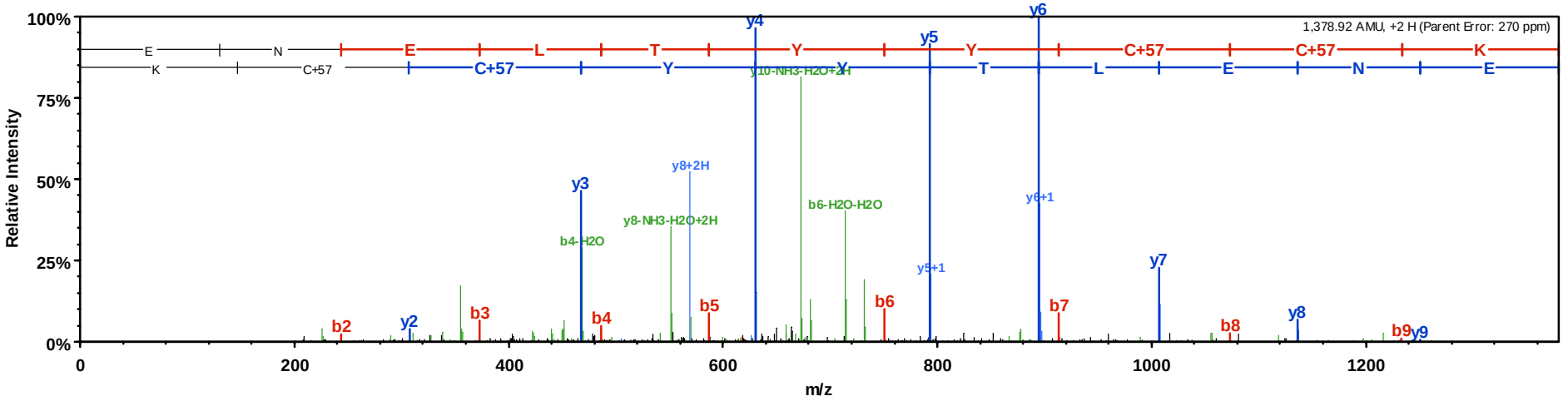
# Supporting MS/MS Spectra and Sequence Coverage for Biomarker Candidates

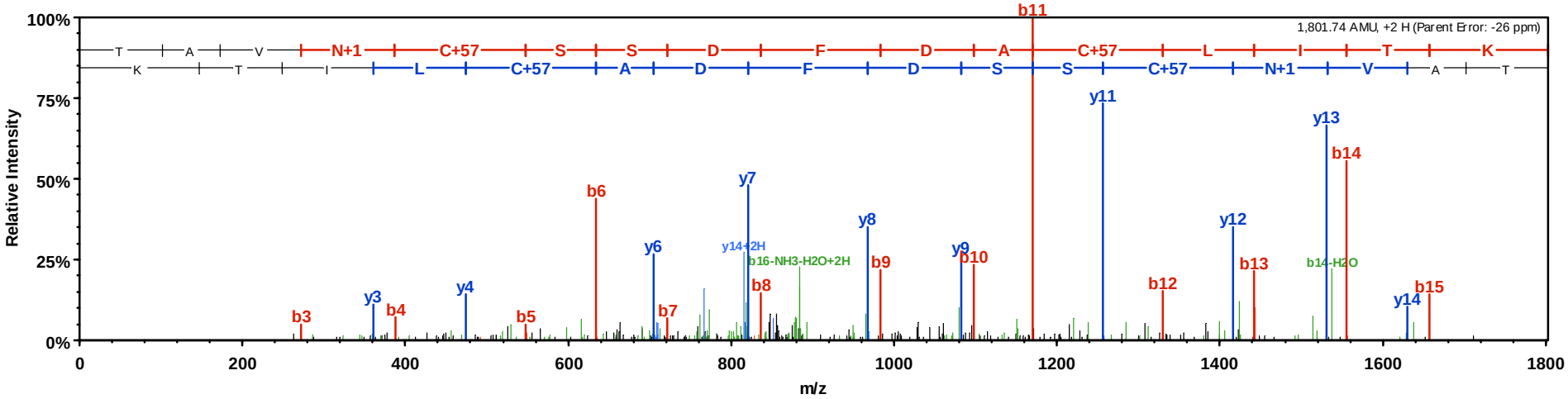
CD59_HUMAN (100%), 14,177.2 Da

(P13987) CD59 glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin) (MEM43 antigen) (Membrane inhibitor of reactive lysis) (MIRL) (20 kDa homologous restriction factor) (HRF-2(

5 unique peptides, 7 unique spectra, 165 total spectra, 48/128 amino acids (38% coverage)

MGIQGGSVLF GLLLVLAVFC HSGHSLQCYN CPNPTADCKT AVNCSSDFDA CLITKAGLQV YNKCWKFEHC NFNDVTTRLR ENELTYYCCK
KDLCNFNEQL ENGGTSLSEK TVLLLVTPFL AAAWSLHP



