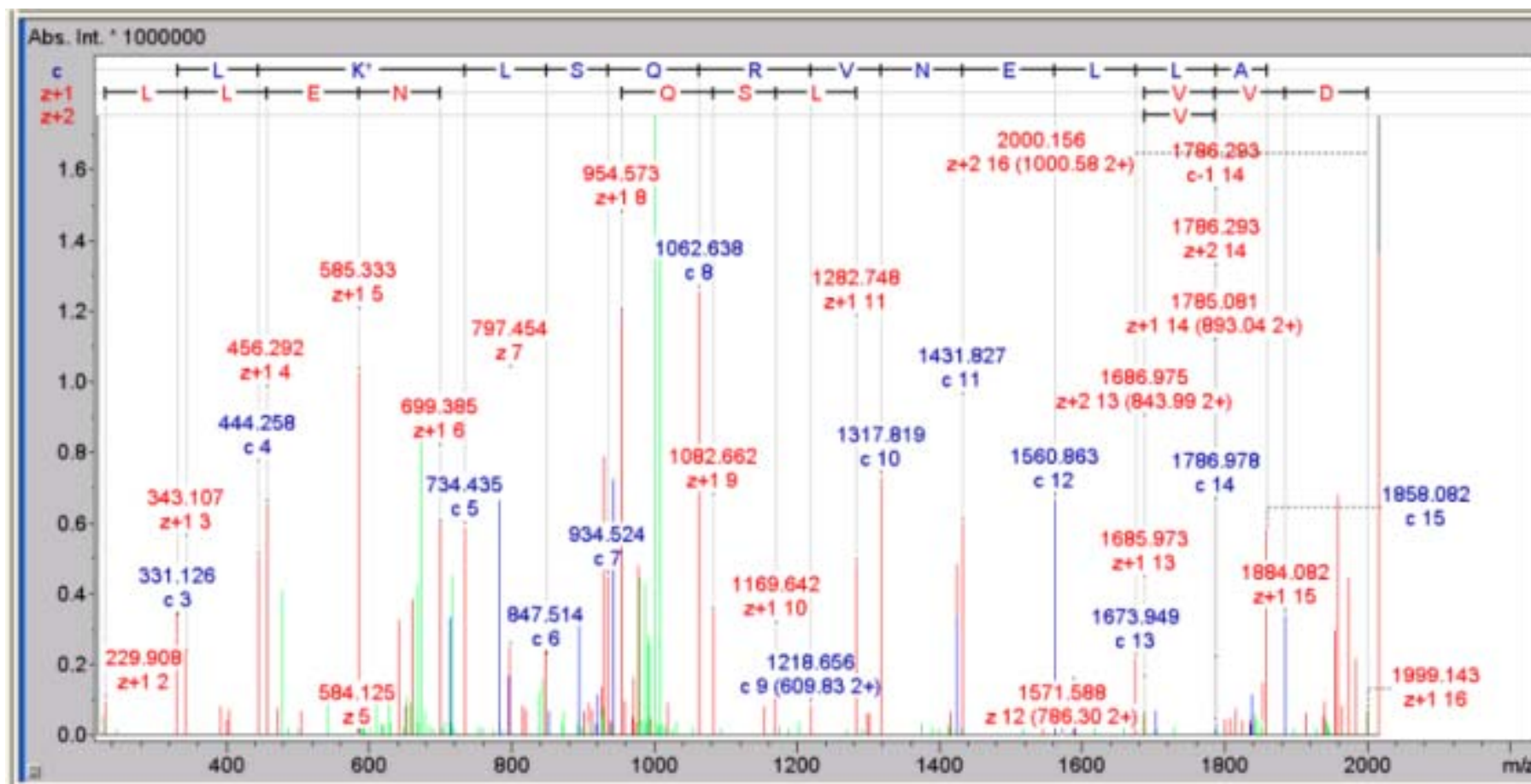
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Hexose: K74	518.5601	4+
sequence (enzyme/ ion score/ mass error)				
58 V.DTLINAVPEVKKLANVK*G.E Hex(K) 75 (AspN/58/0.0541)				



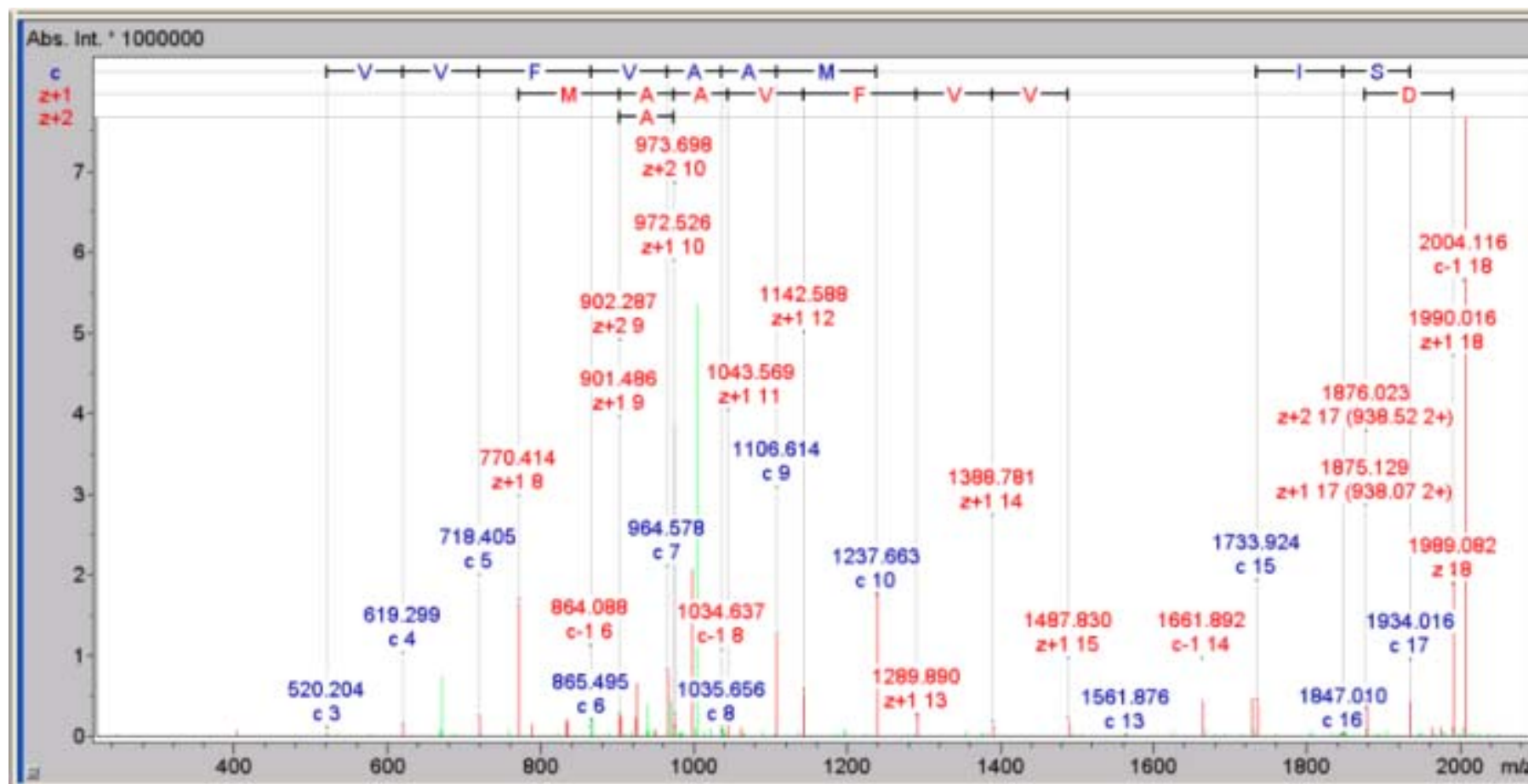
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Hexose: K93	504.5236	4+
sequence (enzyme/ ion score/ mass error)				
89 G.DVVLK*LSQRVNELLAR.D Hex(K) 104 (AspN/94/-0.0769)				



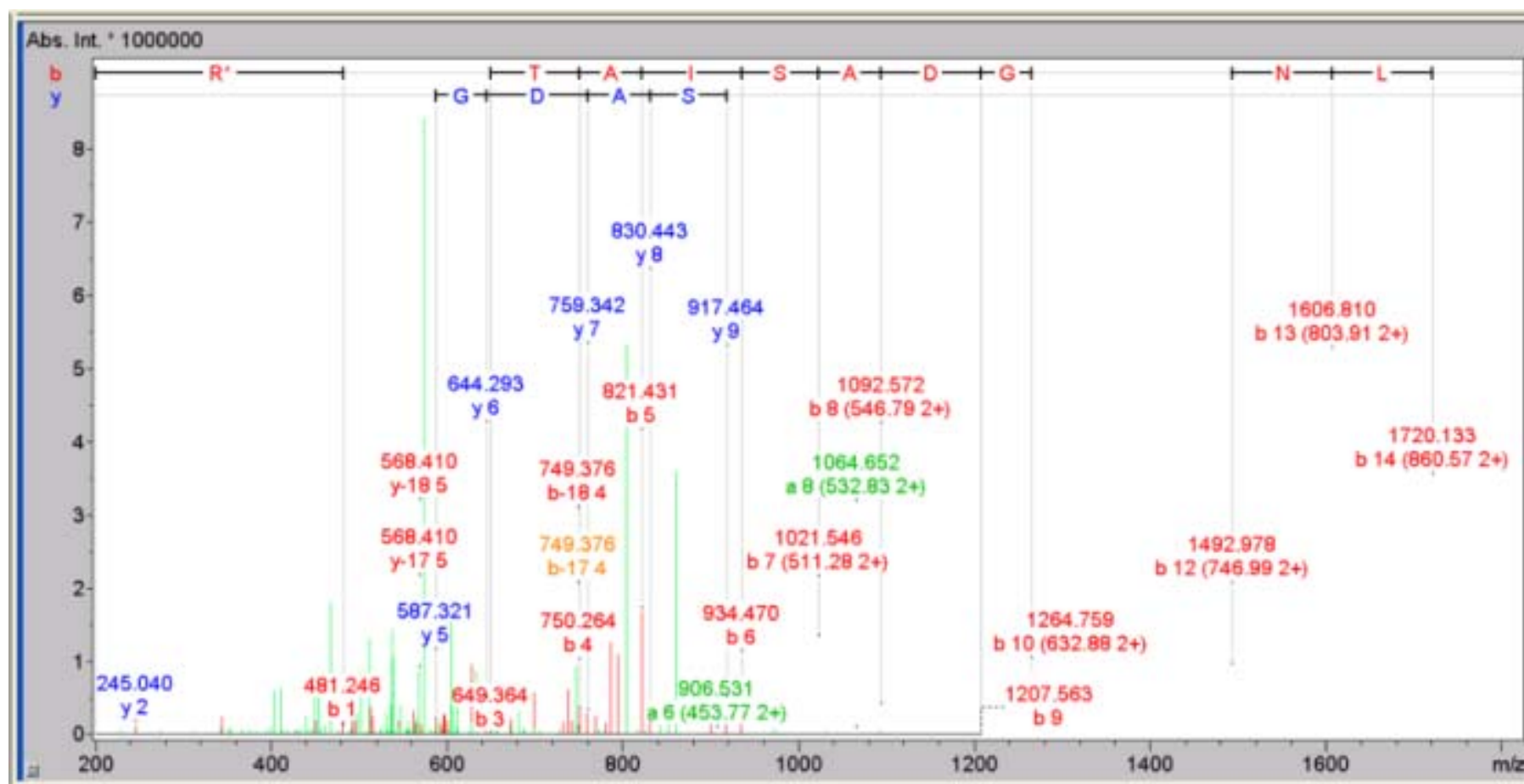
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Hexose: K134	669.3982	3+
sequence (enzyme/ ion score/ mass error)				
133 S.DK*PVVFVAAMRPATAISA.D Hex(K) 150 (AspN/51/0.1174)				



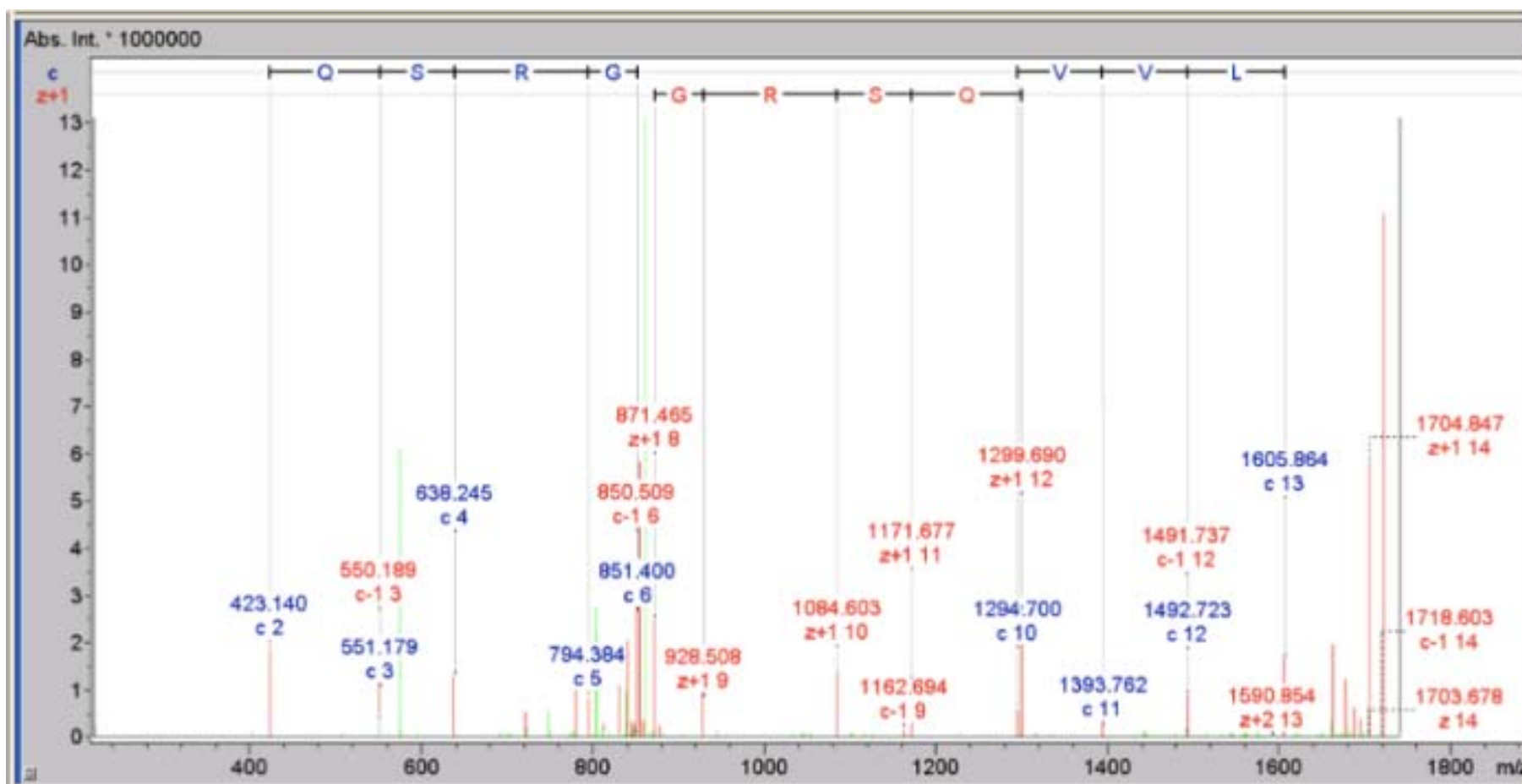
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Hexose: R143	617.6369	3+
sequence (enzyme/ ion score/ mass error)				
143 M.R*PATAISADGPMNLL.E Hex(2)(R) 157 (Chy/68/-0.009)				



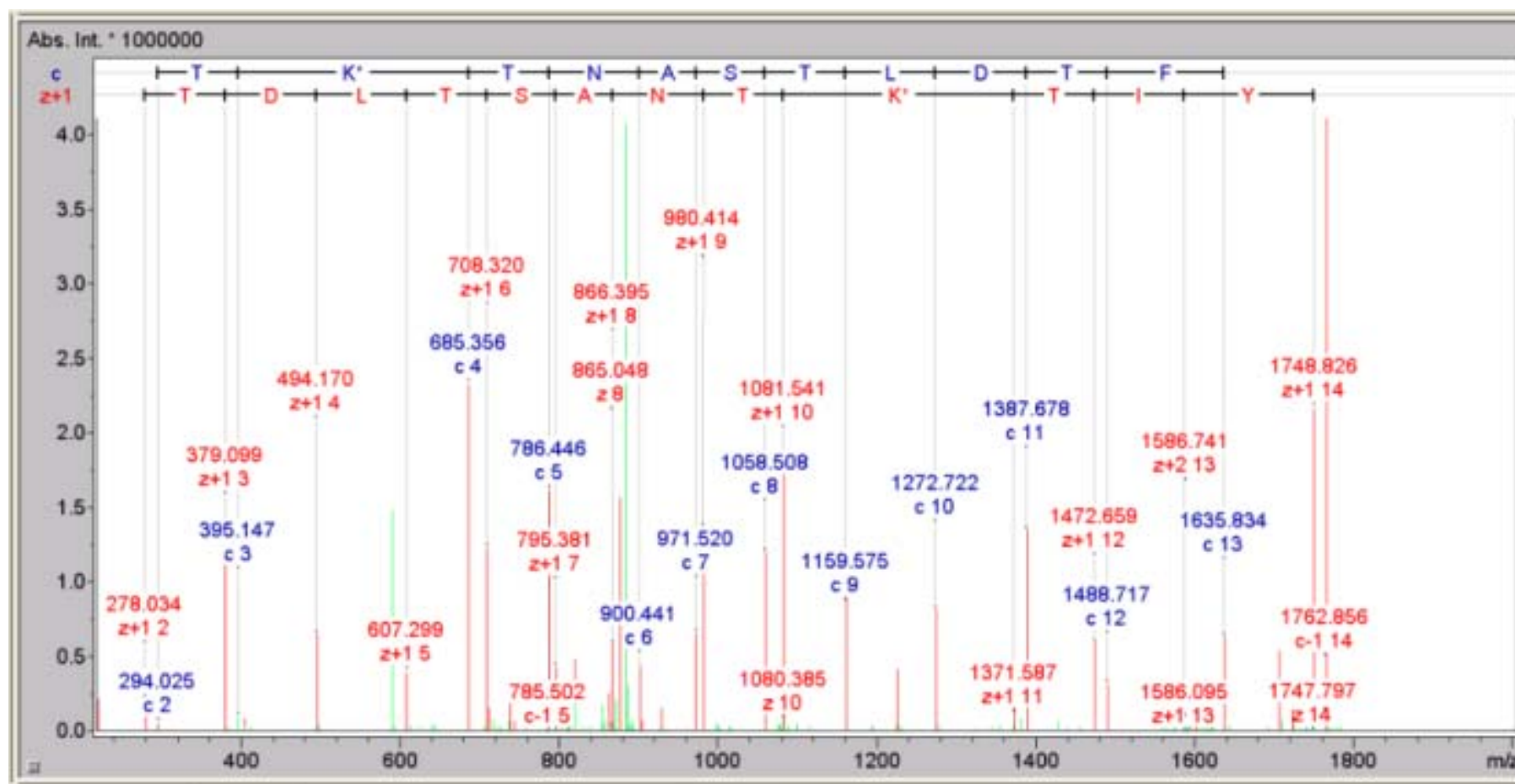
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Hexose: K166	574.2772	3+
sequence (enzyme/ ion score/ mass error)				
165 G.DK*QSRGRGVMVVLN.D Hex(K) 178 (AspN/44/-0.084)				



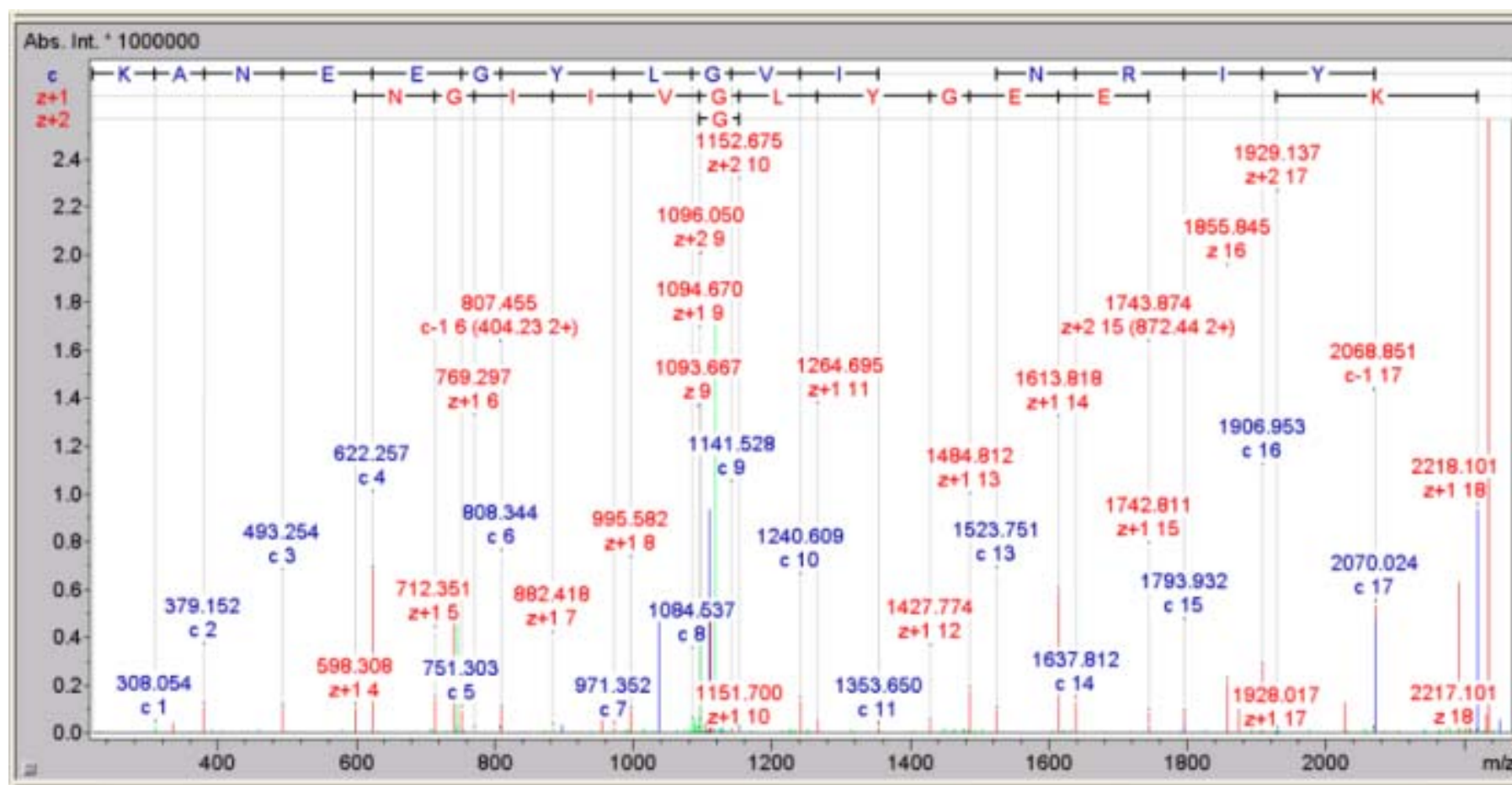
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Hexose: K189	588.9589	3+
sequence (enzyme/ ion score/ mass error)				
186 R.YITK*TNASTLDTFK.A Hex(K) 199 (Try/81/-0.028)				



