

Tb11.01.2200

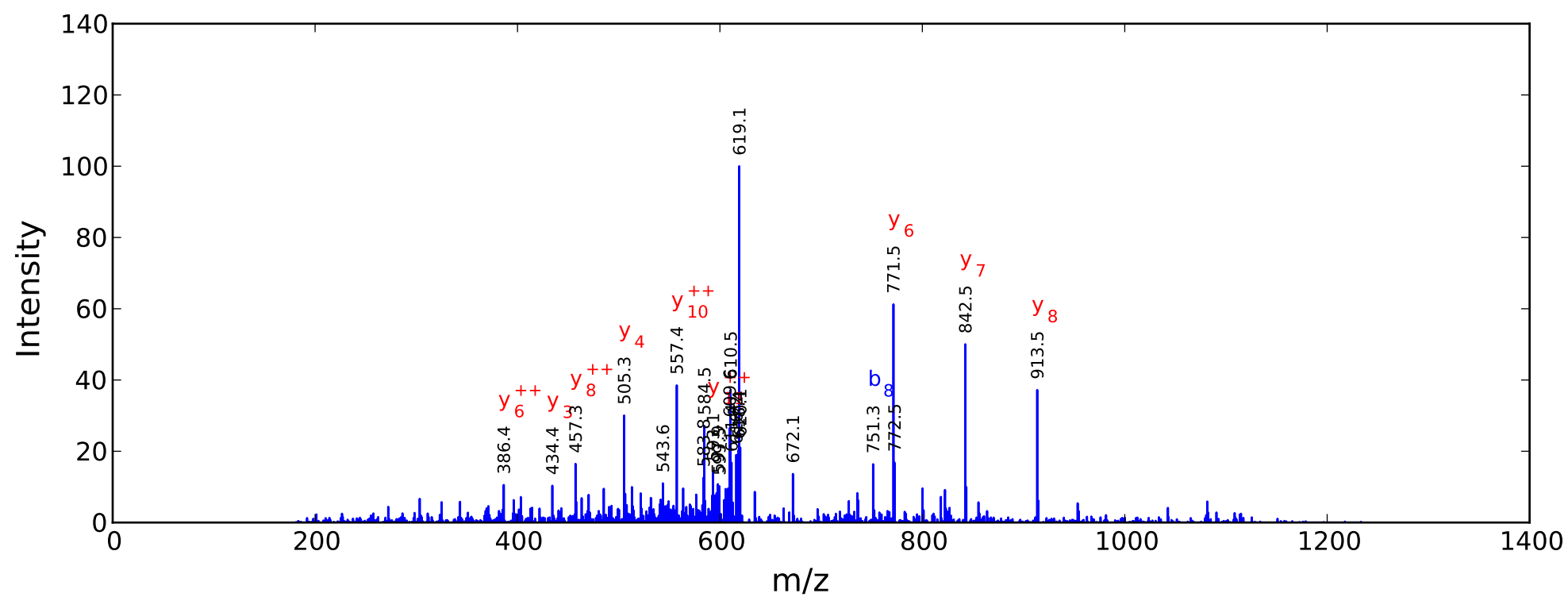
hypothetical protein, conserved

Peptide: AAEEAAHEAMQR

Charge State: 2.0

Modifications: None

m/z: 628.296245



Tb11.02.3930

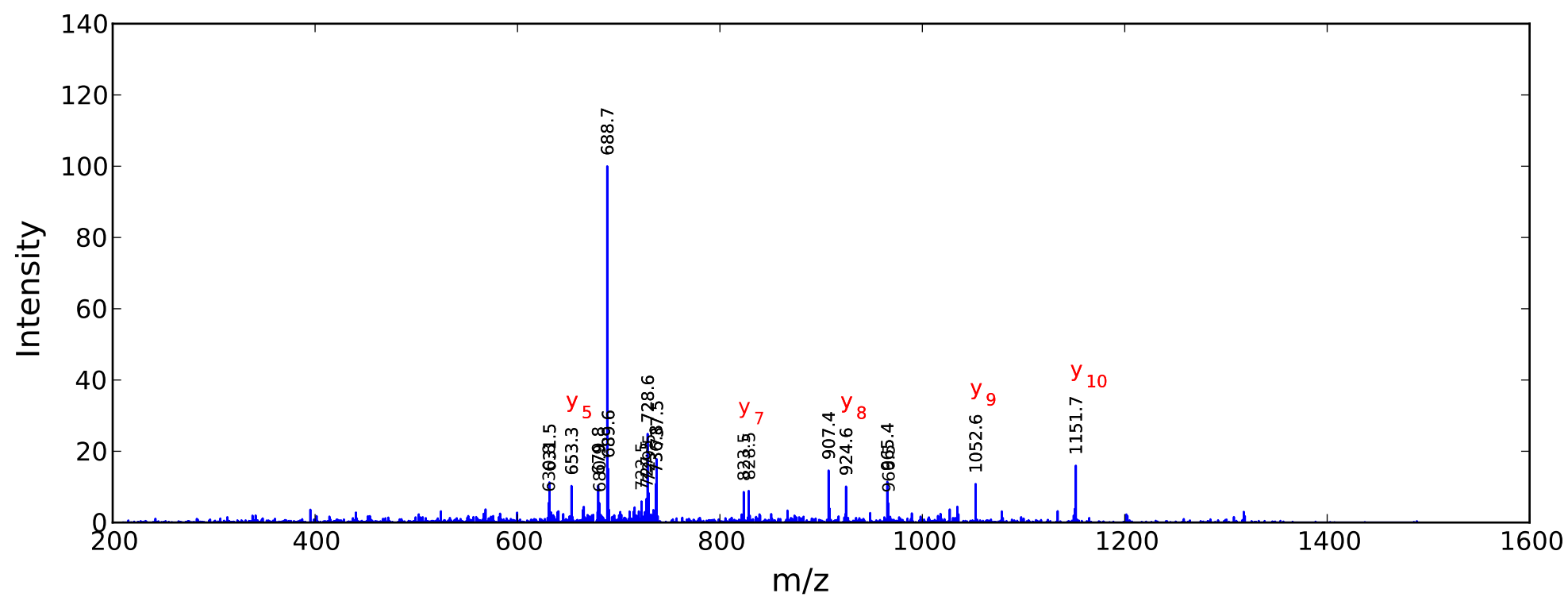
hypothetical protein, conserved

Peptide: ALGVVQTAVEEGYR

Charge State: 2.0

Modifications: None

m/z: 746.393935



Tb927.10.5120

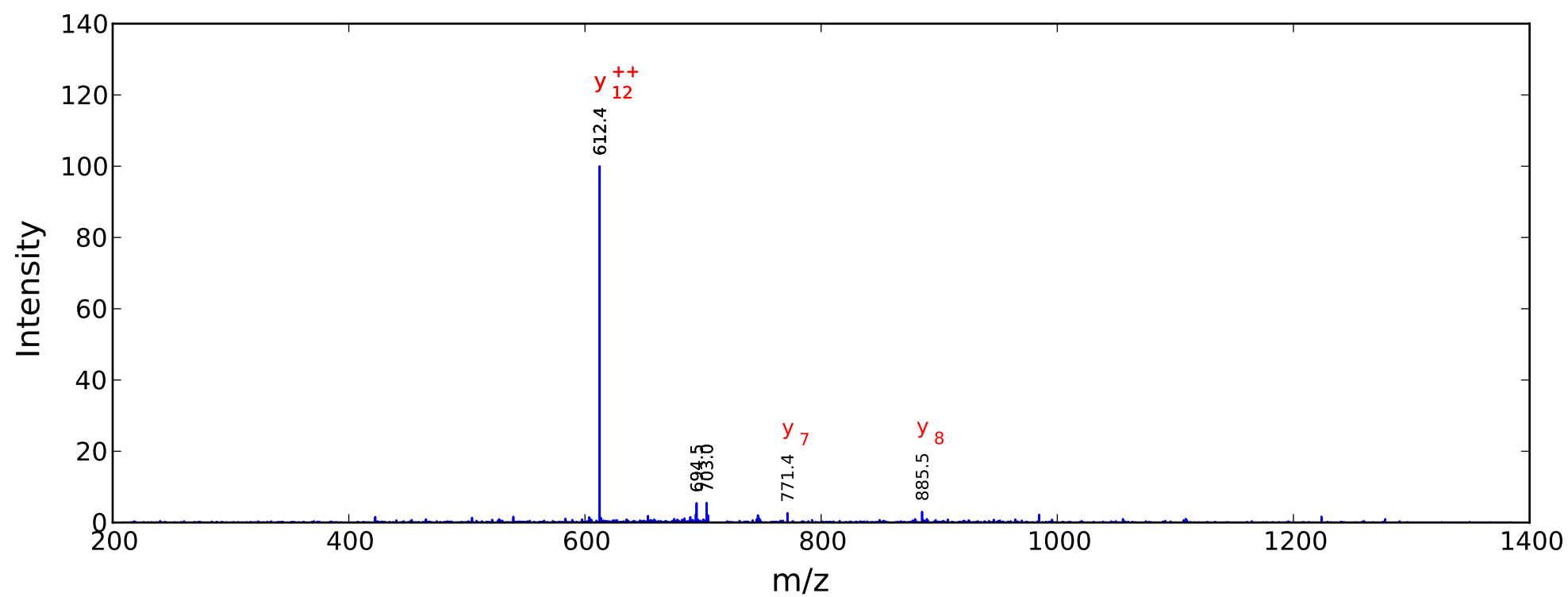
KREPA6

Peptide: TVPAAVNPAVEDIK

Charge State: 2.0

Modifications: None

m/z: 712.3934



Tb927.3.5630

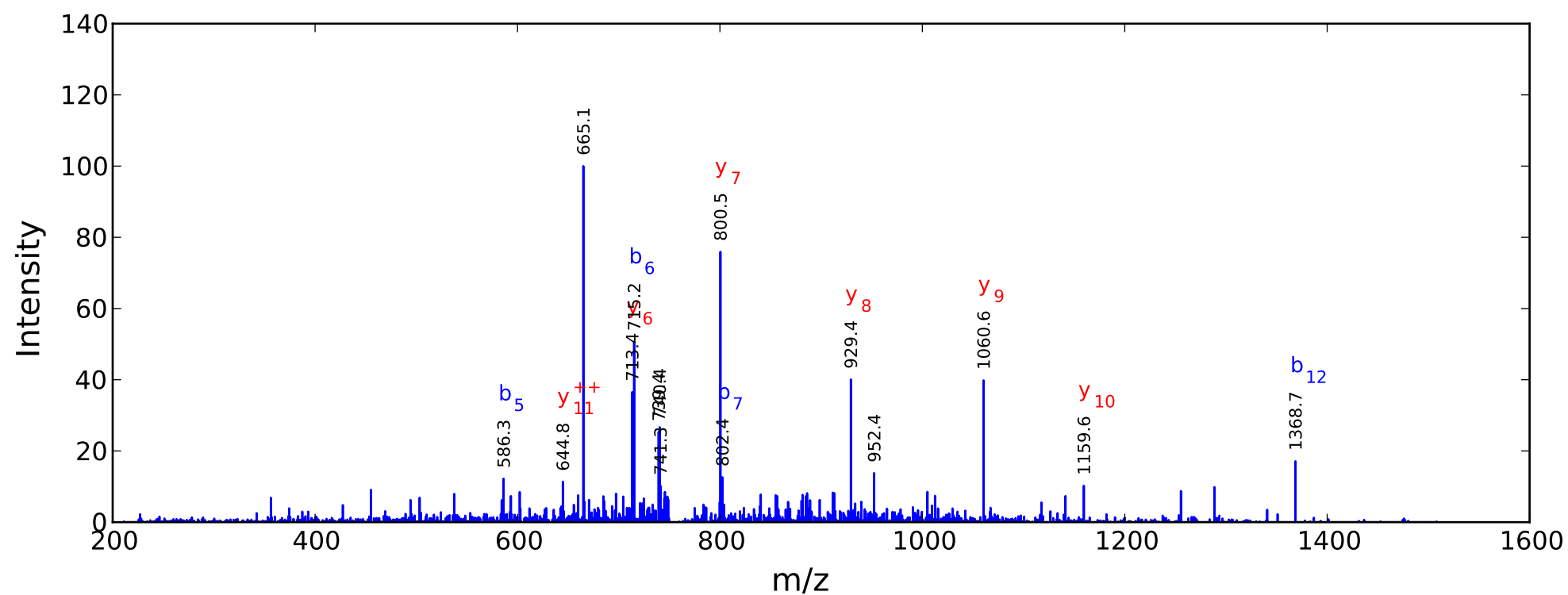
3,2-trans-enoyl-CoA isomerase, mitochondrial precursor, putative