**BASI_HUMAN (100%), 42,199.7 Da**

**(P35613) Basigin precursor (Leukocyte activation antigen M6) (Collagenase stimulatory factor) (Extracellular matrix metalloproteinase inducer) (EMMPRIN) (5F7) (Tumor cell-derived collagenase stimulatory factor) (T**

**11 unique peptides, 17 unique spectra, 116 total spectra, 164/385 amino acids (43% coverage)**

```
MAAALFVLLG FALLGTHGAS GAAGFVQAPL SQQRWVGGSV ELHCEAVGSP VPEIQWWFEG QGPNDTCSQL WDGARLDRVH
IHATYHQHAA STISIDTLVE EDTGTYECRA SNDPDRNHLT RAPRVKWVRA QAVVLVLEPG TVFTTVEDLG SKILLTCSLN
DSATEVTGHR WLKGGVVLKE DALPGQKTEF KVDSDDQWGE YSCVFLPEPM GTANIQLHGP PRVKAVKSSE HINEGETAML
VCKSESVPPV TDWAWYKITD SEDKALMNGS ESRFFVSSSQ GRSELHIENL NMEADPGQYR CNGTSSKGSD QAIITLRVRS
HLAALWPFLG IVAEVLVLVT IIFIYEKRRK PEDVLDDDDA GSAPLKSSGQ HQNDKGKNVR QRNSS
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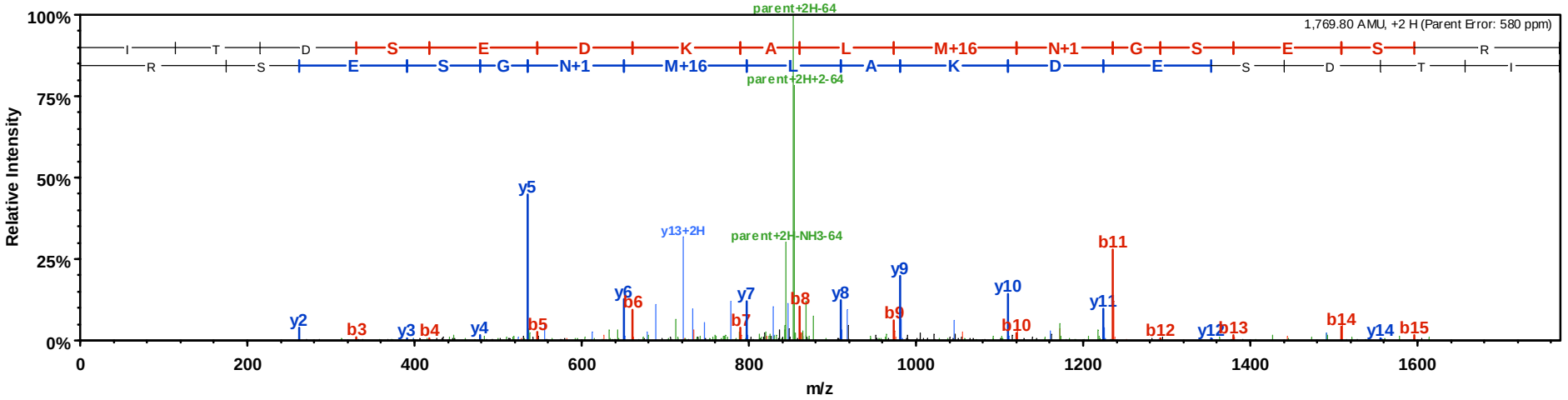
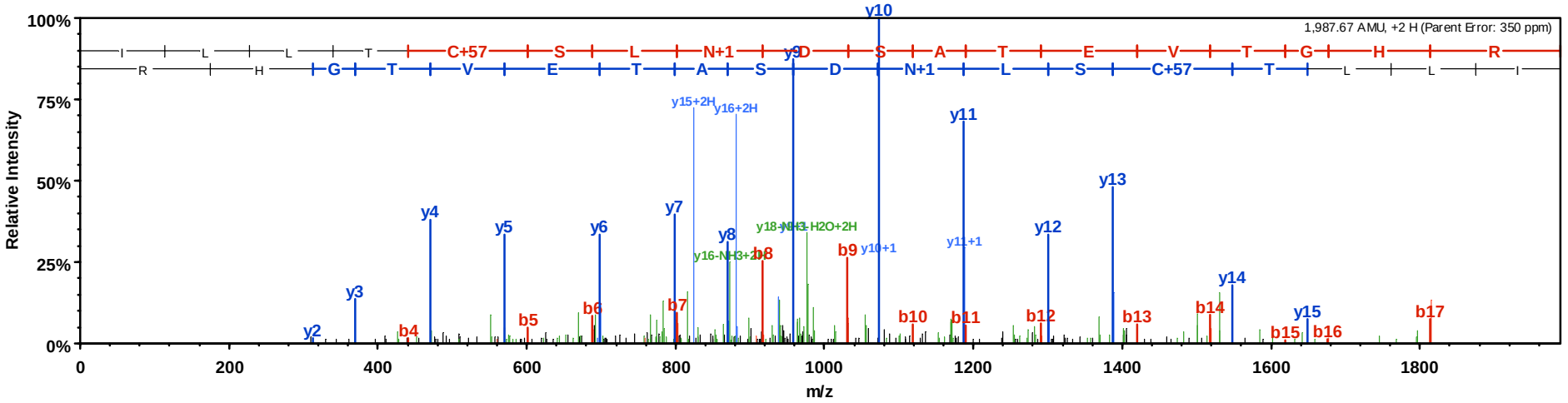


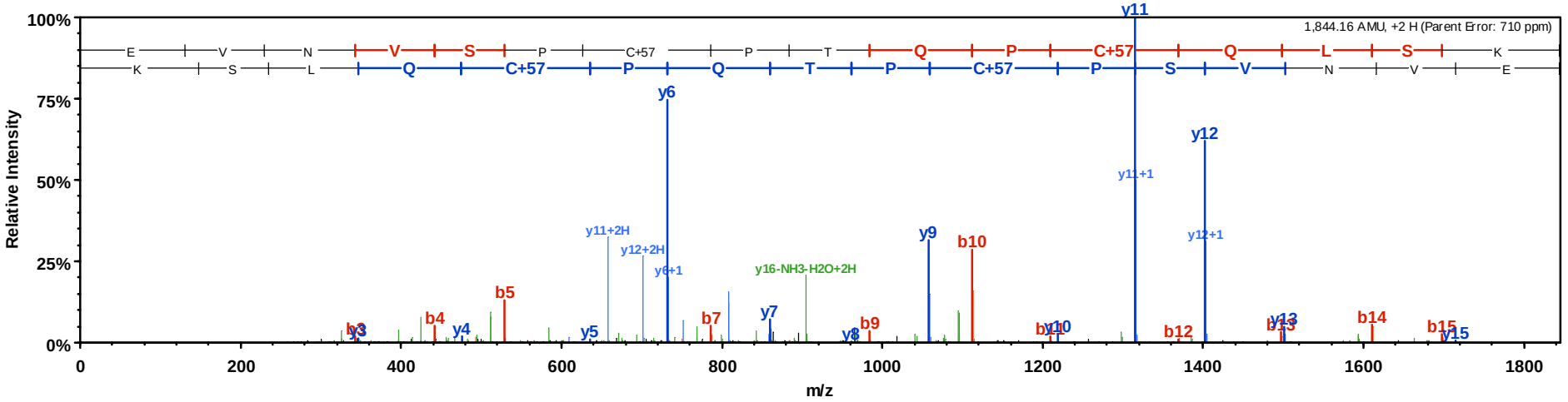



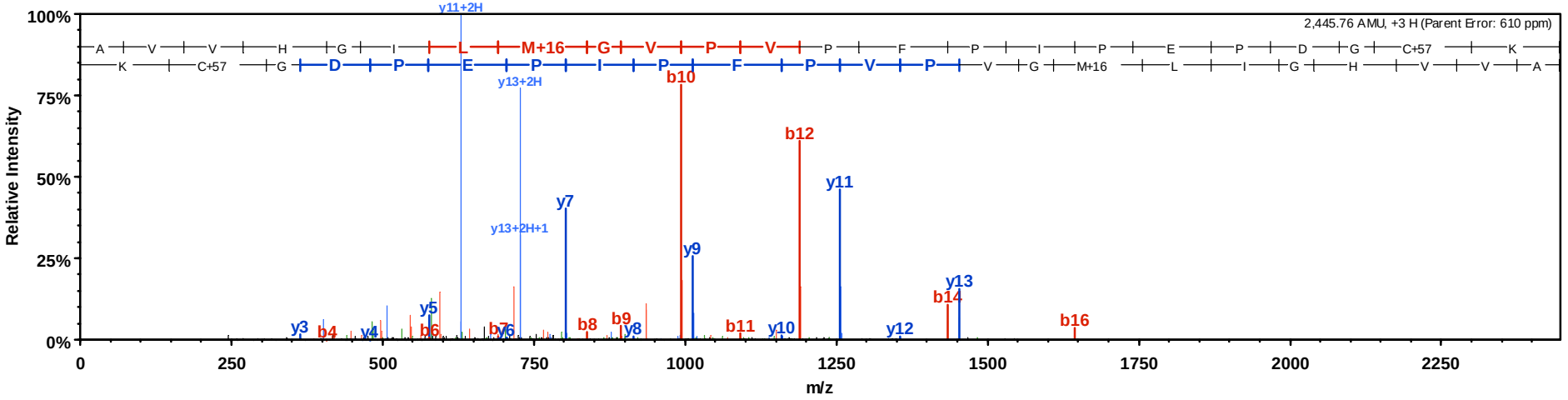
NPC2_HUMAN (100%), 16,570.0 Da

(P61916) Epididymal secretory protein E1 precursor (Niemann-Pick disease type C2 protein) (hE1)