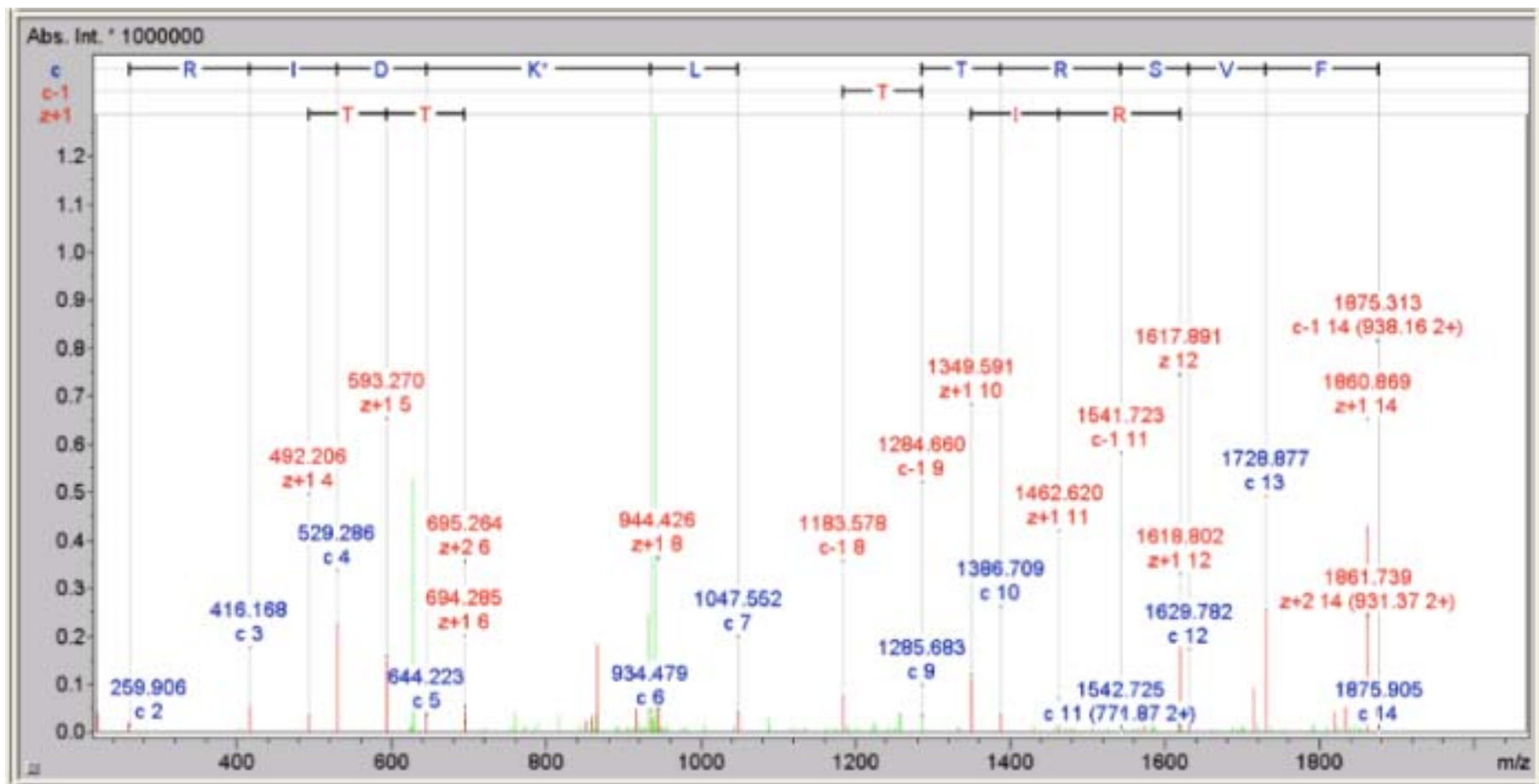
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Hexose: K199	745.364	3+
sequence (enzyme/ ion score/ mass error)				
199 F.K*ANEEGYLGVIIGNRIYY.Q Hex(K) 216 (Chy/91/-0.0564)				



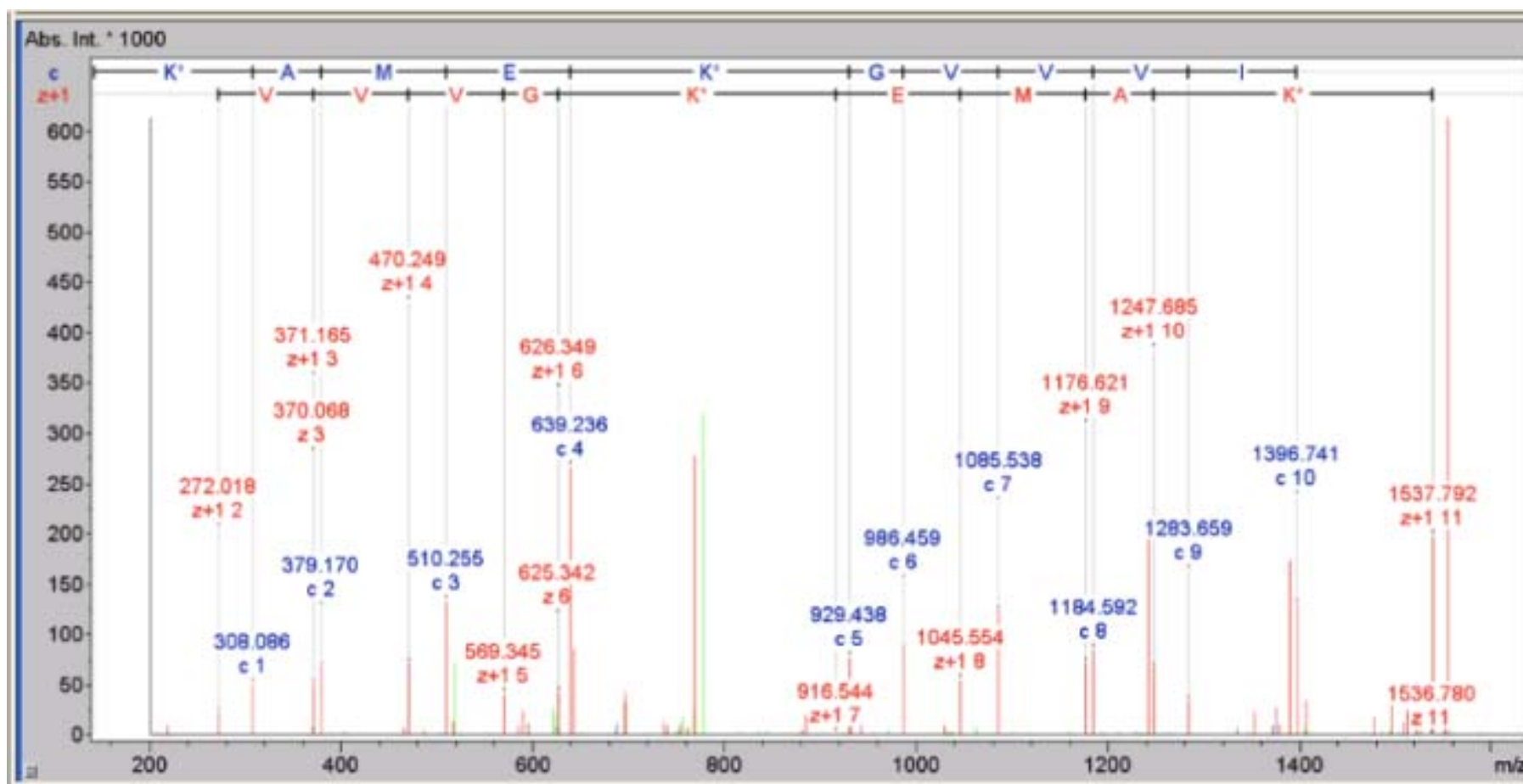
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Hexose: K222	626.2912	3+
sequence (enzyme/ ion score/ mass error)				
217 Y.QNRIDK*LHTTRSVF.D Hex(K) 230 (Chy/50/-0.1285)				



Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Mascot	Hexose: K286, K290	518.5749	3+
sequence (enzyme/ ion score/ mass error)				
286 R.K*AMEK*GVVVIR.S 2 Hex(K) 296 (Try/62/-0.1353)				



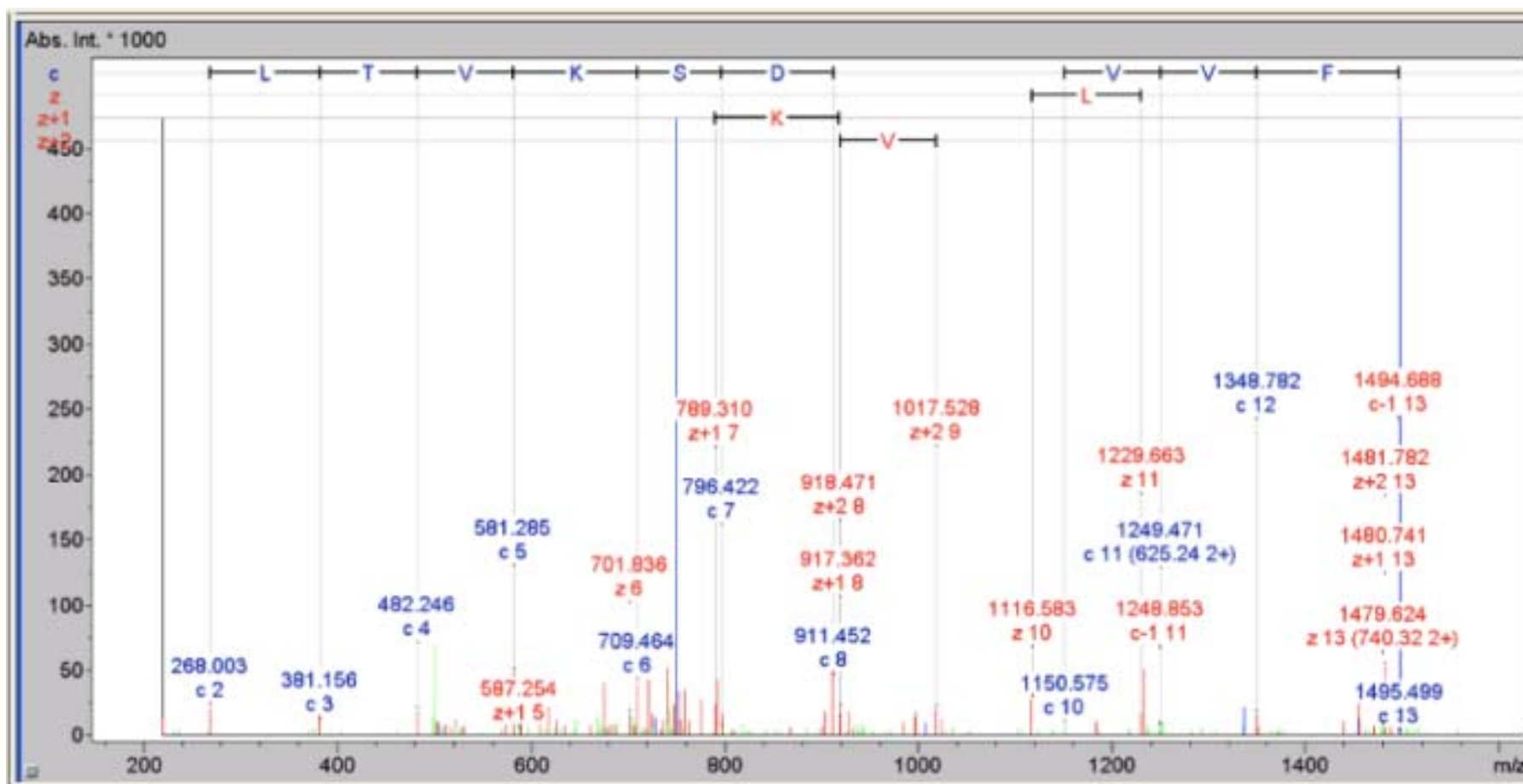
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Pro->pyro-Glu: P65	840.9384	2+
sequence (enzyme/ ion score/ mass error)				
52 K.AGALGVDTLINAVP*EVK.K Pro->pyro-Glu(P) 68 (Try/72/-0.0471)				



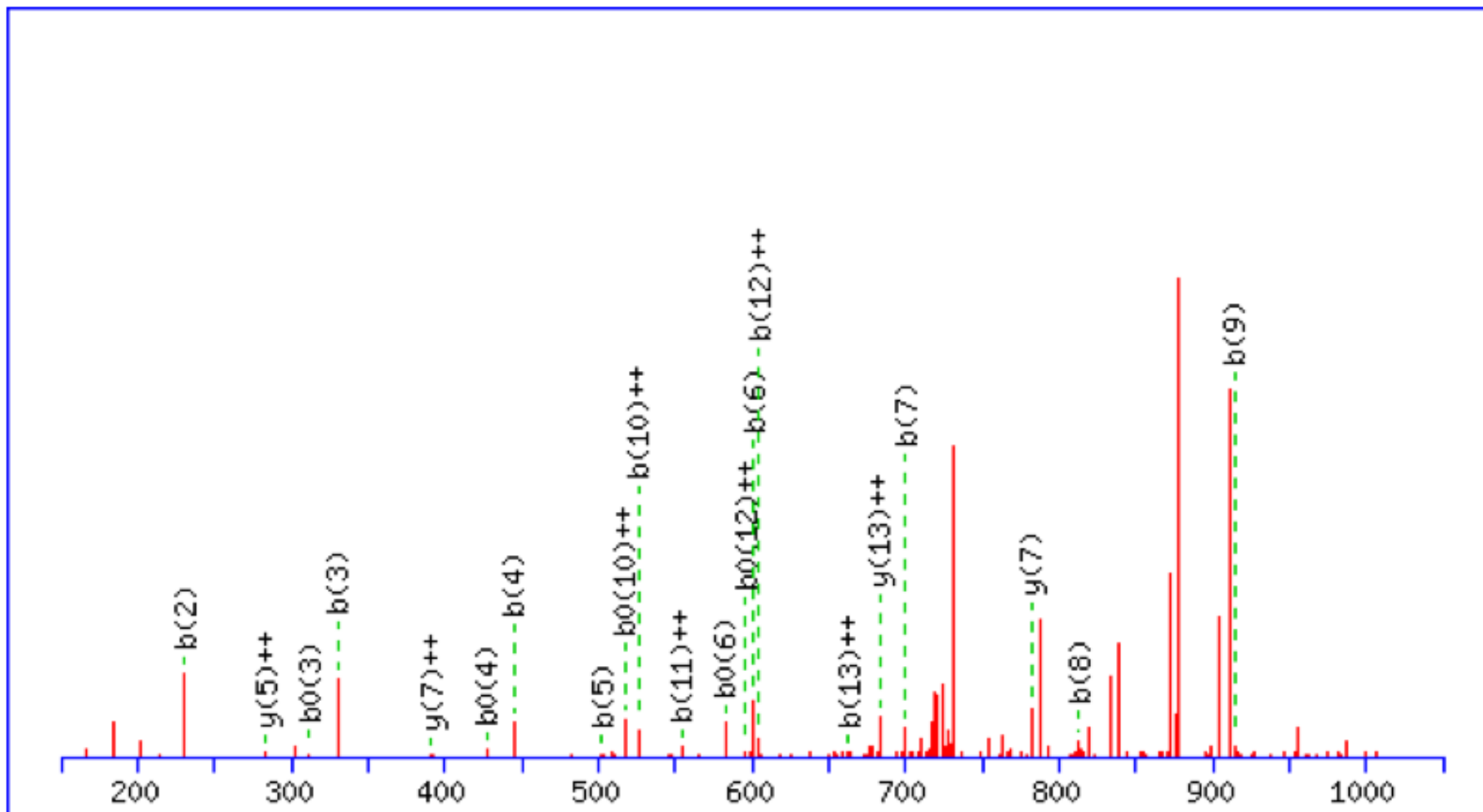
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Pro->pyro-Glu: P135	499.6122	3+
sequence (enzyme/ ion score/ mass error)				
126 F.LHLTVKSDKP*VVF.V Pro->pyro-Glu(P) 138 (Chy/45/-0.0251)				



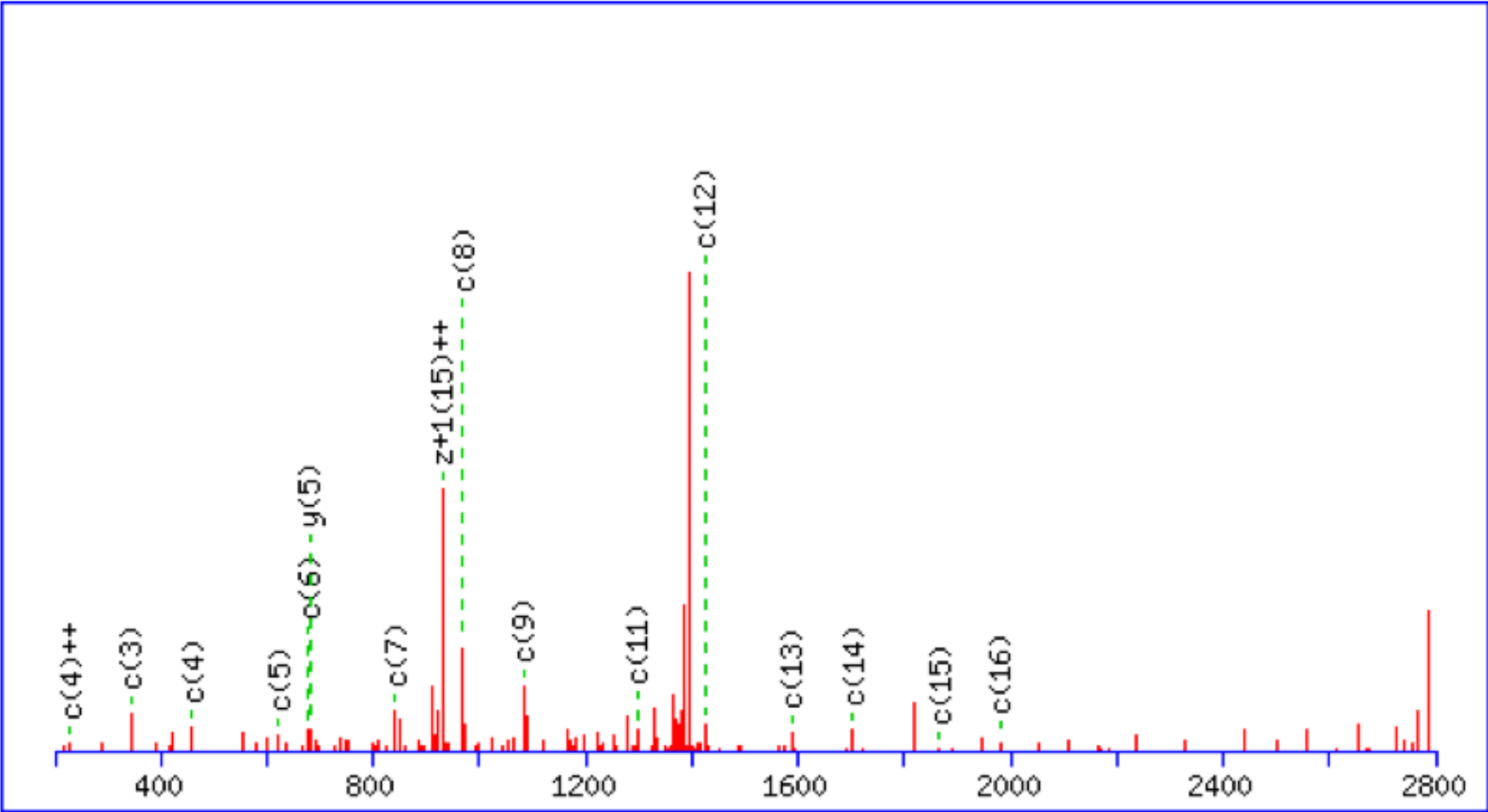
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Propargylamine: T118	740.837	2+
sequence (enzyme/ ion score/ mass error)				
105 R.DDVDGVVITHGTD*.V Propargylamine(T) 118 (Try/34/-0.0248)				



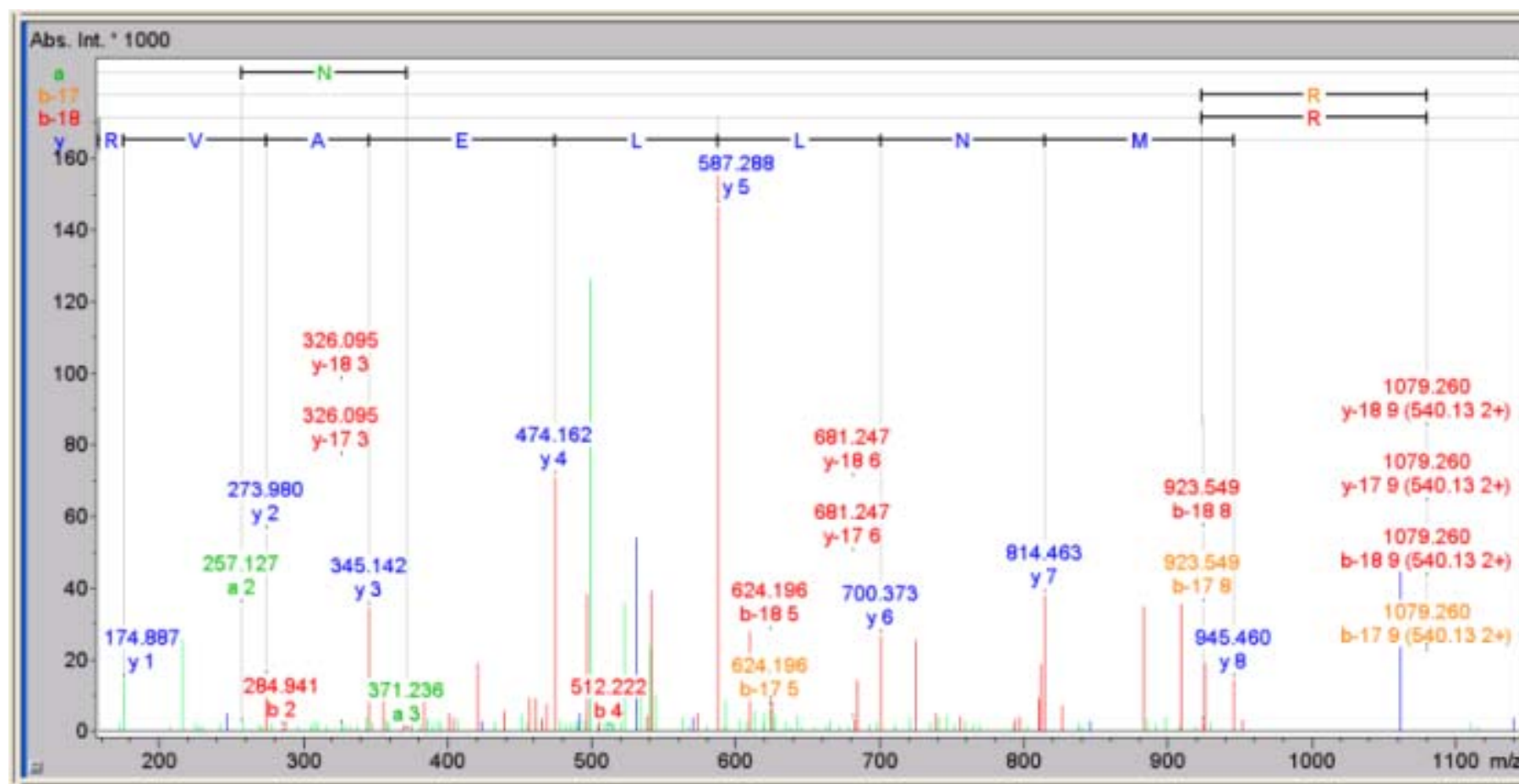
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Propargylamine: A257	696.9841	3+
sequence (enzyme/ ion score/ mass error)				
241 K.VDILYGYQDDPEYLYDA*.A Propargylamine(A) 257 (Try/49/-0.0059)				



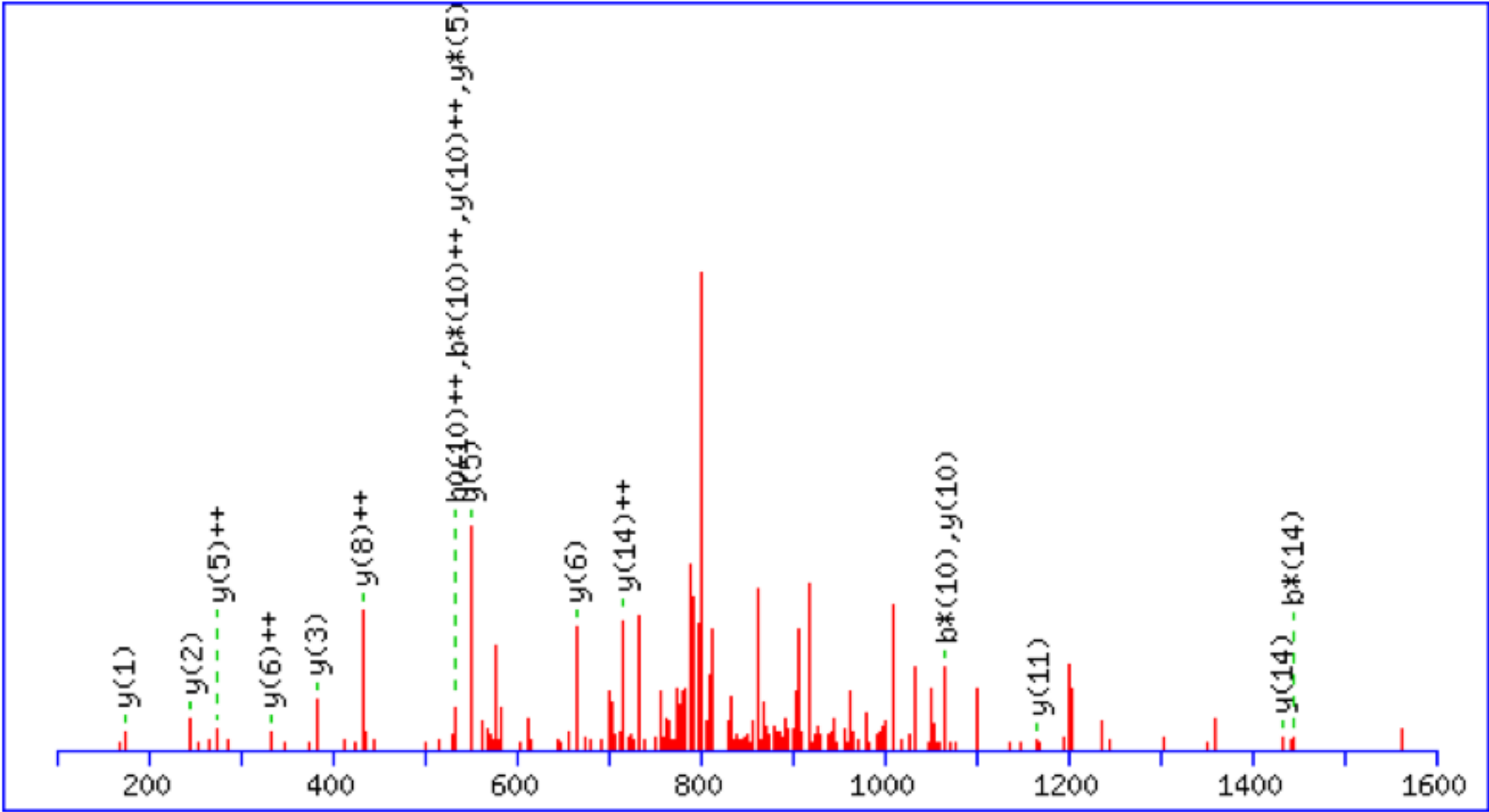
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	Propionyl: P153	549.7854	2+
sequence (enzyme/ ion score/ mass error)				
153 G.P*MNLLEAVR.V Propionyl(P) 161 (Try/44/-0.034)				