Peptide: LIEVMESPIENIK

Charge State: 2.0

Modifications: None

m/z: 757.910575



Tb927.4.1070

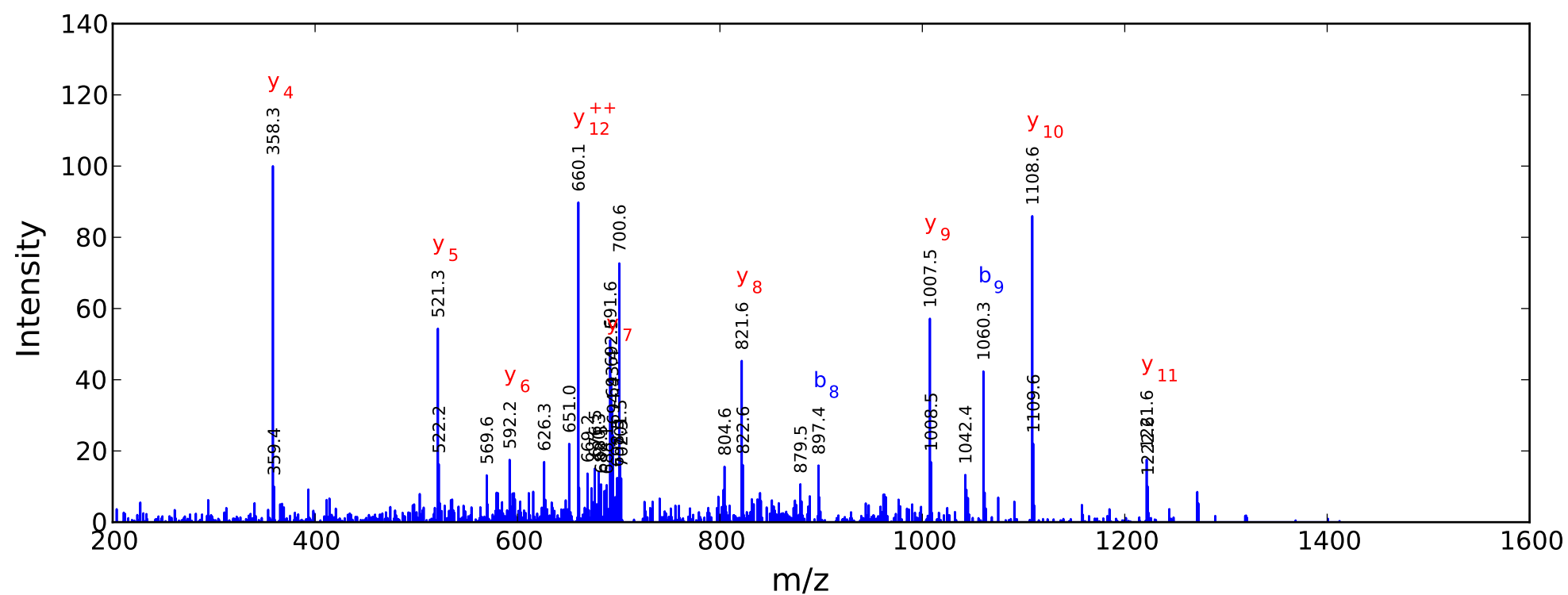
50S ribosomal protein L13, putative

Peptide: VPITWQTAYPGGK

Charge State: 2.0

Modifications: None

m/z: 709.37756



Tb927.4.4620

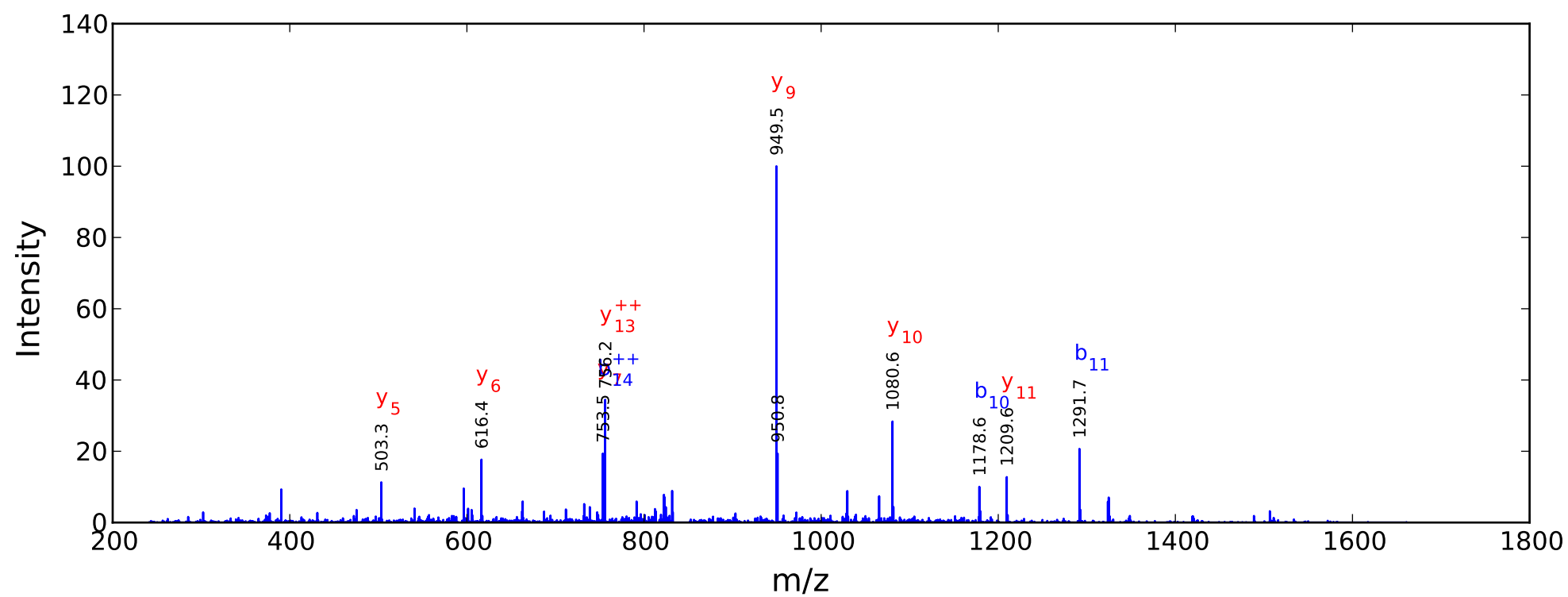
cytochrome oxidase subunit VIII

Peptide: VAWDEMPVHLIGASR

Charge State: 2.0

Modifications: None

m/z: 840.93016



Tb927.6.1890

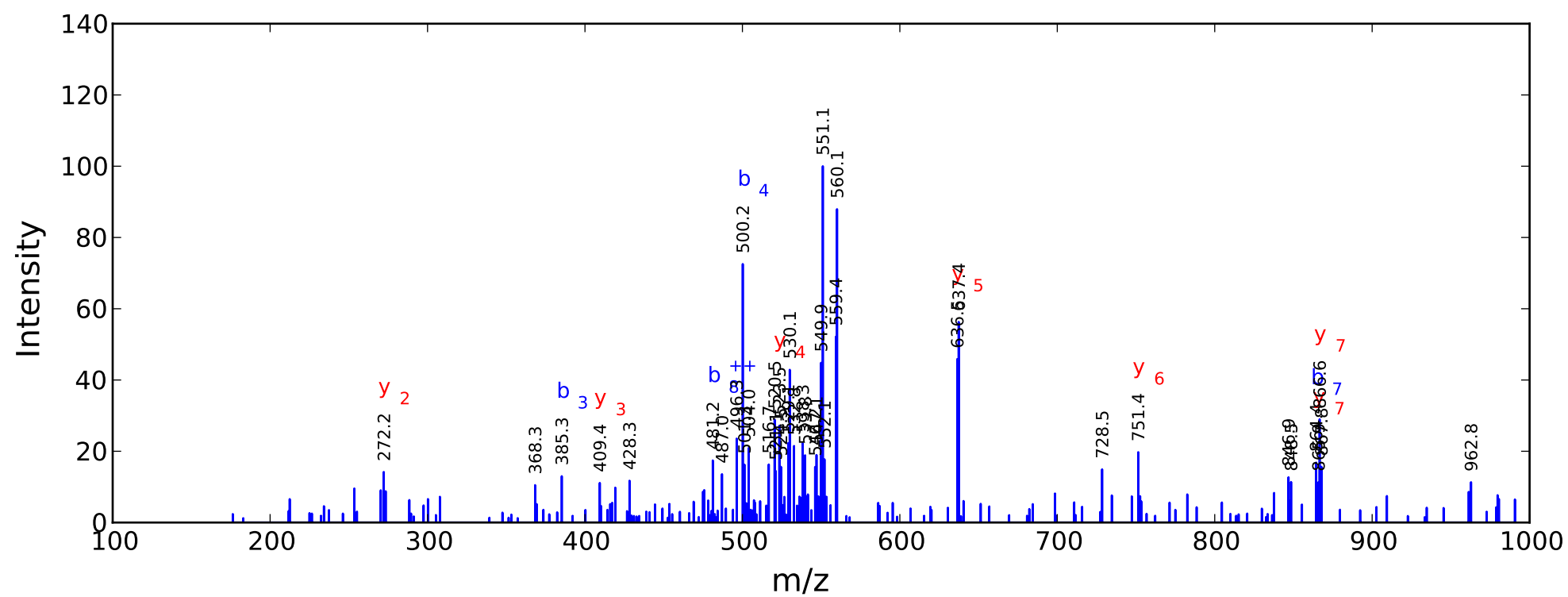
hypothetical protein, conserved

Peptide: LRDDLNHPR

Charge State: 2.0

Modifications: None

m/z: 568.30219



Tb927.6.3360

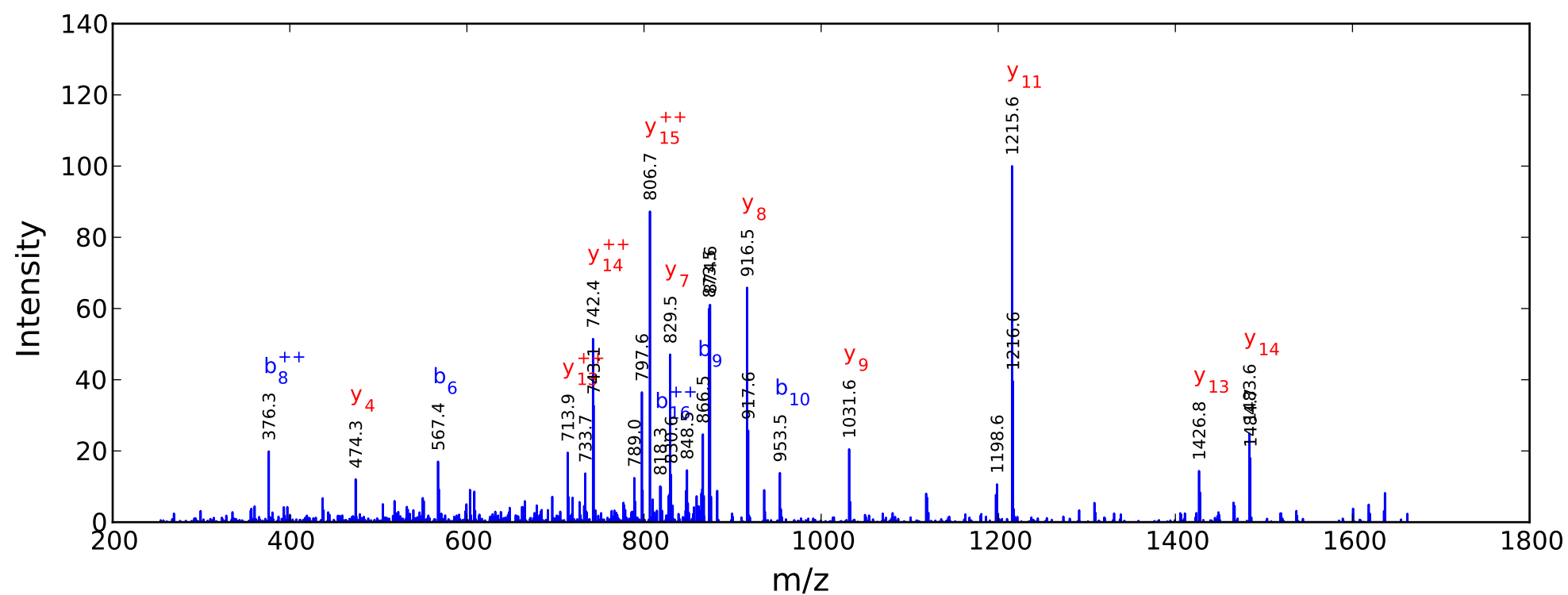
hypothetical protein, conserved

Peptide: GIQGPNPSPDSPEENNVK

Charge State: 2.0

Modifications: None

m/z: 891.41887





Tb927.6.3530

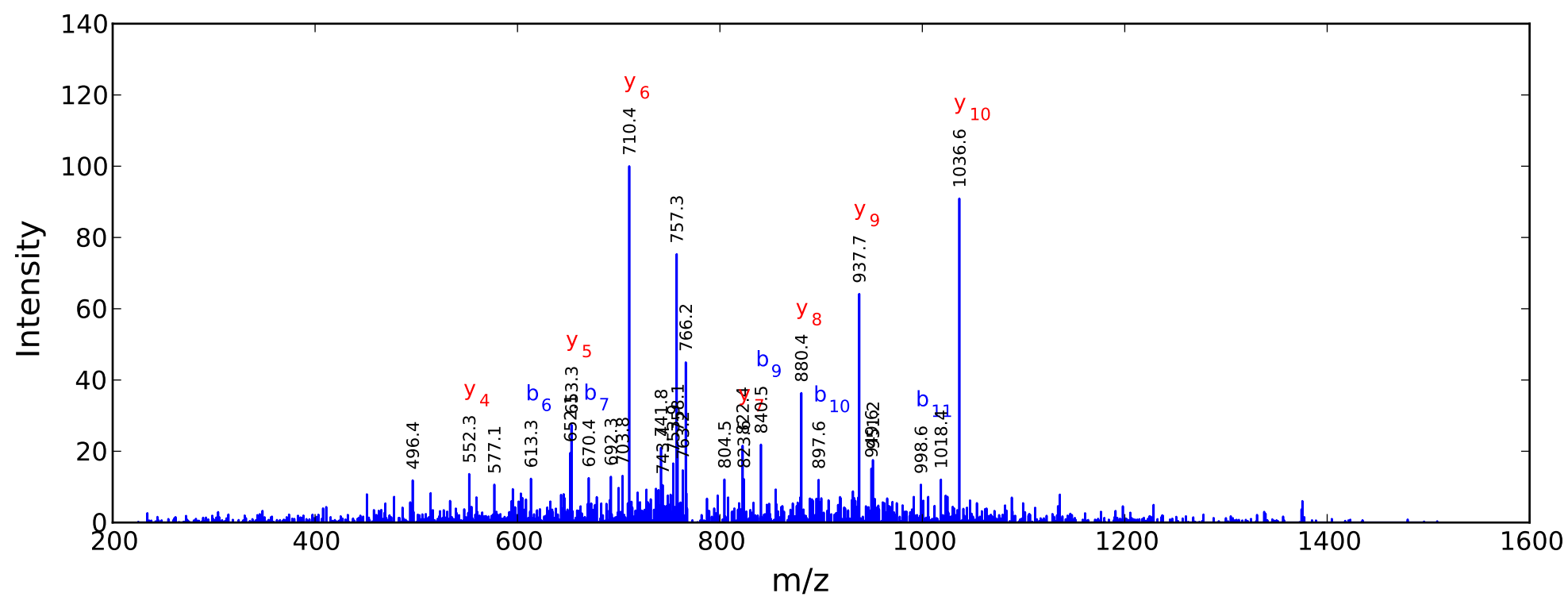
hypothetical protein, conserved

Peptide: VLTTVVGGIGTTFER

Charge State: 2.0

Modifications: None

m/z: 775.43306



Tb927.8.6890

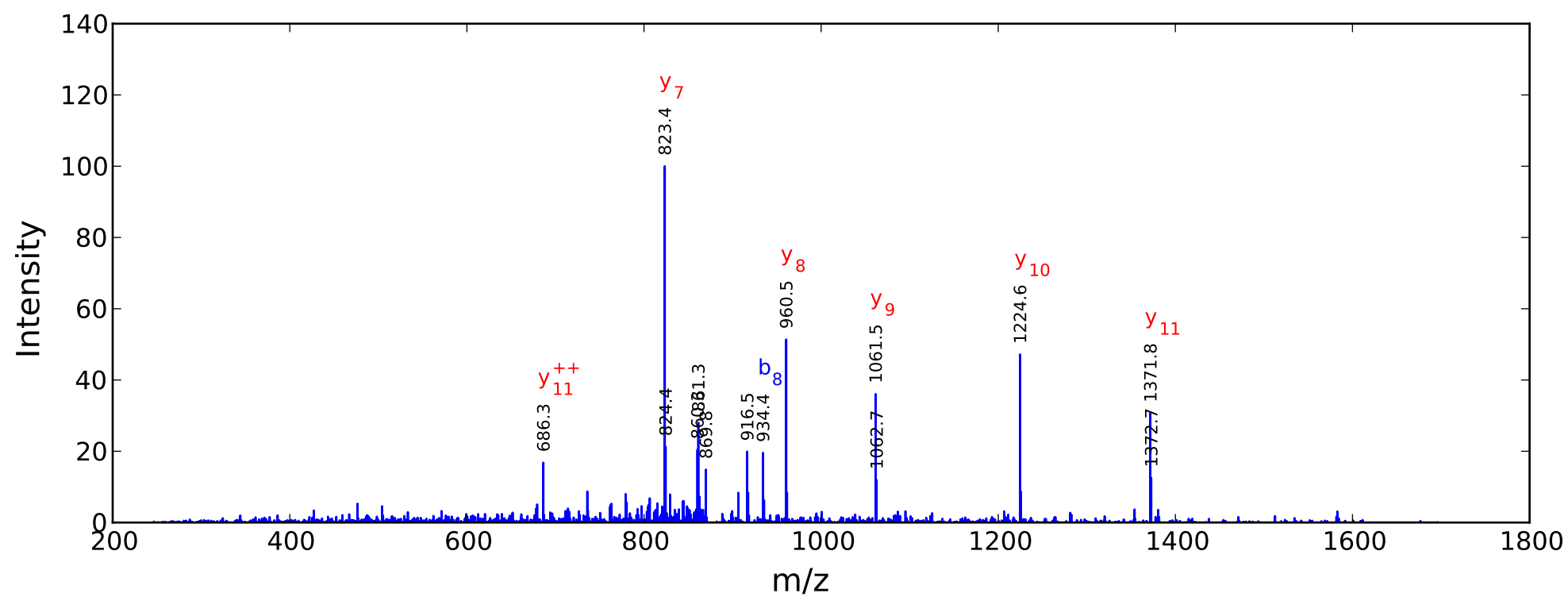
hypothetical protein, conserved

Peptide: ATNVFYTHPSYVMAR

Charge State: 2.0

Modifications: None

m/z: 878.92763



Tb09.211.3200

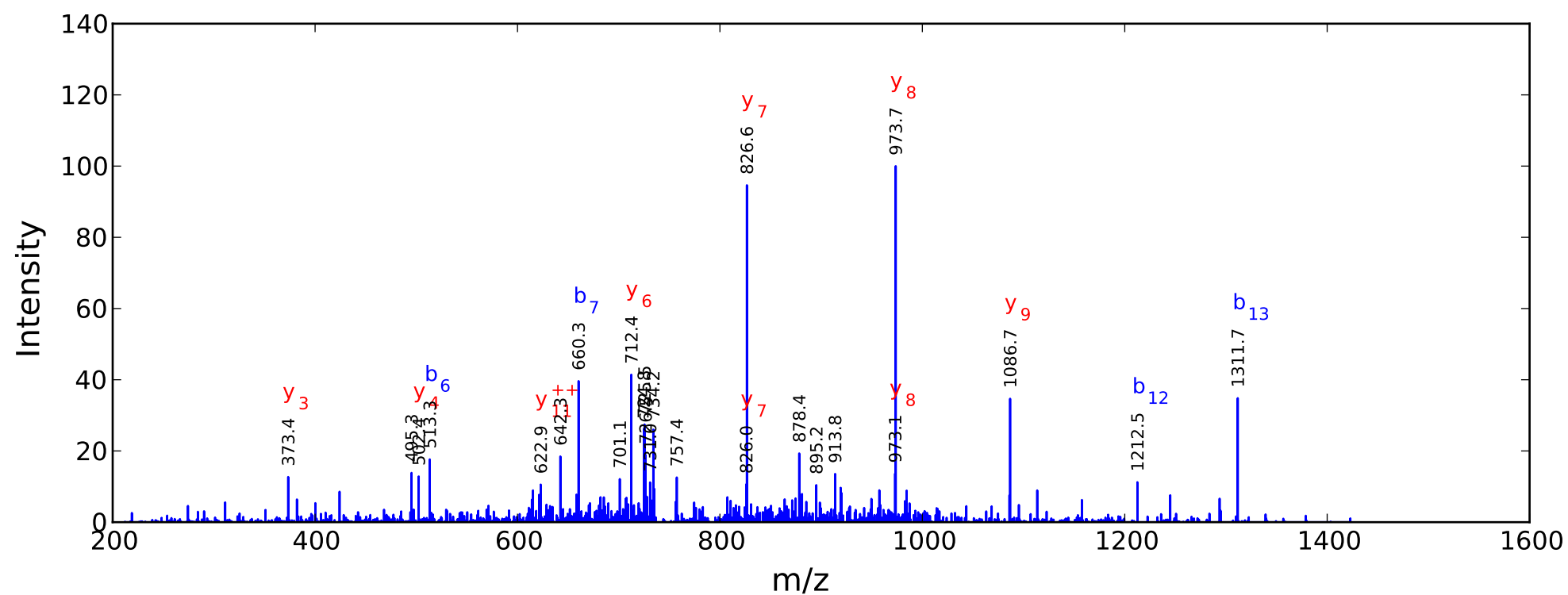
mitochondrial carrier protein, putative

Peptide: AVASALFNPIEVVR

Charge State: 2.0

Modifications: None

m/z: 743.425035



Tb11.01.0500

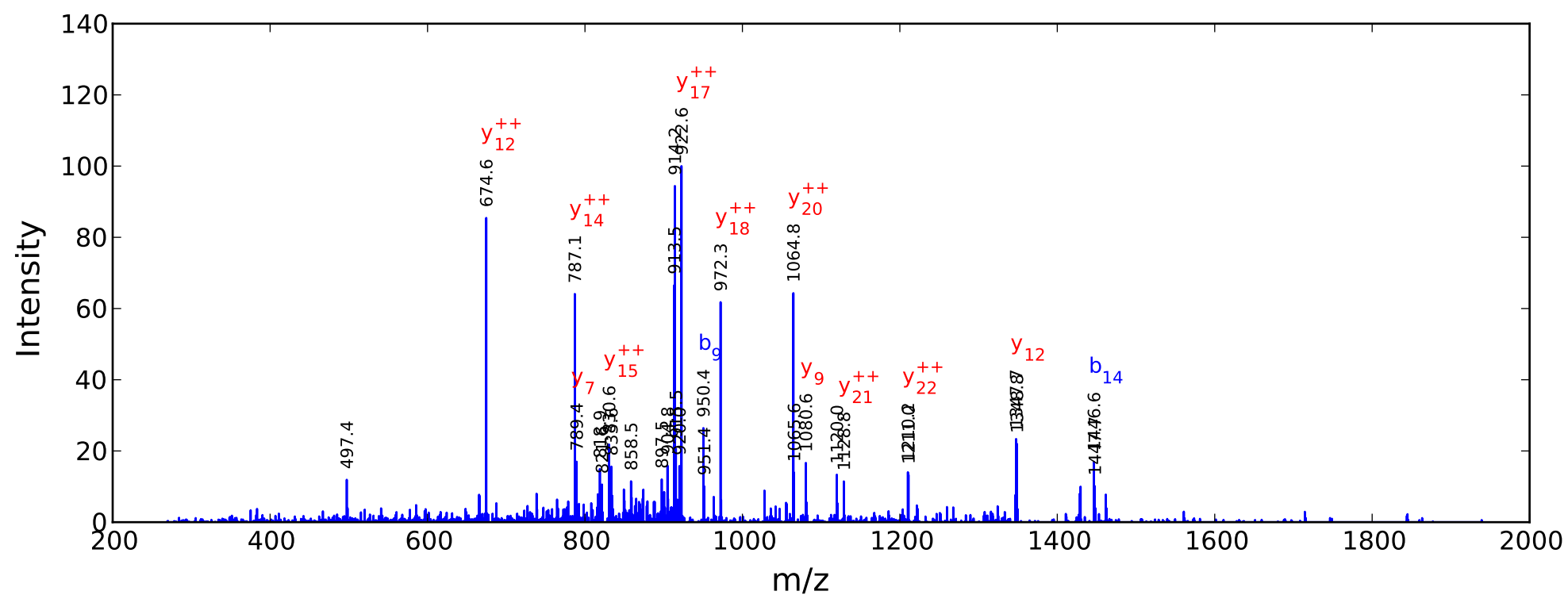
hypothetical protein, conserved

Peptide: TGTDYQGQVPSSPQPGLYQGFSDVHK

Charge State: 3.0

Modifications: None

m/z: 931.775476667



Tb11.01.6780

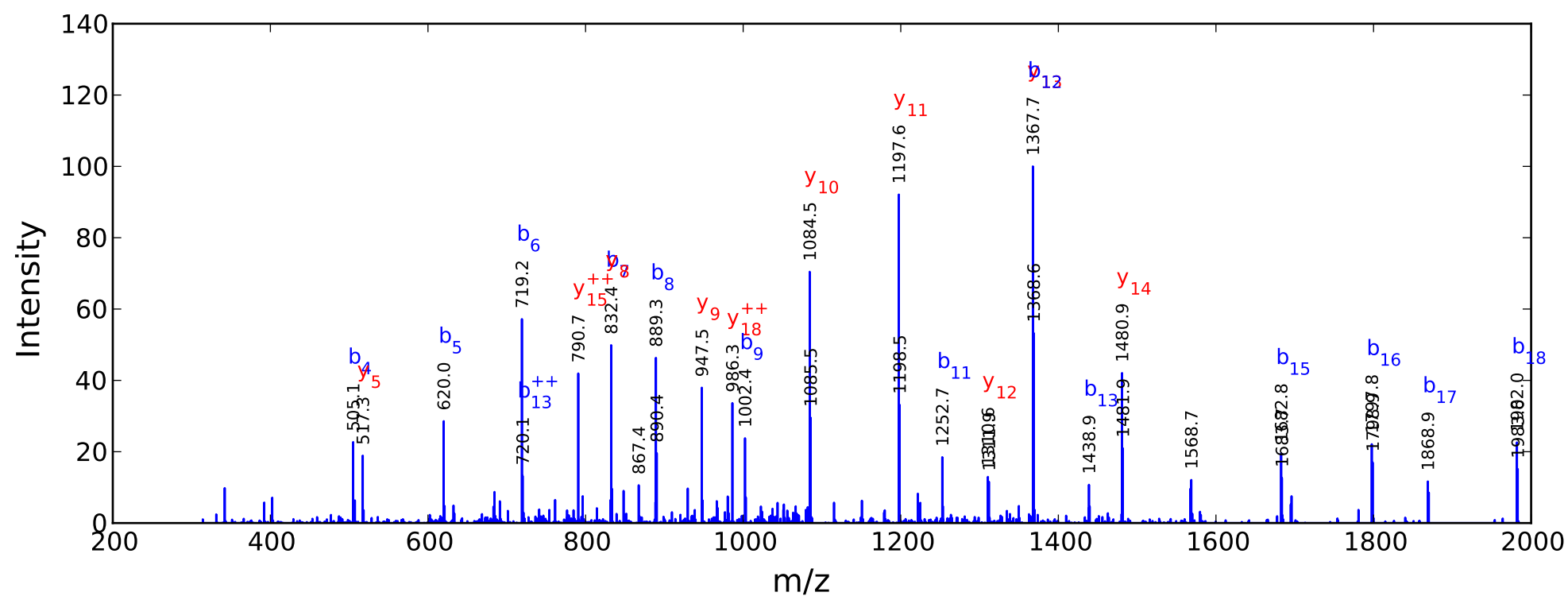
chaperone protein DNAj, putative

Peptide: ADLYDVLGILHDAEDDAIAK

Charge State: 2.0

Modifications: Residue 1, Acetyl (Protein N-term)