7 unique peptides, 8 unique spectra, 49 total spectra, 103/151 amino acids (68% coverage)

MRFLAATFLL LALSTAAQAE PVQFKDCGSV DGVIKEVNVS PCPTQPCQLS KGQSYSVNVT FTSNIQSKSS KAVVHGILMG
VPVPFPIPEP DGCKSGINCP IQKDKTYSYL NKLPVKSEYP SIKLVVEWQL QDDKNQSLFC WEIPVQIVSH L



**LG3BP_HUMAN (100%), 65,332.1 Da**
**(Q08380) Galectin-3-binding protein precursor (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (Mac-2 BP) (MAC2BP) (Tumor-associated antigen 90K)**
**23 unique peptides, 31 unique spectra, 210 total spectra, 320/585 amino acids (55% coverage)**

```
MTPPRLFWVW  LLVAGTQGVN  DGDMRLADGG  ATNQGRVEIF  YRGQWGTVCD  NLWDLTDASV  VCRALGFENA  TQALGRAAFG
QGSGPIMLDE  VQCTGTEASL  ADCKSLGWLK  SNCRHERDAG  VVCTNETRST  HTLDLSRELS  EALGQIFDSQ  RGCDLSISVN
VQGEDALGFC  GHTVILTANL  EAQALWKEPG  SNVTMSVDAE  CVPMVRDLLR  YFYSRRIDIT  LSSVKCFHKL  ASAYGARQLQ
GYCASLFAIL  LPQDPSFQMP  LDLYAYAVAT  GDALLEKLCL  QFLAWNFEAL  TQAEAWPSVP  TDLLQLLLPR  SDLAVPSELA
LLKAVDTWSW  GERASHEEVE  GLVEKIRFPM  MLPEELFELQ  FNLSLYWSHE  ALFQKKTLQA  LEFHTVPFQL  LARYKGLNLT
EDTYKPRIYT  SPTWSAFVTD  SSWSARKSQL  VYQSRRGPLV  KYSSDYFQAP  SDYRYYPYQS  FQTPQHPSFL  FQDKRVSWSL
VYLPTIQSCW  NYGFSCSSDE  LPVLGLTKSG  GSDRTIAYEN  KALMLCEGLF  VADVTDFEGW  KAAIPSALDT  NSSKSTSSFP