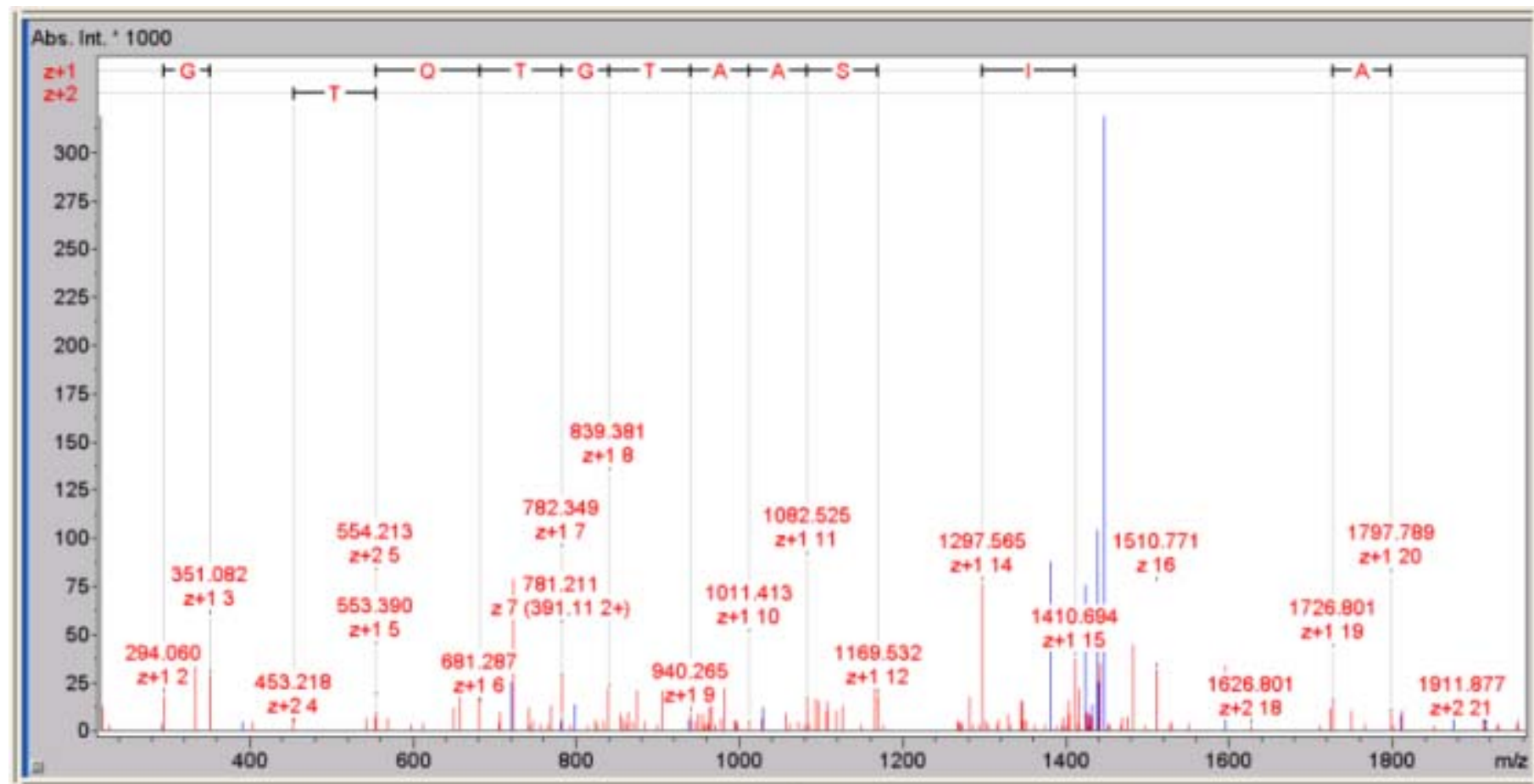
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Mascot	Thioacyl: L311	817.9049	2+
sequence (enzyme/ ion score/ mass error)				
311 E.L*PGLVSDSLNPAHAR.I Thioacyl(L) 325 (Chy/40/-0.0294)				



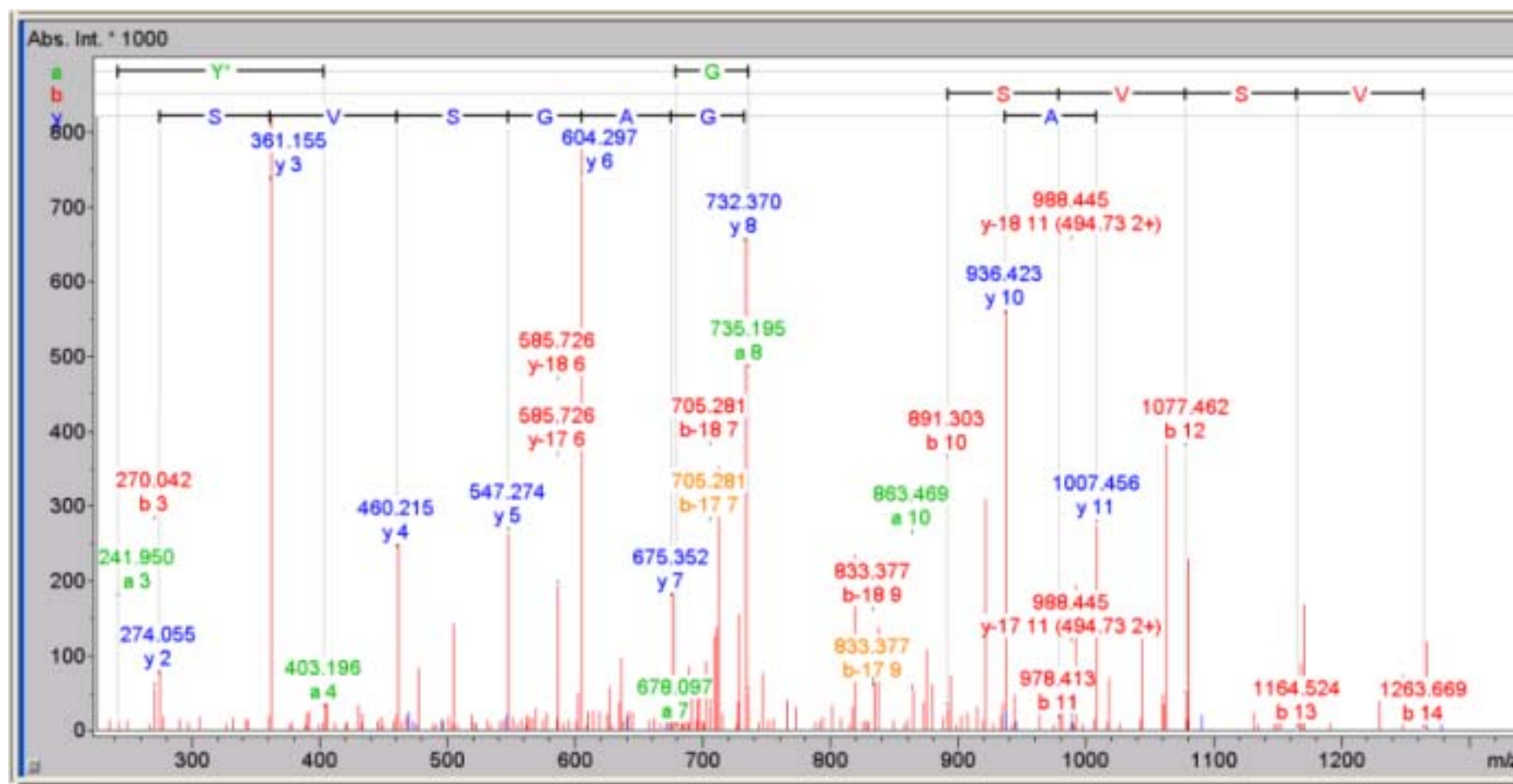
Mascot/ pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Mascot	TMAB: I30	723.3426	3+
sequence (enzyme/ ion score/ mass error)				
30 V.I*LATGGTIAGSAATGTQTTGYK.A TMAB(I) 51 (Try/52/-0.1551)				



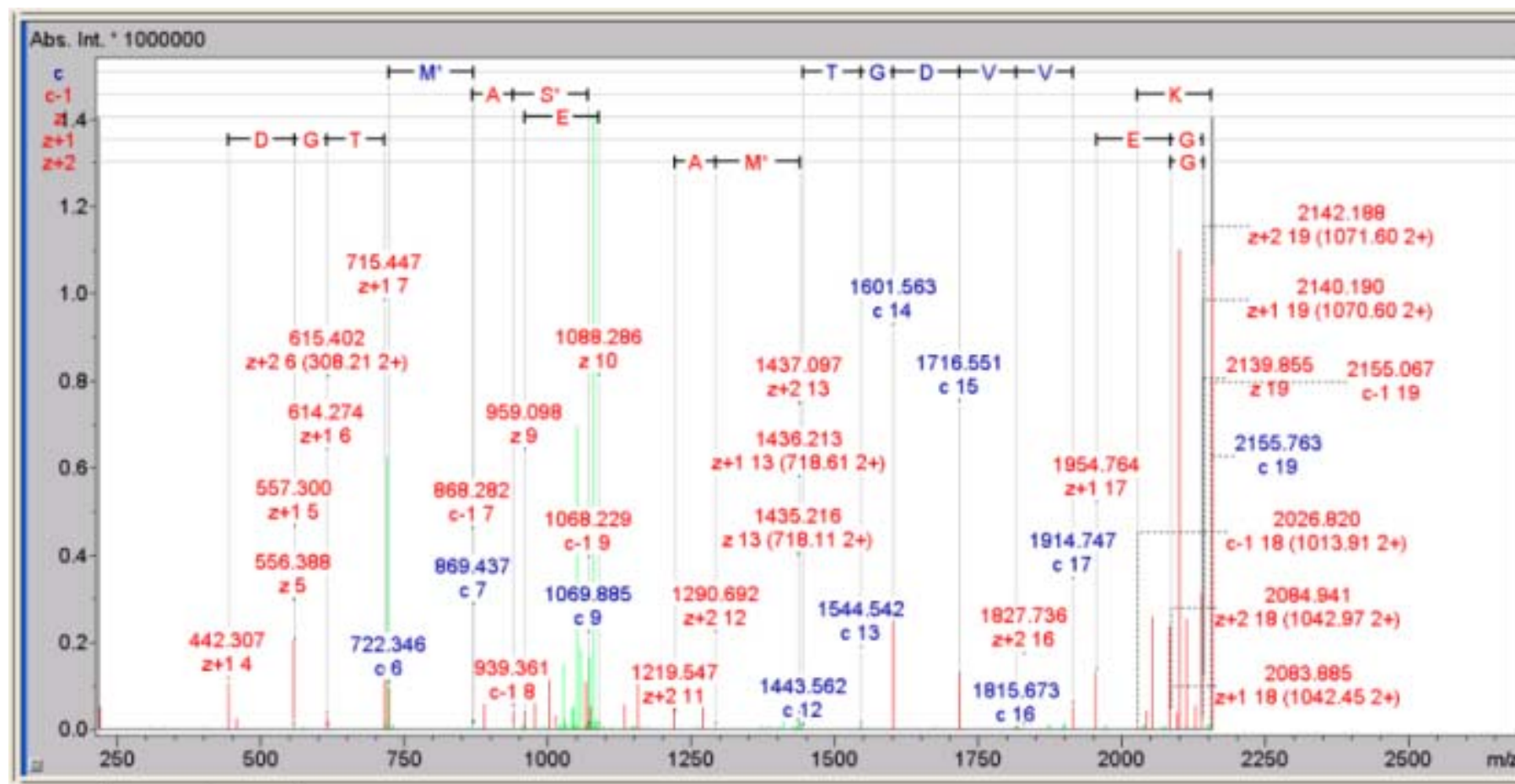
Modiro/ Untreated / L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Modiro	2-amino-3-oxo-butanoic_acid: Y268	719.33	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
265 K.GIVY*AGM*GAGSVSVR.G 2-amino-3-oxo-butanoic_acid(Y) Oxidation(M) 279 (Try/CID/313/98.8/-0.0314)				



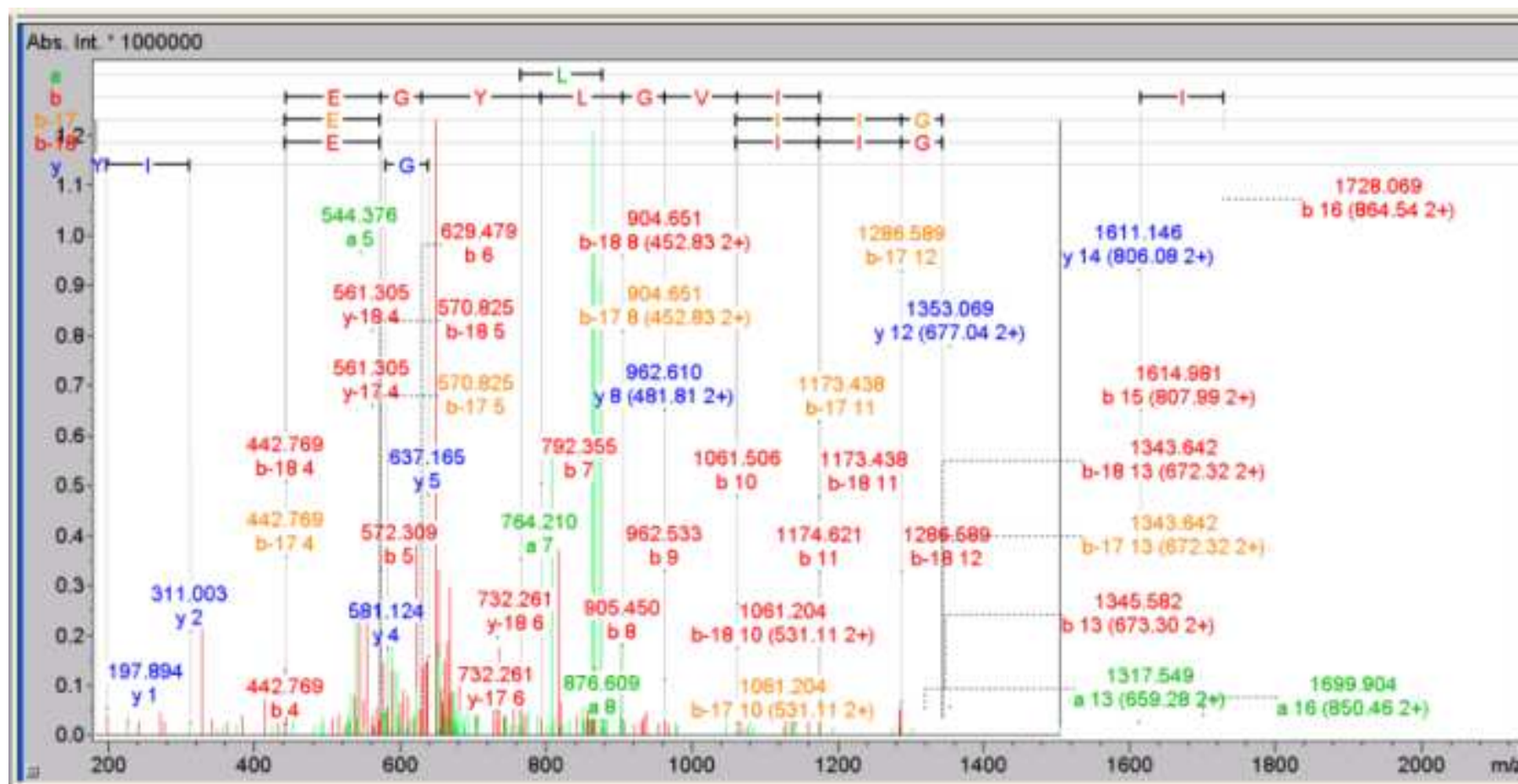
Modiro/ Untreated / L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Modiro	Acetylation: S79, S83	719.61	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
75 K.GEQFS*NM*AS*ENMTGDVVLK.L 2 Acetylation(S) Oxidation(M) 93 (Try/ETD/372/93.6/-0.044)				



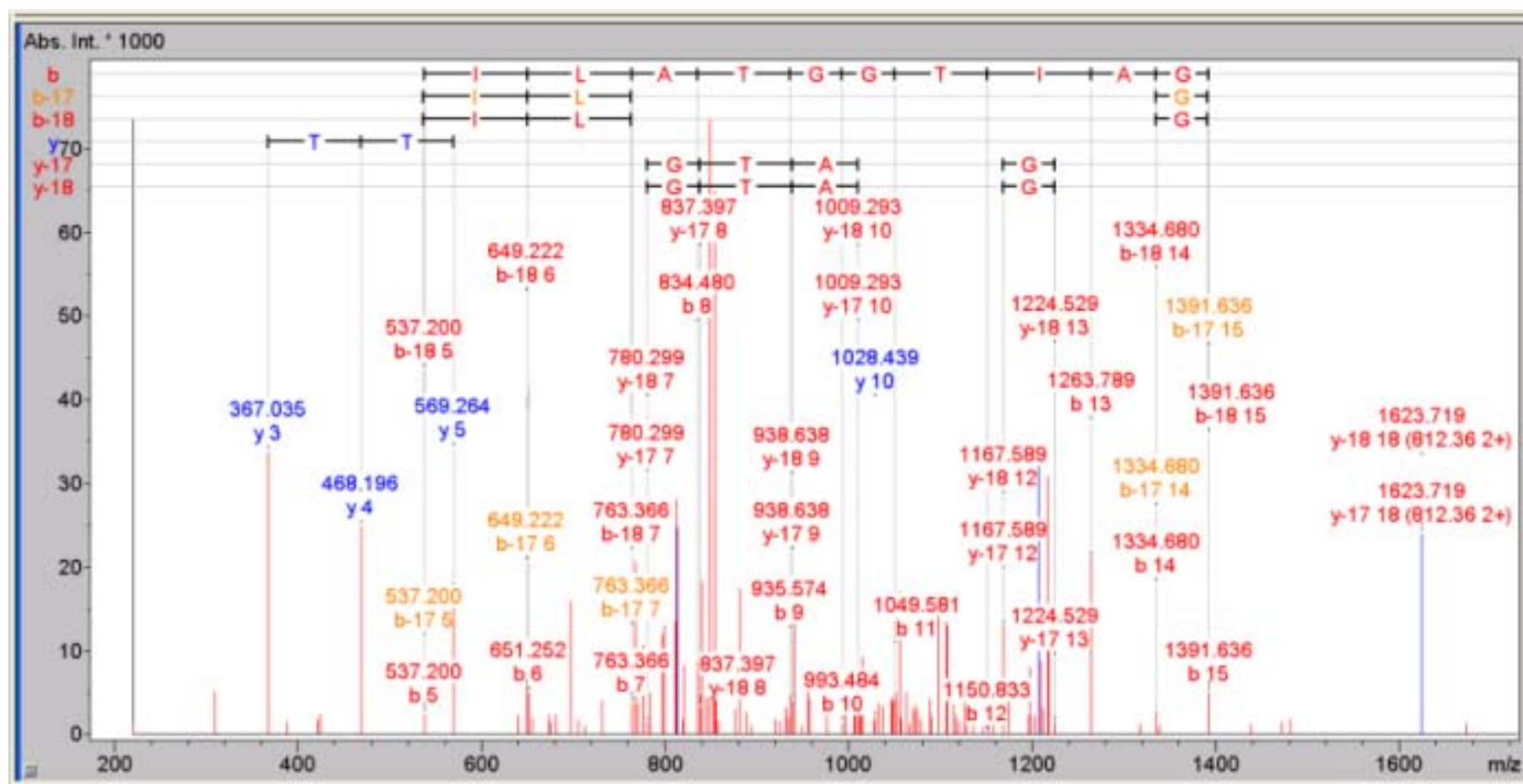
Modiro/ Untreated / L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Modiro	Amino: Y215	641.97	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
199 F.KANEEGYLGVIIGNRIY*.Y Amino(Y) 215 (Chy/ETD/323/97.4/-0.0444)				



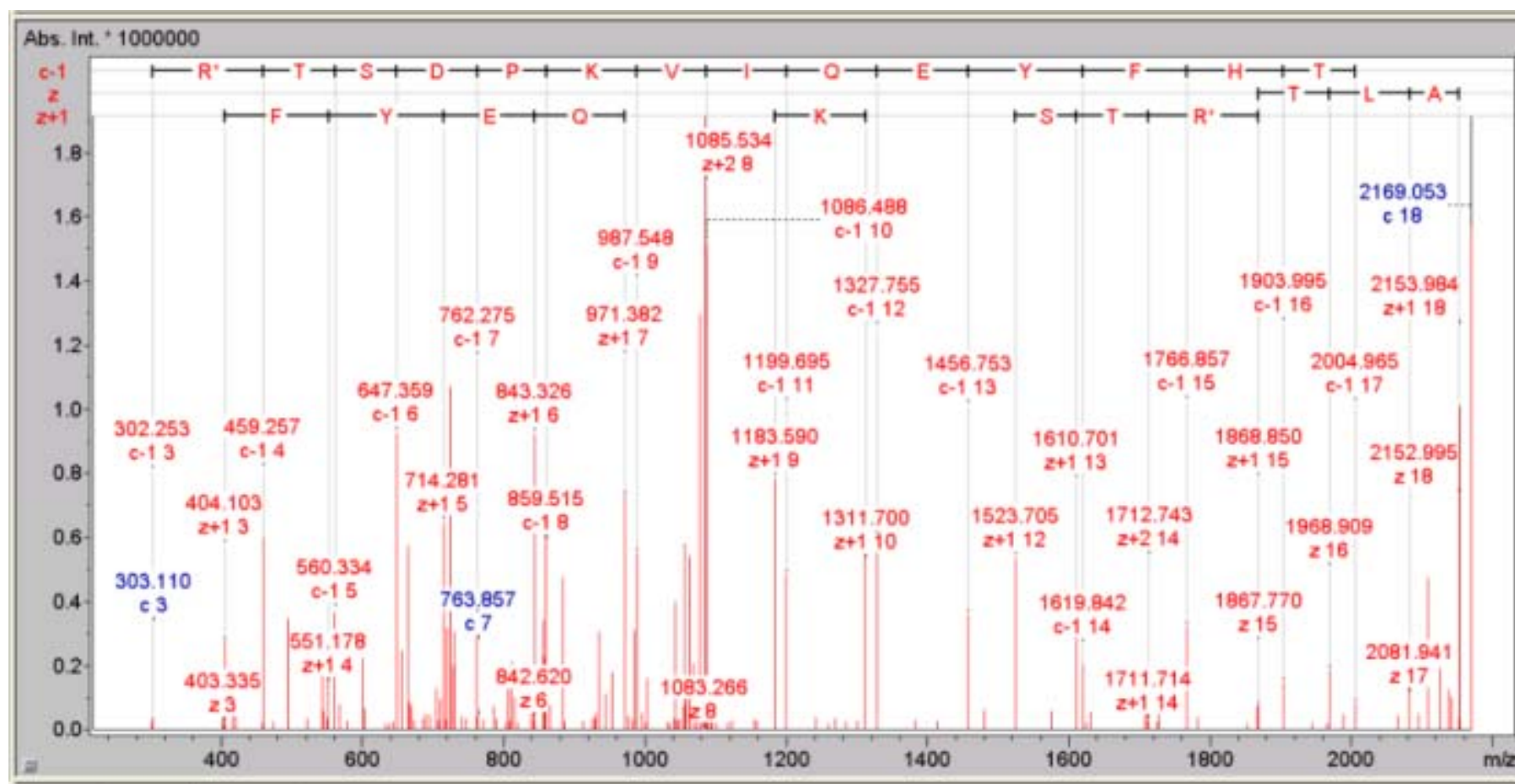
Modiro/ Untreated / L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Modiro	Deamidation: Q46	859.72	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
25 K.LPNIVILATGGTIAGSAATGTQ*TTGYK.A Deamidation(Q) 51 (Try/CID/327/97.1/-0.0772)				