m/z: 1100.0446125



Tb11.01.7430

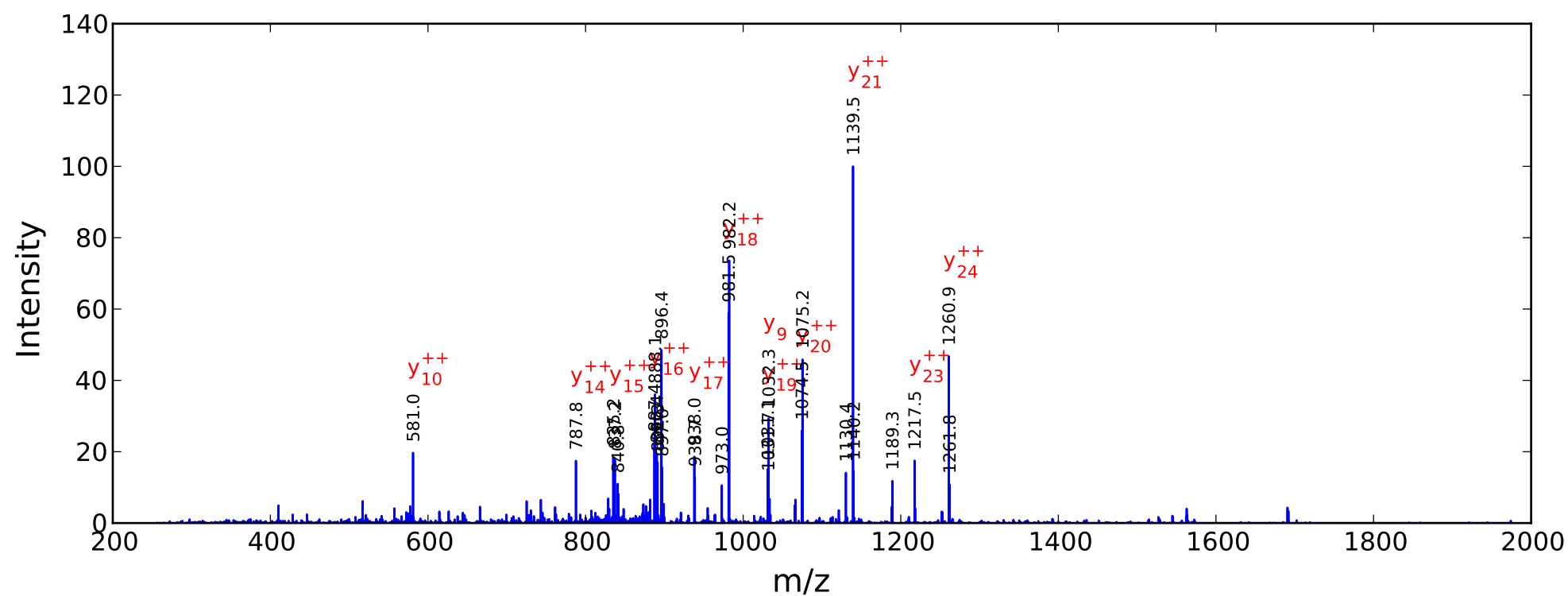
hypothetical protein, conserved

Peptide: TTSGVESVSTTVNEGLKPQTEGSEER

Charge State: 3.0

Modifications: None

m/z: 908.10544



Tb11.02.3065

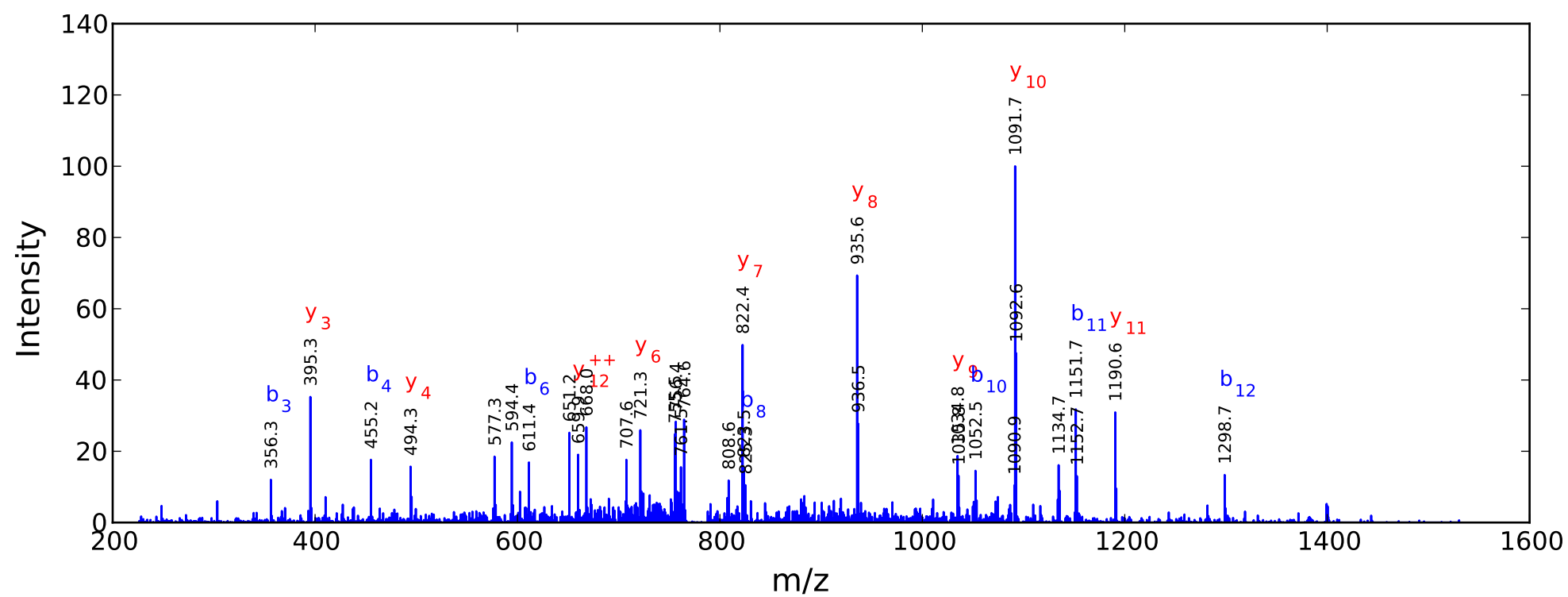
hypothetical protein, conserved

Peptide: LNQVGvitNIVFTK

Charge State: 2.0

Modifications: None

m/z: 773.4538



Tb11.02.5290

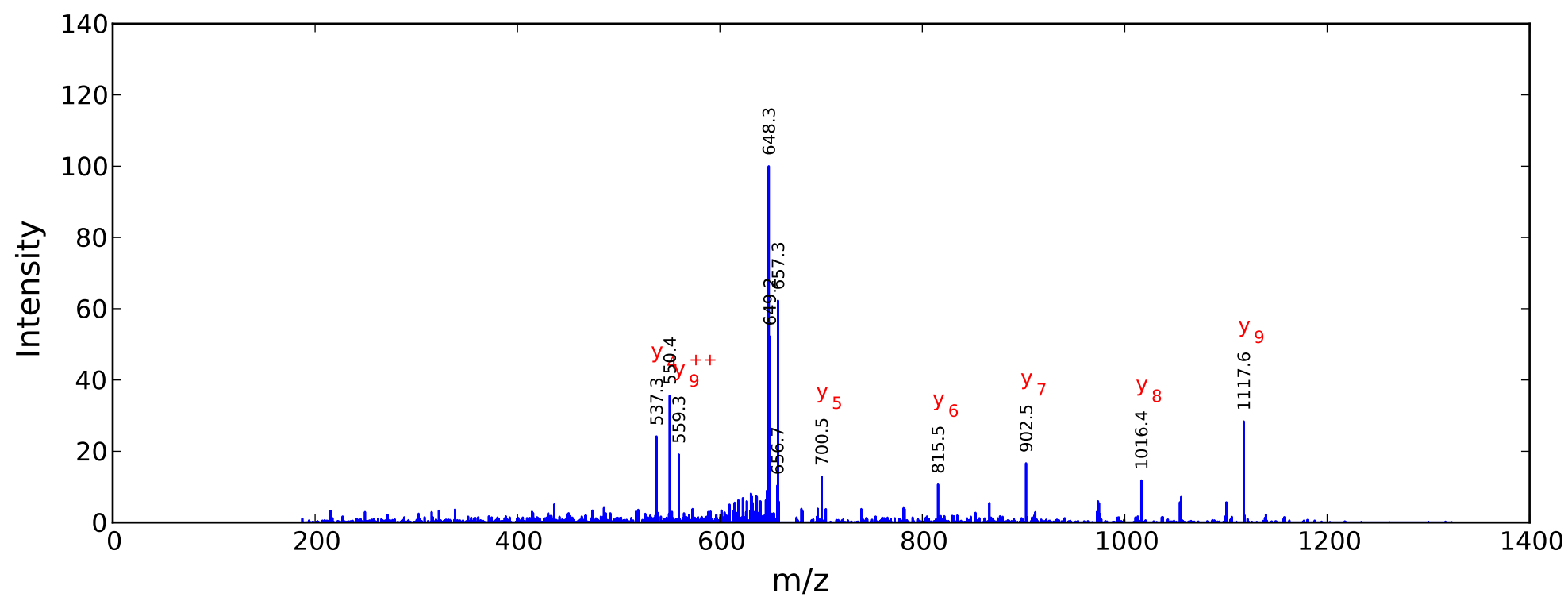
hypothetical protein, conserved

Peptide: TLTNSDYTNFR

Charge State: 2.0

Modifications: None

m/z: 666.31517





Tb11.03.0490

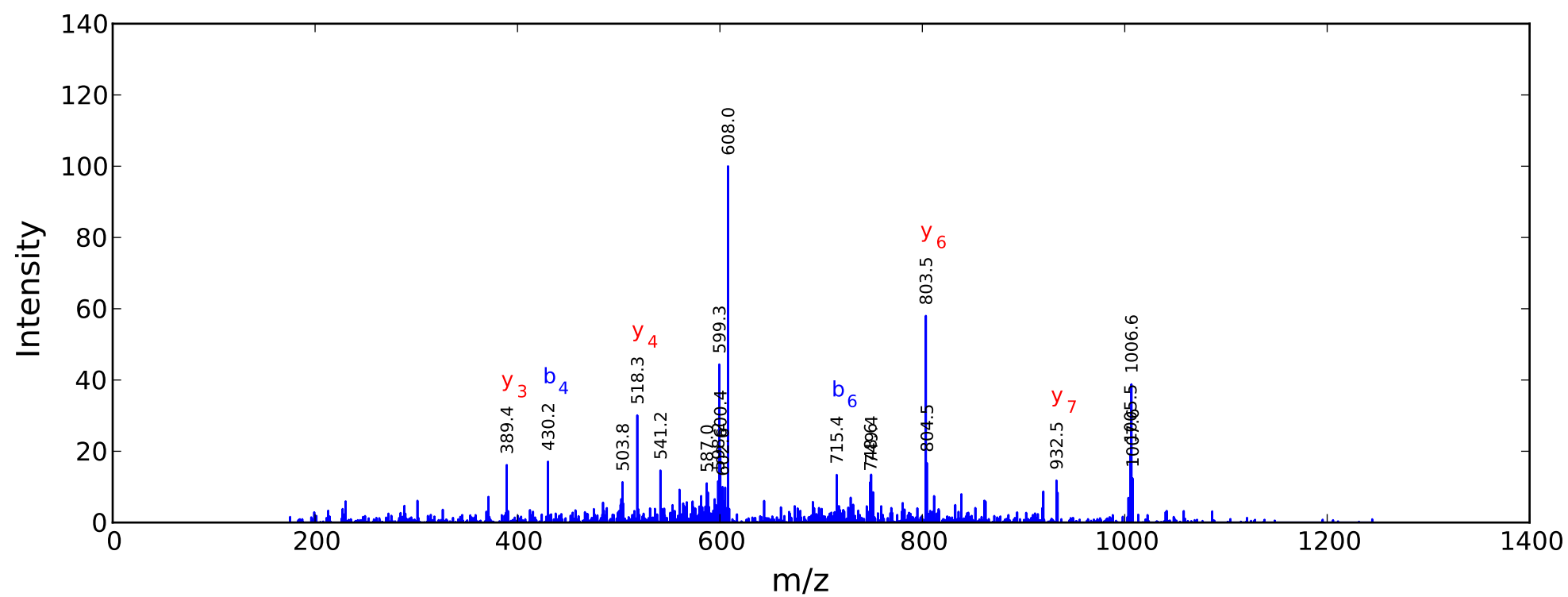
hypothetical protein, conserved

Peptide: NDAEWVETLR

Charge State: 2.0

Modifications: None

m/z: 616.799145



Tb11.52.0019

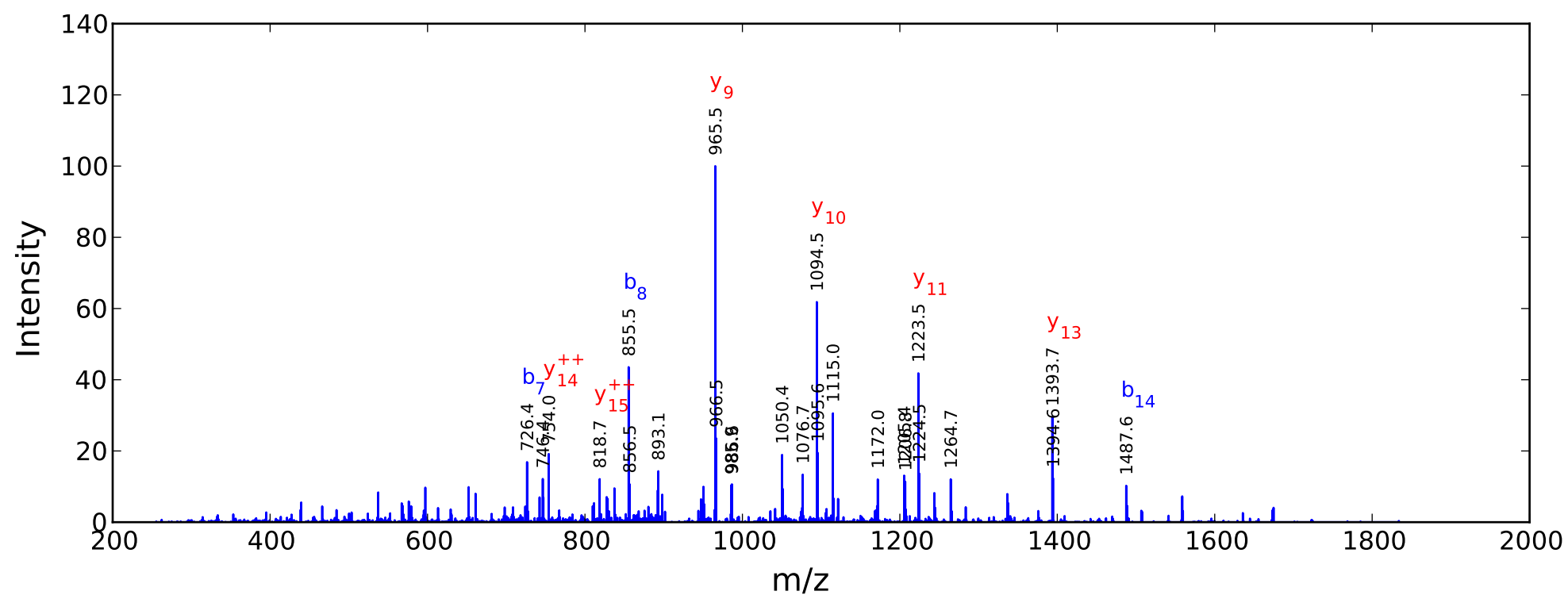
hypothetical protein, conserved

Peptide: ALELGLEEPTDDGFADK

Charge State: 2.0

Modifications: None

m/z: 910.43364



Tb927.1.1210

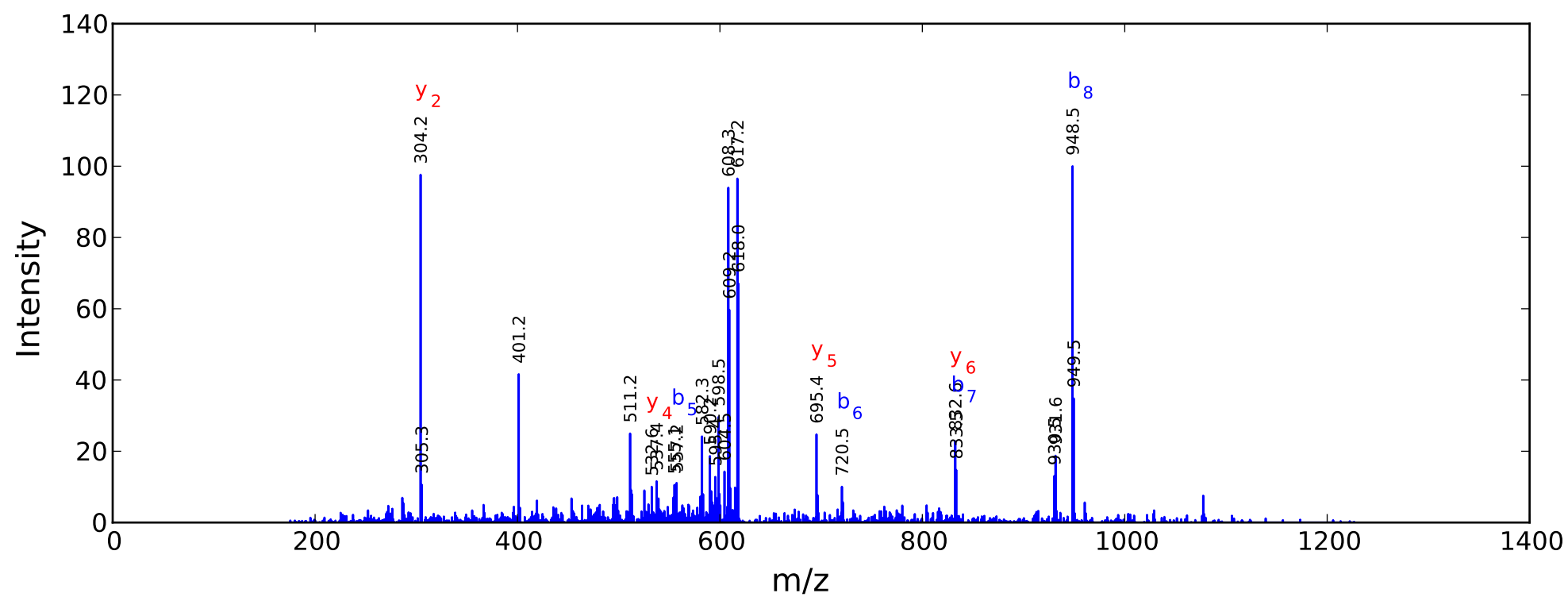
hypothetical protein, conserved

Peptide: GSFQHYLDER

Charge State: 2.0

Modifications: None

m/z: 626.29149



Tb927.10.13990

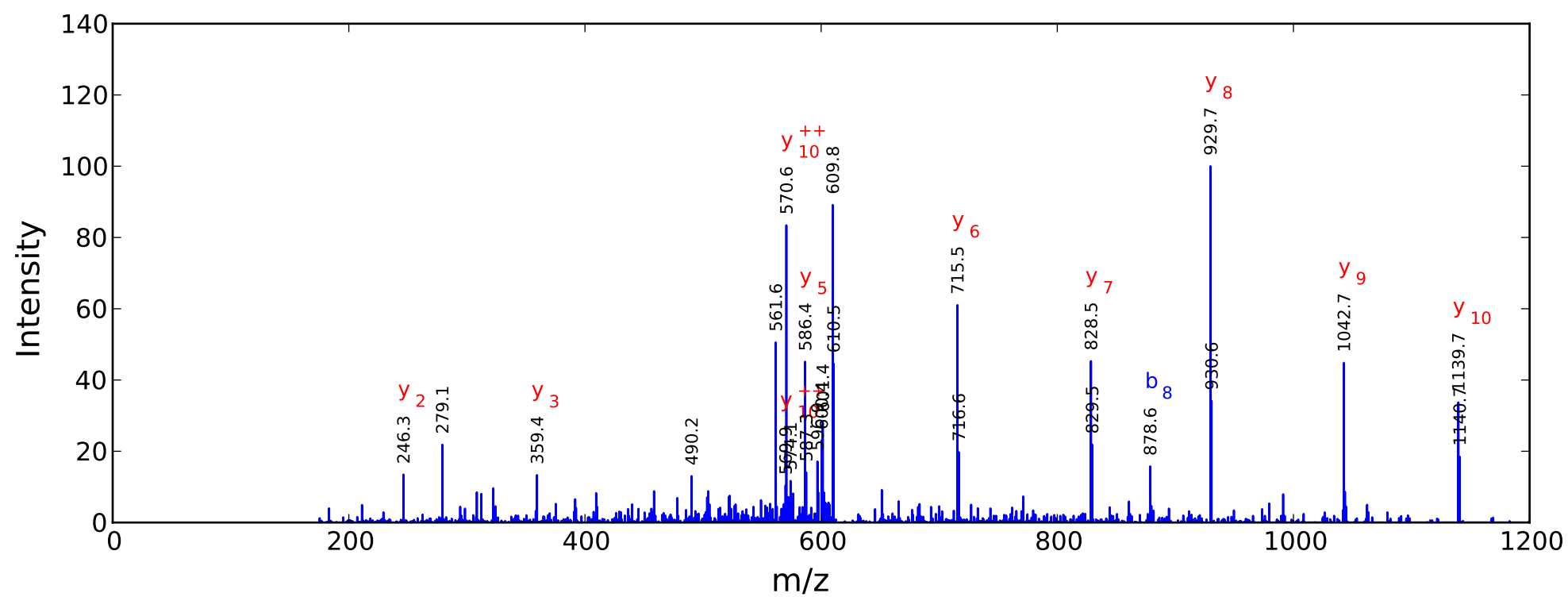
hypothetical protein, conserved

Peptide: PPLTLEQVLAR

Charge State: 2.0

Modifications: None

m/z: 618.86937



Tb927.10.14370

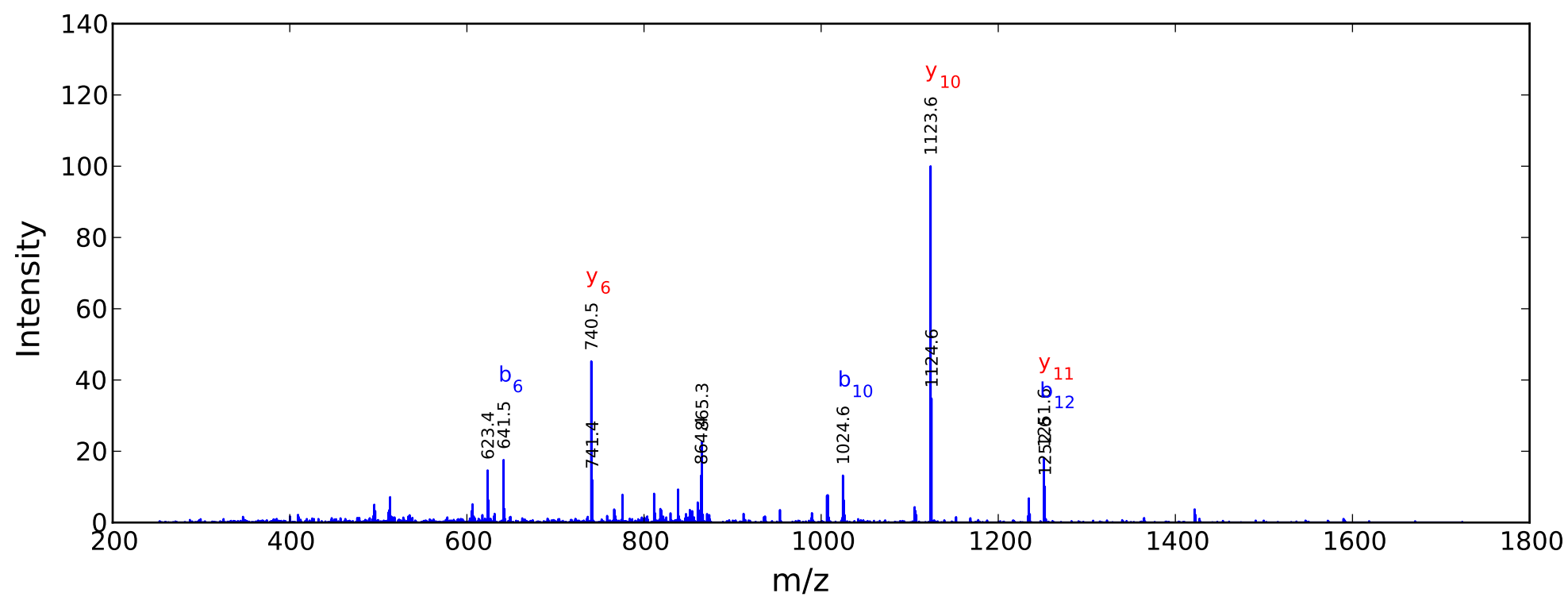
hypothetical protein, conserved

Peptide: LTQGLQPNTAPMSSYR

Charge State: 2.0

Modifications: None

m/z: 882.441105



Tb927.10.15400

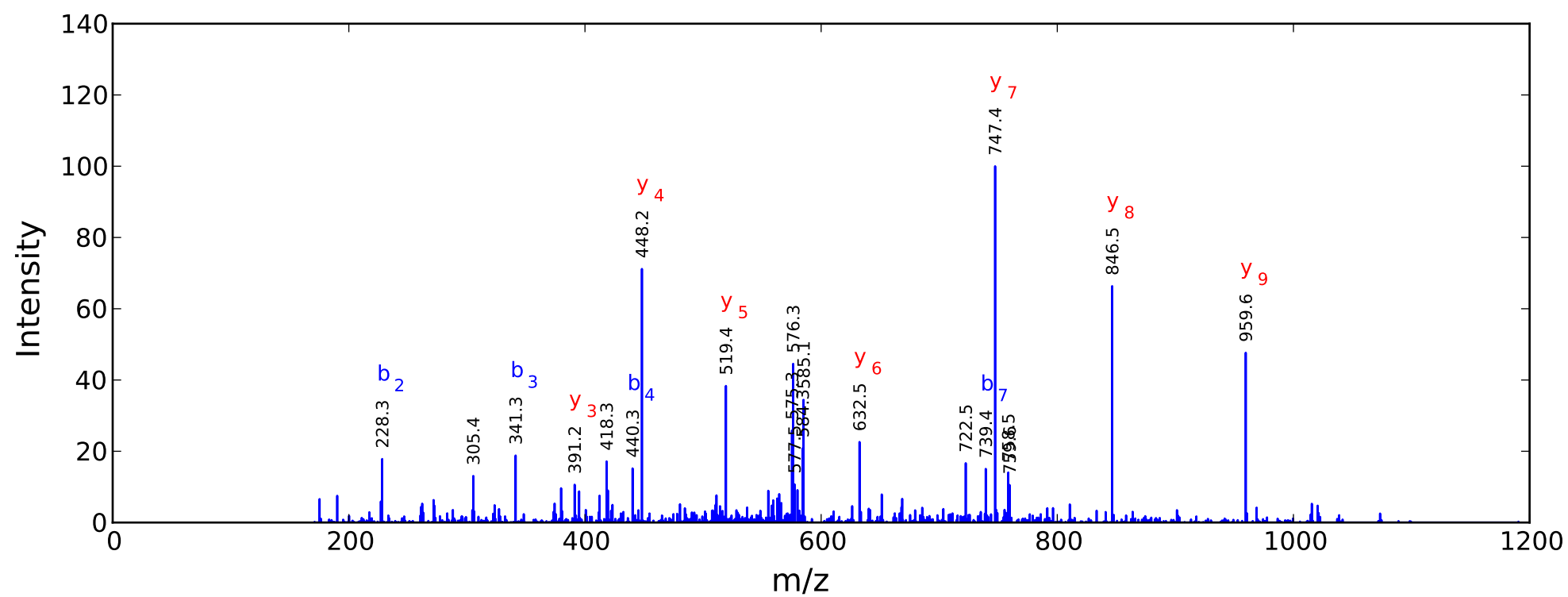
kinesin, putative

Peptide: LNLVDLAGSER

Charge State: 2.0

Modifications: None

m/z: 593.82516



Tb927.10.1870

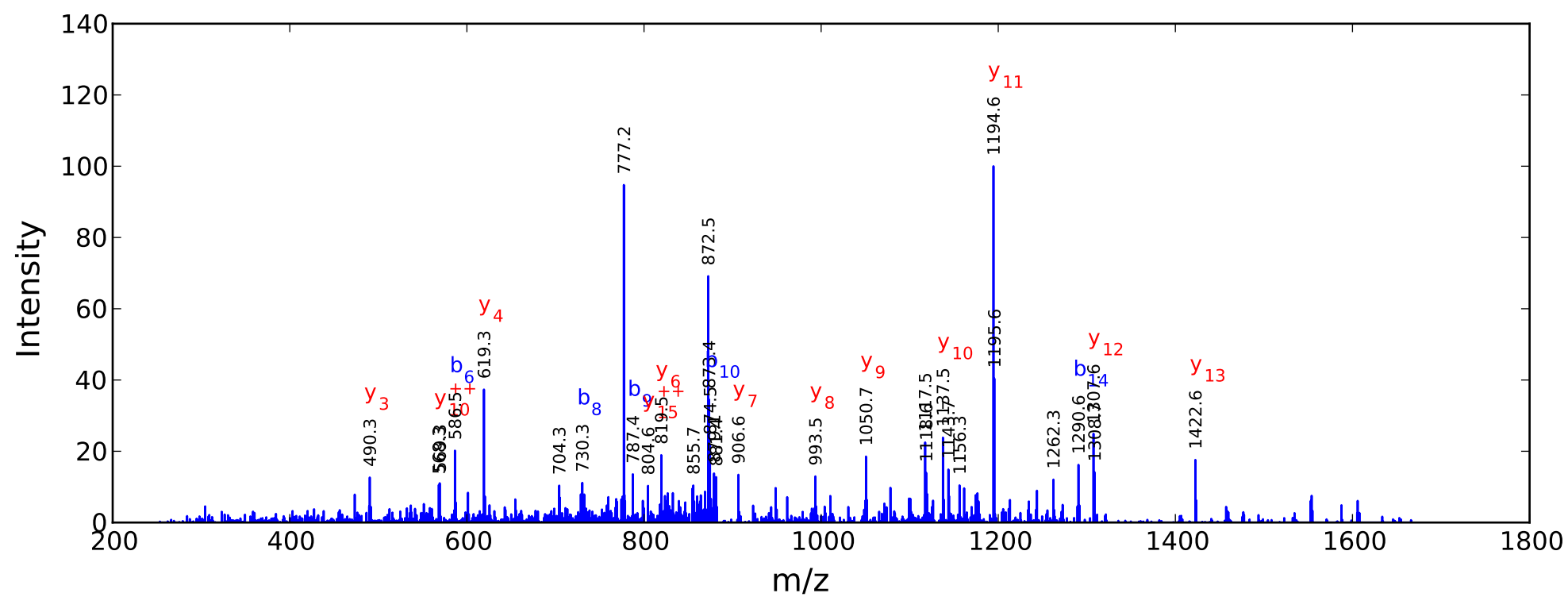
hypothetical protein, conserved

Peptide: ATNADIGSGSSSIEWER

Charge State: 2.0

Modifications: None

m/z: 890.411045



Tb927.10.3120

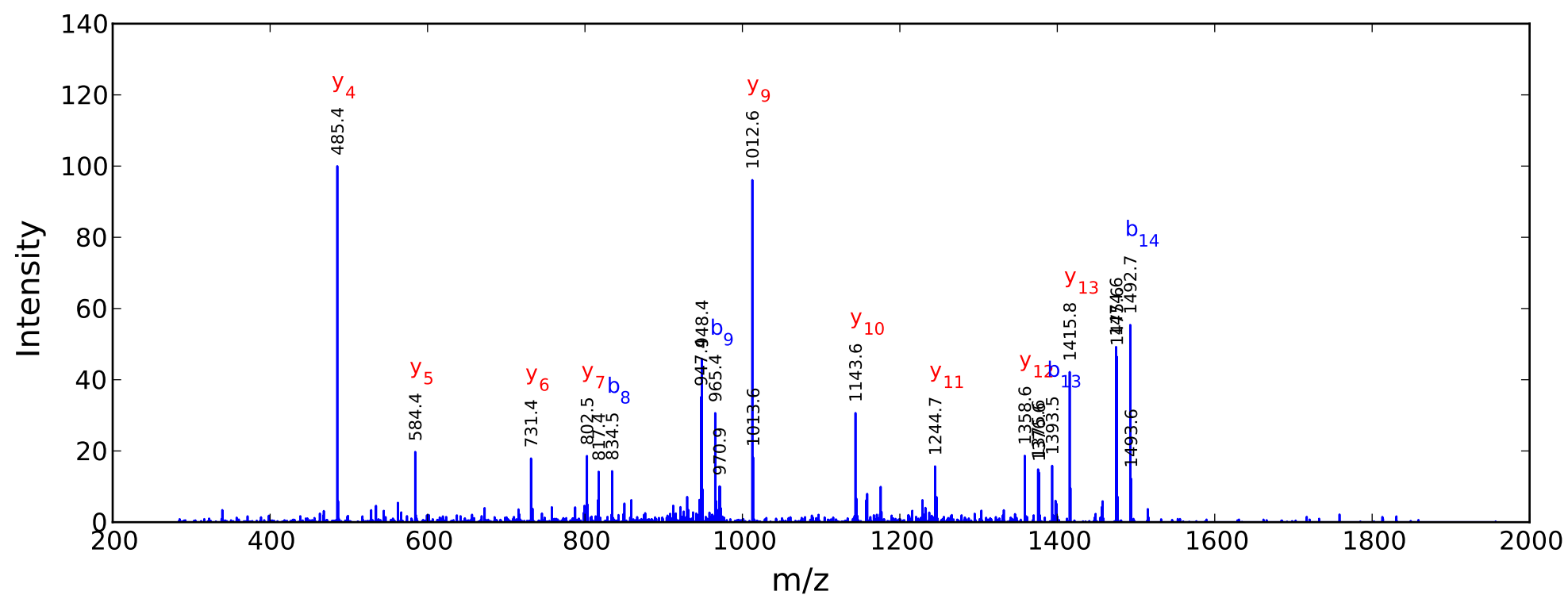
cytochrome c oxidase assembly protein, putative

Peptide: FLSDVGNTMPIAFVPLQK

Charge State: 2.0

Modifications: None

m/z: 989.02954





Tb927.10.8110

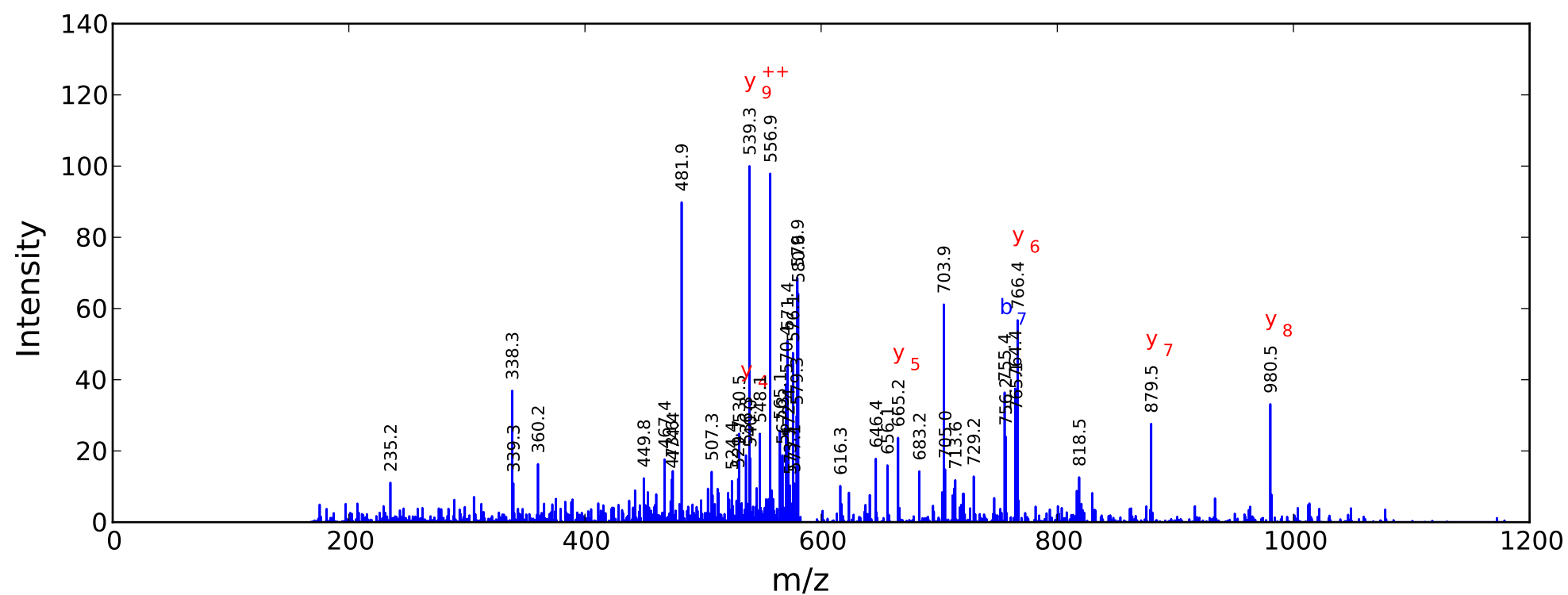
hypothetical protein, conserved

Peptide: VPTLTENQMK

Charge State: 2.0

Modifications: Residue 9, Oxidation (M)

m/z: 588.79985



Tb927.2.2140

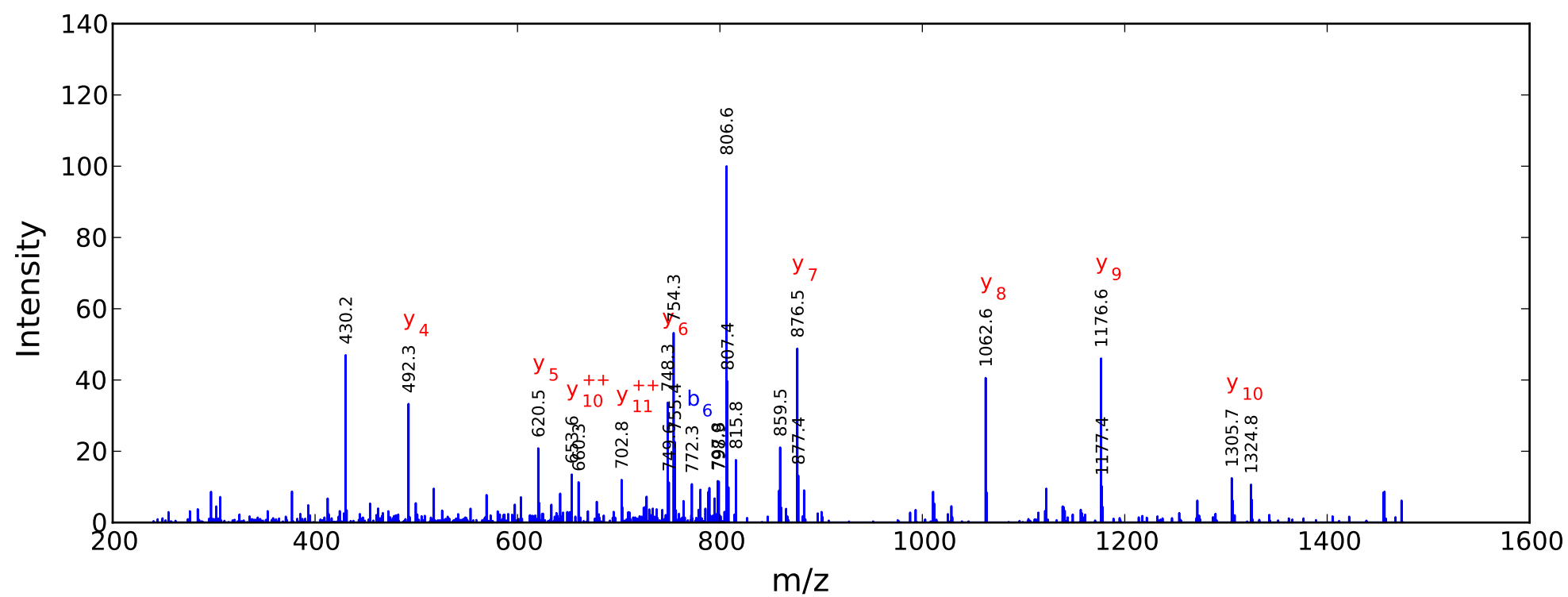
hypothetical protein, conserved

Peptide: ENVENWQQQDAMR

Charge State: 2.0

Modifications: None

m/z: 824.362855



Tb927.2.4445

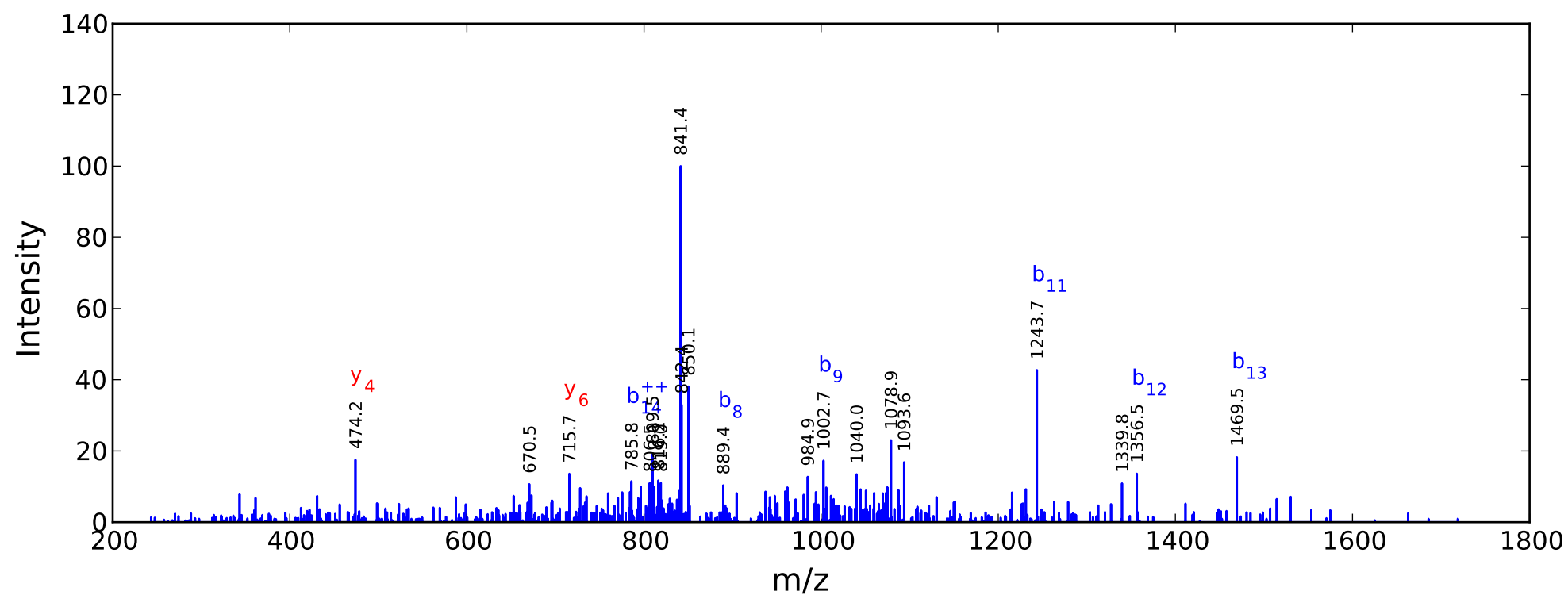
hypothetical protein, conserved

Peptide: STEATNENLQILLTK

Charge State: 2.0

Modifications:    Residue 1, Acetyl (Protein N-term)

m/z: 858.9545625



Tb927.3.2880

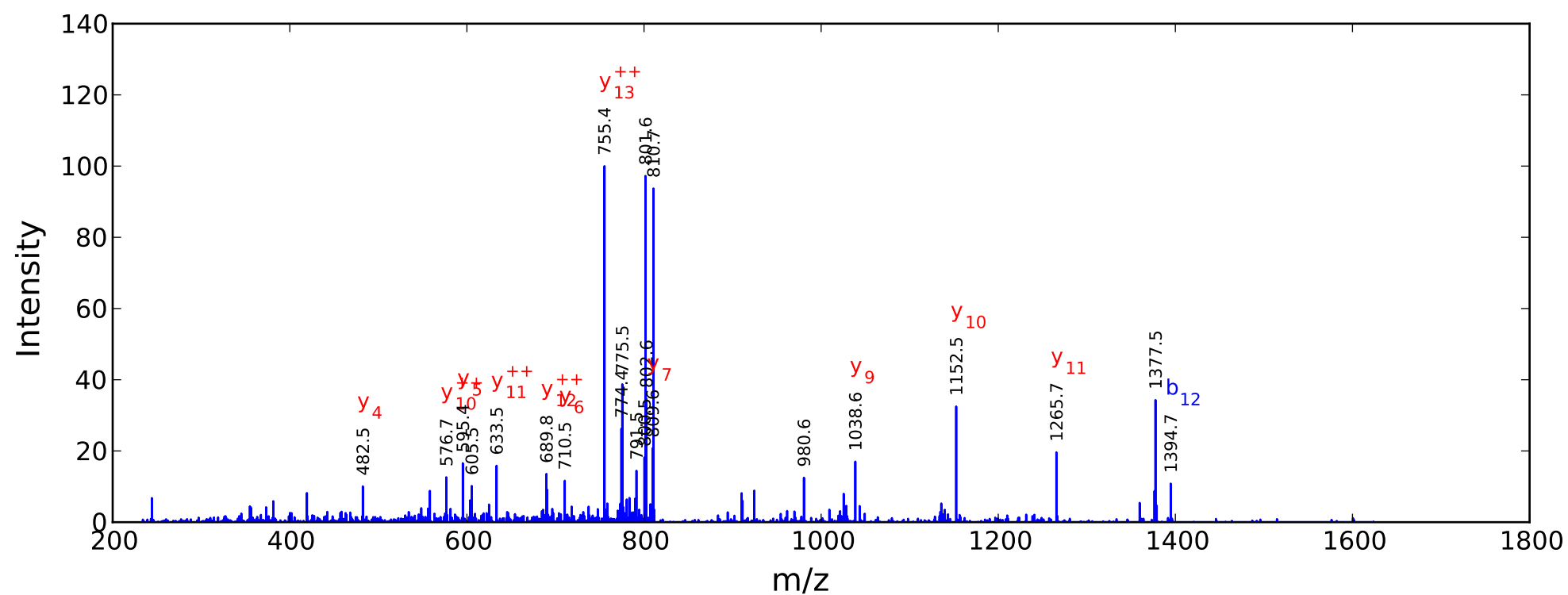
hypothetical protein, conserved

Peptide: QMIINNDVDITHPK

Charge State: 2.0

Modifications: None

m/z: 819.419635



Tb927.3.5600

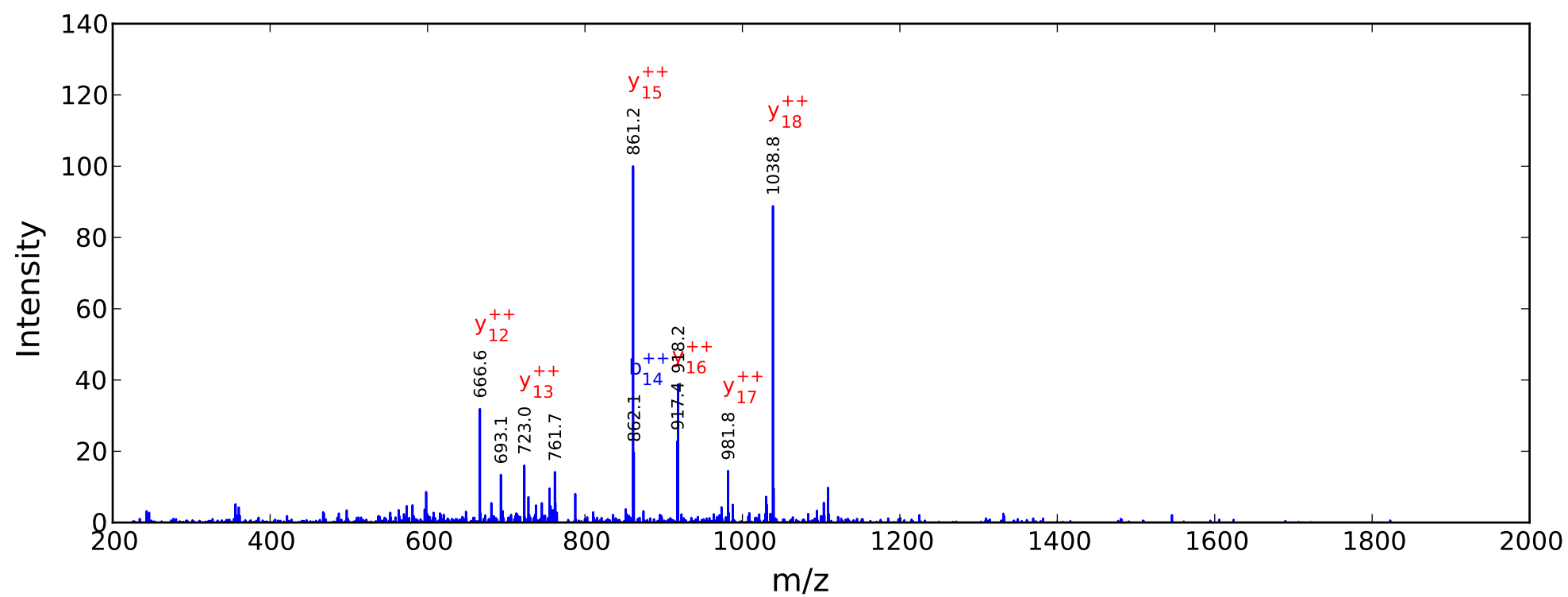
hypothetical protein, conserved

Peptide: LENQLFEITQEYDVVHAGGR

Charge State: 3.0

Modifications: None

m/z: 773.38537



Tb927.3.700

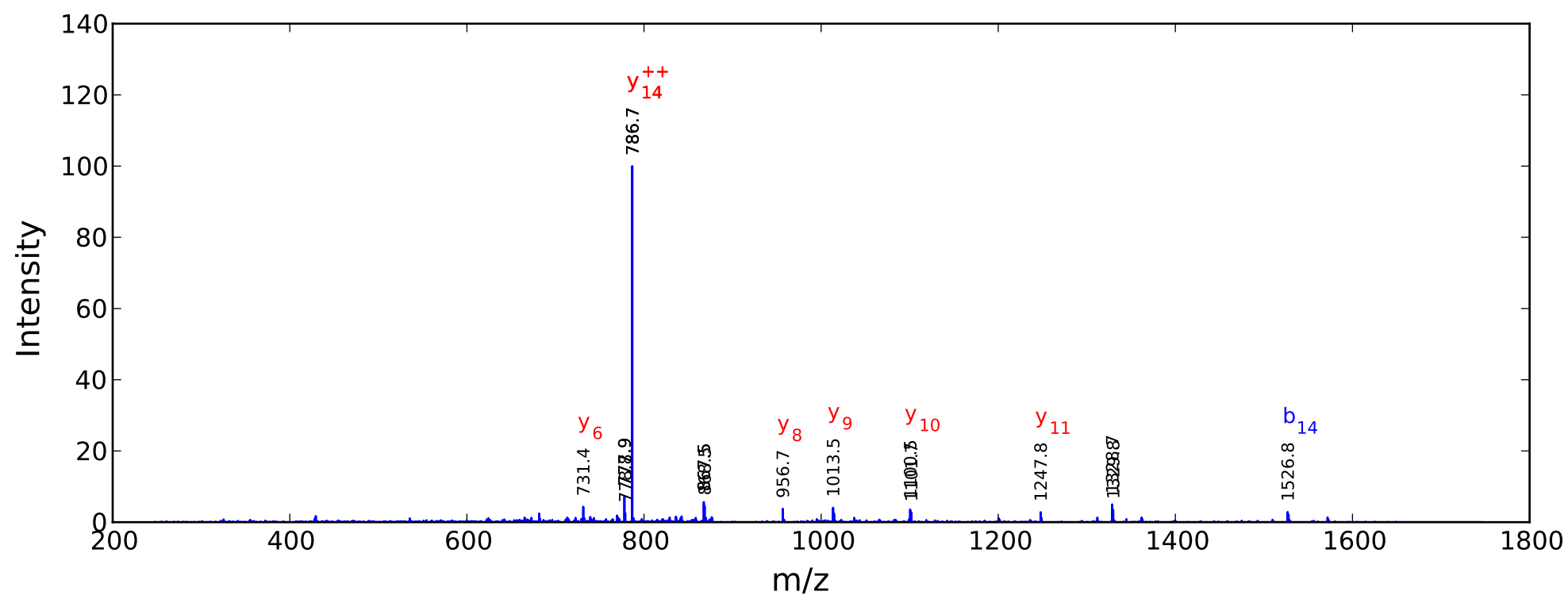
hypothetical protein, conserved

Peptide: VVPLNFSGPKPVYQPK

Charge State: 2.0

Modifications: None

m/z: 885.501275



Tb927.3.820

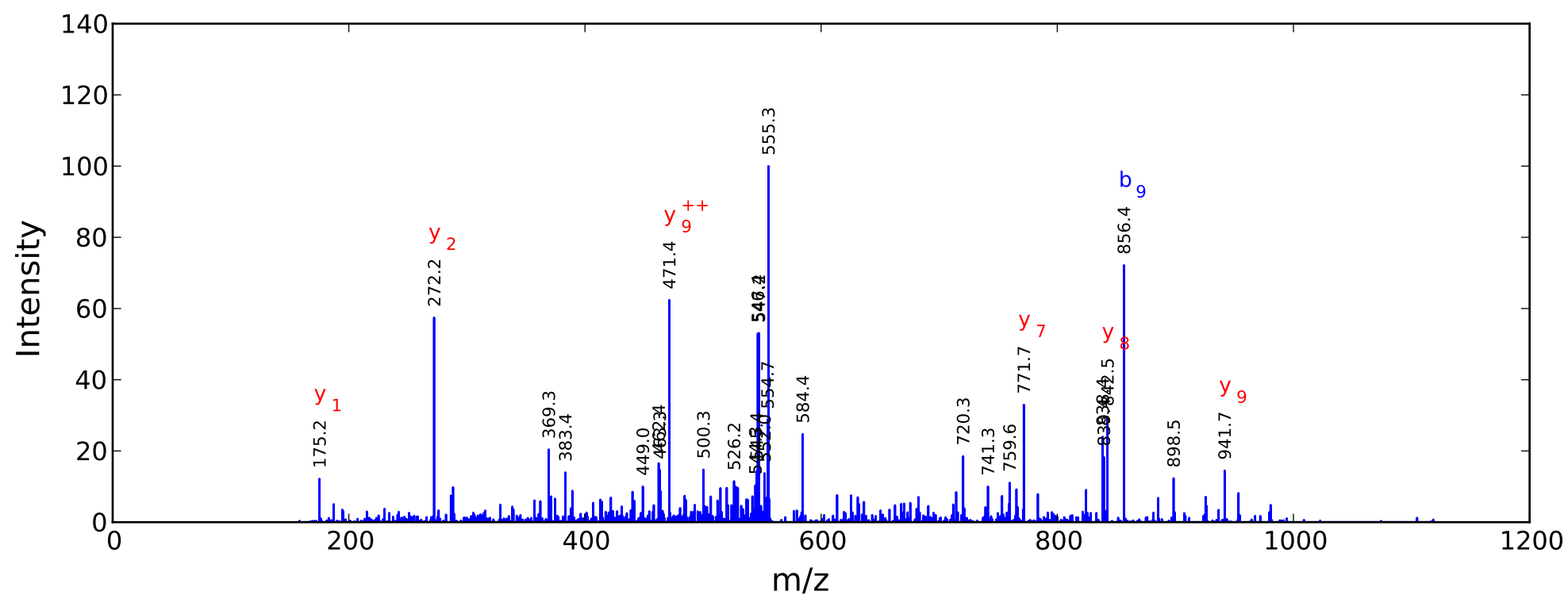
hypothetical protein, conserved

Peptide: SVVAGTQNVPR

Charge State: 2.0

Modifications: None

m/z: 564.312225



Tb927.4.3060

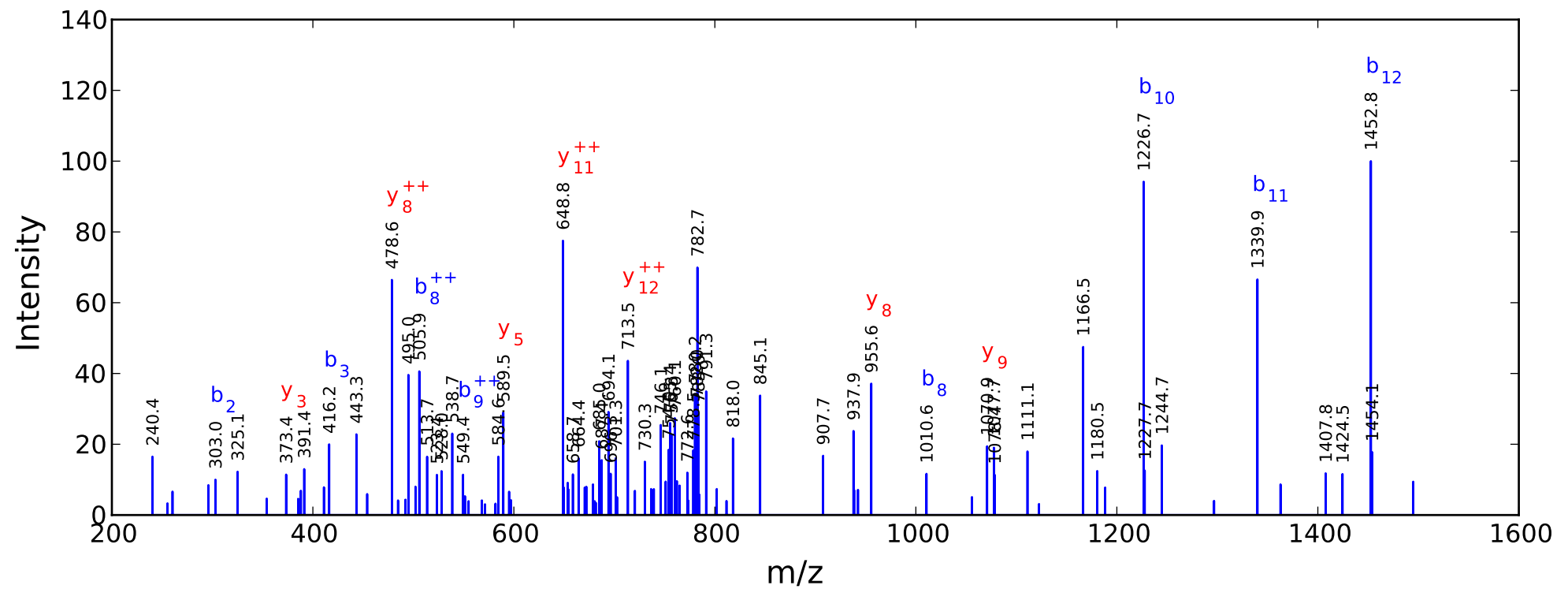
hypothetical protein, conserved

Peptide: MEIIDRPLSEIIK

Charge State: 2.0

Modifications: Residue 1, Acetyl (Protein N-term)