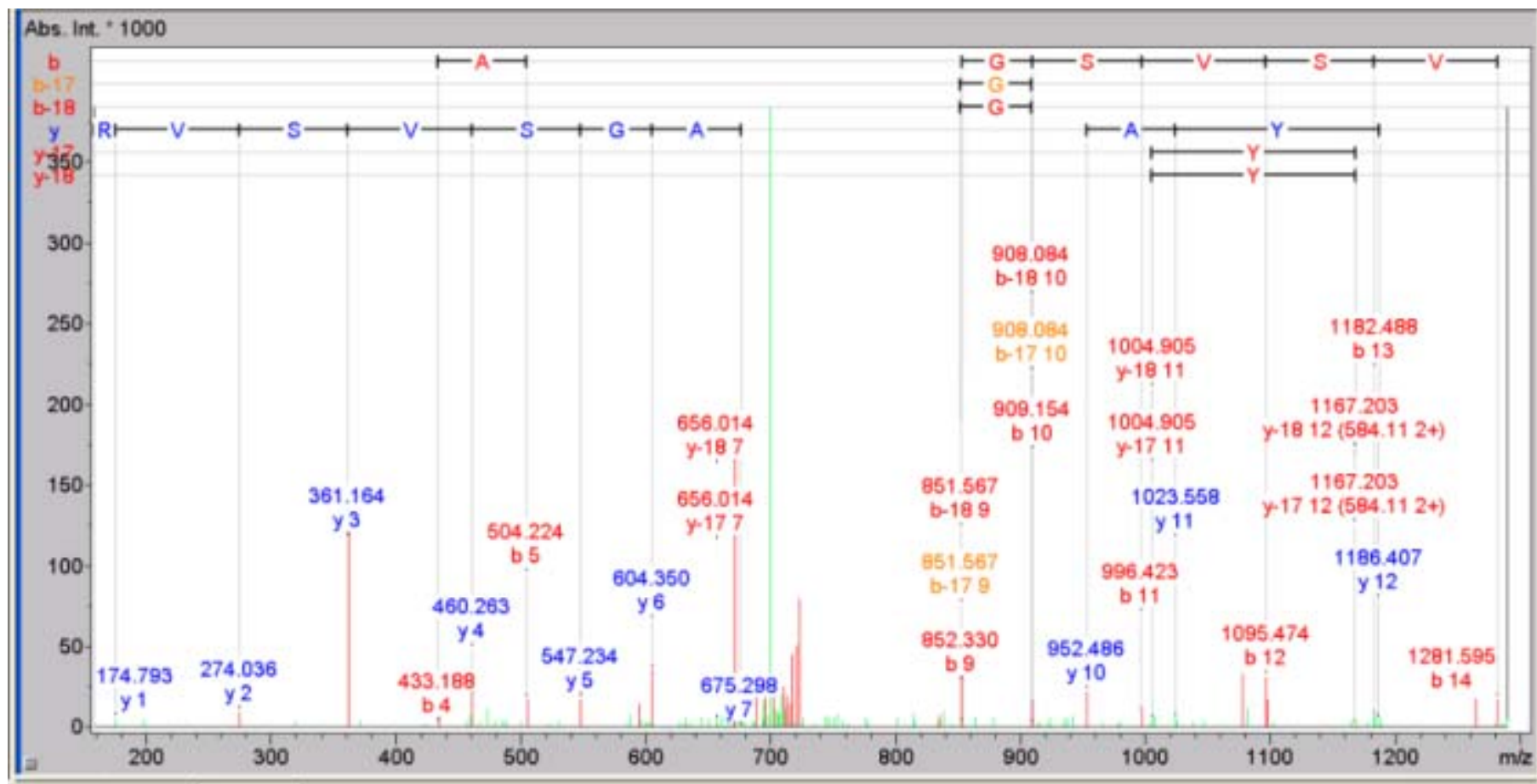
Modiro/ Untreated / L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Modiro	Deamidation: R334	543.29	4+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
331 L.ALTR*TSDPKVIEYFHTY.- Deamidation(R) 348 (Chy/ETD/494/96.1/0.0142)				



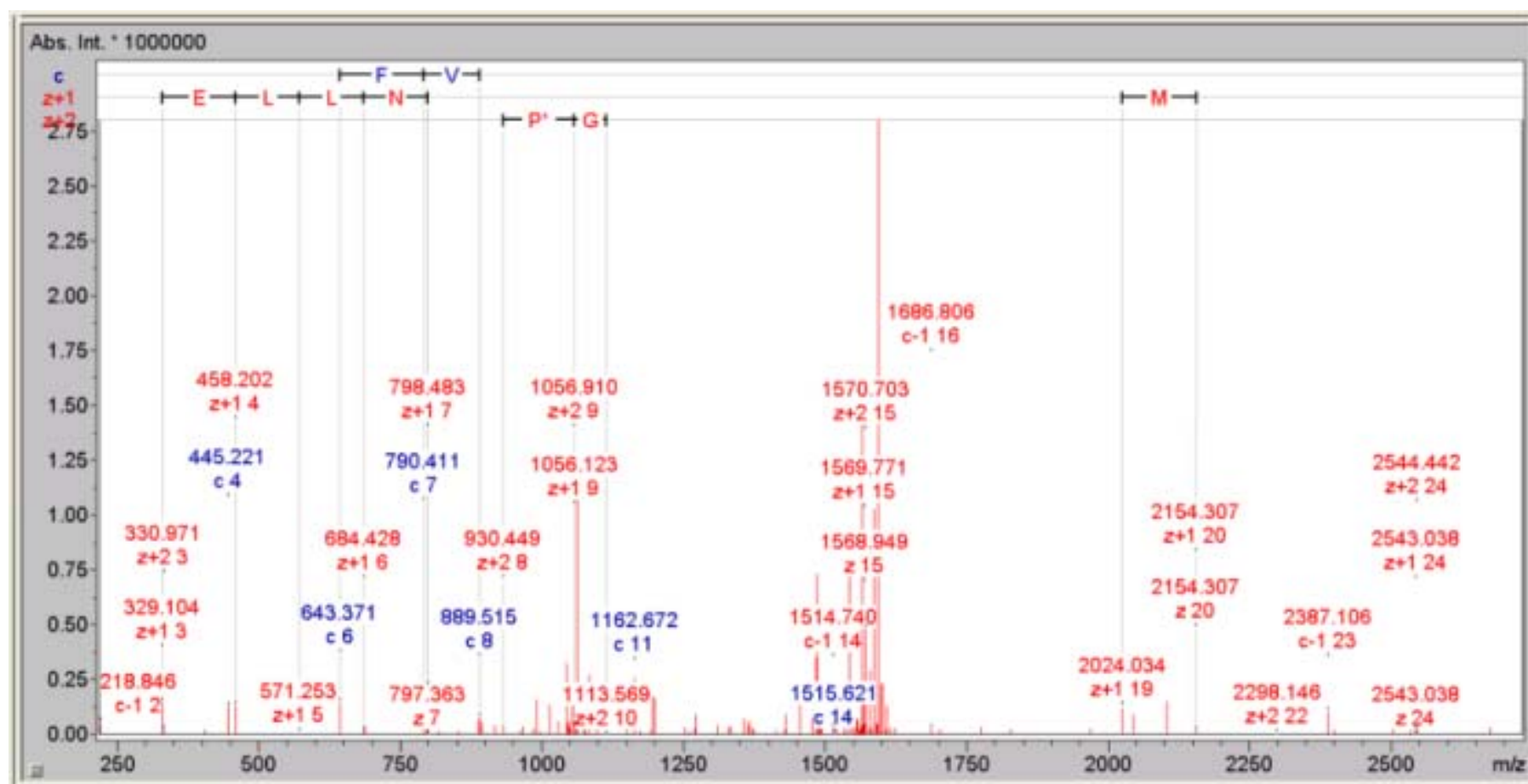
Modiro/ Untreated / L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Modiro	Dihydroxylation: M271	728.25	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
265 K.GIVYAGM*GAGSVSVR.G Dihydroxylation(M) 279 (Try/CID/394/100/-0.1167)				



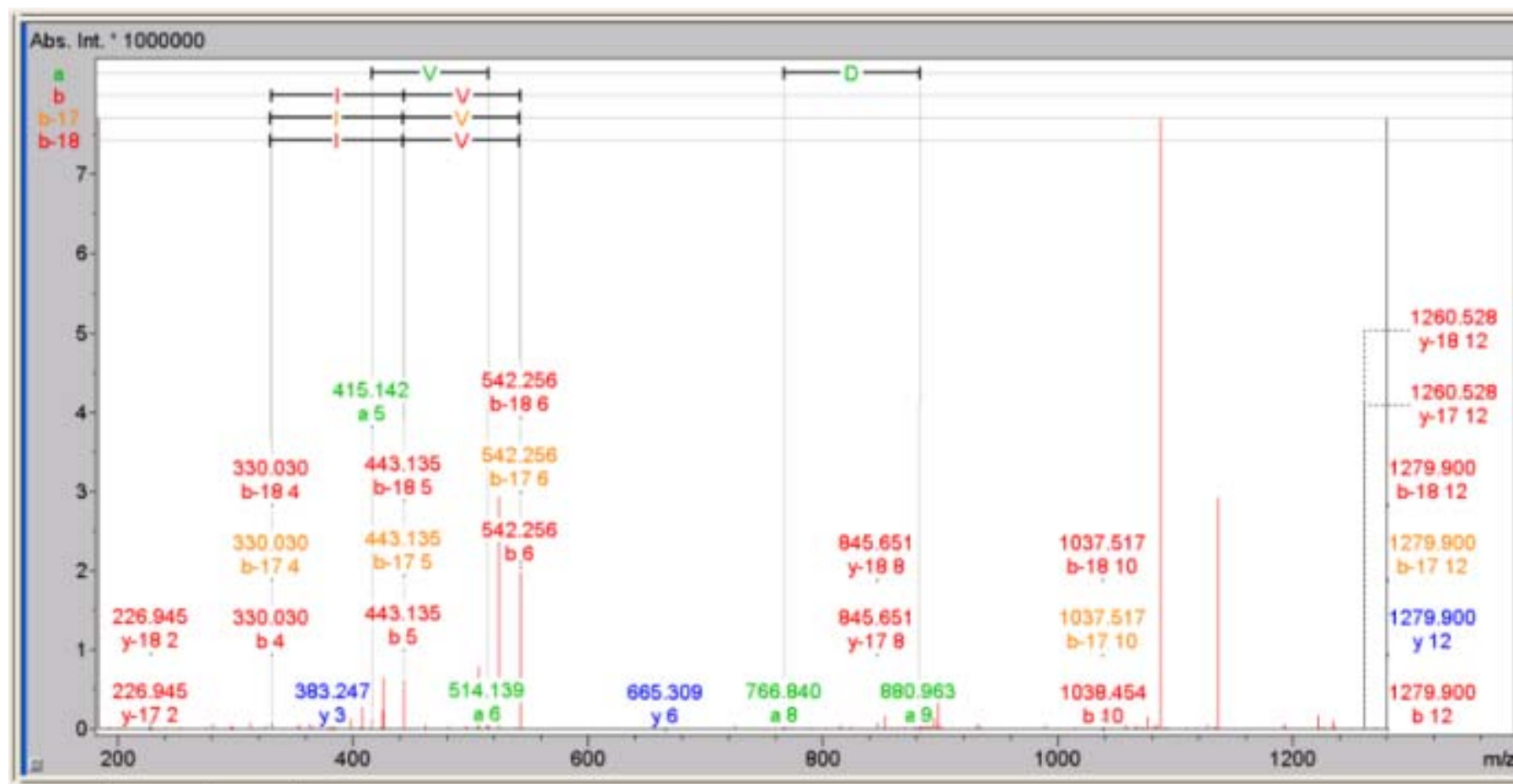
Modiro/ Untreated / L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Modiro	Dimethylation: P144, P153	797.08	4+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
132 K.SDKPVVFVAAMRP*ATAISADGP*MNLLEAVR.V Dimethylation(P) 161 (Try/ETD/428/89.1/0.144)				



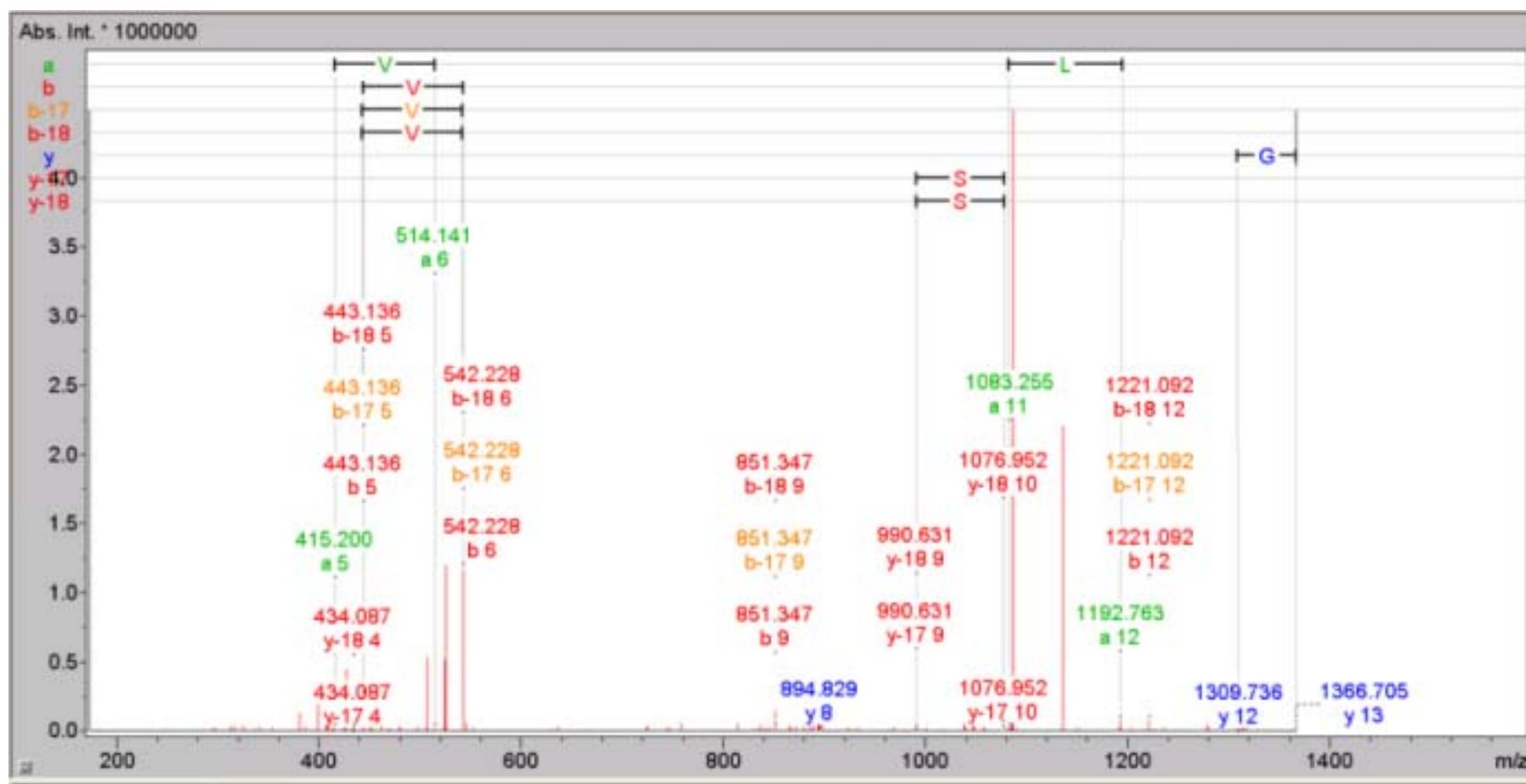
Modiro/ Untreated / L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Modiro	Dimethylation: P306,P307	905.07	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
300 R.TGNGIVP*P*DEELPGLVSDSLNPAHAR.I 2 Dimethylation(P) 325 (Try/CID/352/93.1/-0.0734)				



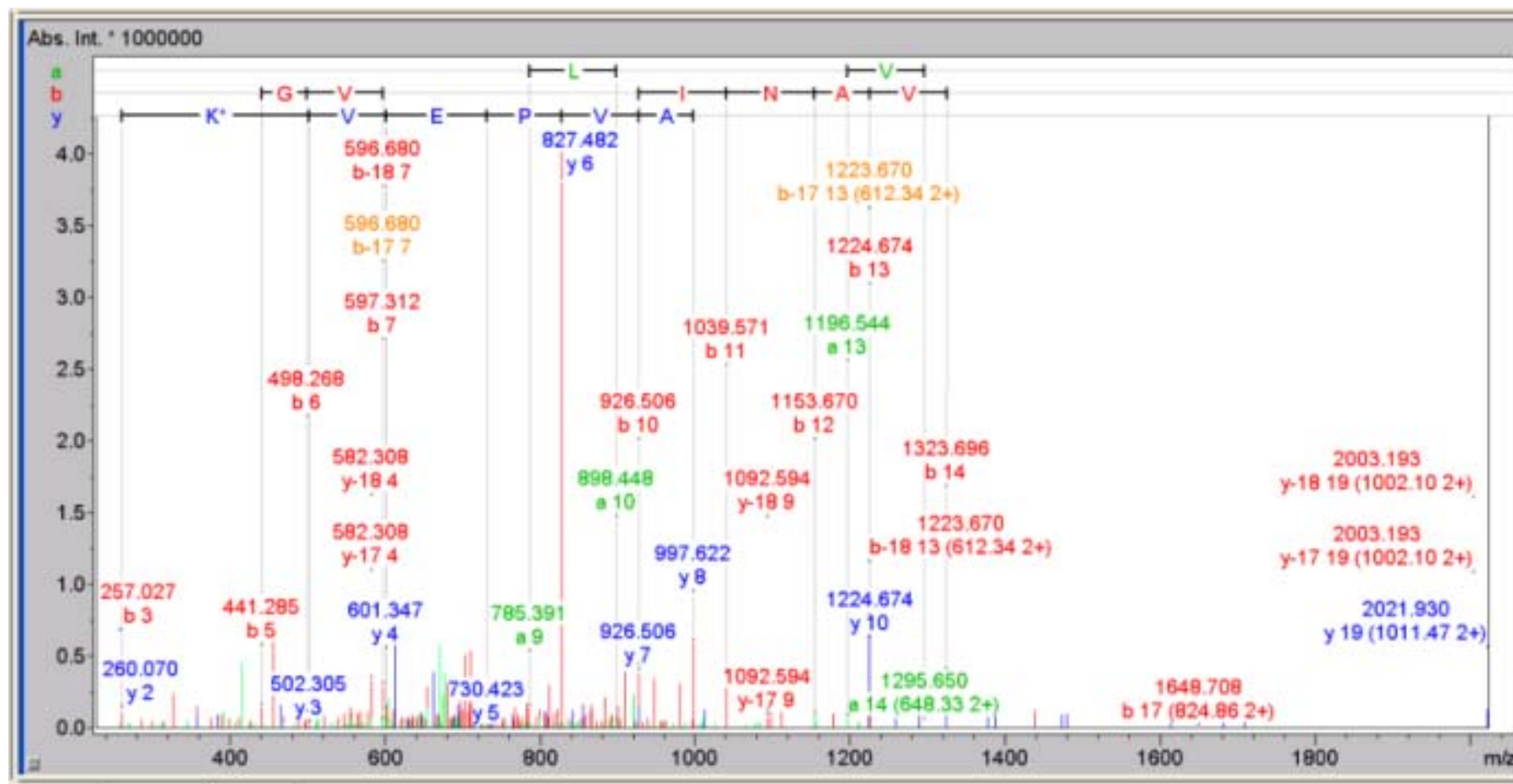
Modiro/ Untreated / L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Modiro	Dimethylation: P312, P321	905.09	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
300 R.TGNGIVPPDEELP*GLVSDSLNP*AHAR.I 2 Dimethylation(P) 325 (Try/CID/305/95.1/-0.0534)				



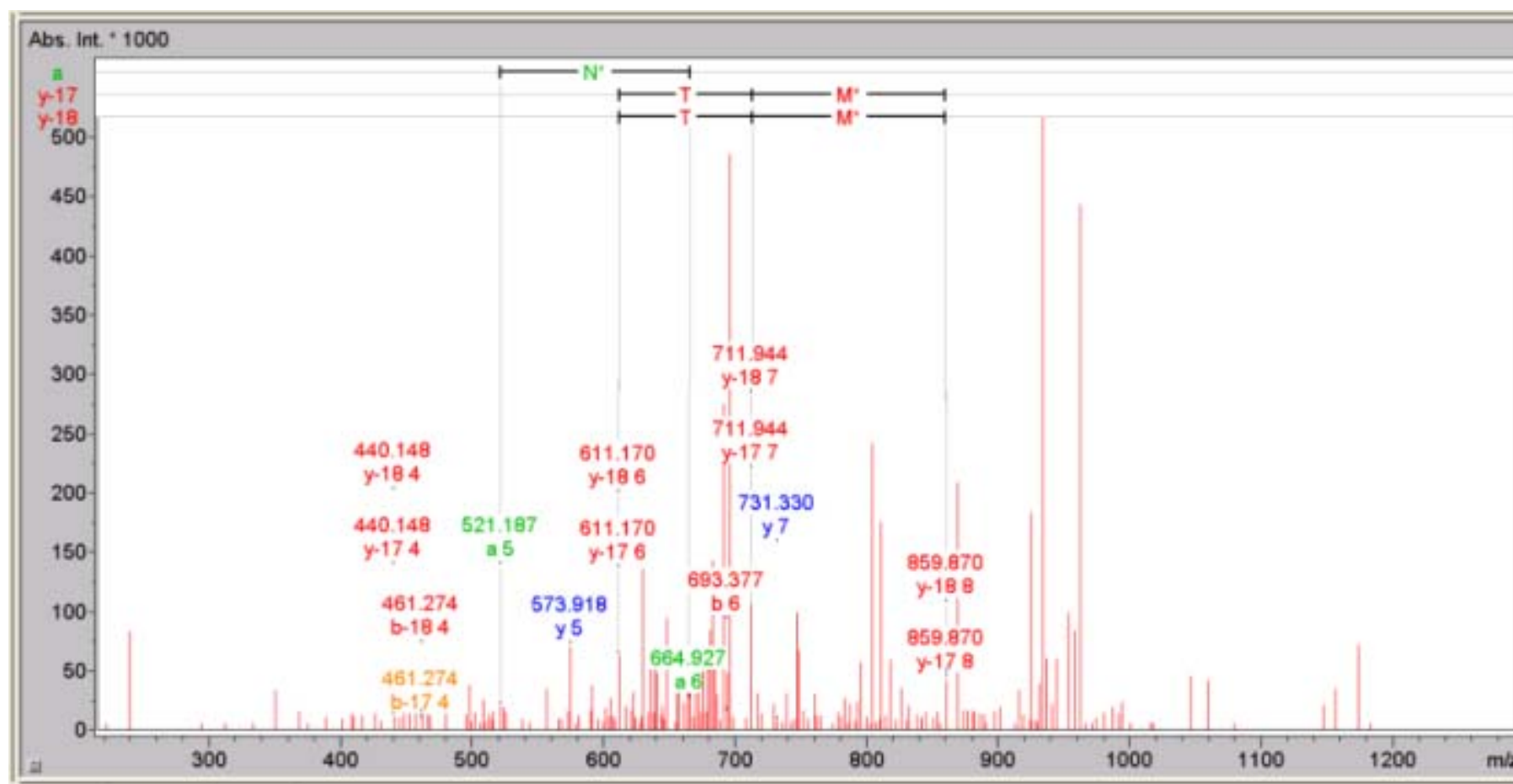
Modiro/ Untreated / L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Modiro	GlyGly: K68	717.44	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
51 Y.KAGALGVDTLINAVPEVK*KL.A GlyGly(K) 70 (Chy/CID/288/92.6/0.017)				



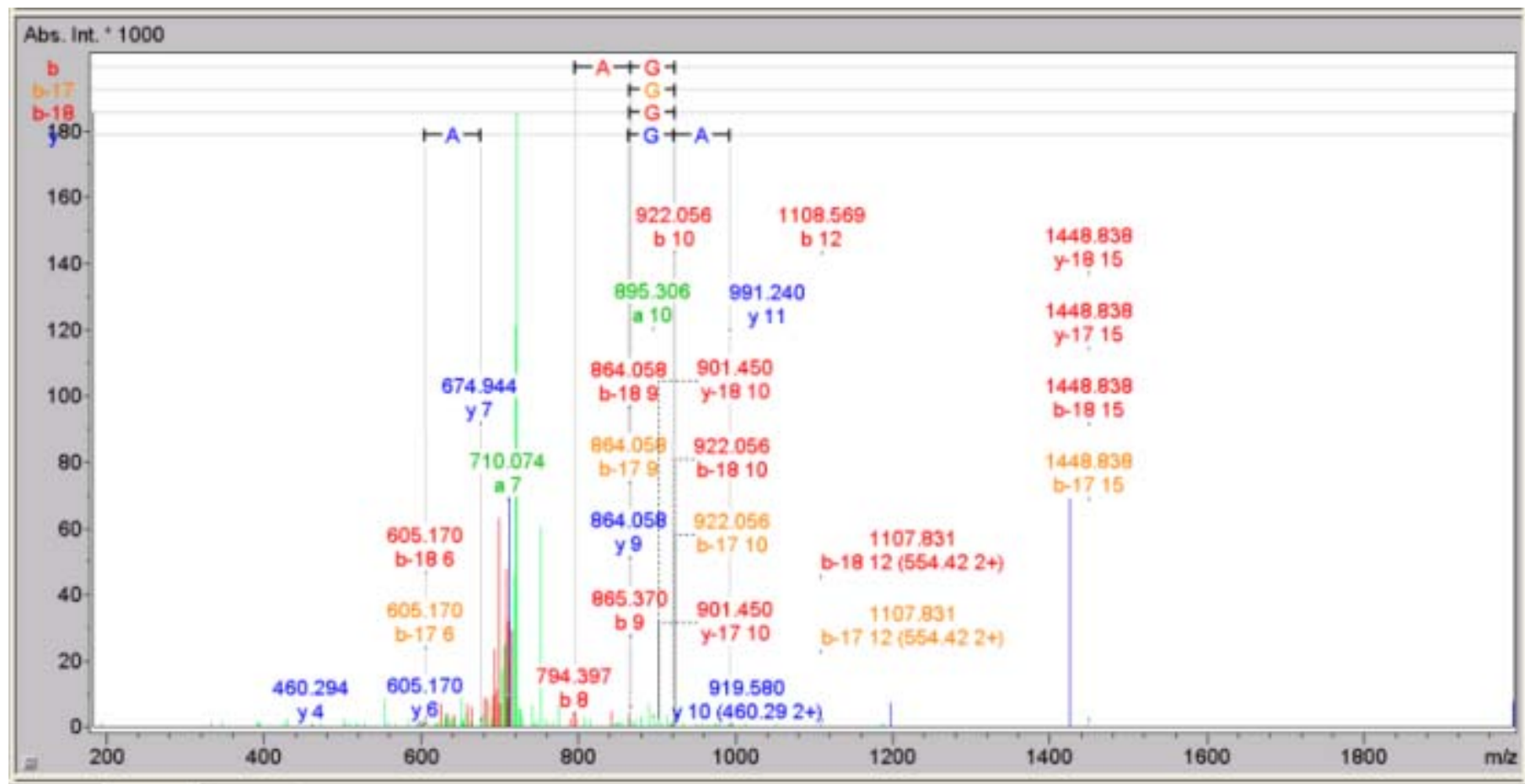
Modiro/ Untreated / L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Modiro	Hydroxymethyl: N80	701.62	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
75 K.GEQFSN*MASENM*TGDVVLK.L Hydroxymethyl(N) Oxidation(M) 93 (Try/CID/316/100/-0.0305)				



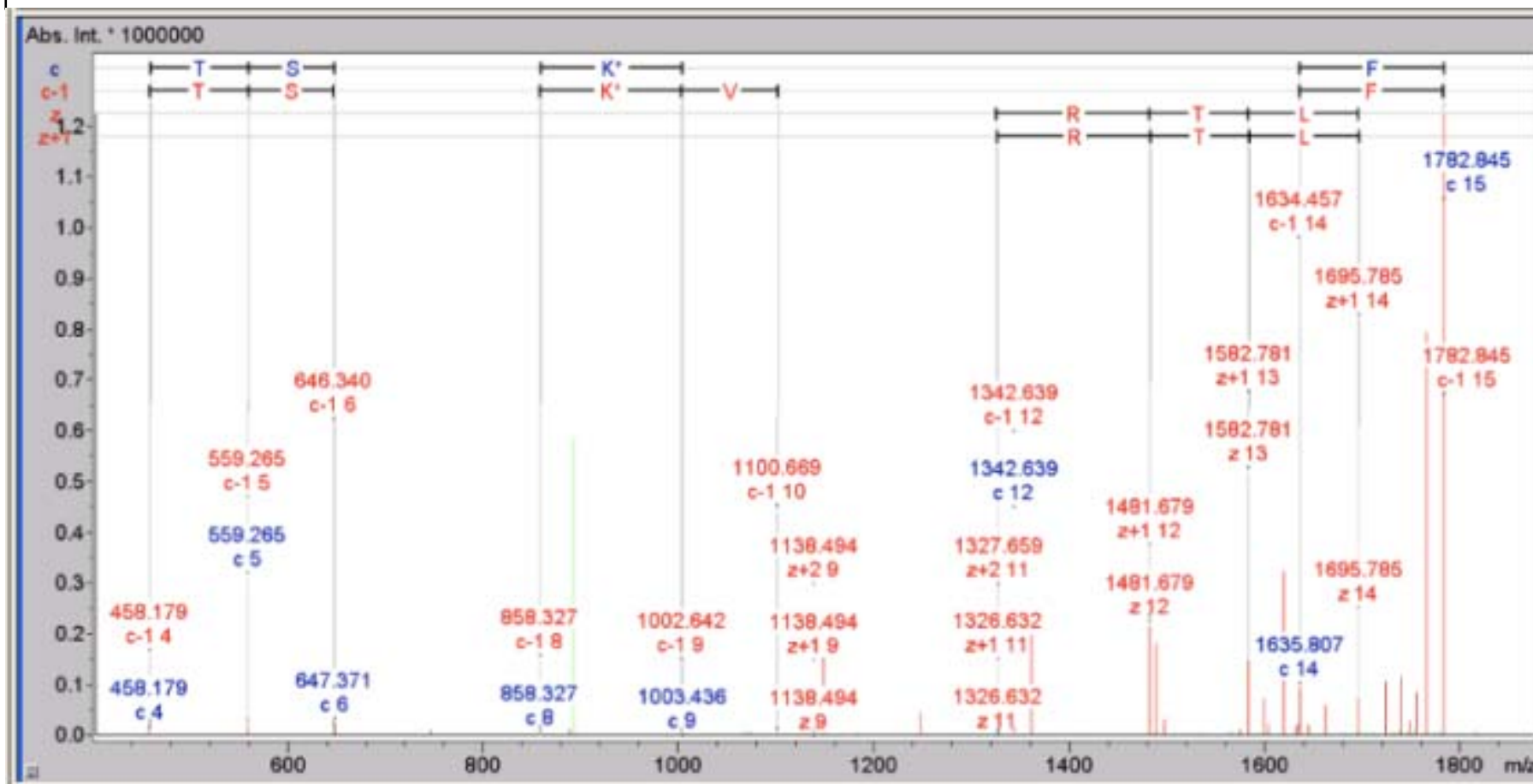
Modiro/ Untreated / L-ASNase

Sample	Search engine	Modification	m/z	charge
Untreated L-ASNase sample 1	Modiro	Nitro: Y268	734.83	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
265 K.GIVY*AGMGAGSVSVR.G Nitro(Y) 279 (Try/CID/264/85.9/-0.0343)				



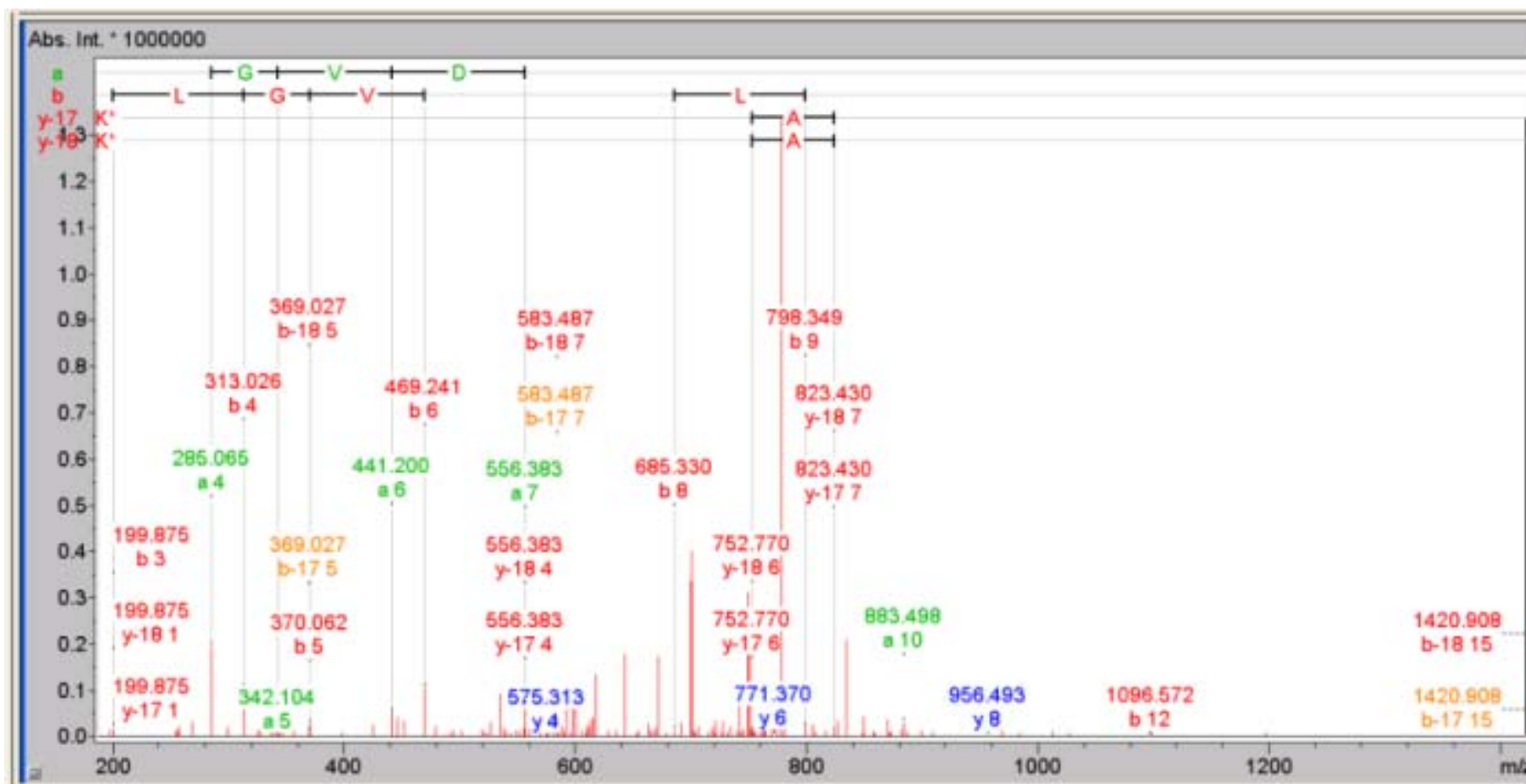
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Modiro	Alpha-amino adipic acid: K339	891.93	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
331 L.ALTRTSDPK*VIQEYF.H Alpha-amino adipic acid(K) 345 (Chy/ETD/228/81.3/-0.0191)				



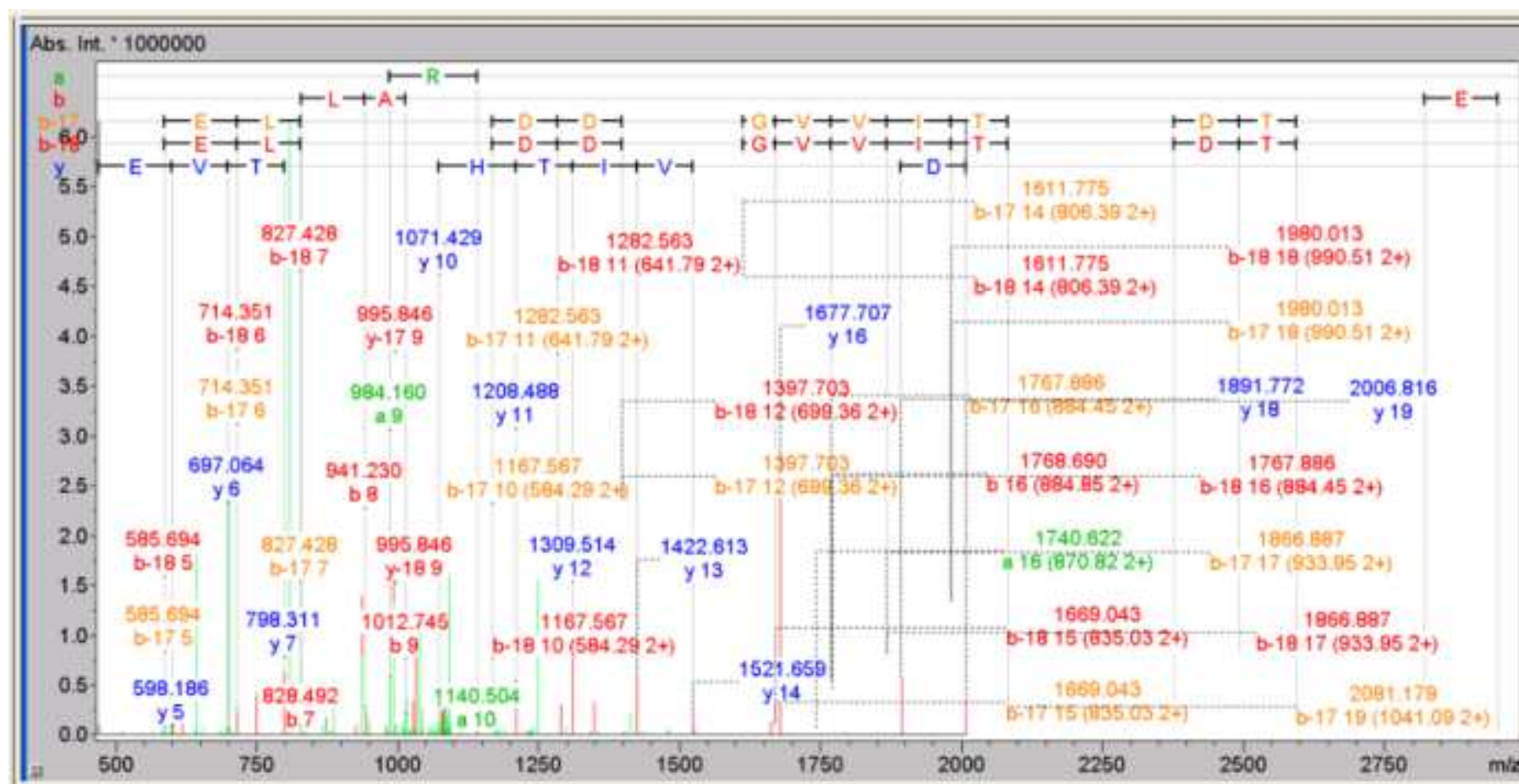
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Carboxyethyl: K69	623.01	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
52 K.AGALGVDTLINAVPEVKK*.L Carboxyethyl(K) 69 (Try/CID/354/92.7/-0.0127)				



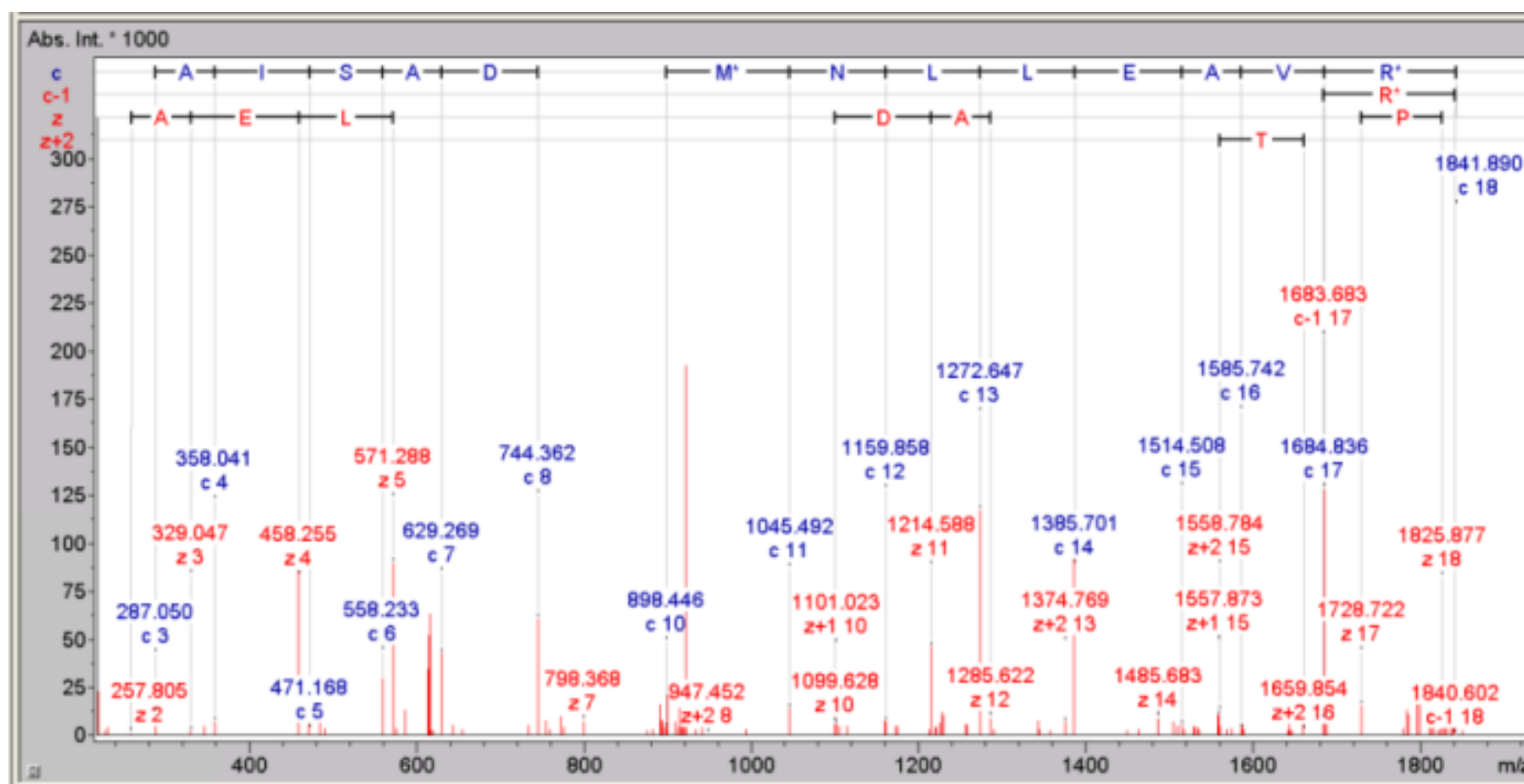
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Deamidation: R97	1097.13	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
95 L.SQR*VNELLARDDVDGVVITHGTDTVVEESAY.F Deamidation(R) 124 (Chy/CID/458/98.8/-0.0688)				



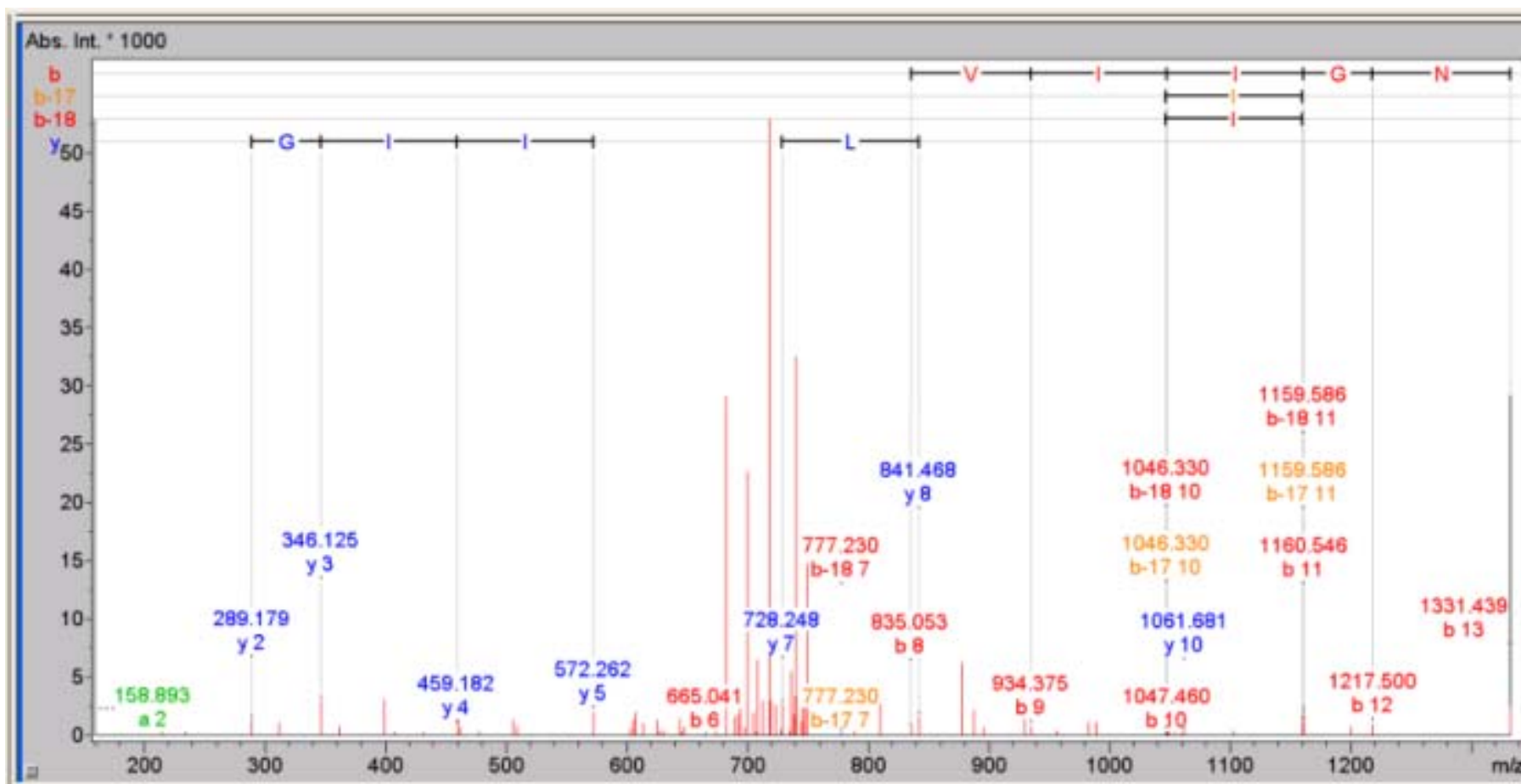
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Deamidation: R161	614.99	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
144 R.PATAISADGPM*NLLEAVR*.V Oxidation(M) Deamidation(R) 161 (Try/ETD/346/96.1/0.0096)				



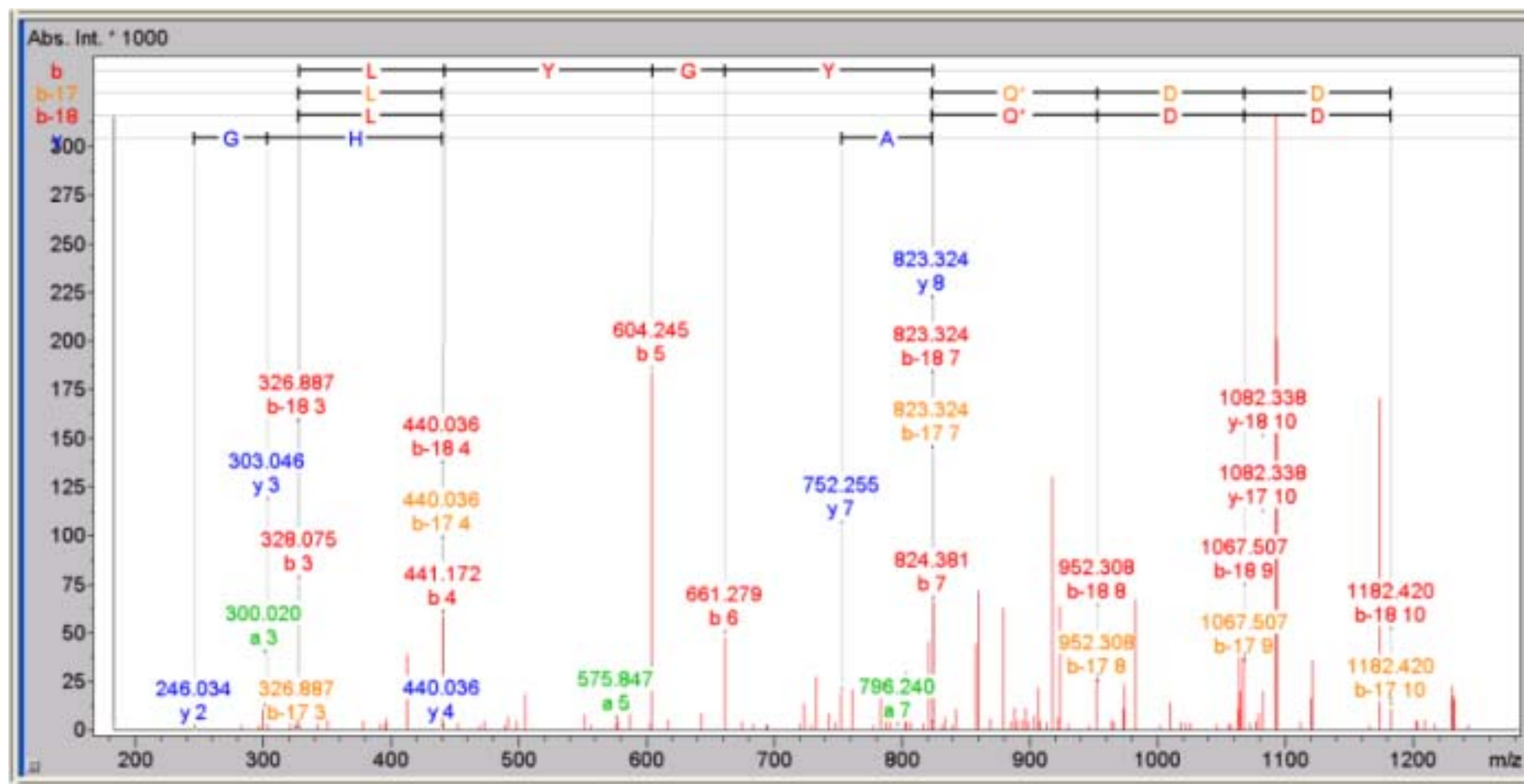
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Modiro	Deamidation: N201	753.58	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
200 K.AN*EEGYLGVIIGNR.I Deamidation(N) 213 (Try/CID/235/97.8/0.1966)				