m/z: 799.9449475





Tb927.6.2610

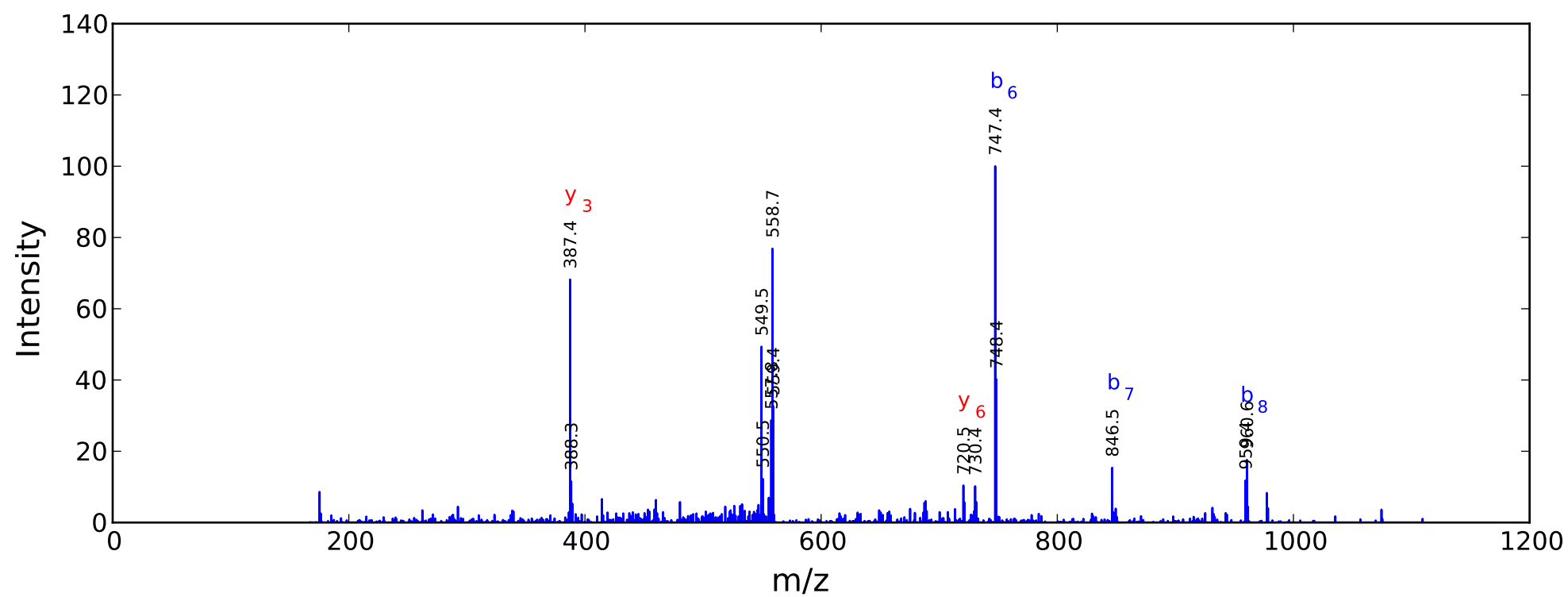
hypothetical protein, conserved

Peptide: RQEFADVIR

Charge State: 2.0

Modifications: None

m/z: 567.30694



Tb927.6.4580

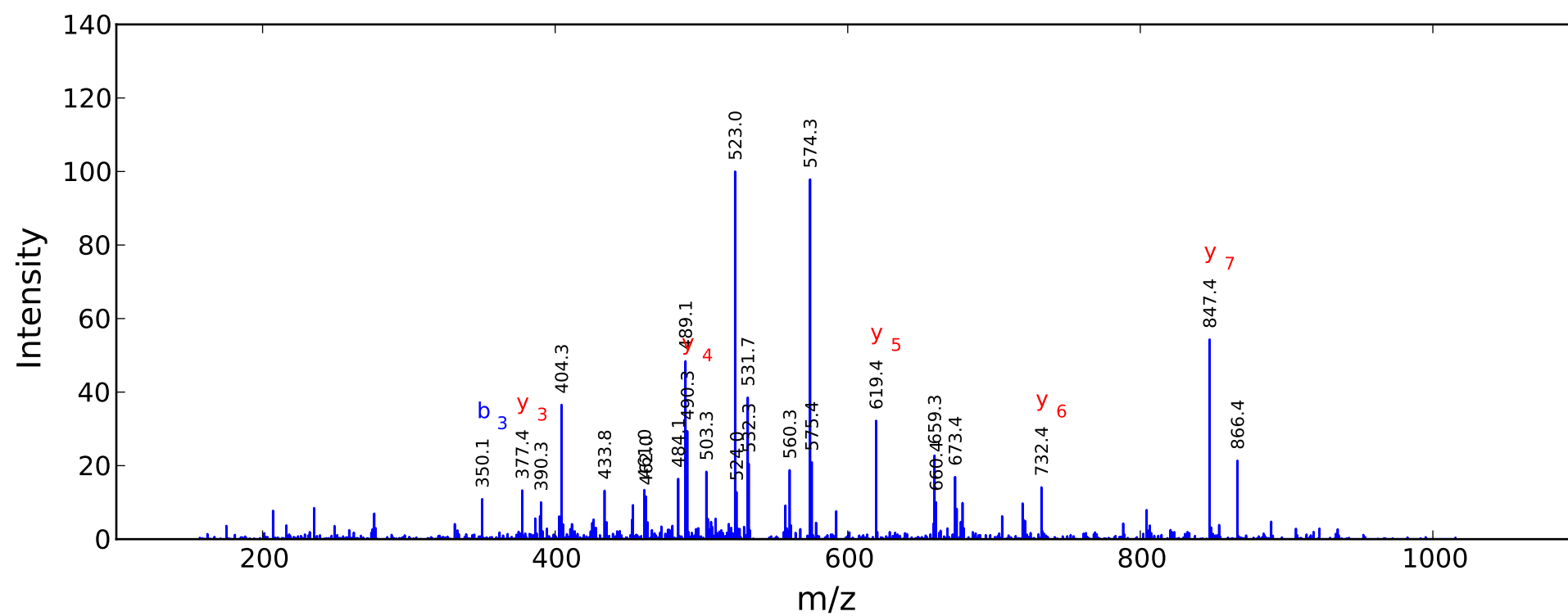
hypothetical protein, conserved

Peptide: YADLELTTR

Charge State: 2.0

Modifications: None

m/z: 541.28006



Tb927.7.1030

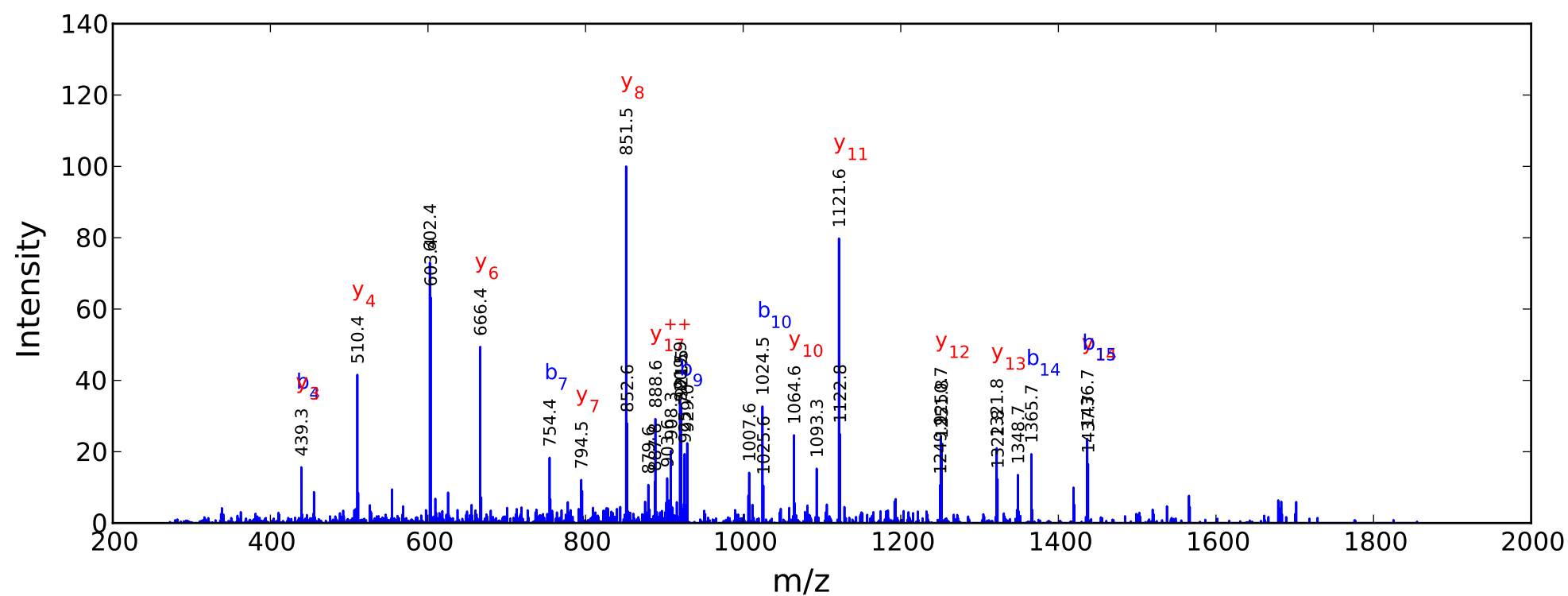
heat shock 70 kDa protein, putative

Peptide: VPLEDAEGNVGQGVATYR

Charge State: 2.0

Modifications: None

m/z: 937.96598



Tb927.7.4810

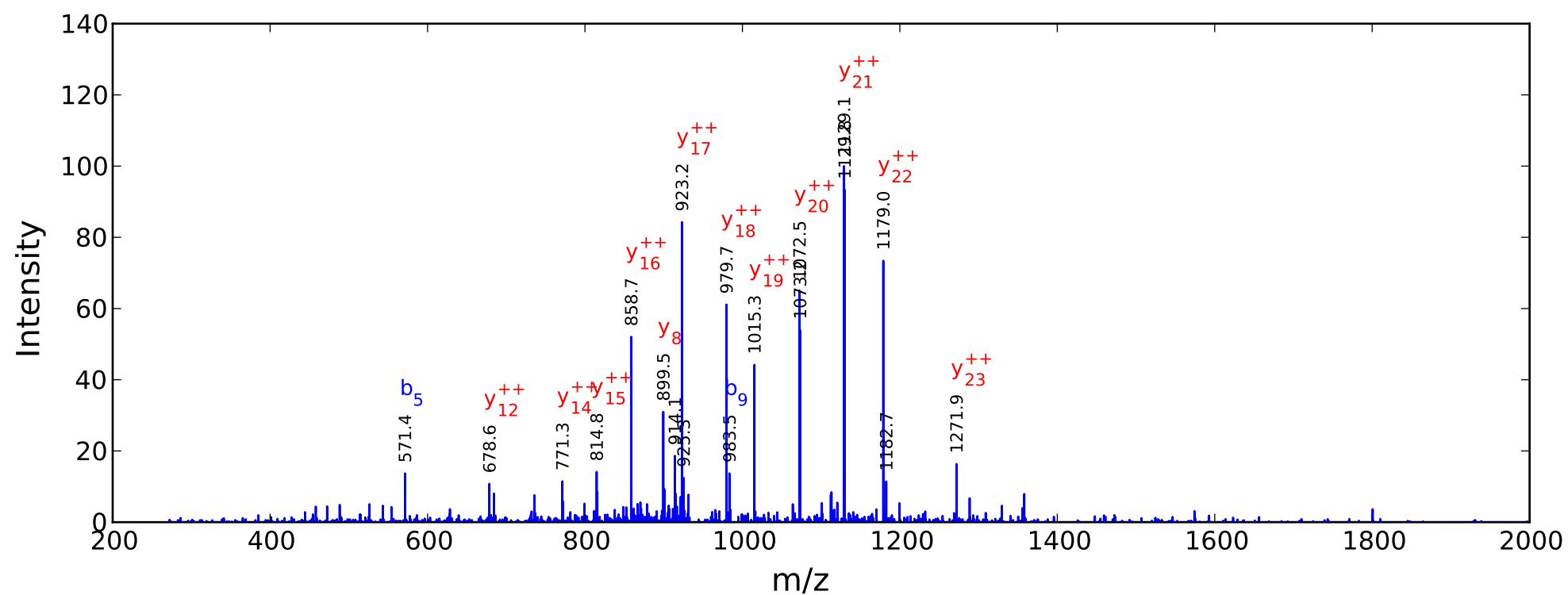
hypothetical protein, conserved

Peptide: LGDWVLDAIESSADTNLKPAQDIISR

Charge State: 3.0

Modifications: None

m/z: 943.154056667



Tb927.7.4910

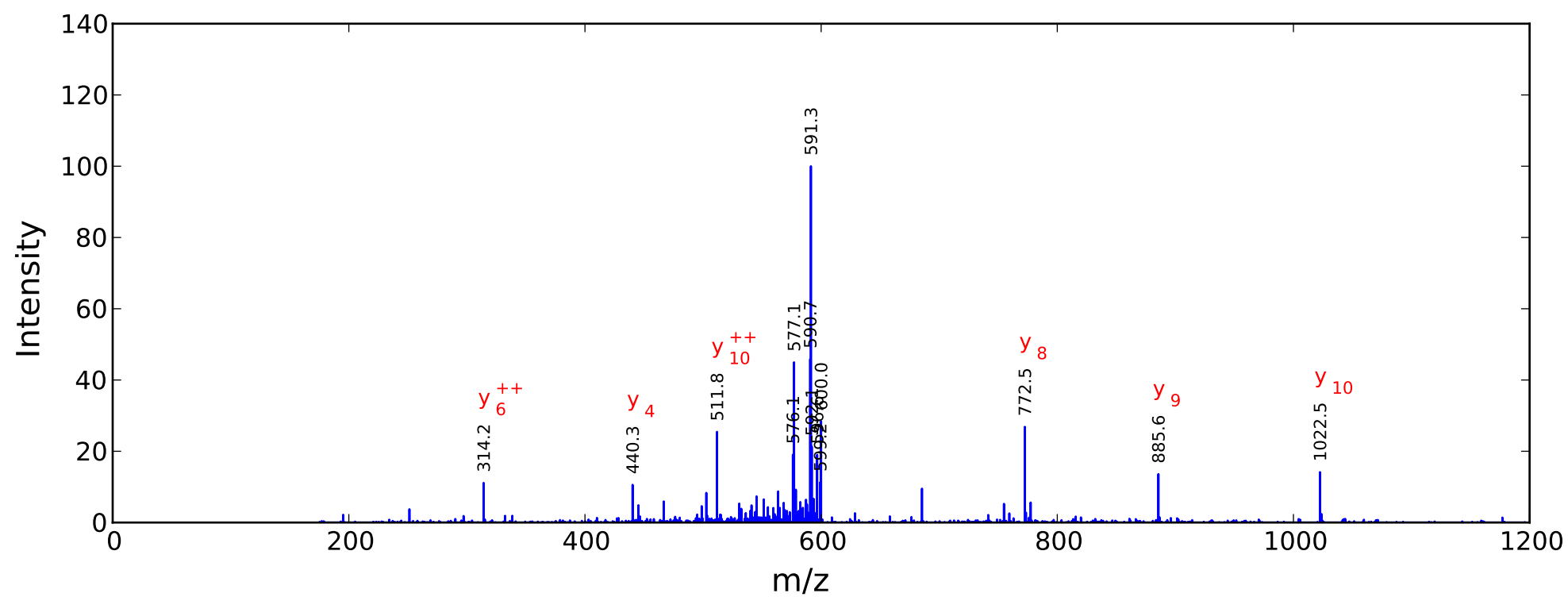
hypothetical protein, conserved

Peptide: GHHLSGSTPPAR

Charge State: 2.0

Modifications: None

m/z: 608.81292



Tb927.7.5260

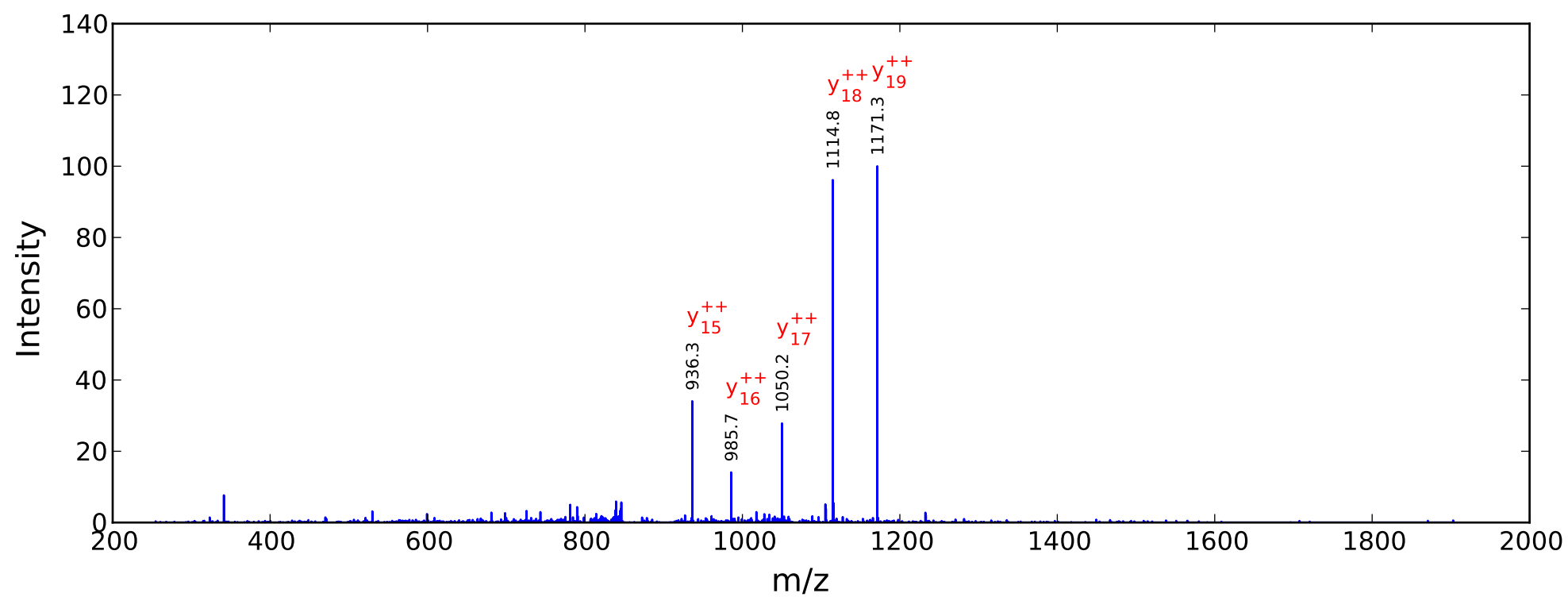
hypothetical protein, conserved

Peptide: NLIEEVYEEDFESVDHVSQMR

Charge State: 3.0

Modifications: None

m/z: 856.723613333



Tb927.7.5540

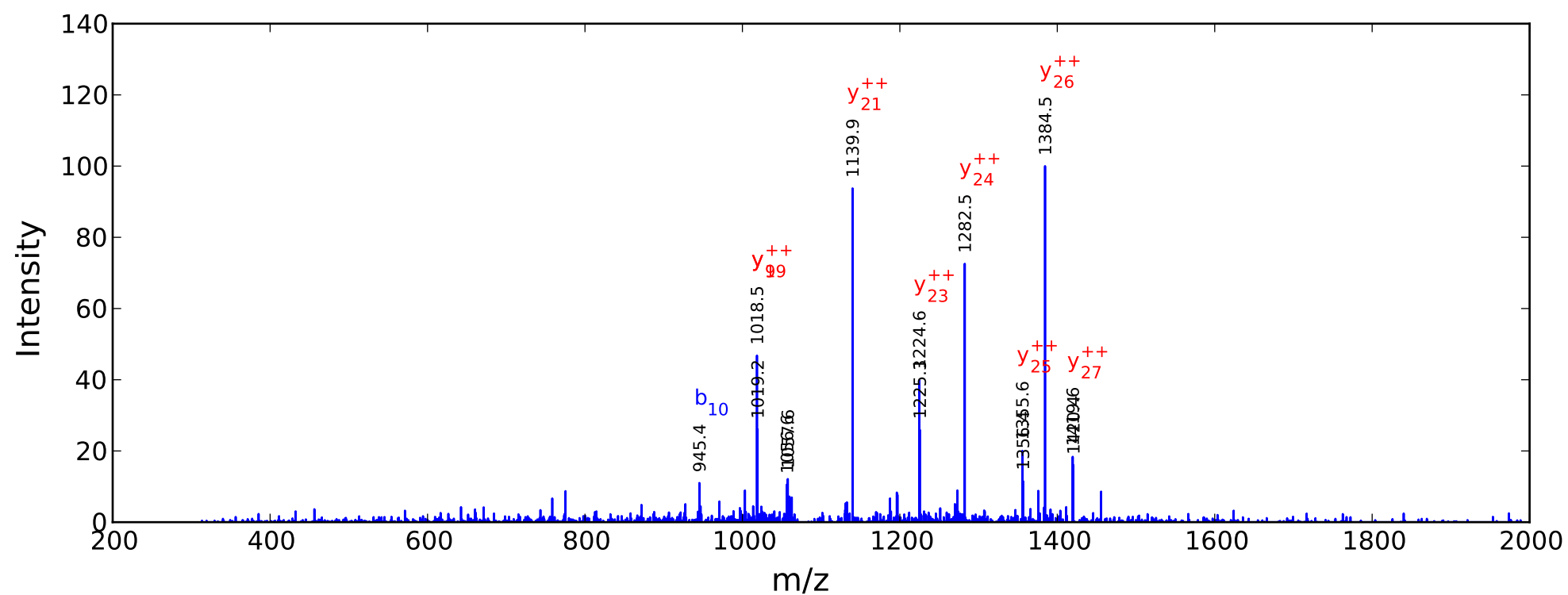
2,4-dienoyl-coa reductase-like protein

Peptide: LAEAAGFDGIEIPVSEGALLHNFLSPAVNDR

Charge State: 3.0

Modifications: None

m/z: 1074.88596



Tb927.8.2530

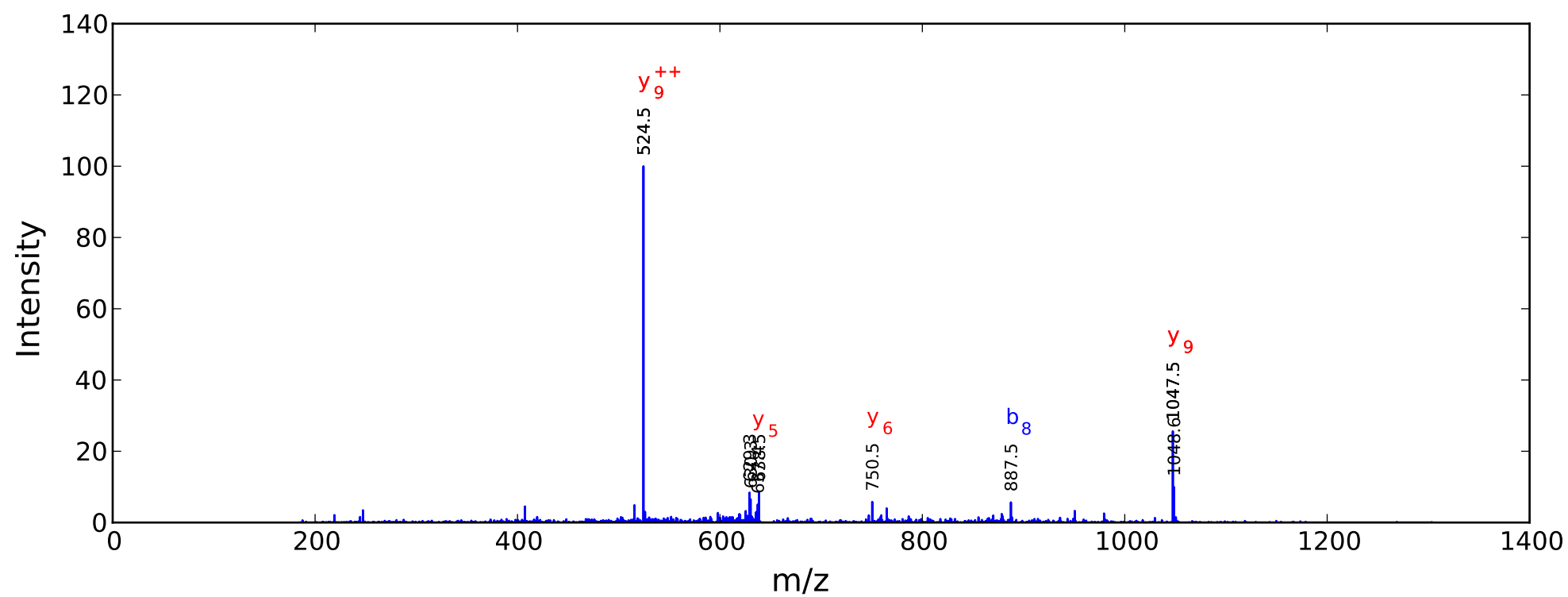
hypothetical protein, conserved

Peptide: VFPSILTEYPK

Charge State: 2.0

Modifications: None

m/z: 647.358305





Tb927.10.7760