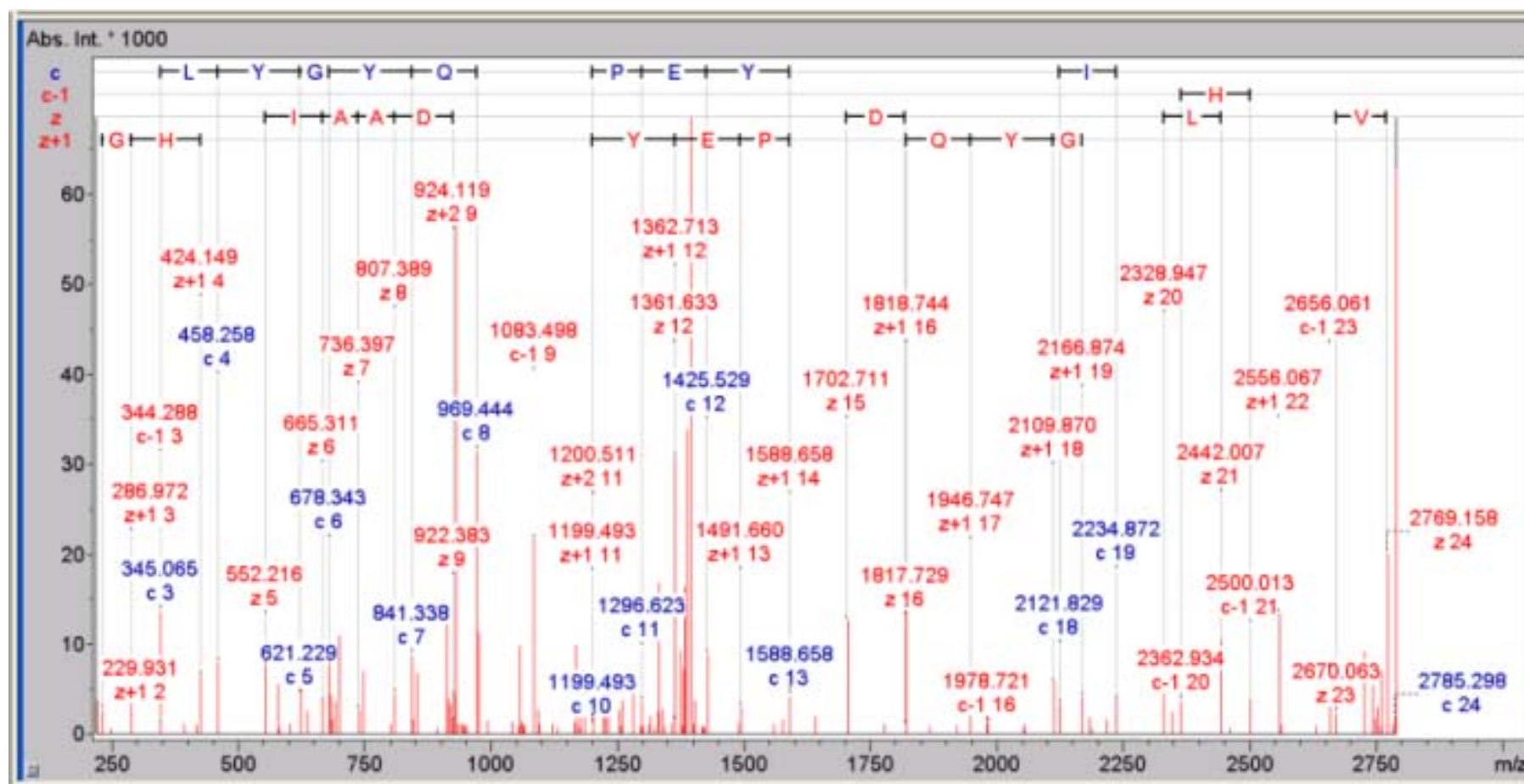
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Modiro	Deamidation: Q248	929.44	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
241 K.VDILYGYQ*DDPEYLYDAAIQHGVK.G Deamidation(Q) 264 (Try/CID/367/99.1/-0.0047)				



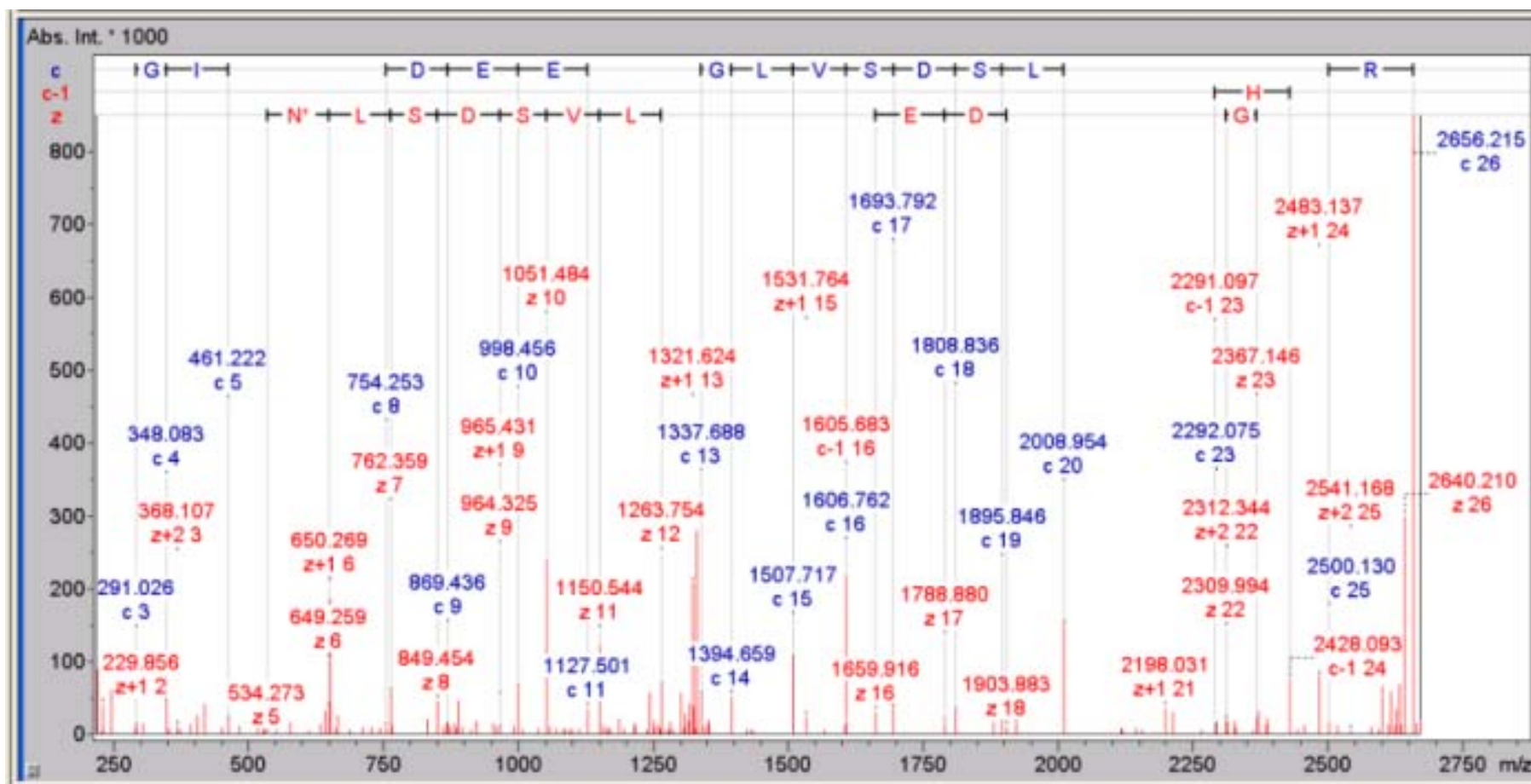
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Modiro	Deamidation: Q260	697.29	4+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
241 K.VDILYGYQDDPEYLYDAAIQ*HGVK.G Deamidation(Q) 264 (Try/ETD/445/97.3/-0.0453)				



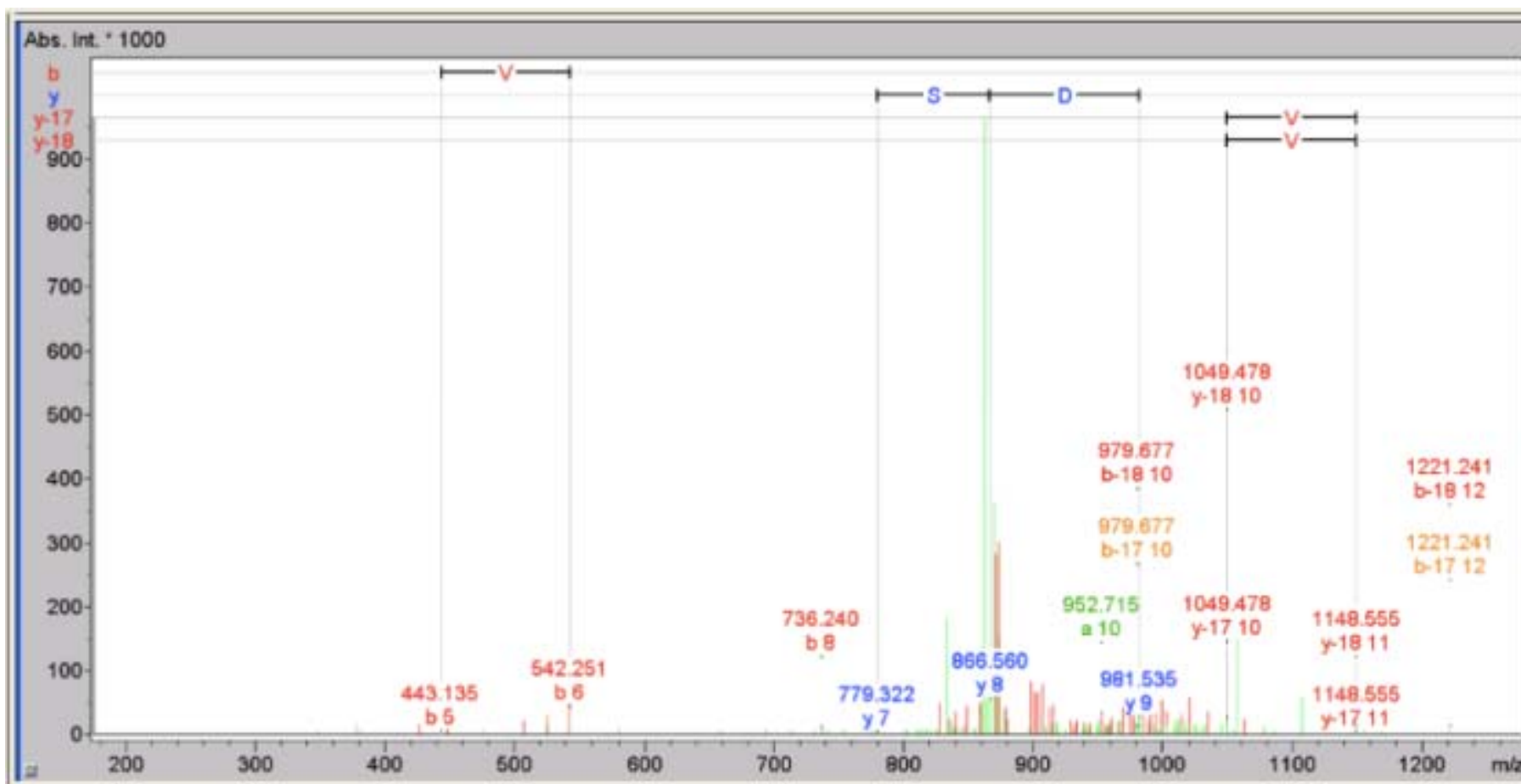
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Deamidation: N320	665.07	4+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
300 R.TGN*GIVPPDEELPGLVSDSLN*PAHAR.I 2 Deamidation(N) 325 (Try/ETD/433/100/-0.0118)				



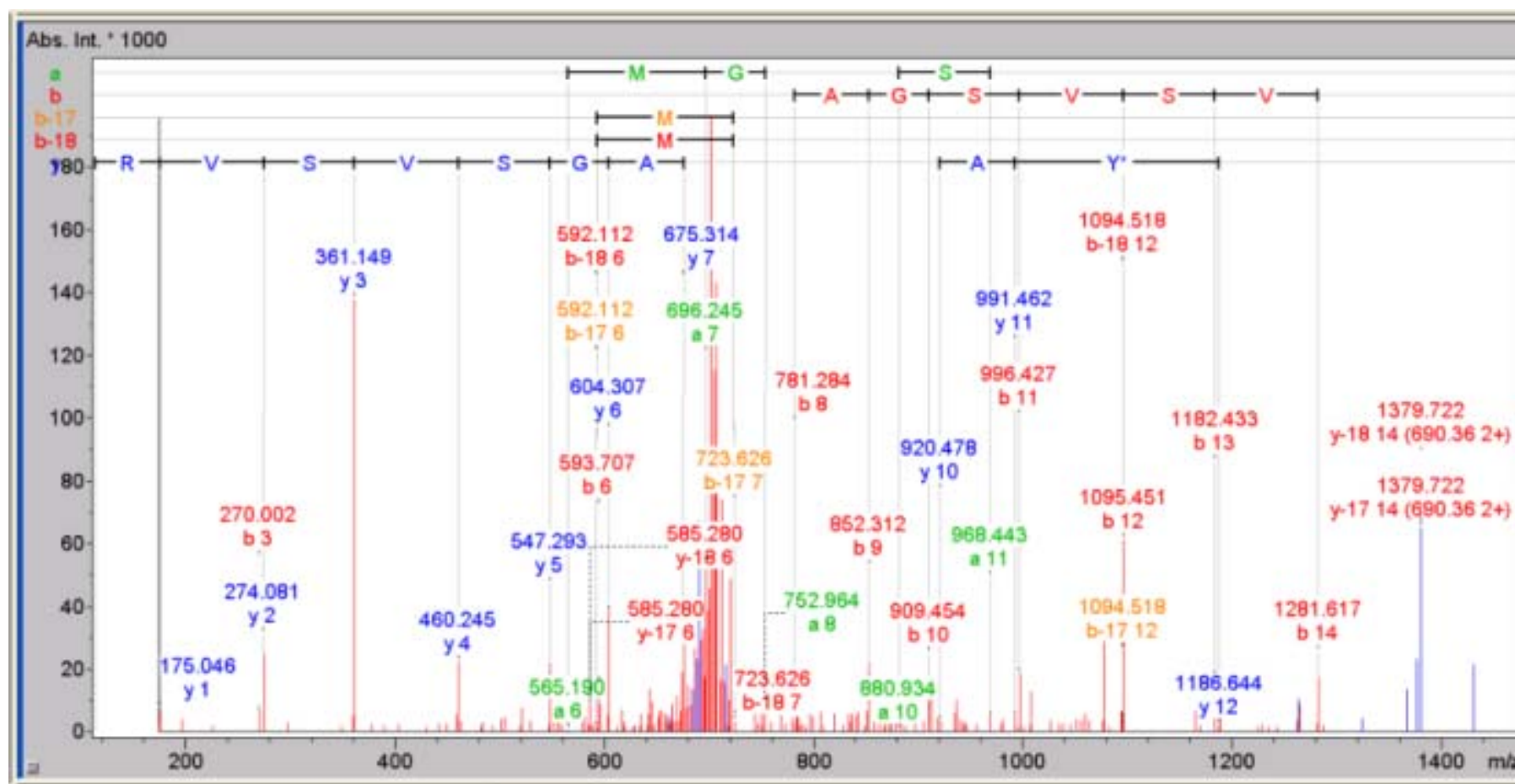
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Deamidation: R325	886.05	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
300 R.TGNGIVPPDEELPGLVSDSLNPAHAR*.I Deamidation(R) 325 (Try/CID/362/96.9/-0.062)				



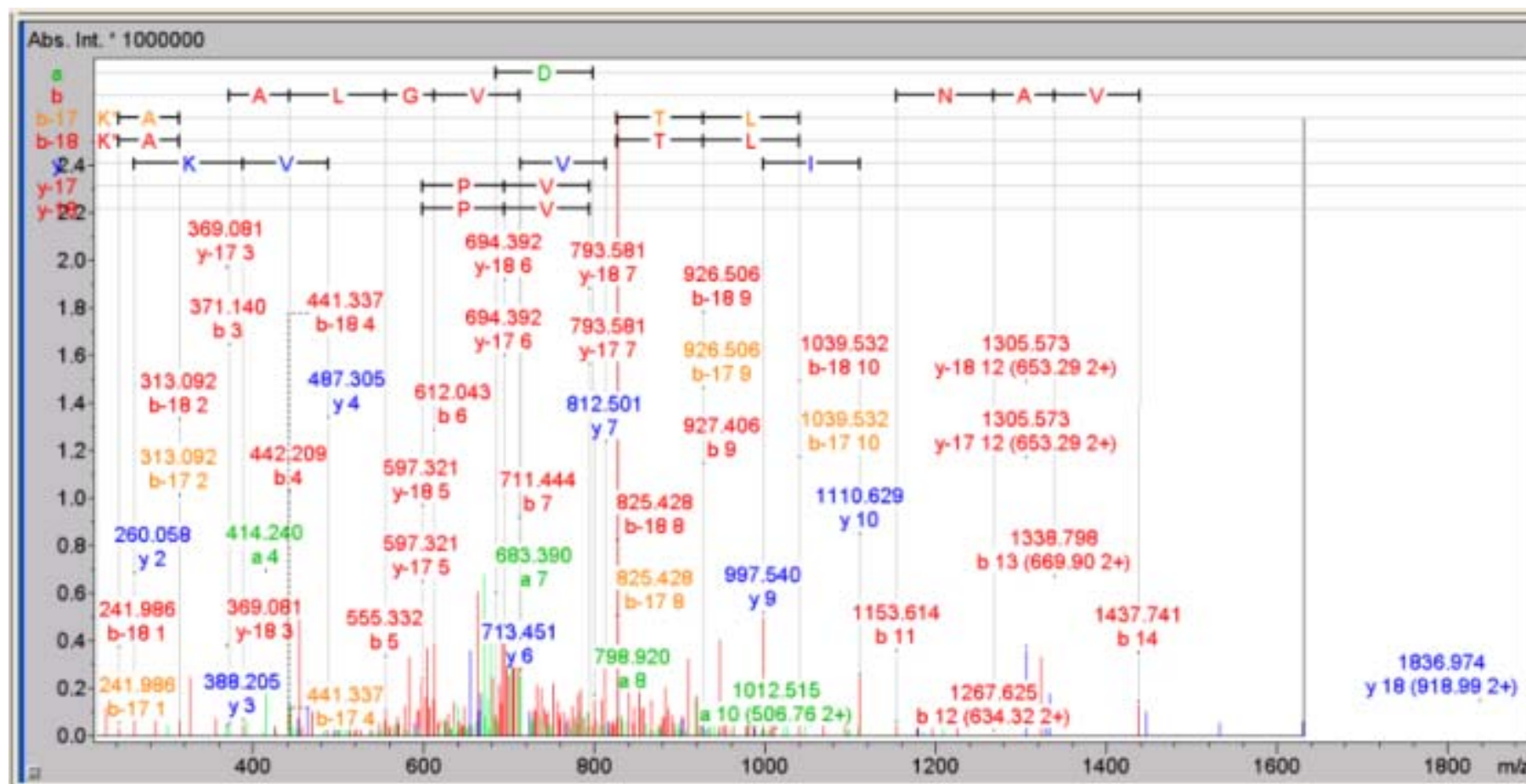
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Modiro	Dihydroxylation: Y268	728.48	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
265 K.GIVY*AGMGAGSVSVR.G Dihydroxylation(Y) 279 (Try/CID/297/100/0.1133)				



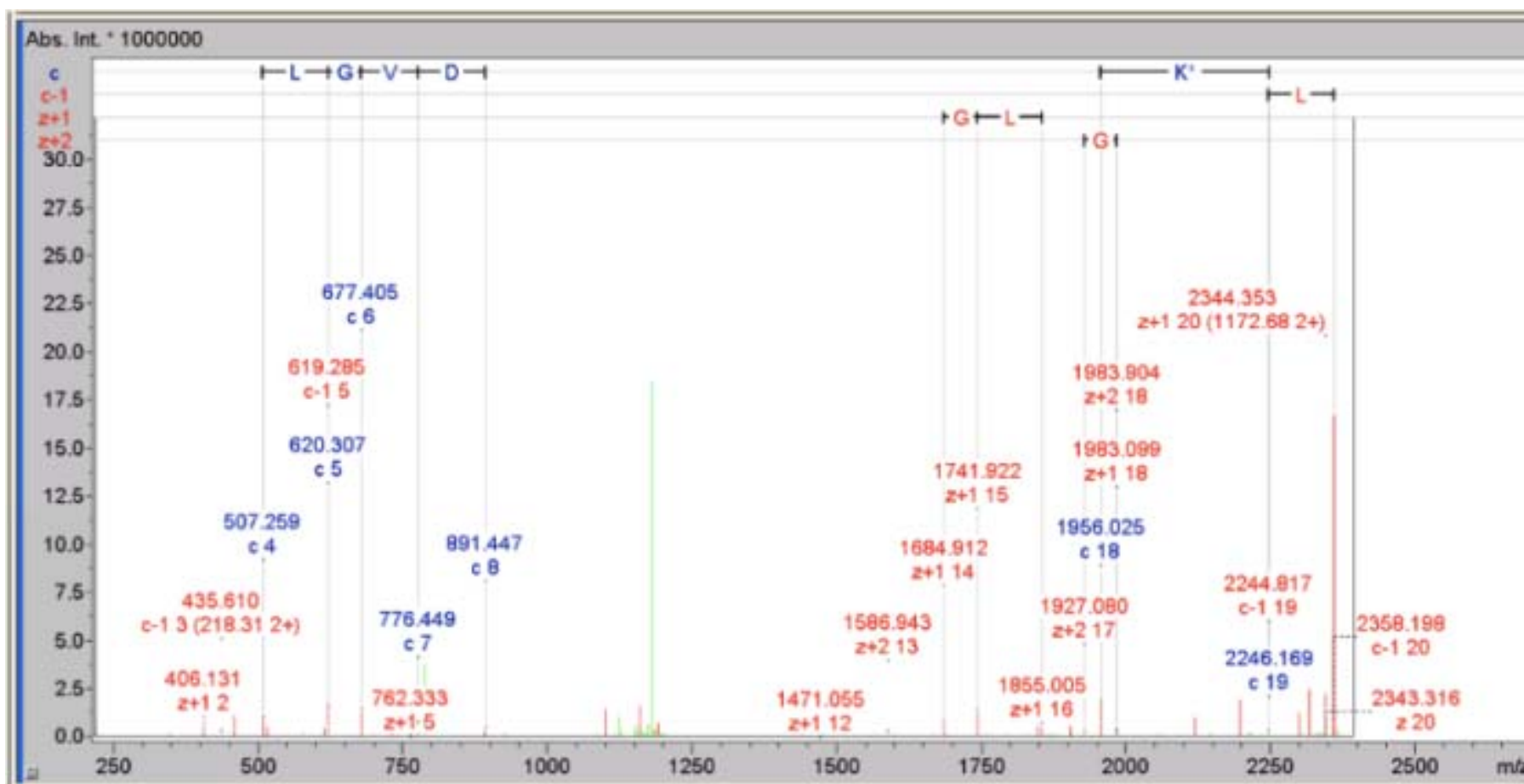
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	GlyGly: K51	717.42	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
51 Y.K*AGALGVDTLINAVPEVKKL.A GlyGly(K) 70 (Chy/CID/255/88.9/-0.003)				



Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Hexose: K51	787.40	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
51 Y.K*AGALGVDTLINAVPEVKK*L.A 2Hex(K) 70 (Chy/ETD/449/99.6/0.0153)				



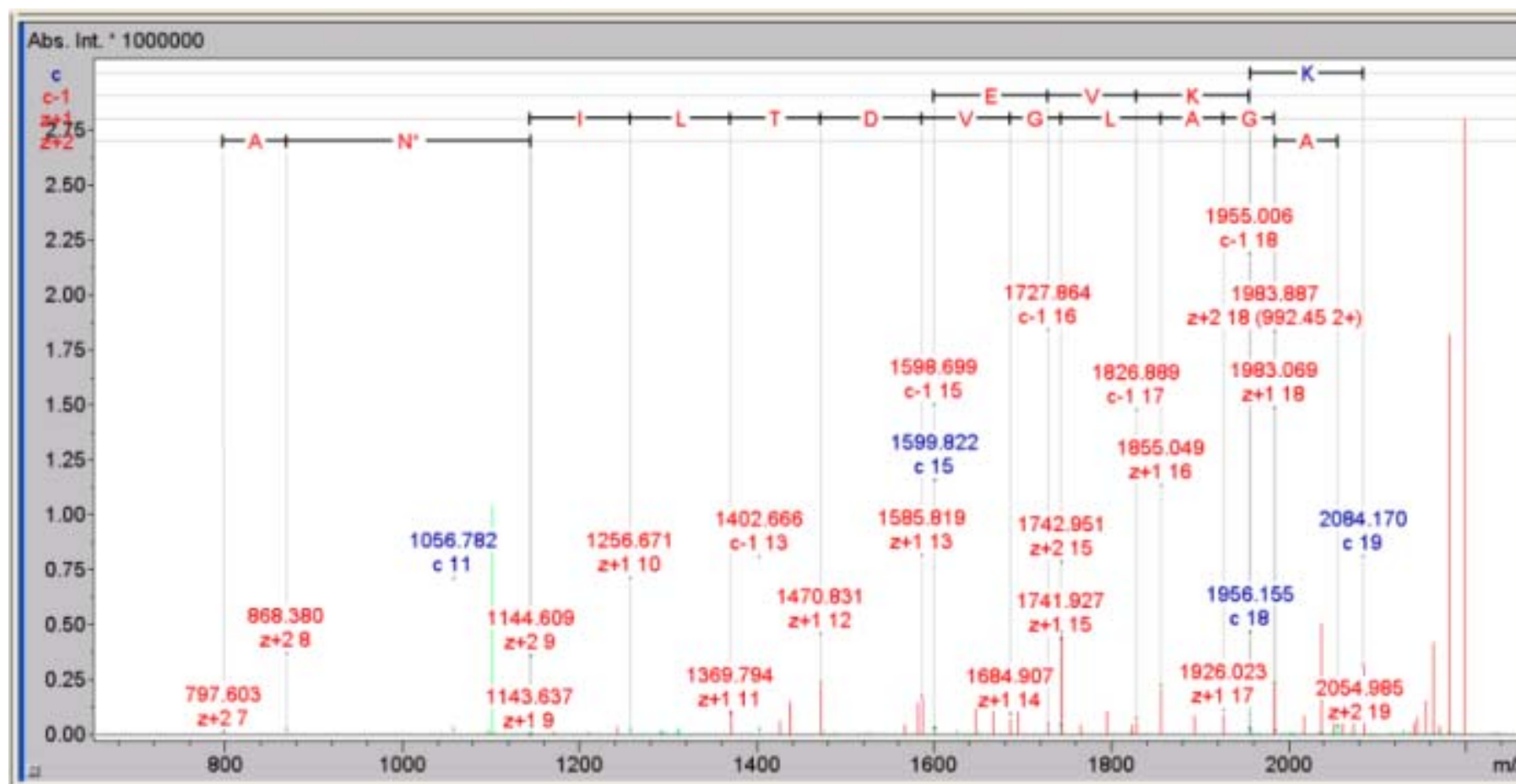
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Hexose: T59	1099.59	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
51 Y.KAGALGVDT*LINAVPEVKKL.A Hex(T) 70 (Chy/ETD/314/99/-0.0457)				



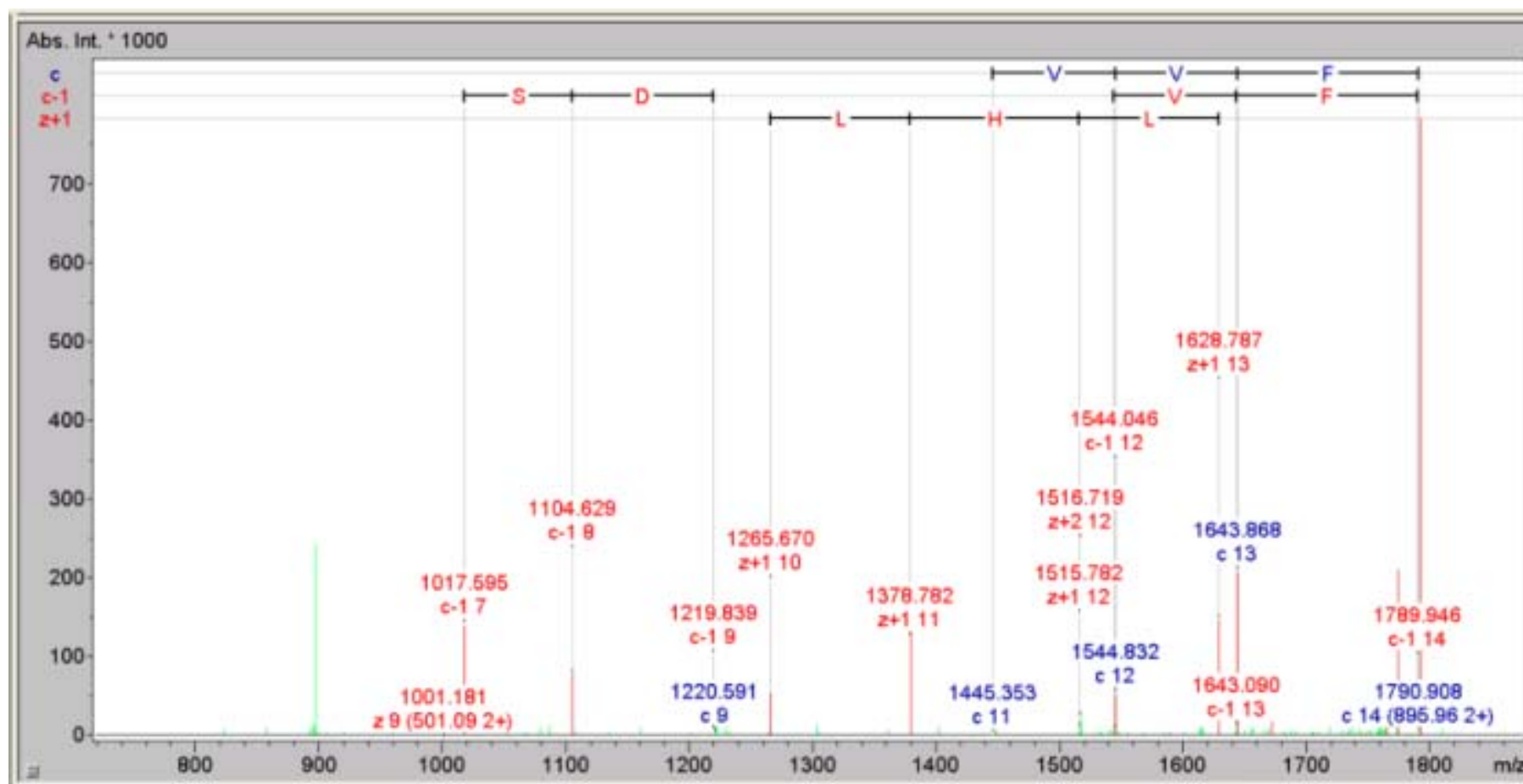
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Hexose: N62	1099.59	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
51 Y.KAGALGVDTLIN*AVPEVKKL.A Hex(N) 70 (Chy/ETD/276/96.9/-0.0457)				



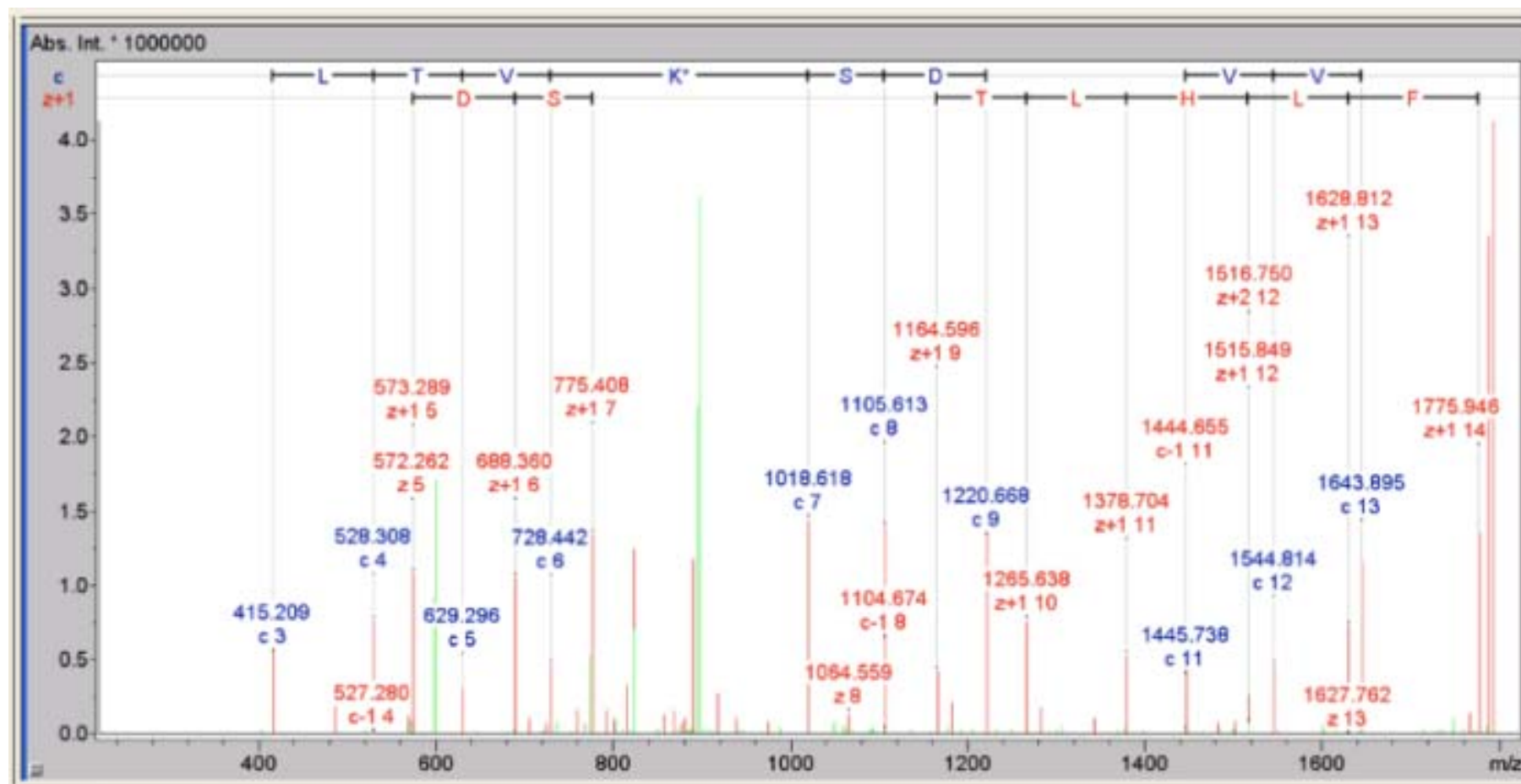
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 3	Modiro	Hexose: T129	896.50	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
125 Y.FLHLT*VKSDKPVVF.V Hex(T) 138 (Chy/ETD/255/81.1/0.0018)				



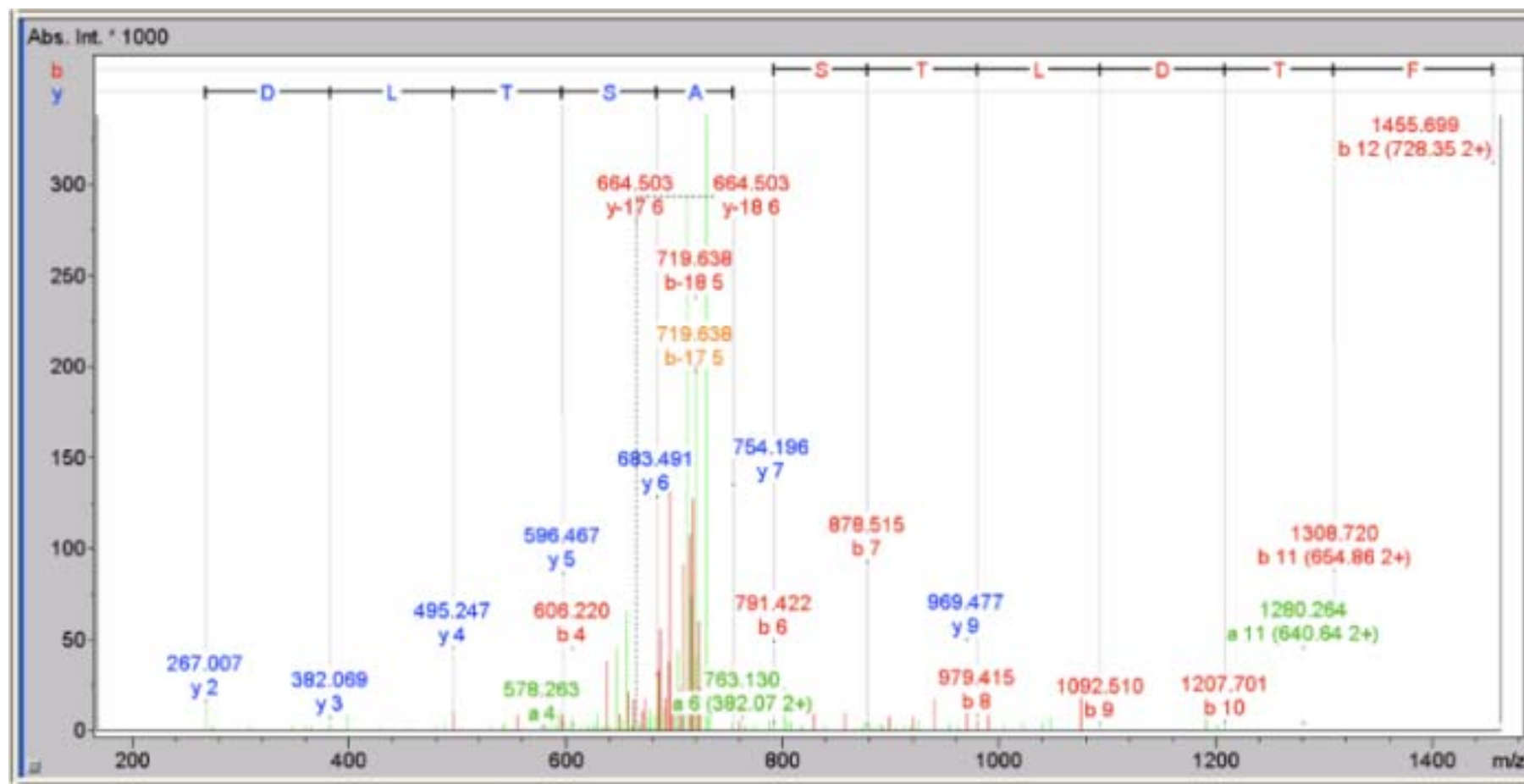
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Hexose: K131	597.98	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
125 Y.FLHLTVK*SDKPVVF.V Hex(K) 138 (Chy/ETD/479/100/-0.0212)				



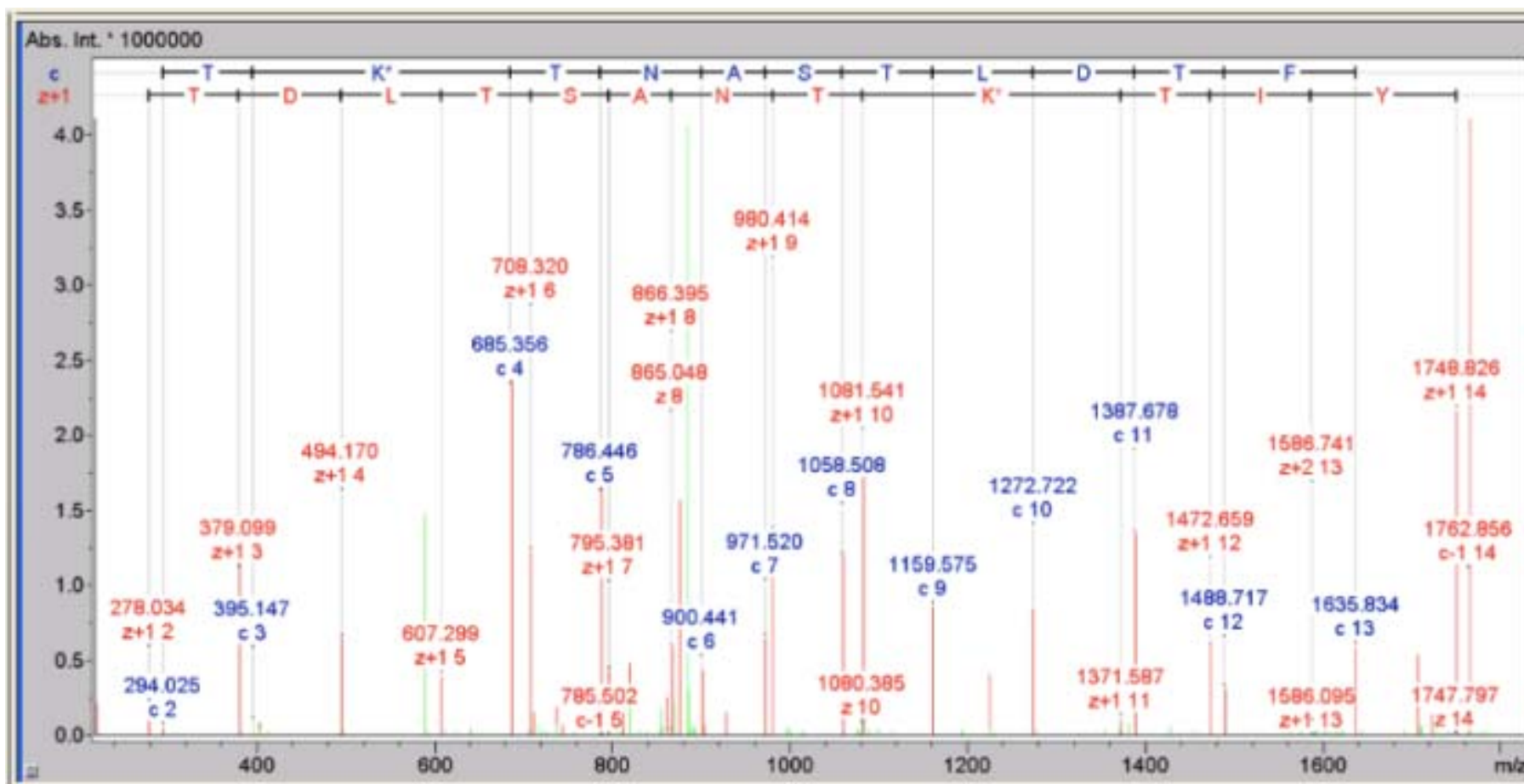
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Modiro	Hexose: T188	737.31	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
187 Y.IT*KTNASTLDTF.K Hex(T) 198 (Chy/CID/205/93.6/-0.0596)				



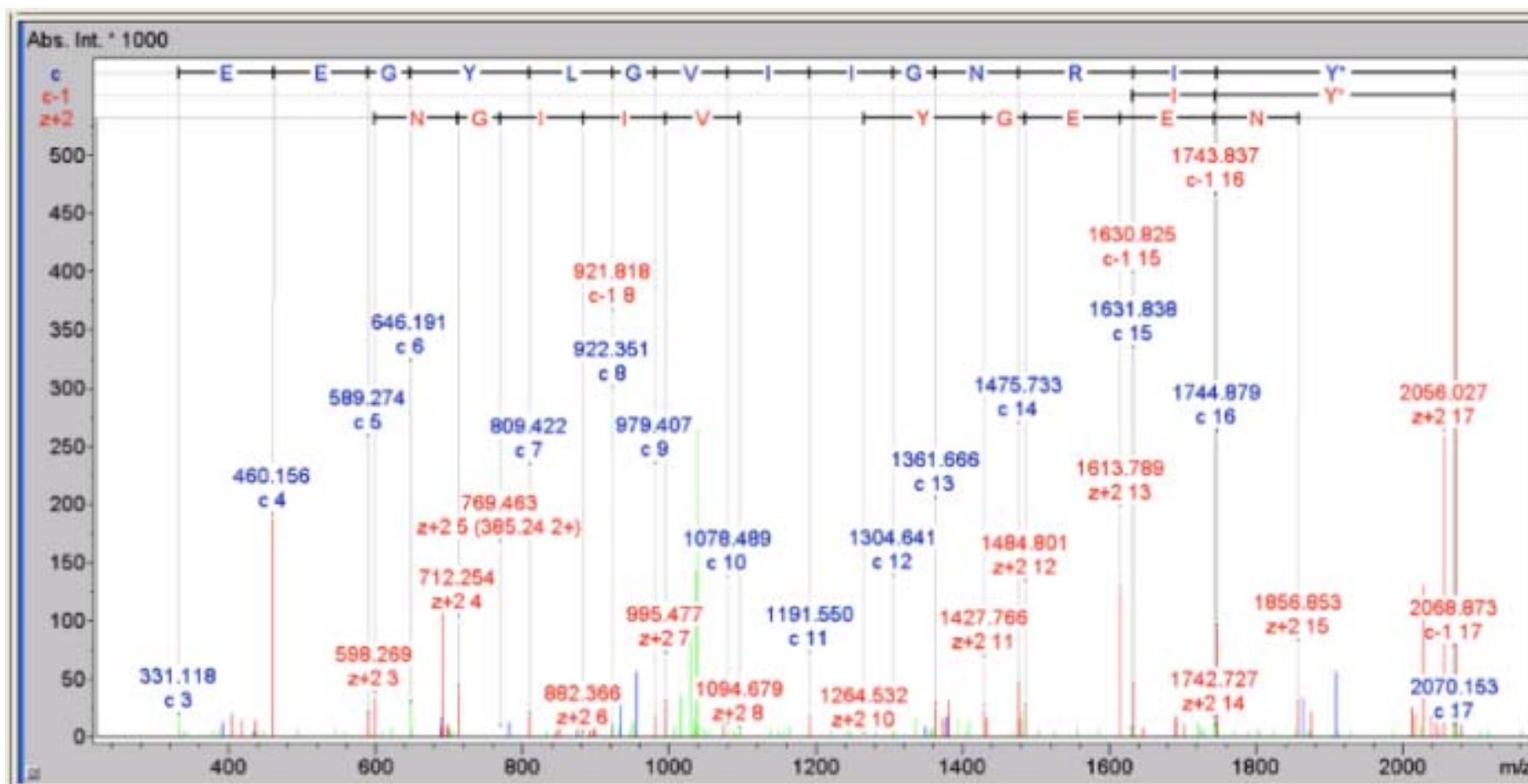
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Hexose: K189	588.96	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
186 R.YITK*TNASTLDTFK.A Hex(K) 199 (Try/ETD/515/99.9/-0.0082)				



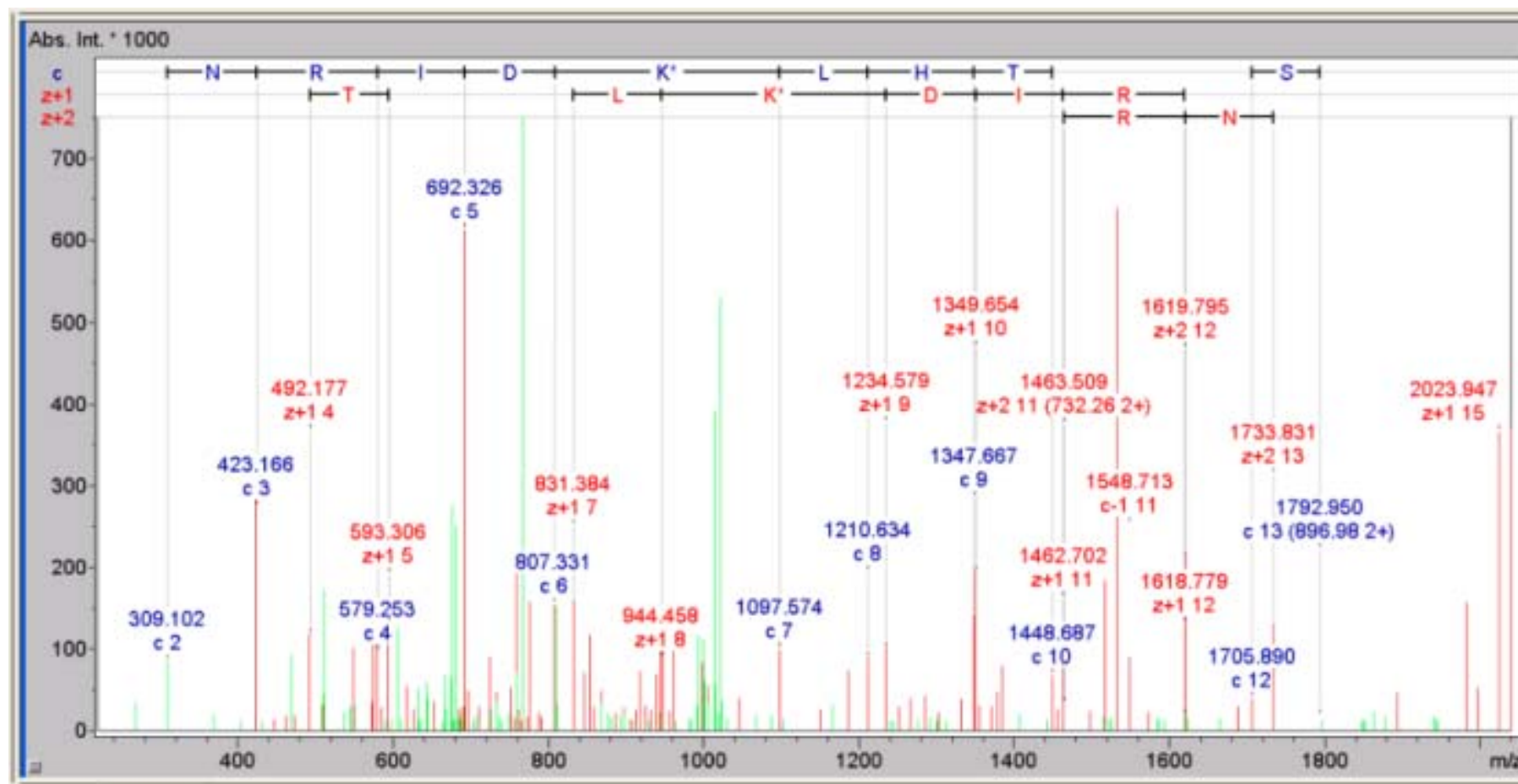
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Hexose: Y215	691.08	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
199 F.KANEEGYLGVIIGNRIY*.Y Hex(Y) 215 (Chy/ETD/278/90.1/0.0516)				