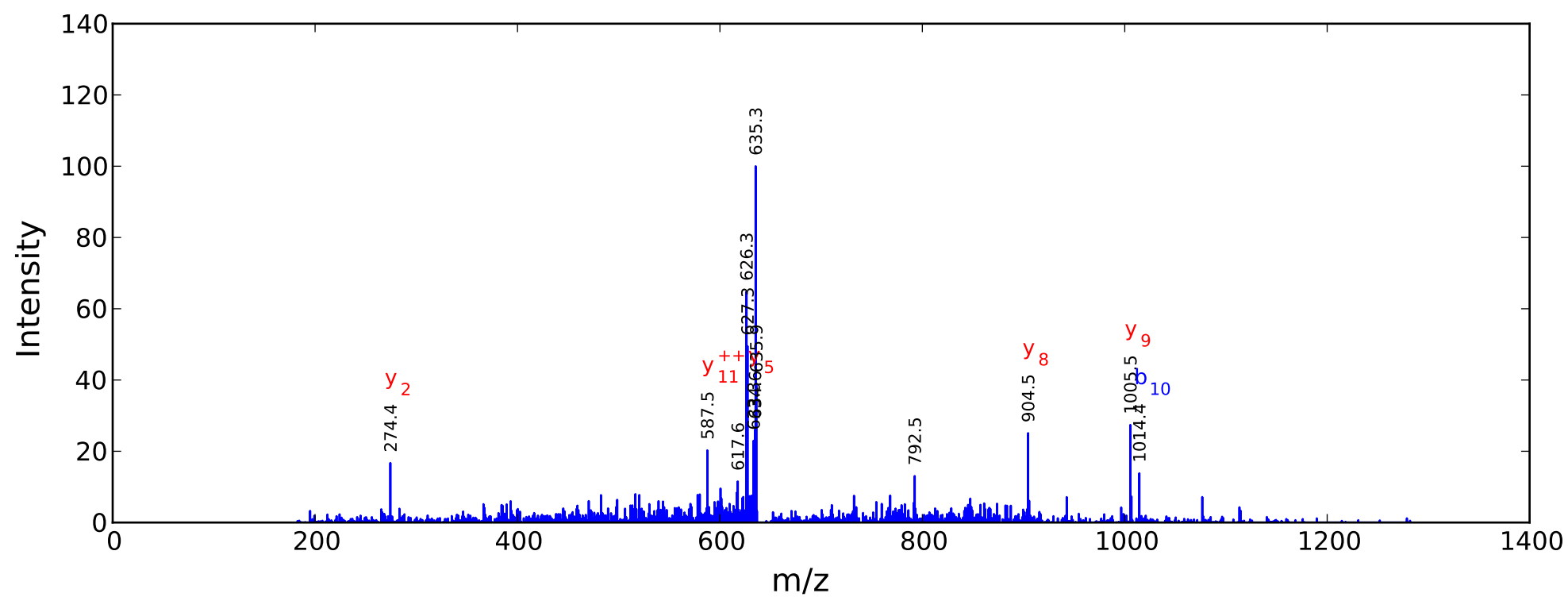
hypothetical protein, conserved

Peptide: NPATGDVLMDVR

Charge State: 2.0

Modifications: None

m/z: 644.32193



Tb11.01.6660

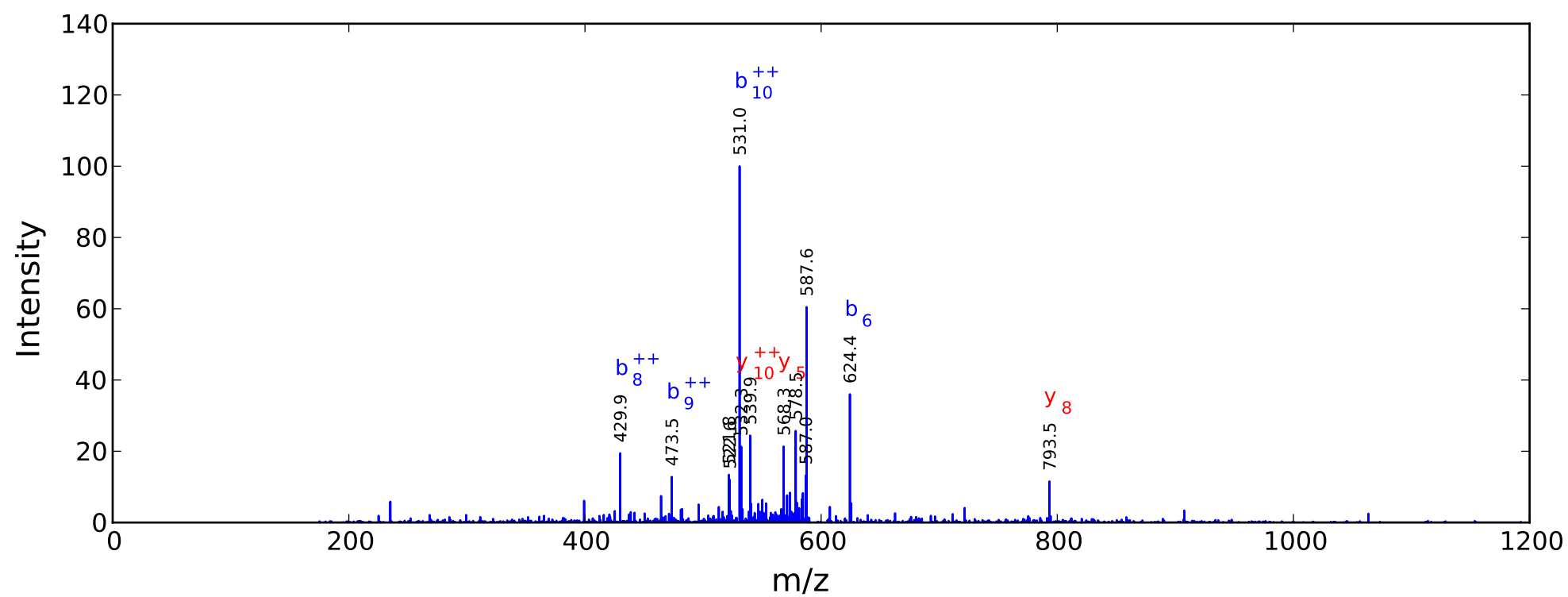
iron superoxide dismutase

Peptide: KRNP GAPHSDL

Charge State: 2.0

Modifications: None

m/z: 596.315295



Tb11.02.3390

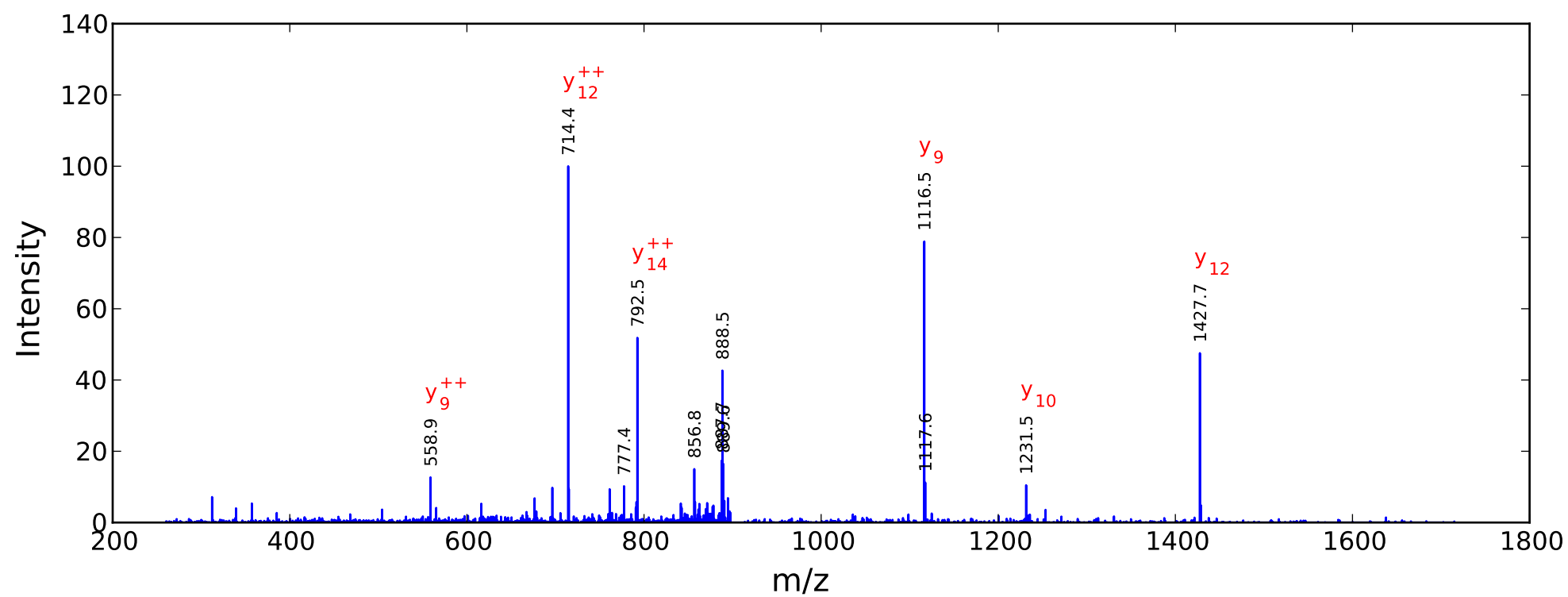
dynein light chain, putative

Peptide: LDGVPVDPEEKEEAER

Charge State: 2.0

Modifications: None

m/z: 906.436715



Tb927.1.880

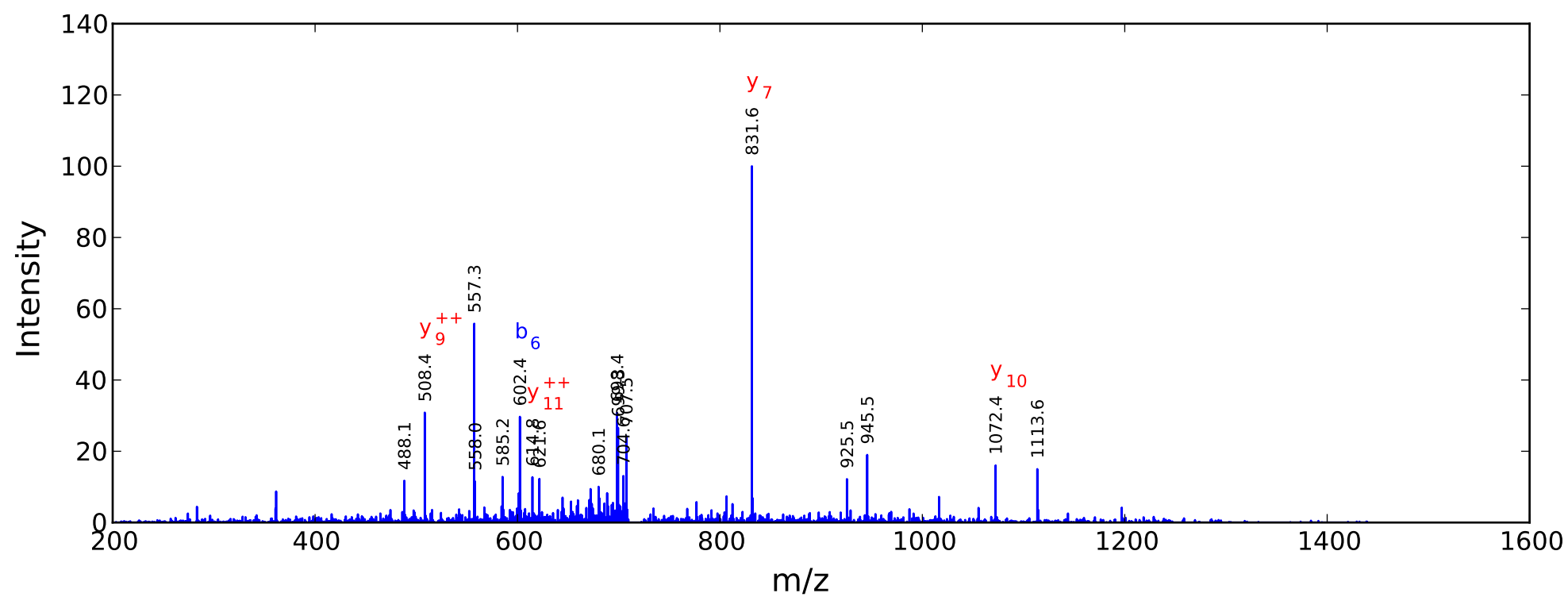
hypothetical protein, conserved

Peptide: MGRGLASLEDVLR

Charge State: 2.0

Modifications: Residue 1, Oxidation (M)

m/z: 716.882225



Tb927.10.12970

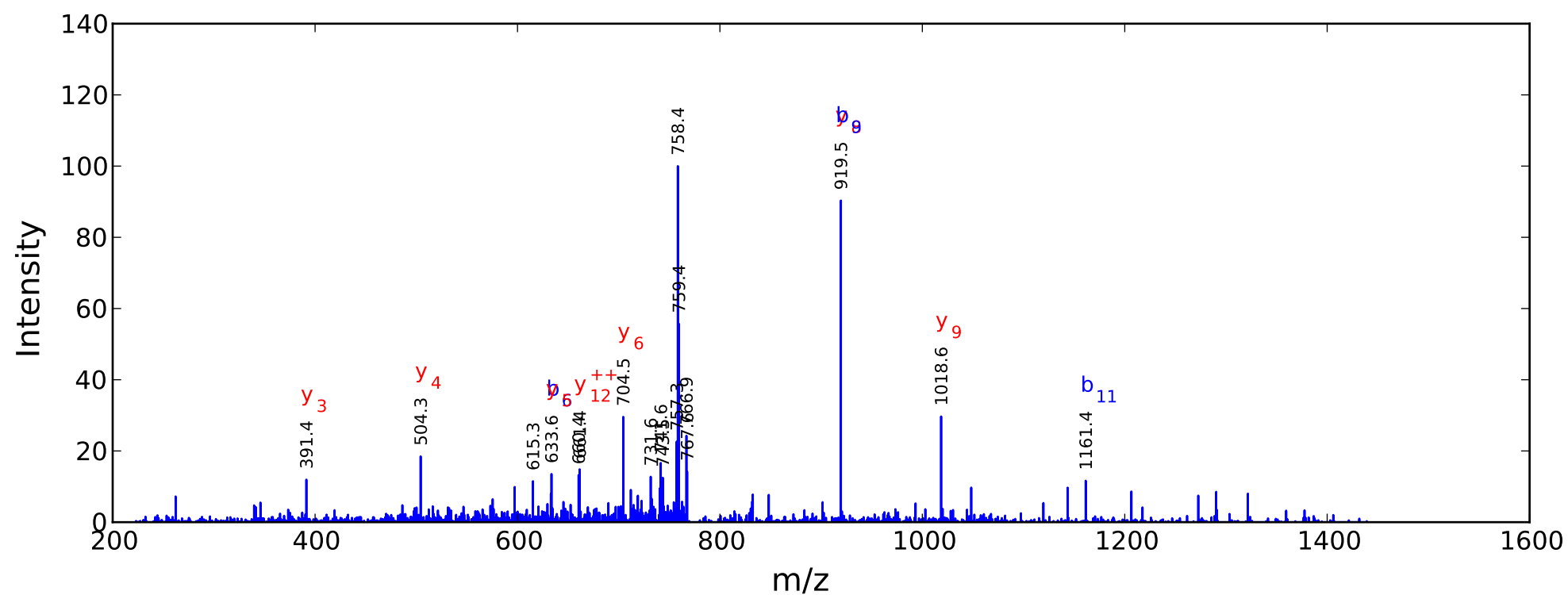
hypothetical protein, conserved

Peptide: MVDSTVSQAELESR

Charge State: 2.0

Modifications: None

m/z: 776.36981



Tb927.5.2700

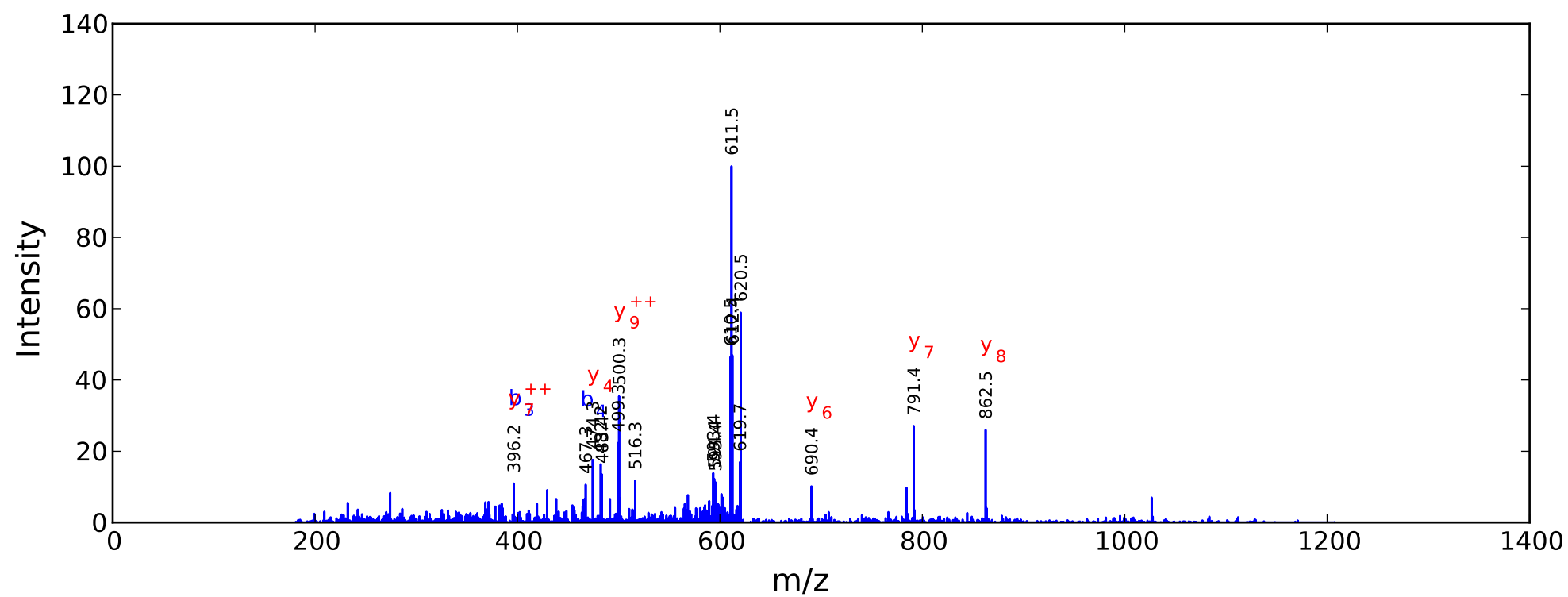
otubain, putative

Peptide: SEHATTDLEGR

Charge State: 2.0

Modifications: Residue 1, Acetyl (Protein N-term)

m/z: 629.2891425



Tb927.8.1120

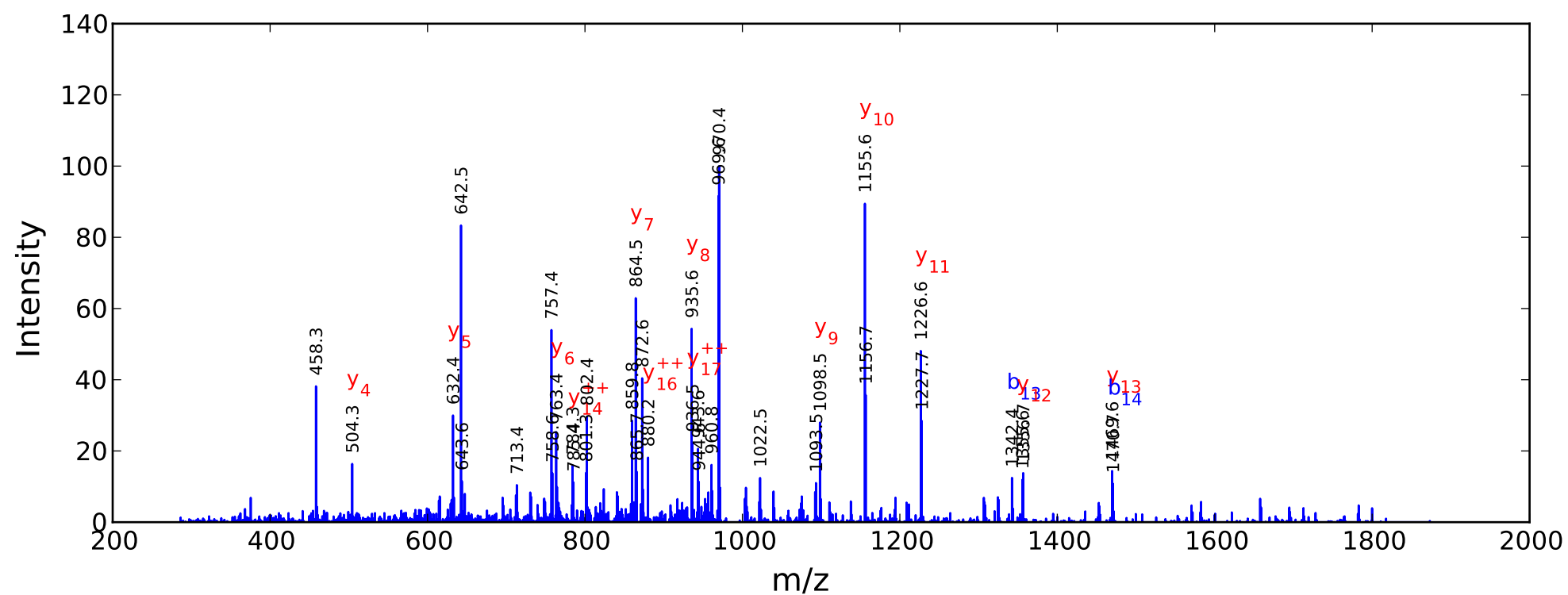
hypothetical protein, conserved

Peptide: TNTSTNEAGYATMQELSR

Charge State: 2.0

Modifications: None

m/z: 987.447315



Tb927.8.3840

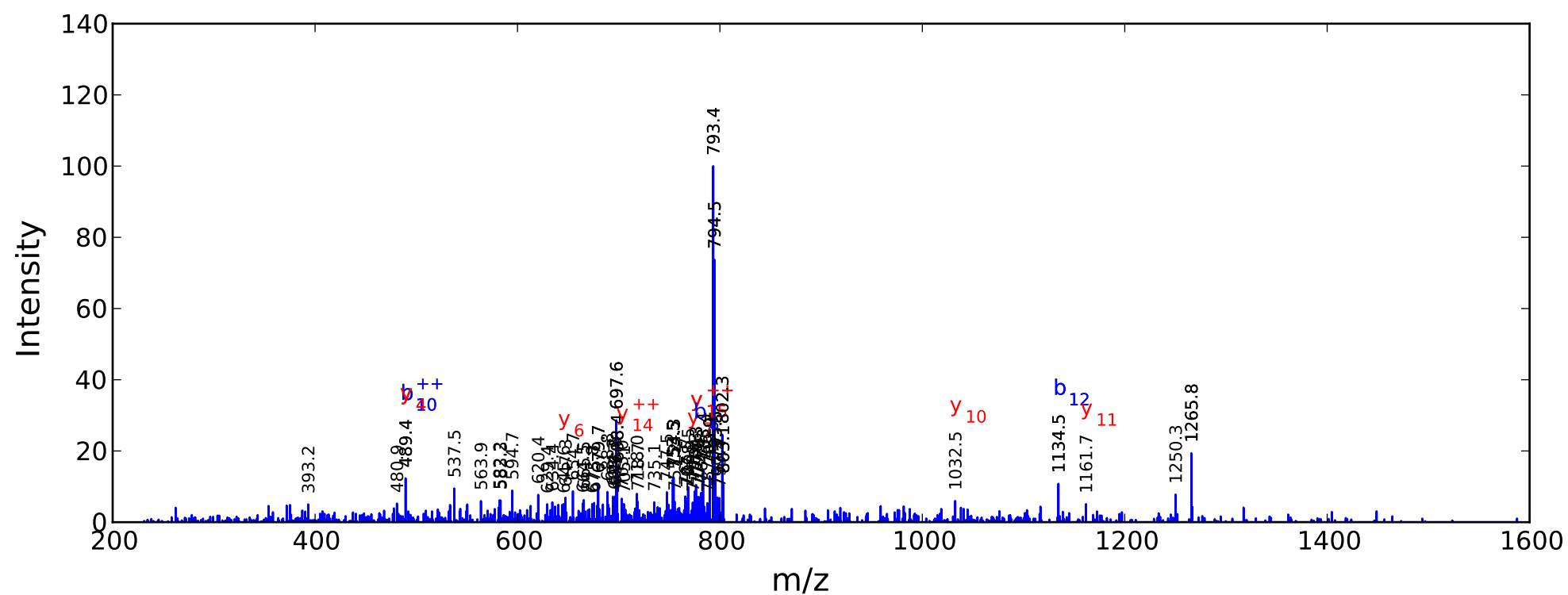
hypothetical protein, conserved

Peptide: AFSGVEGMAQGVVQSR

Charge State: 2.0

Modifications: None

m/z: 811.901605





Tb09.211.2020

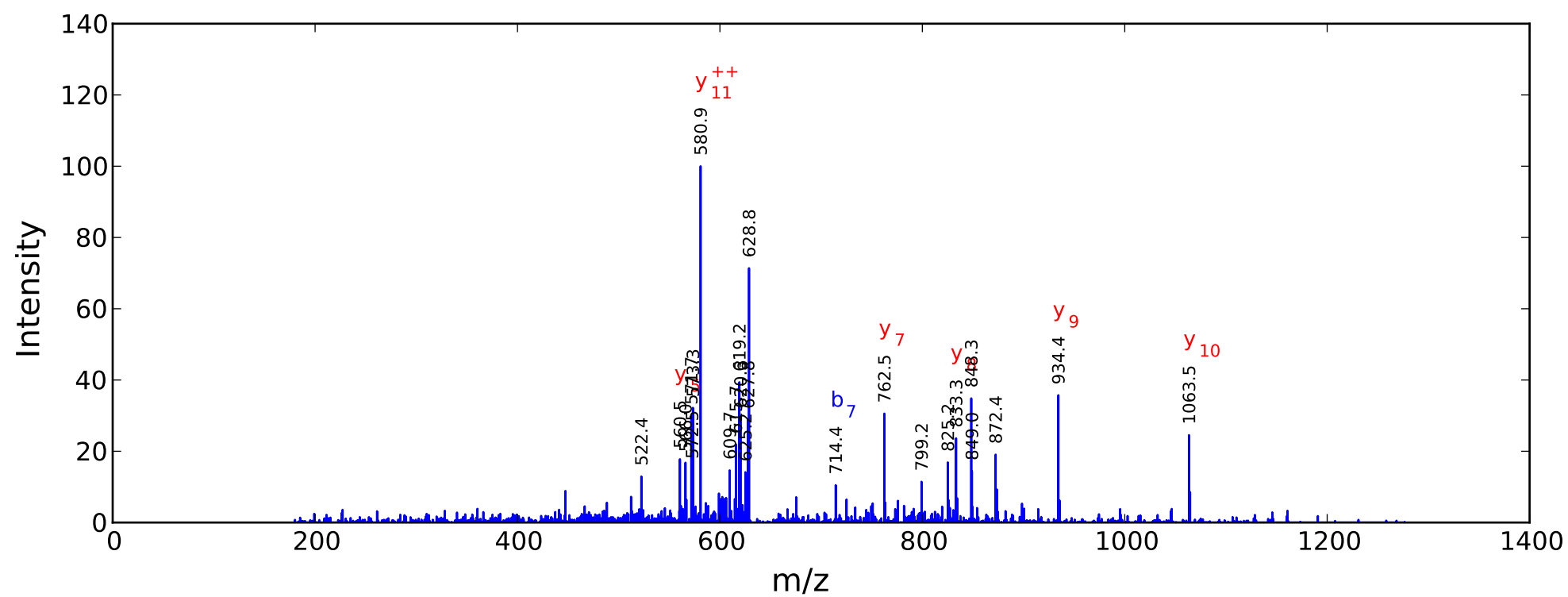
synaptojanin (N-terminal domain), putative