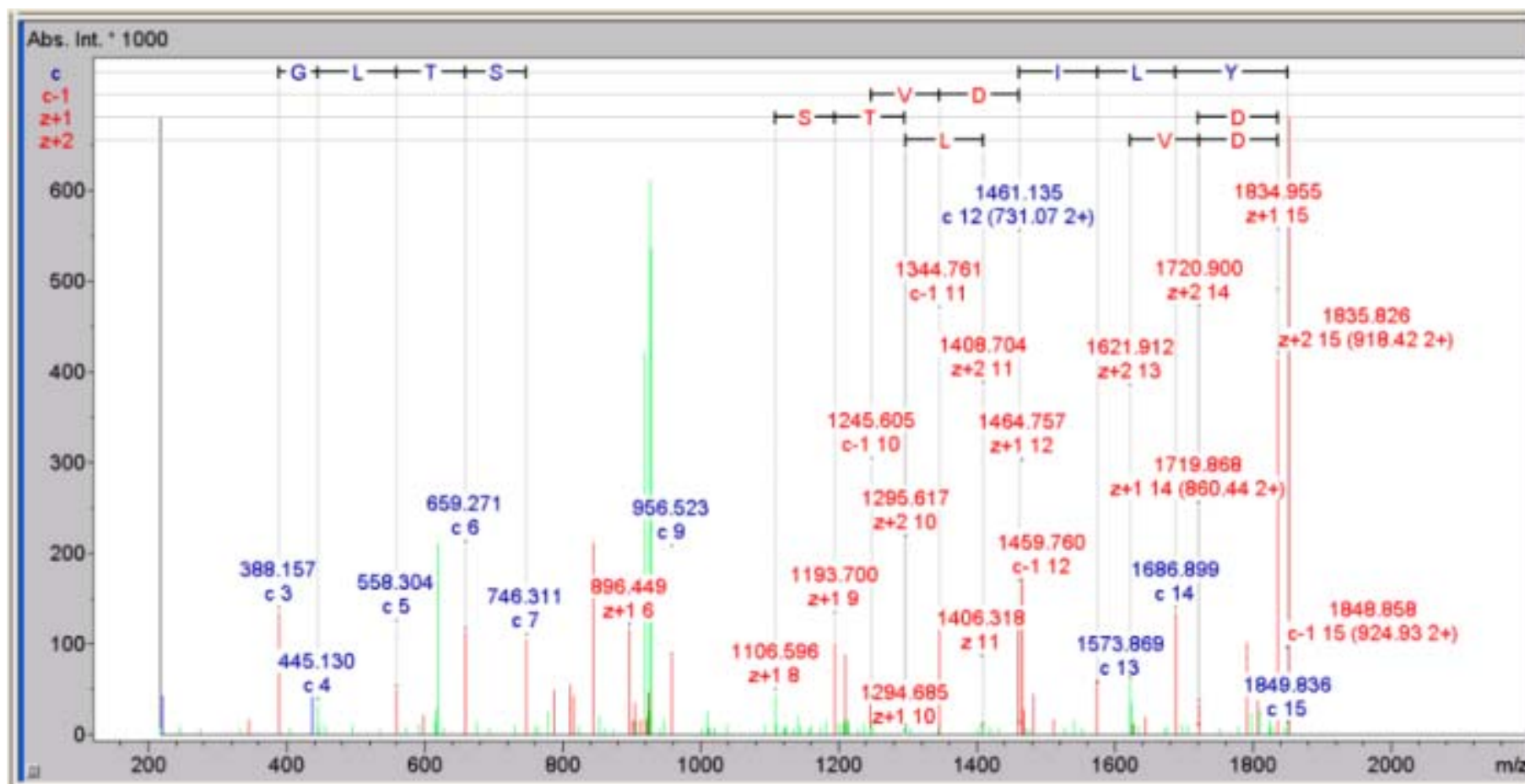
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Hexose: K222	510.75	4+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
216 Y.YQNRIDK*LHTTRSVF.D Hex(K) 230 (Chy/ETD/429/83.9/-0.0182)				



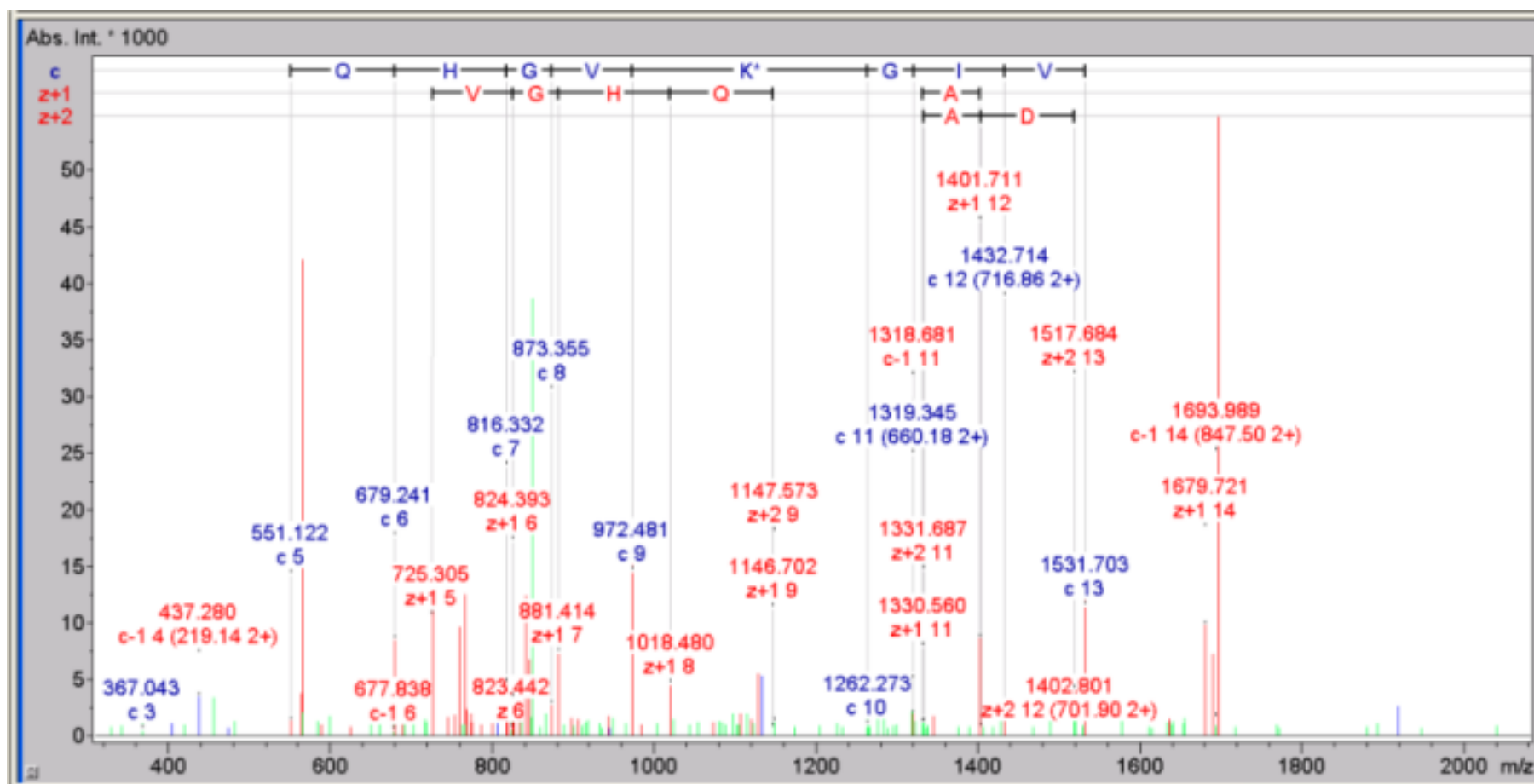
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Hexose: K240	617.66	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
231 F.DVRGLTSLPK*VDILY.G Hex(K) 245 (Chy/ETD/487/99.6/-0.0152)				



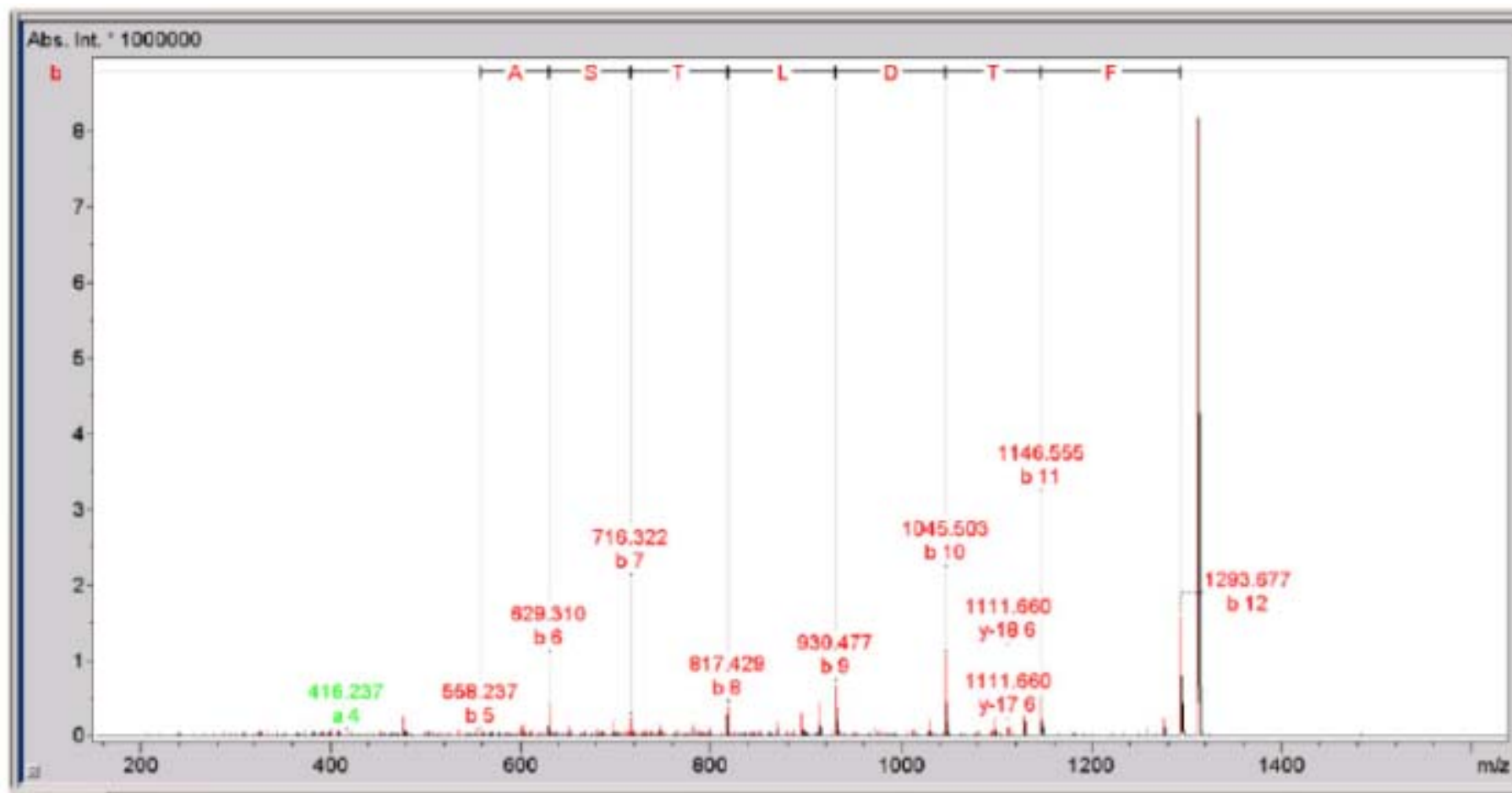
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Modiro	Hexose: K264	565.94	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
255 L.YDAAIQHGVK*GIVY.A Hex(K) 268 (Chy/ETD/279/88.9/-0.0178)				



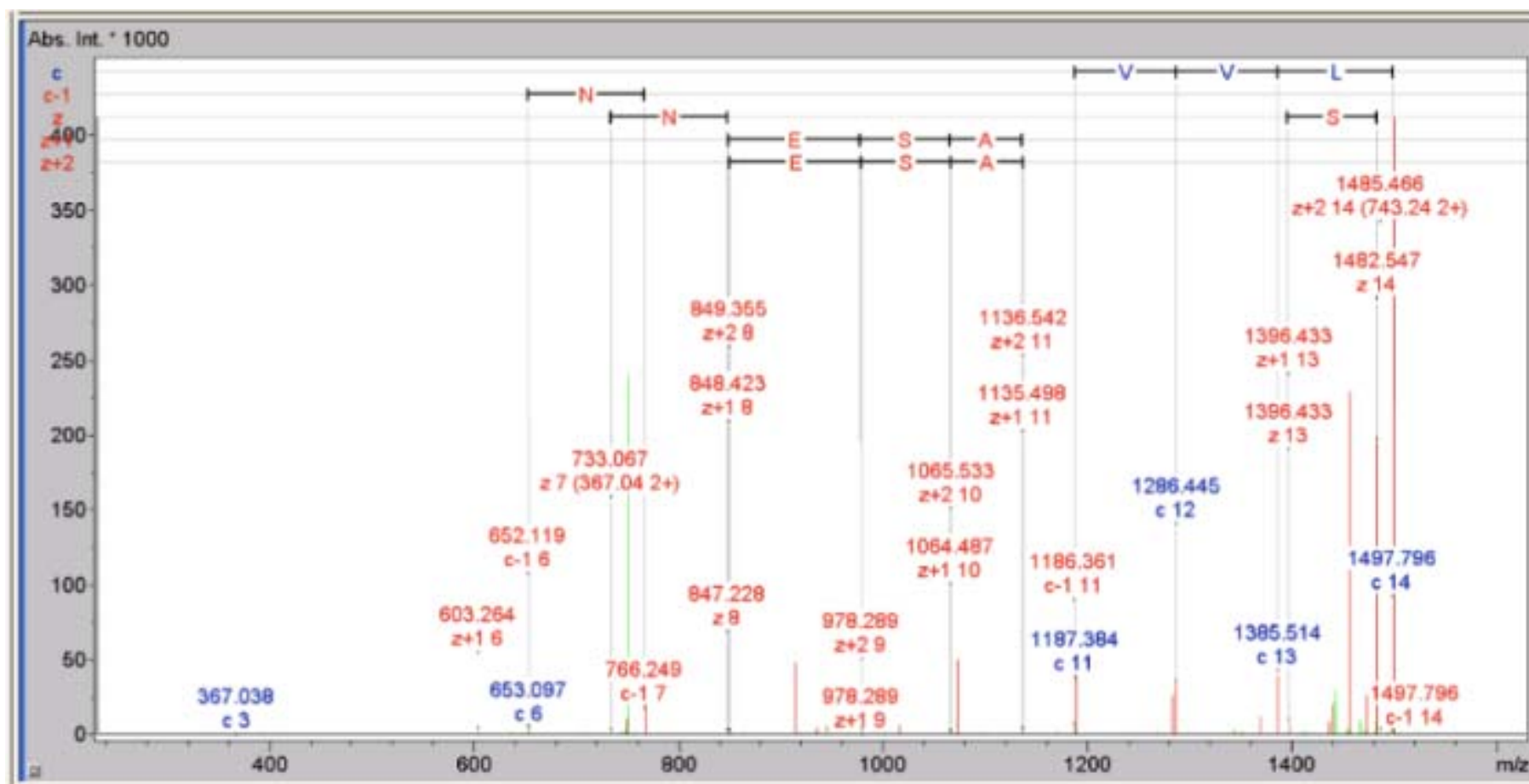
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	HexNAc2: N201	1311.61	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
187 Y.ITKTNASTLDTFKAN*EEGYL.G HexNac2(N) 206 (Chy/CID/226/98.3/-0.0271)				



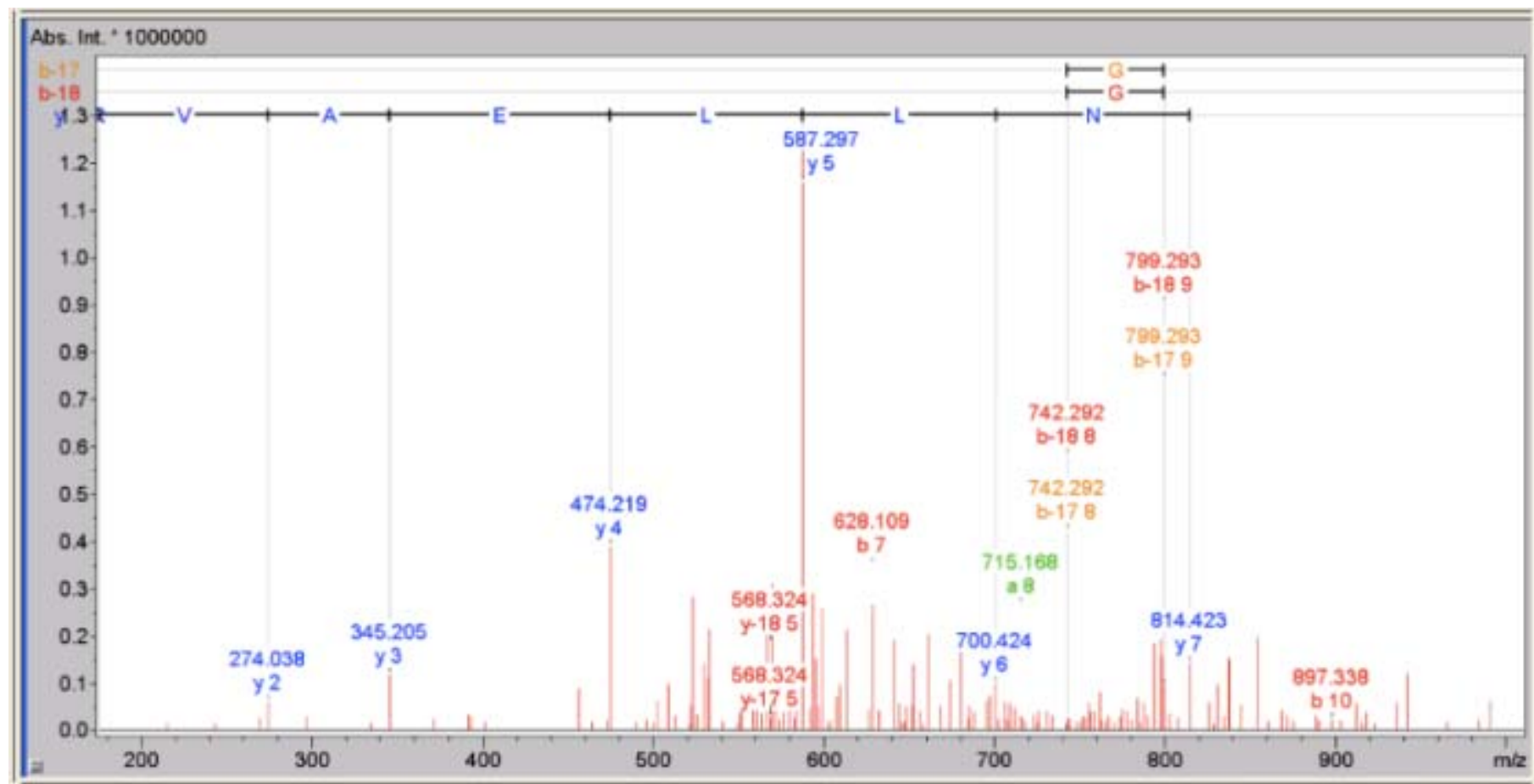
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Modiro	Hydroxylation: D89	750.29	2+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
79 F.SN*MASENMTGD*VVL.K Hydroxylation(ND) 92 (Chy/ETD/286/98.9/-0.0313)				



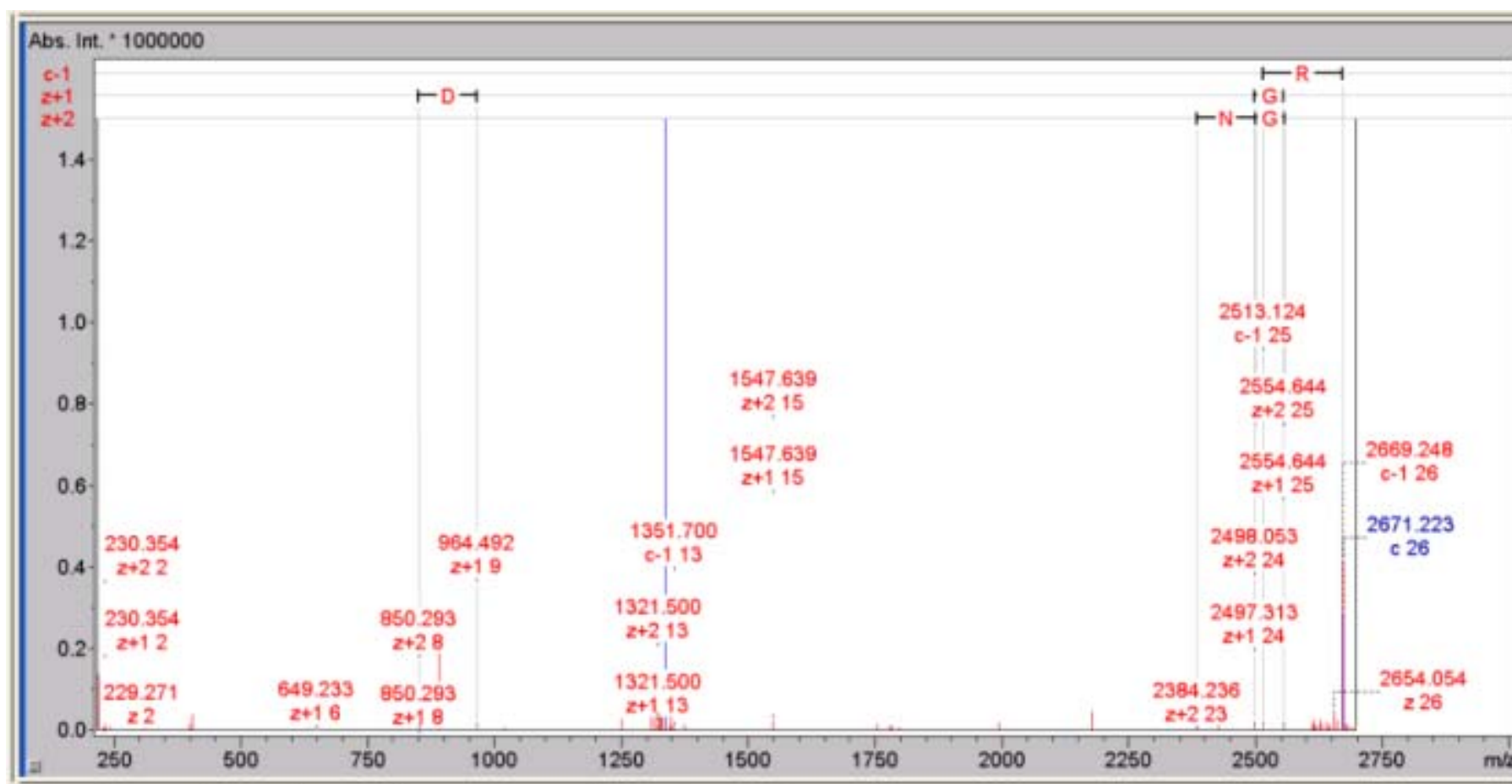
Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Hydroxylation: P144	620.01	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
144 R.P*ATAISADGPM*NLLEAVR.V Hydroxylation(P) Oxidation(M) 161 (Try/CID/282/82.4/0.026)				



Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 1	Modiro	Hydroxylation: P312	891.12	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
300 R.TGNGIVPPDEELP*GLVSDSLNPAHAR.I Hydroxylation(P) 325 (Try/ETD/337/92.6/0.0044)				



Modiro/ Pressurized / L-ASNase

Sample	Search engine	Modification	m/z	charge
Pressurized L-ASNase sample 2	Modiro	Palmitoylation: S40	1018.16	3+
sequence (enzyme/fragmentation/ ion score/sig. score/ mass error)				
25 K.LPNIVILATGGT*IAGS*AATGTQTTGYK.A Palmitoylation(TS) 51 (Try/CID/467/97.7/-0.129)				