Peptide: LPETASDLSVNK

Charge State: 2.0

Modifications: None

m/z: 637.33556



Tb09.211.2600

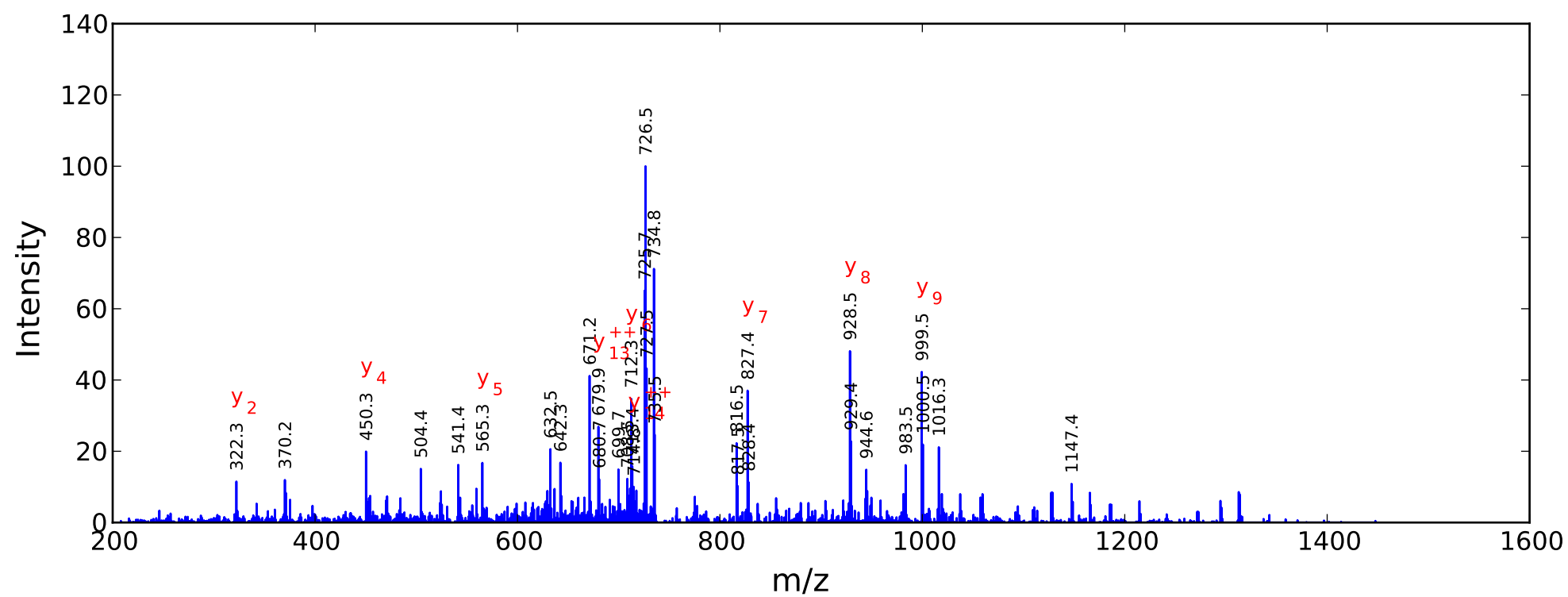
hypothetical protein, conserved

Peptide: GASGSQATDFDGAFR

Charge State: 2.0

Modifications: None

m/z: 743.8317



Tb11.02.3670

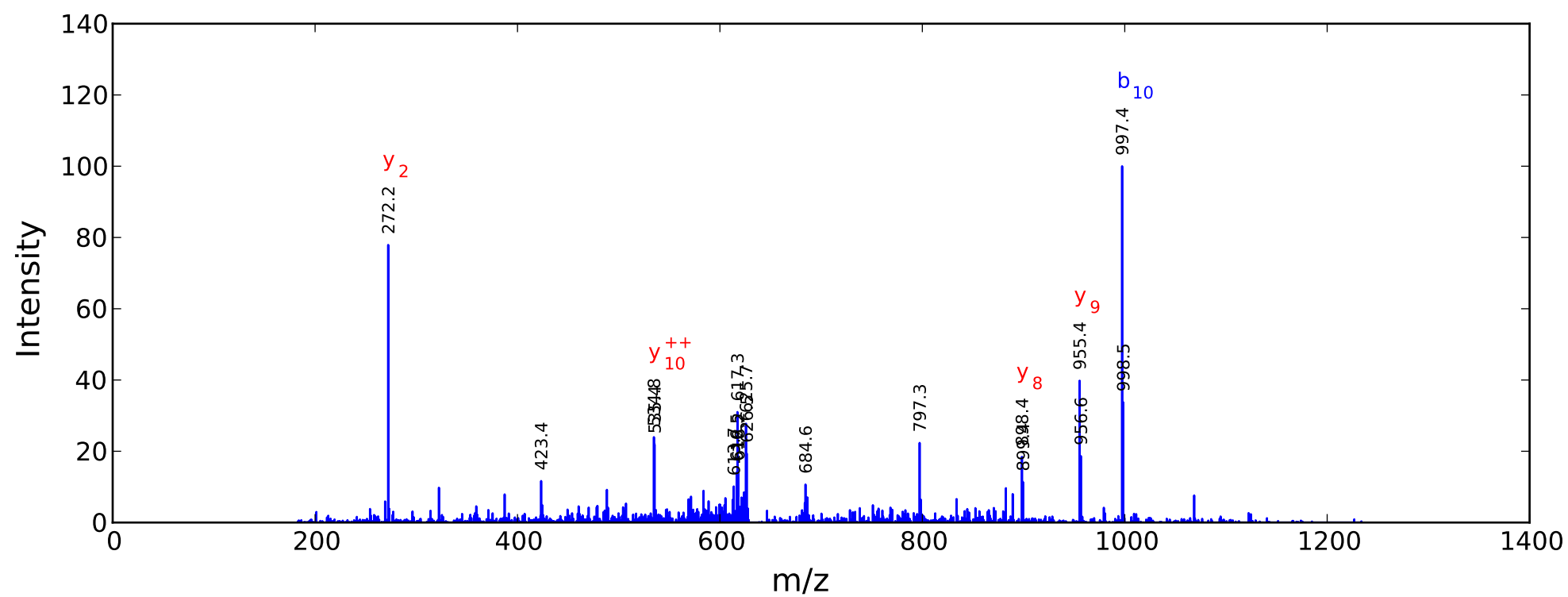
hypothetical protein, conserved

Peptide: SLIGPDGEIDPR

Charge State: 2.0

Modifications: None

m/z: 634.827895



Tb11.02.3860

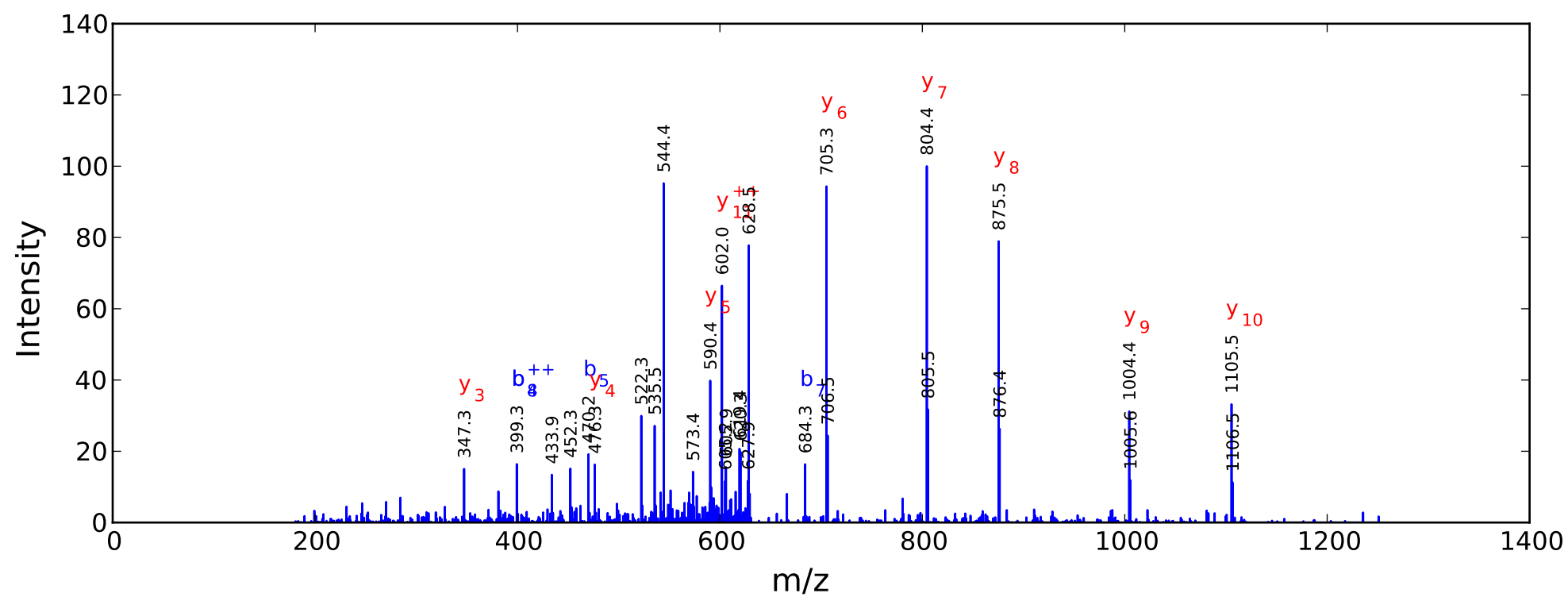
hypothetical protein, conserved

Peptide: APTEAVDNETAR

Charge State: 2.0

Modifications: None

m/z: 637.30479



Tb927.2.6070

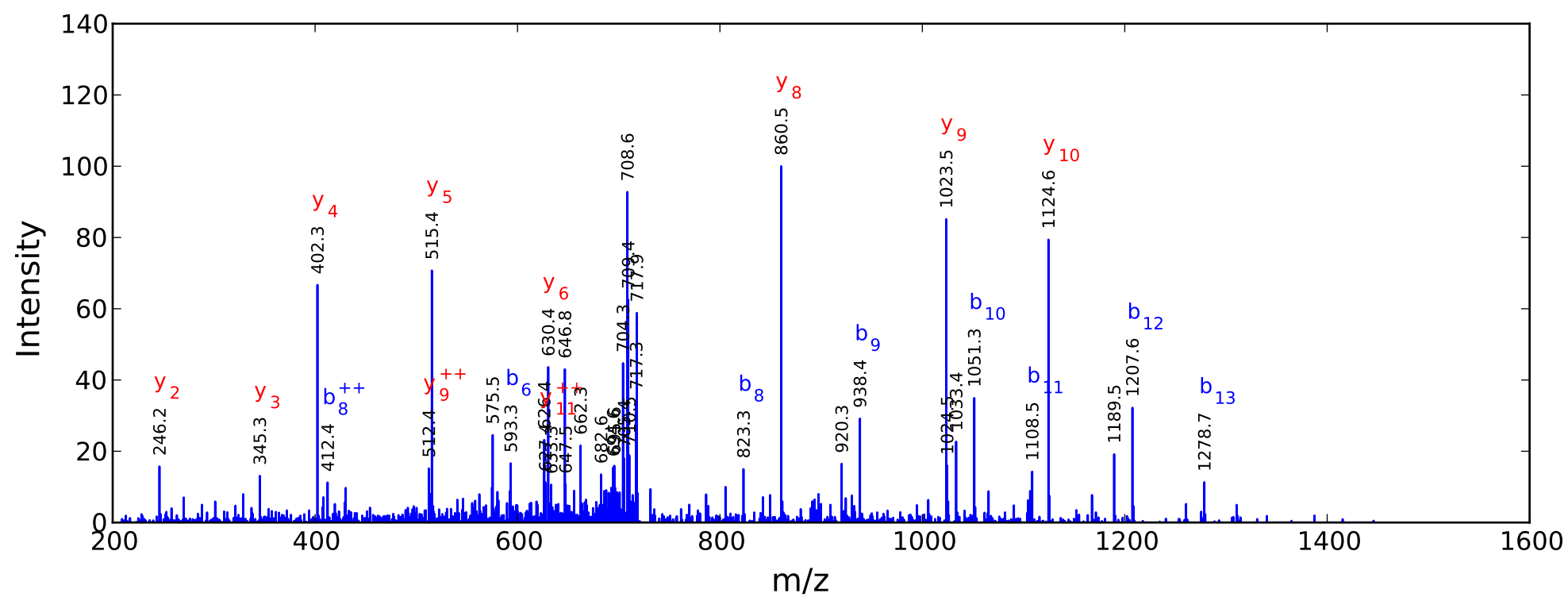
hypothetical protein, conserved

Peptide: AAGETYETDIGVAR

Charge State: 2.0

Modifications: None

m/z: 726.8521



Tb927.5.770

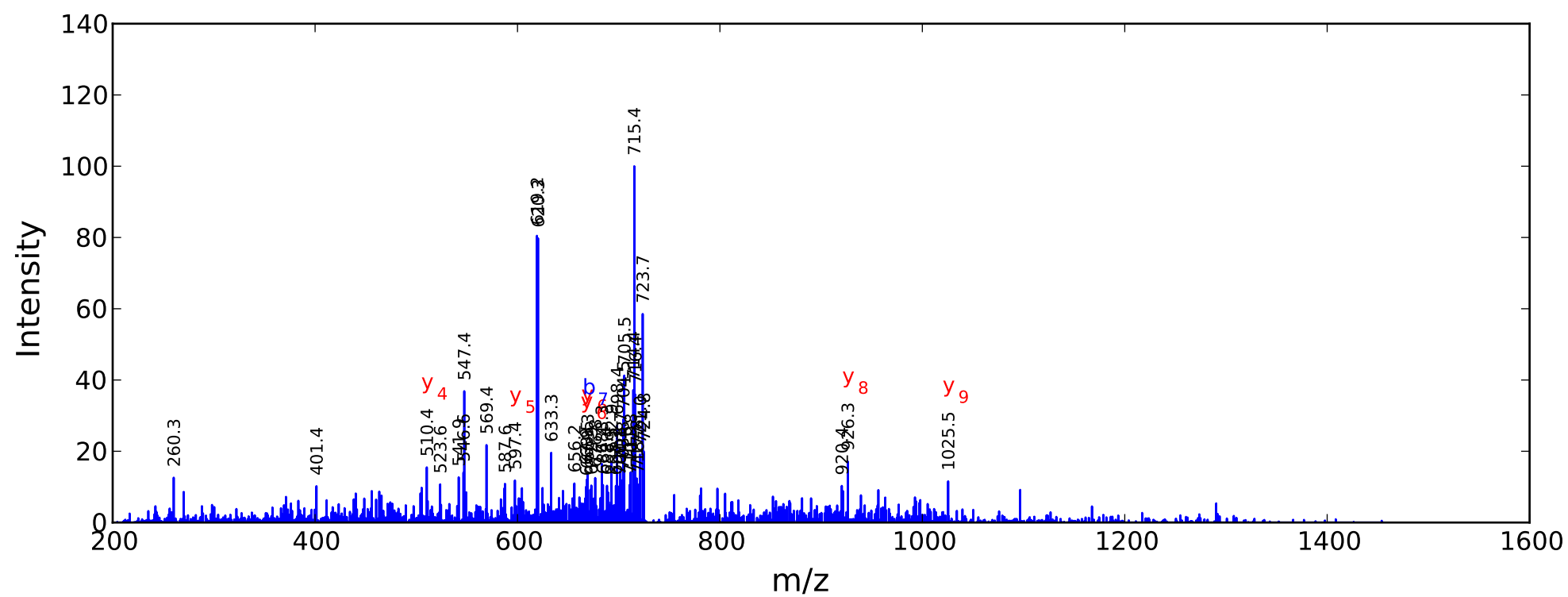
hypothetical protein, conserved

Peptide: ANLAAVEEASSTFR

Charge State: 2.0

Modifications: None

m/z: 733.36792



Tb927.7.3100

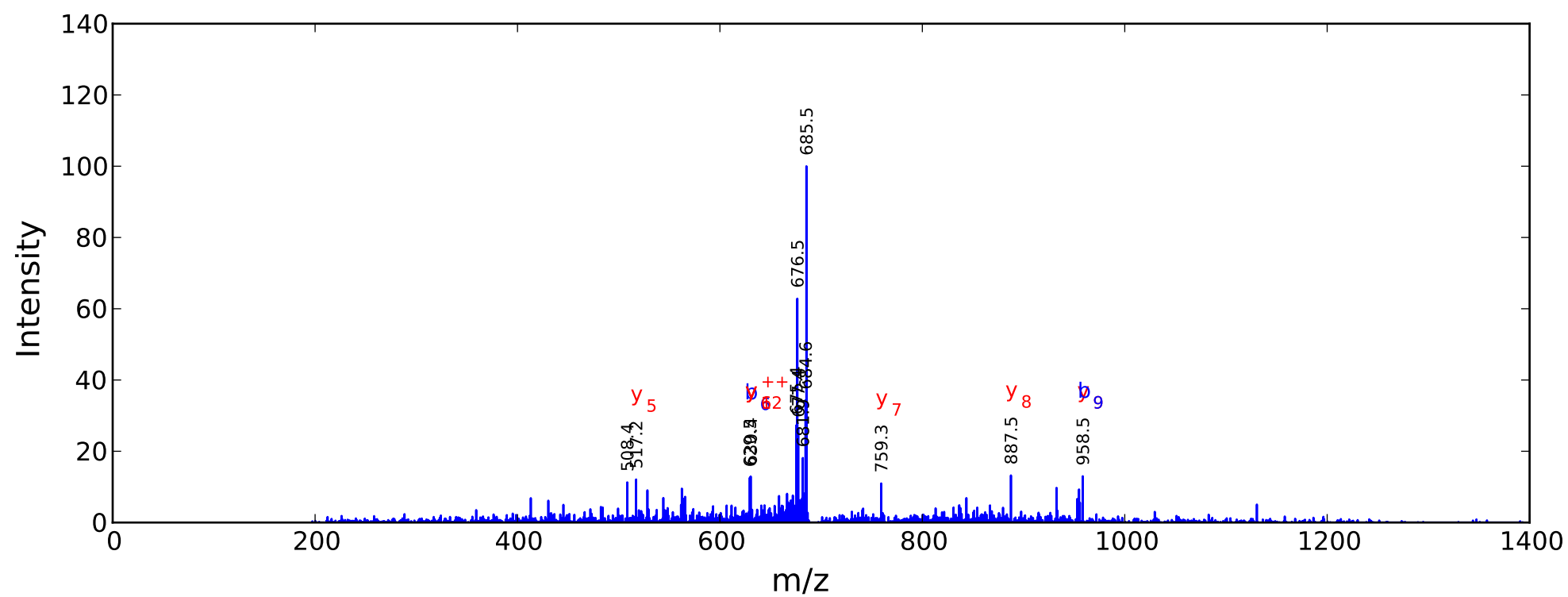
hypothetical protein, conserved

Peptide: QETAAQEISAALR

Charge State: 2.0

Modifications: None

m/z: 694.36264



Tb927.7.2960

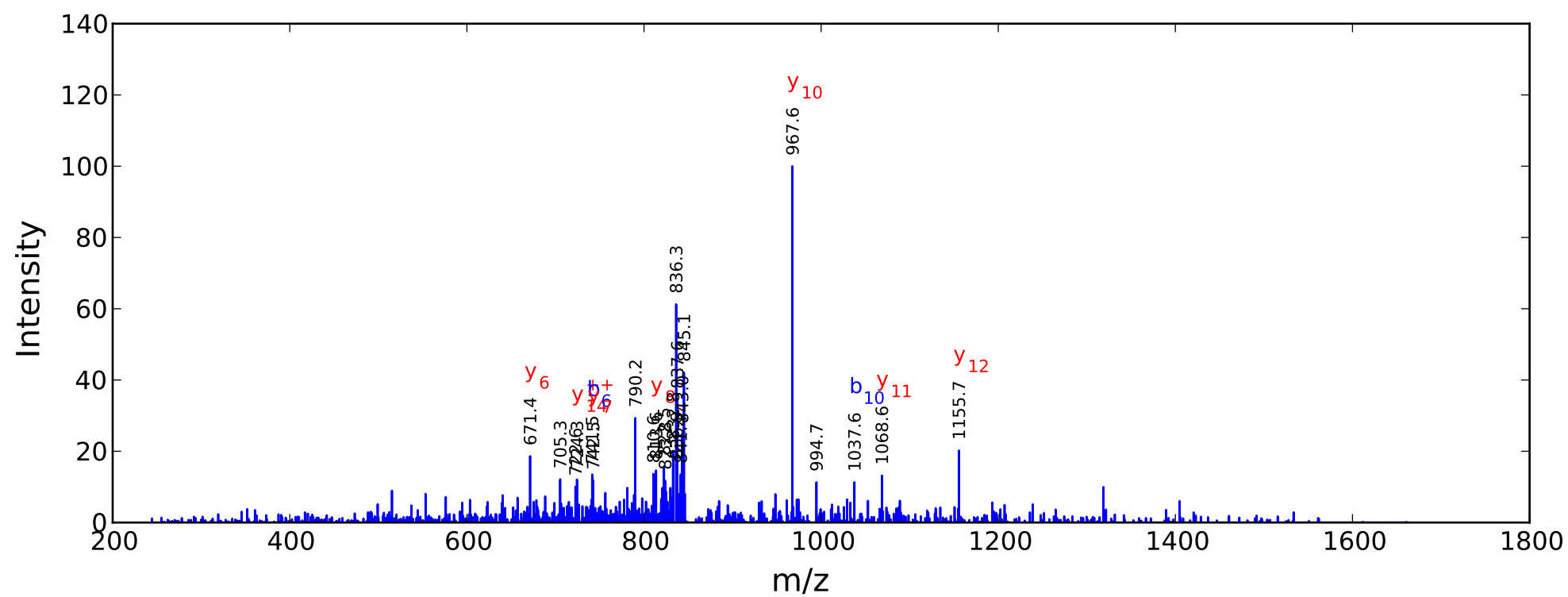
hypothetical protein, conserved

Peptide: FNQYSTPGAAGVQVLR

Charge State: 2.0

Modifications: None

m/z: 854.444495





Tb927.7.7170

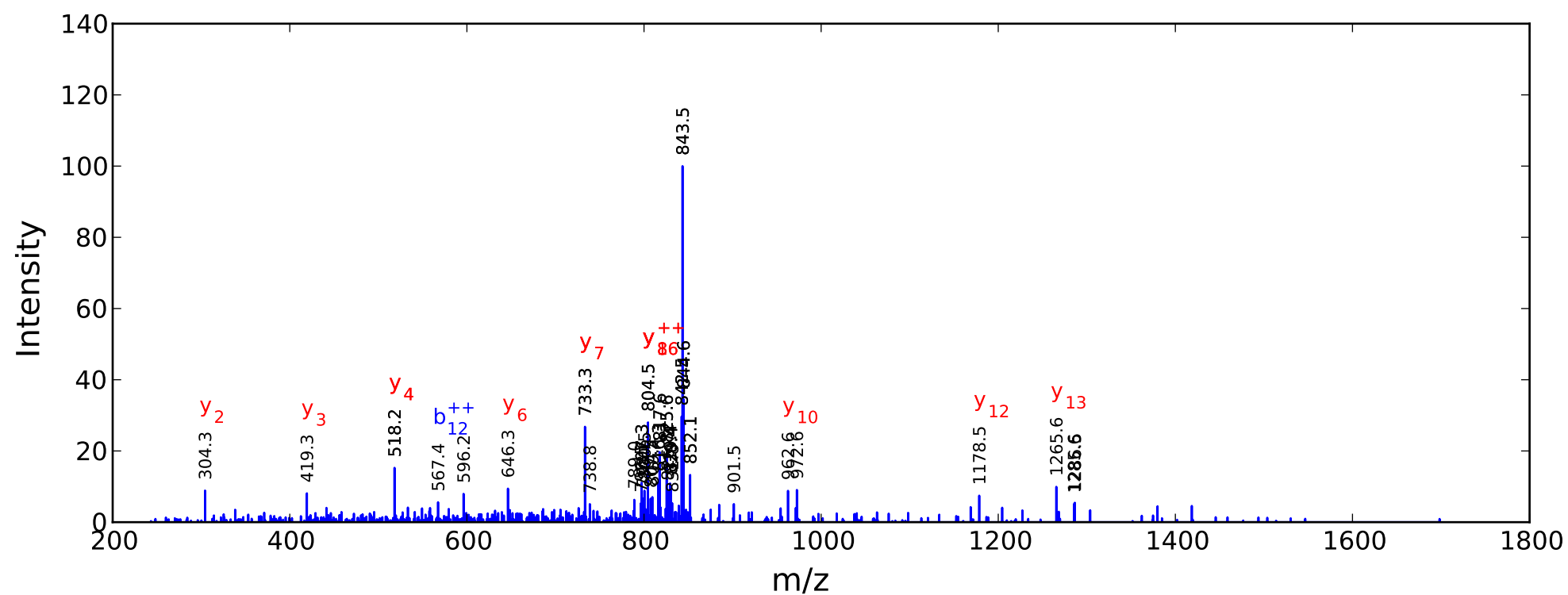
CYC2-like cyclin, putative

Peptide: NNNNSDTSAASGAVDER

Charge State: 2.0

Modifications: None

m/z: 861.369915



Tb927.8.1850

hypothetical protein, conserved

Peptide: SADDGAMLMTMEDFVR

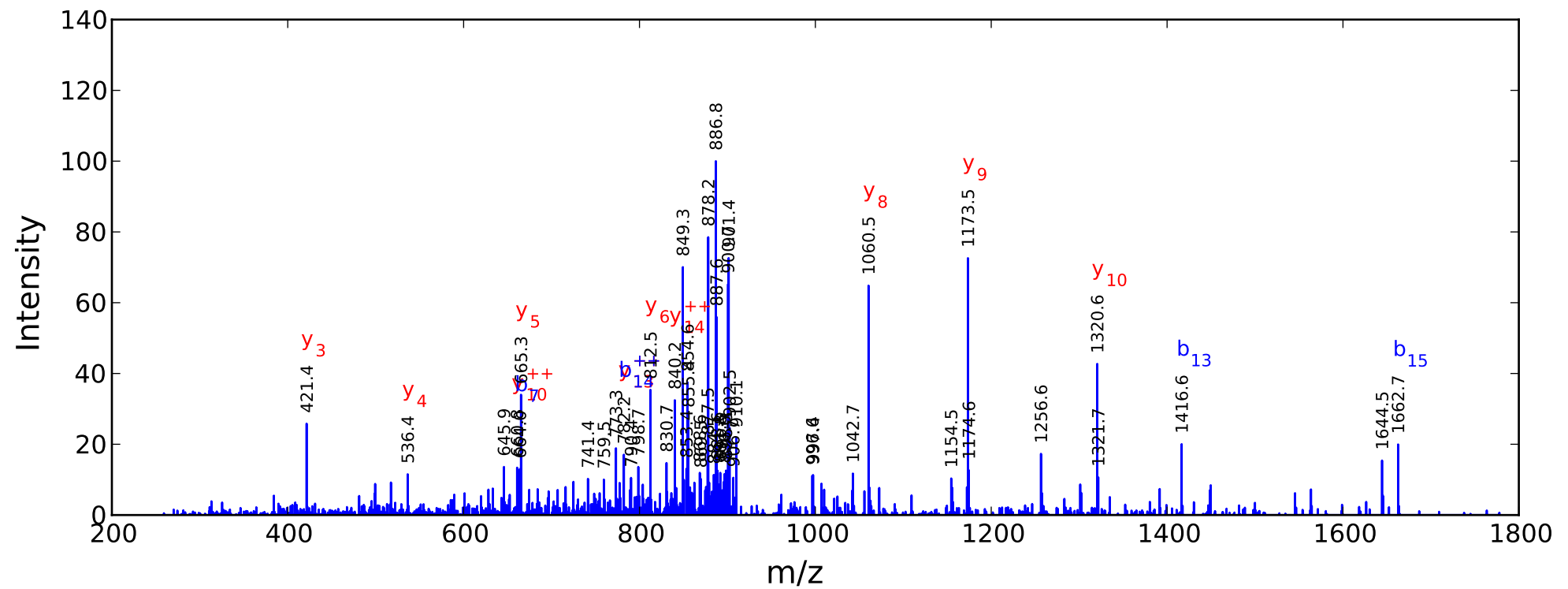
Charge State: 2.0

Modifications: Residue 7, Oxidation (M)

m/z: 918.87491

Residue 9, Oxidation (M)

Residue 11, Oxidation (M)



Tb927.8.6600

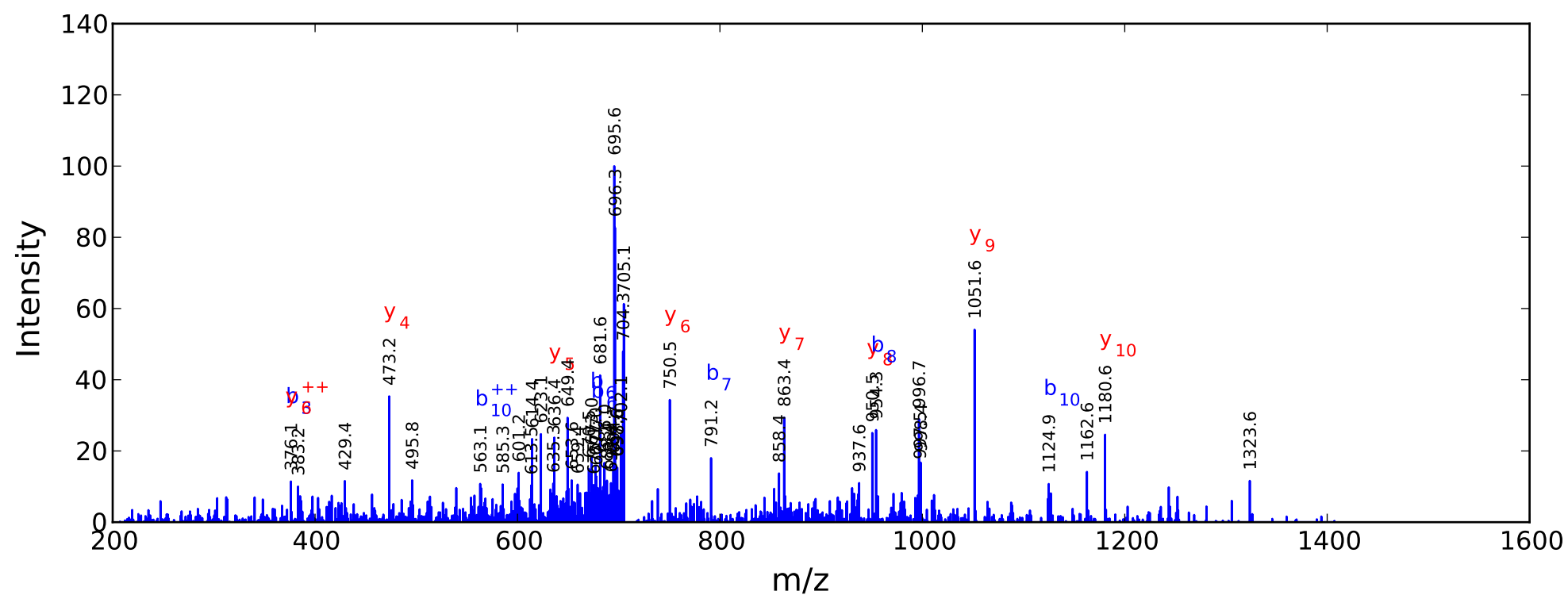
hypothetical protein, conserved

Peptide: MVETSLNYGLQR

Charge State: 2.0

Modifications: Residue 1, Oxidation (M)

m/z: 713.853145



Tb927.7.3060

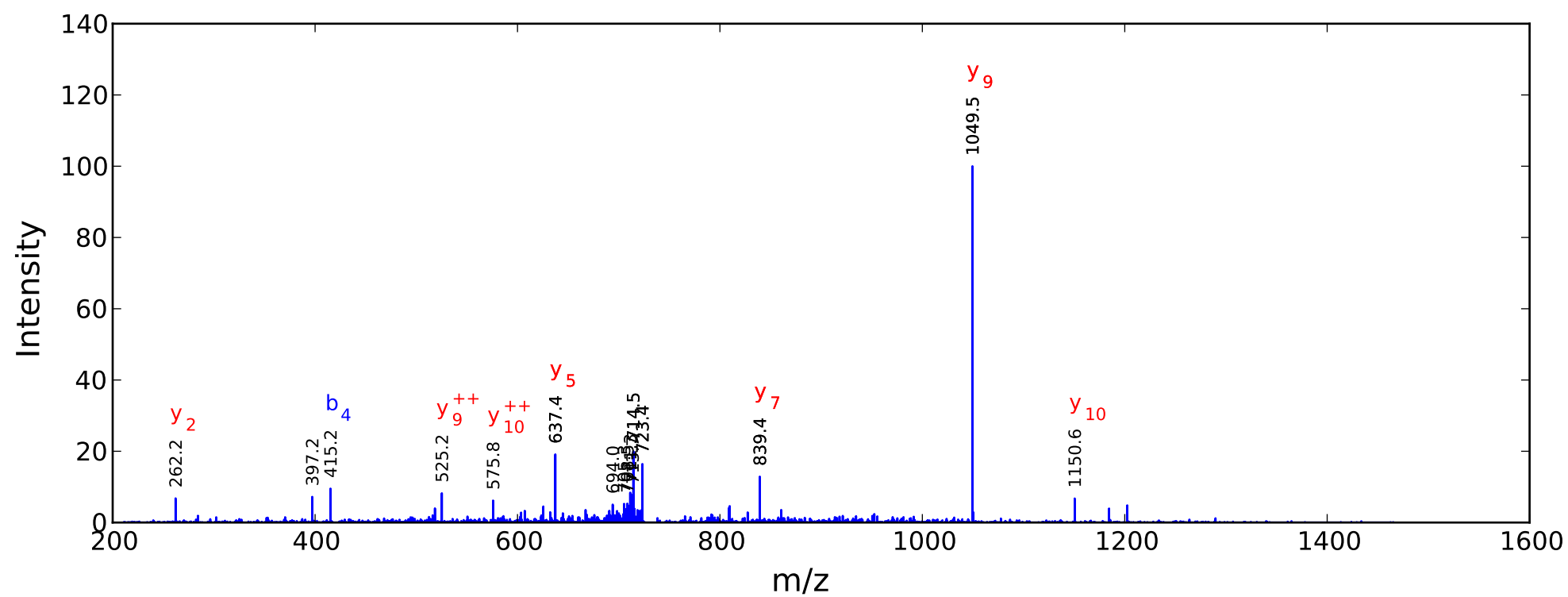
hypothetical protein, conserved

Peptide: ISLTPITTPYDSR

Charge State: 2.0

Modifications: None

m/z: 732.39087



Tb11.01.4430

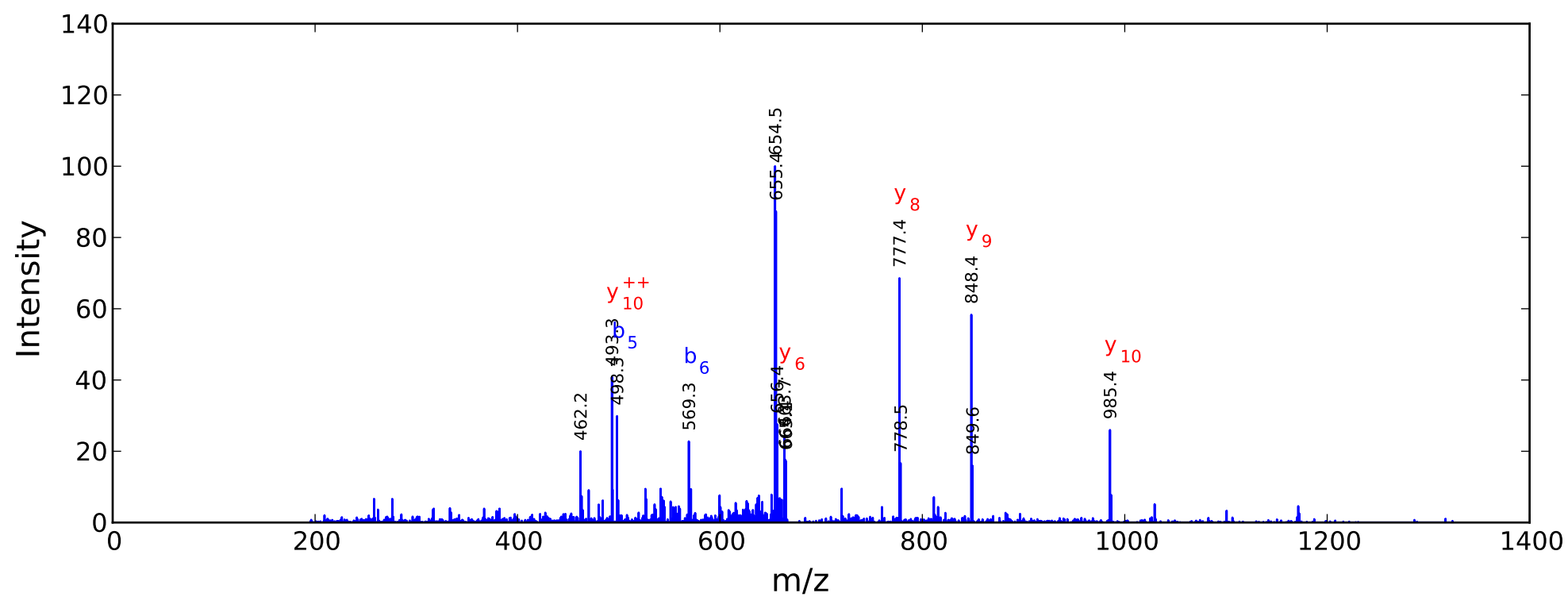
hypothetical protein, conserved

Peptide: FGGVHAGGQAFAAR

Charge State: 2.0

Modifications: None

m/z: 673.341835



Tb11.02.3050

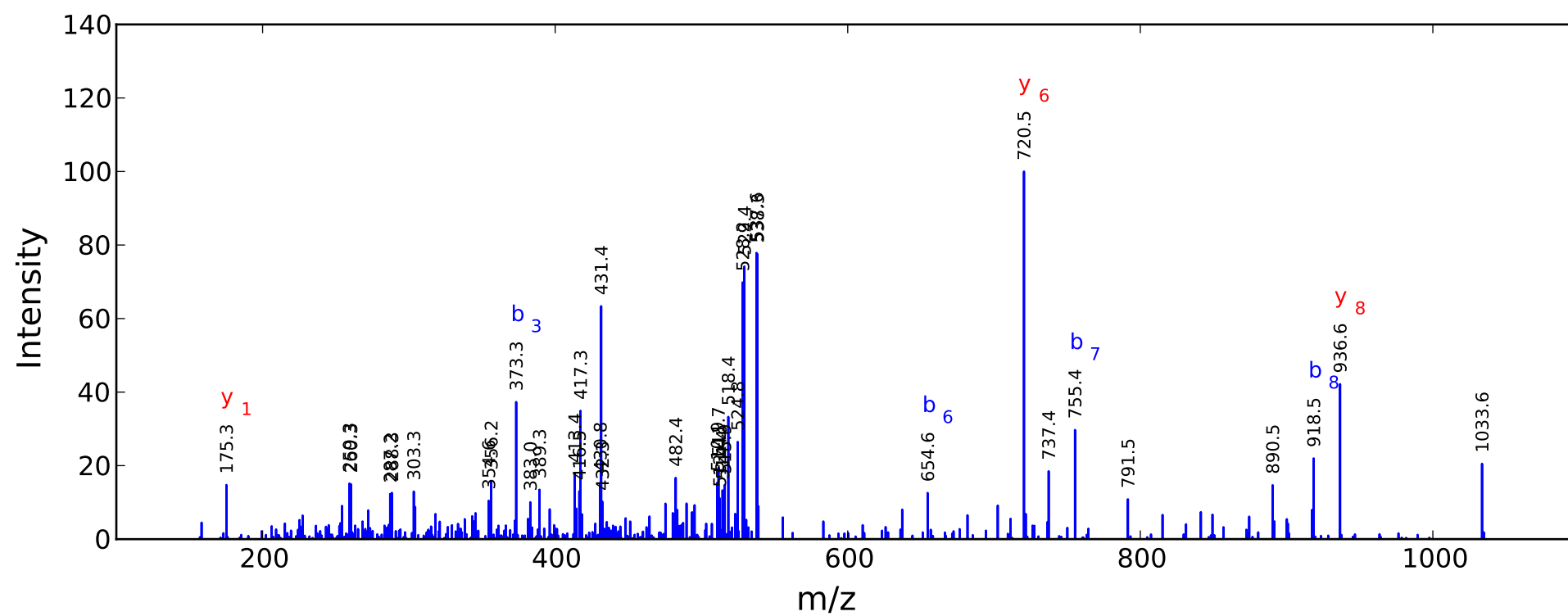
hypothetical protein, conserved

Peptide: RSEPLATYR

Charge State: 2.0

Modifications: None

m/z: 546.79367



Tb927.10.12930

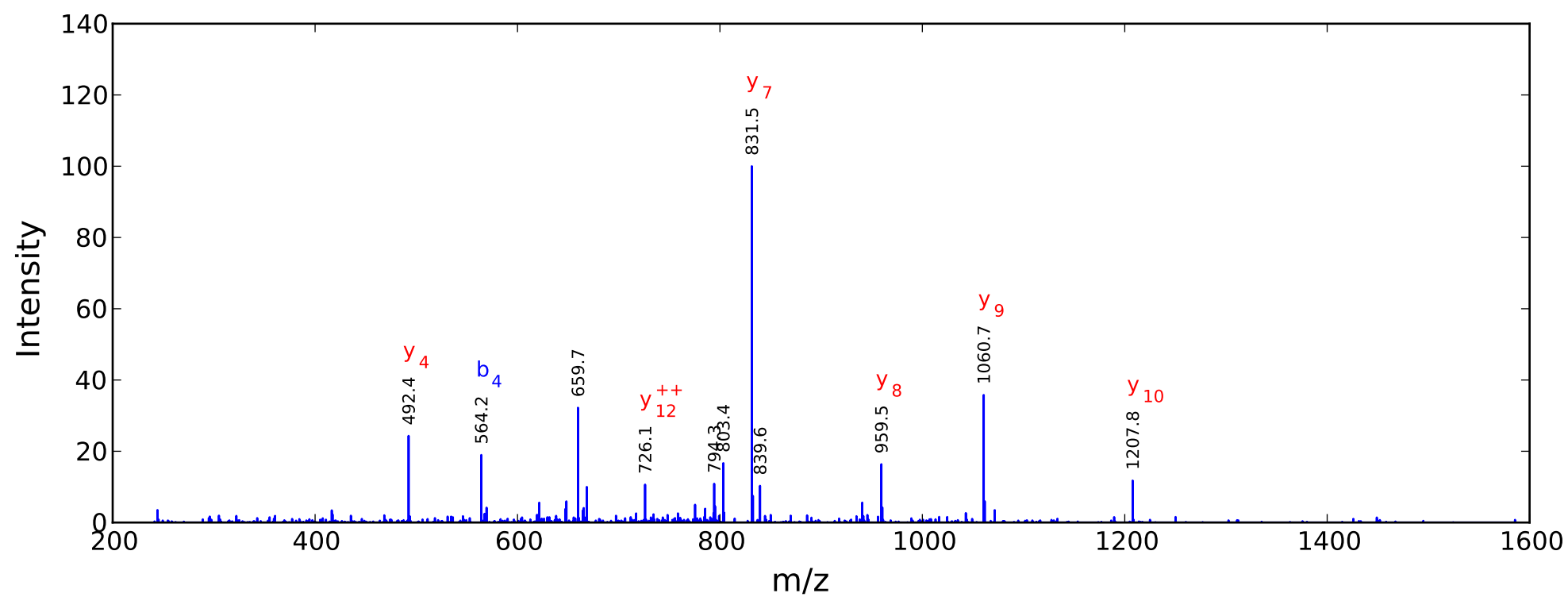
hypothetical protein, conserved

Peptide: MDQFTKPLEGIFR

Charge State: 2.0

Modifications: Residue 1, Acetyl (Protein N-term)

m/z: 812.4138175



Tb927.10.210

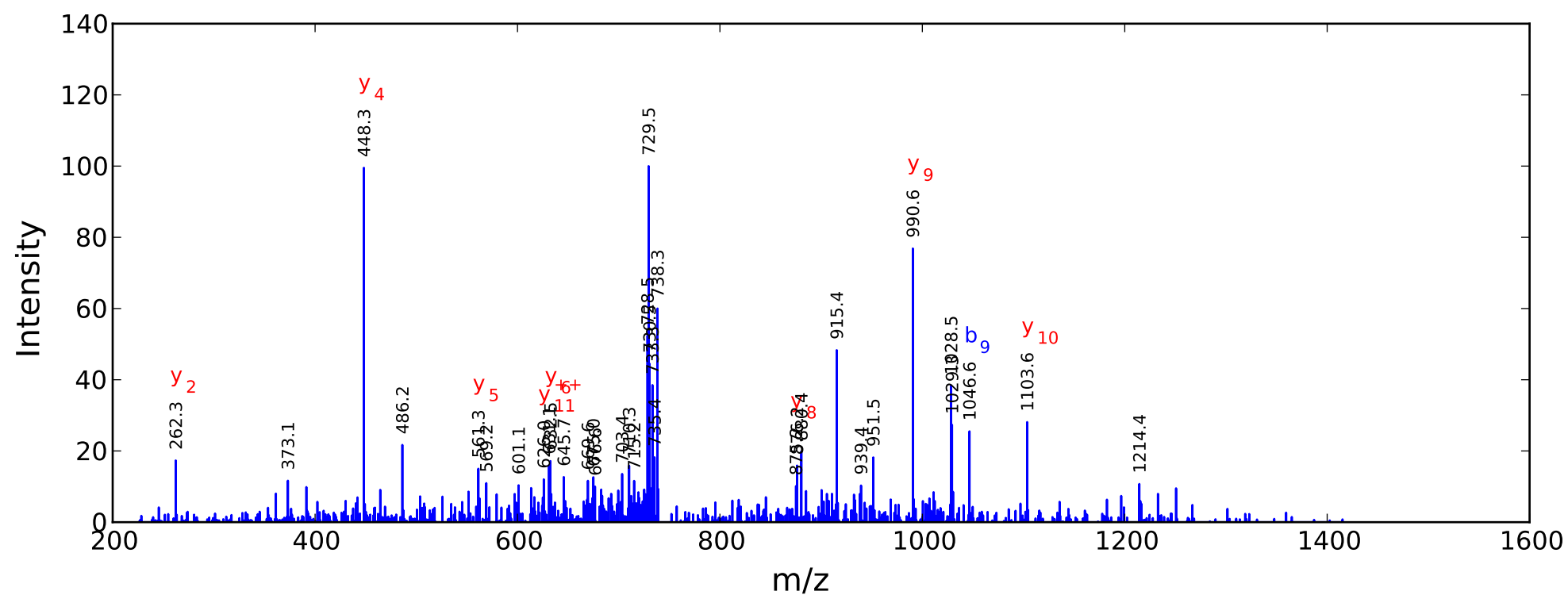
GPI transamidase component GAA1

Peptide: ENFIDENAI SVSR

Charge State: 2.0

Modifications: None

m/z: 747.36538





Tb927.2.3460

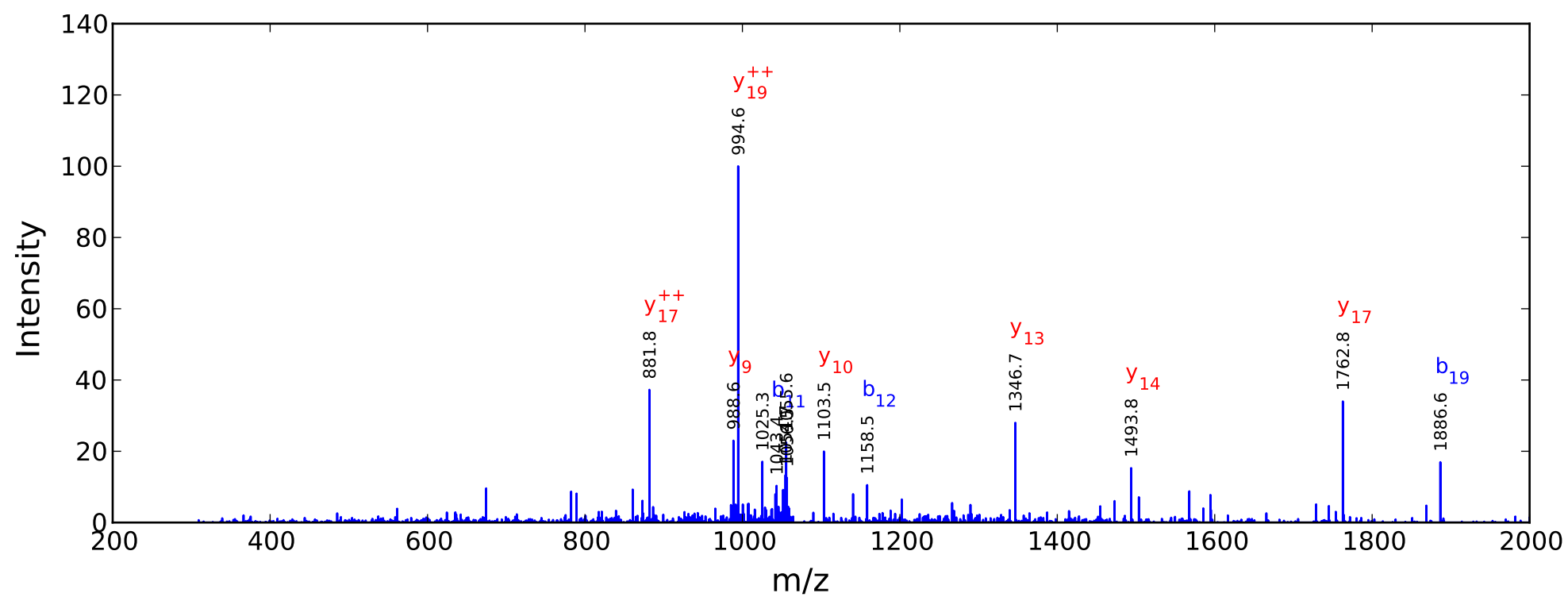
D-alanyl-glycyl endopeptidase-like protein,cysteine peptidase, Clan C

Peptide: GTPQPATFGSVDGAADIWDLK

Charge State: 2.0

Modifications: None

m/z: 1073.526395



Tb927.2.5180

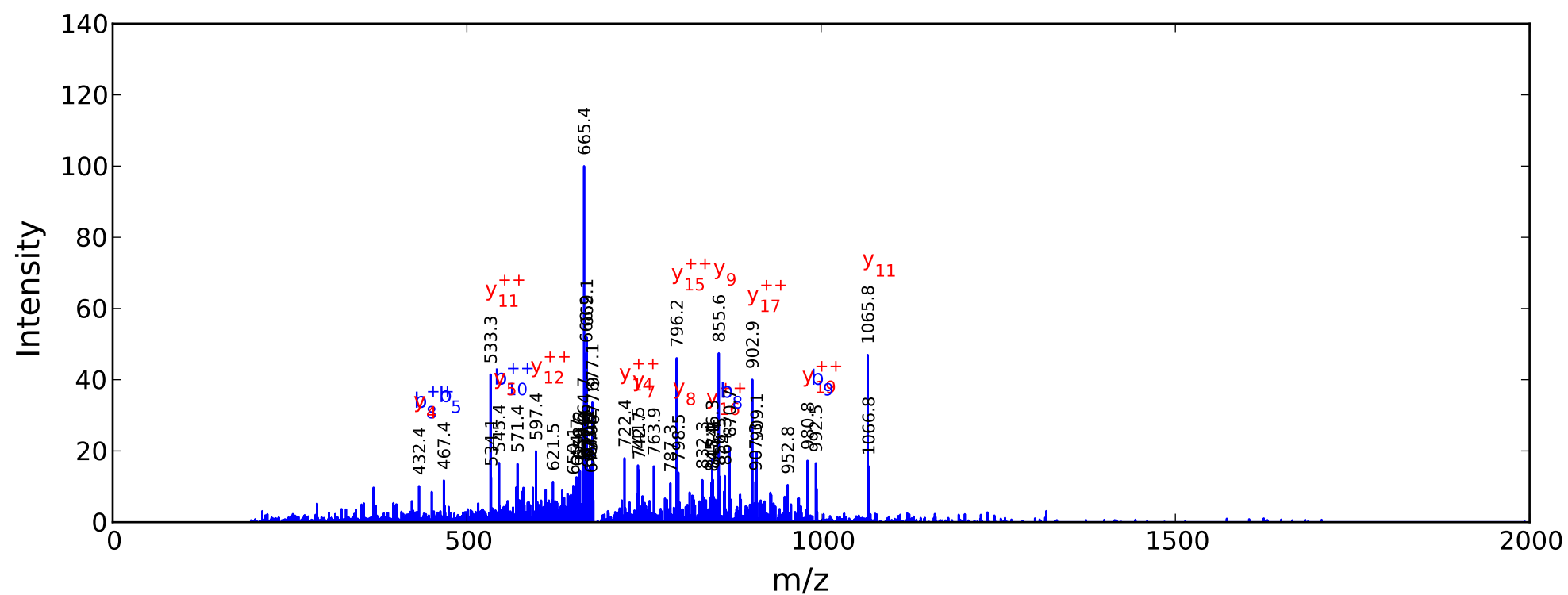
aldo-keto reductase, putative

Peptide: PGVNVMSYKPLGGPVLGVTR

Charge State: 3.0

Modifications: Residue 6, Oxidation (M)

m/z: 686.378416667



Tb927.8.6010

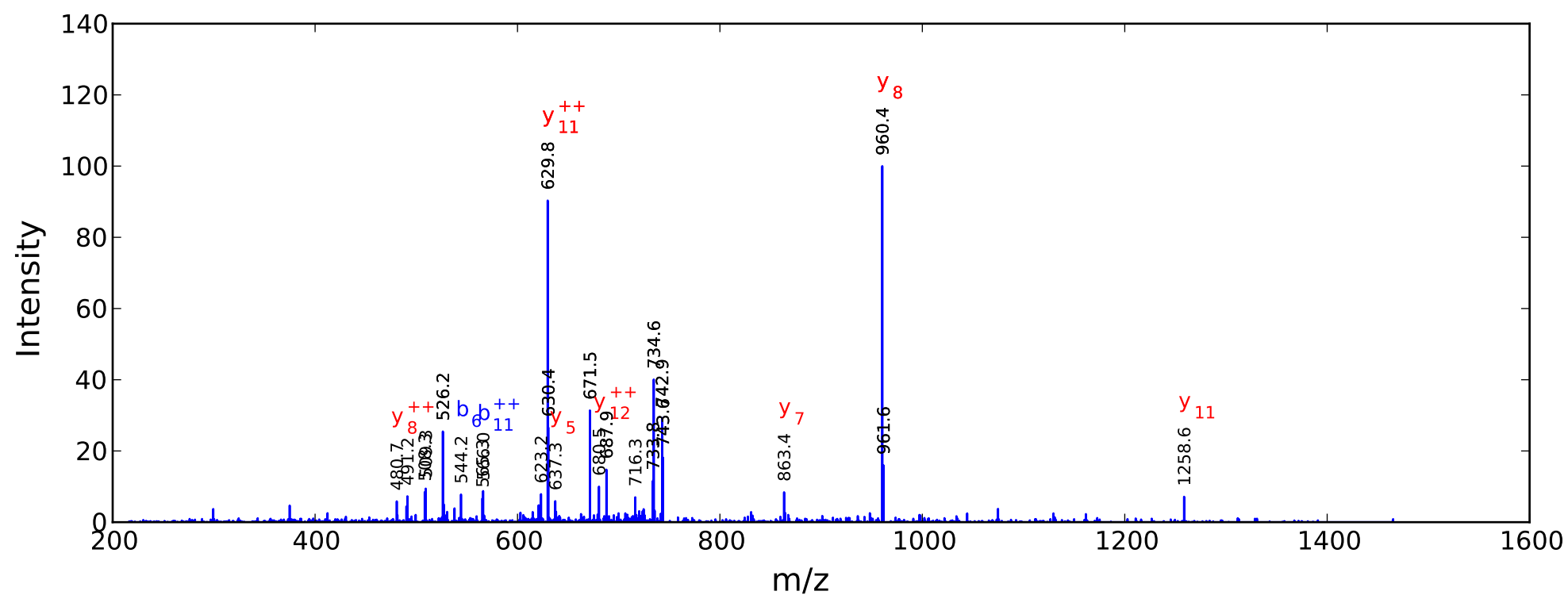
hypothetical predicted multi-pass transmembrane protein

Peptide: SGTPSNPPEFDSLRL

Charge State: 2.0

Modifications: None

m/z: 752.357555



Tb927.3.4820

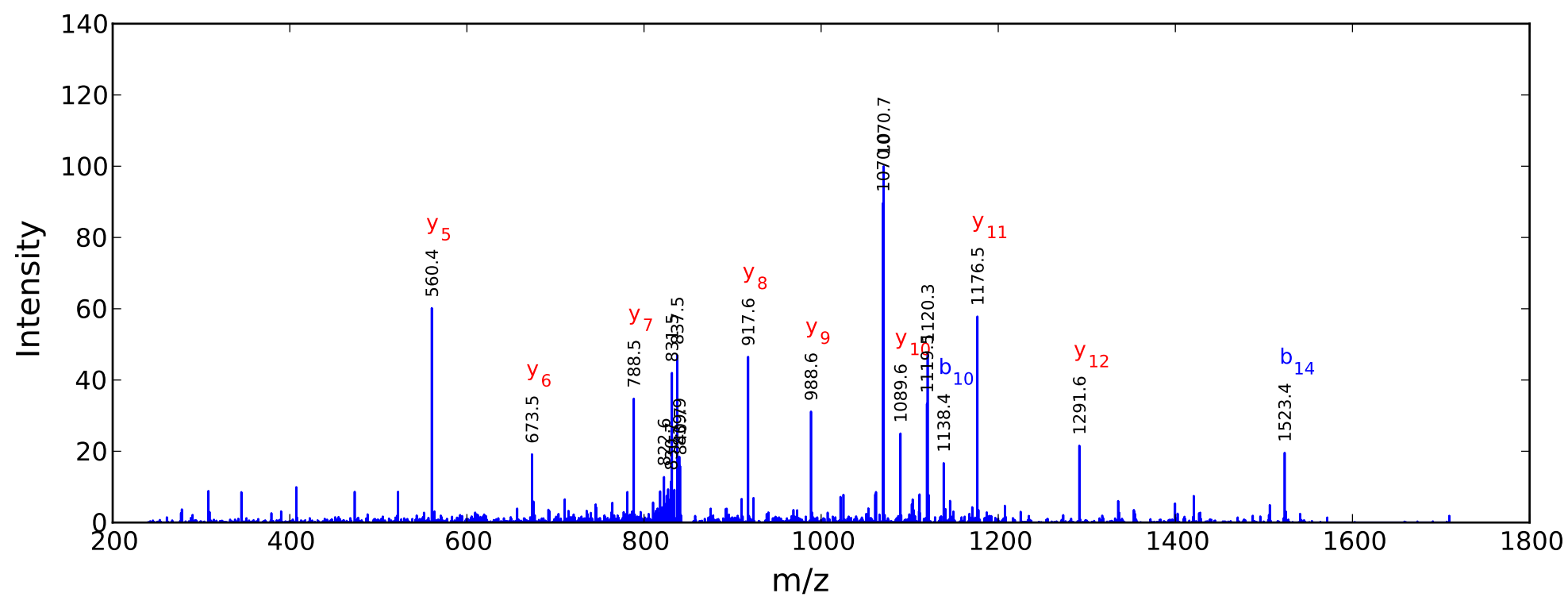
acyltransferase, putative

Peptide: YNEDSTAEDISQGLR

Charge State: 2.0

Modifications: None

m/z: 849.3845



Tb927.7.3520

hypothetical protein, conserved

Peptide: YGVVAYLNSVYNLAPSFK

Charge State: 2.0

Modifications: None

m/z: 1003.025315