CPAGHFNGFR  TVIRPFYLTN  SSGVD
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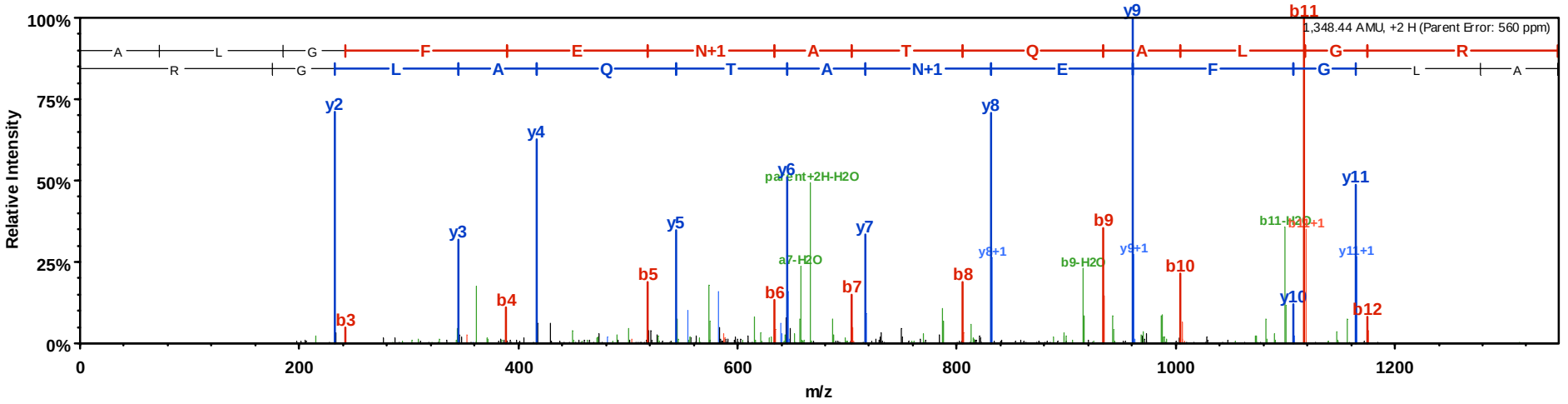
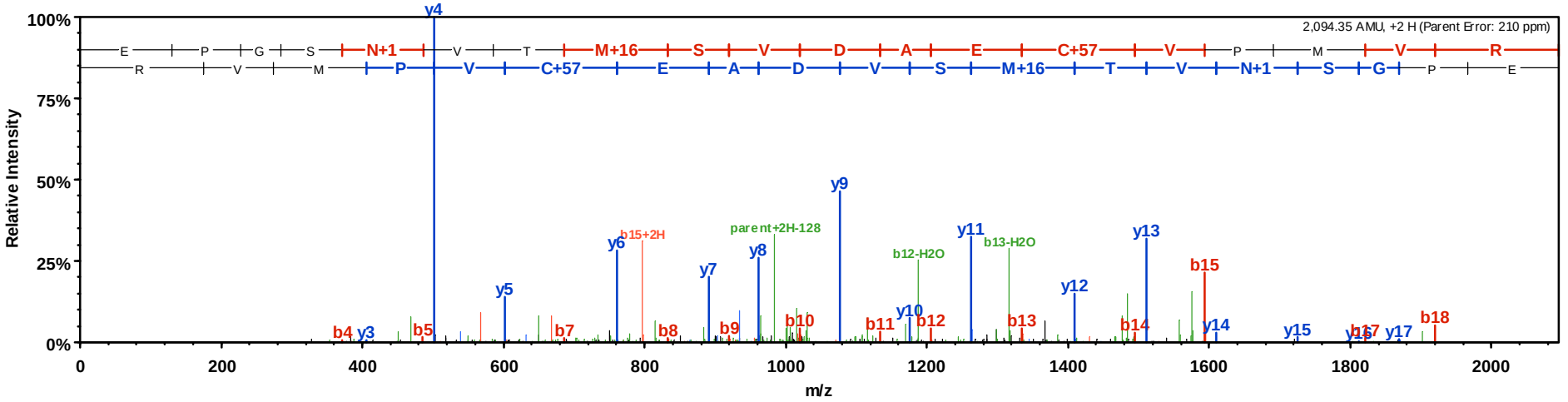
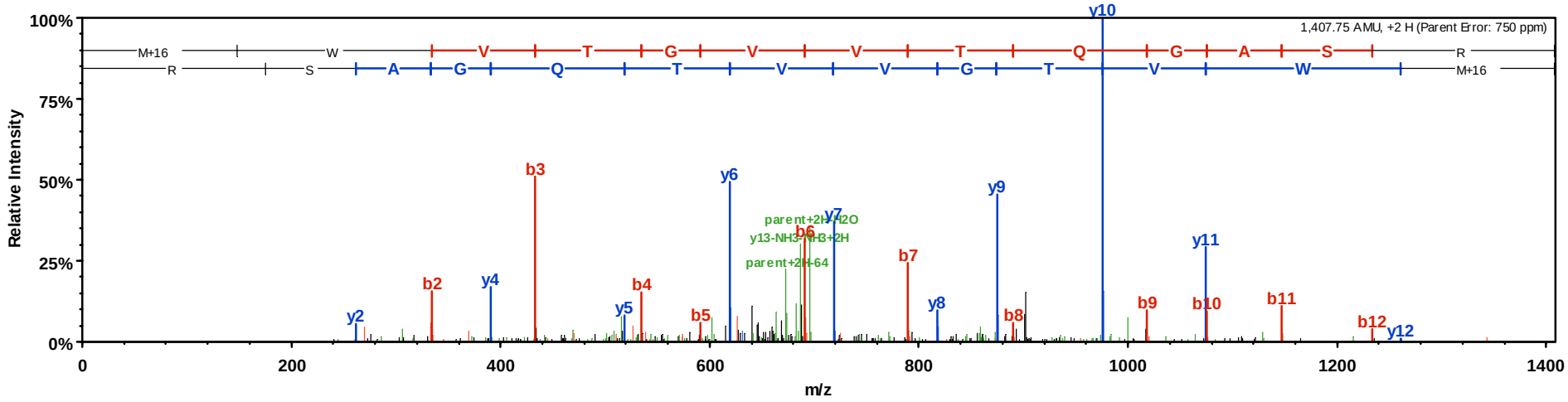
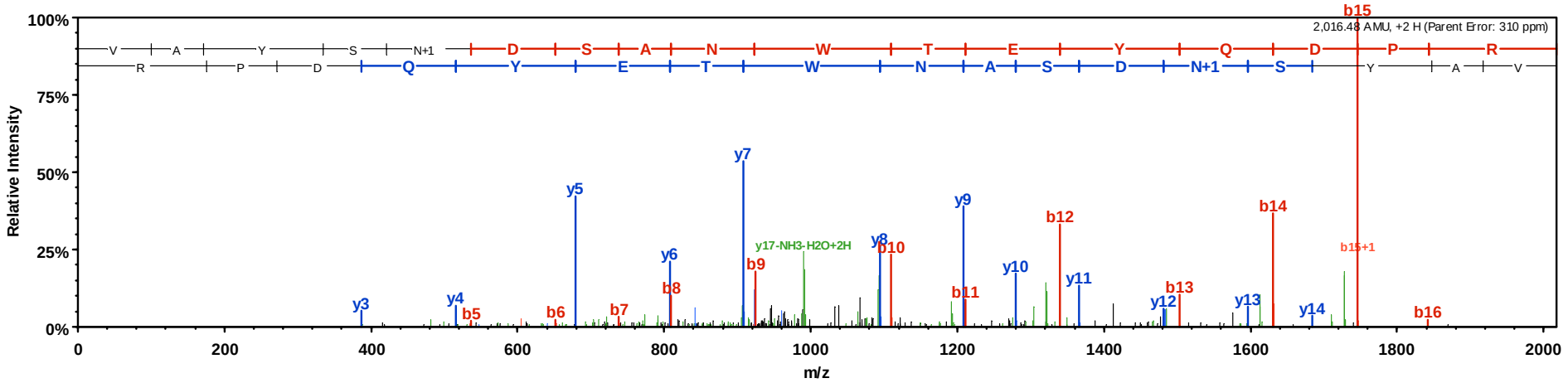


**MFGM_HUMAN (100%), 43,122.9 Da**
**(Q08431) Lactadherin precursor (Milk fat globule-EGF factor 8) (MFG-E8) (HMFG) (Breast epithelial antigen BA46) (MFGM) [Contains: Lactadherin short form; Medin]**
**12 unique peptides, 14 unique spectra, 24 total spectra, 173/387 amino acids (45% coverage)**

```
MPRPRLLAAL  CGALLCAPSL  LVALDICSKN  PCHNGGLCEE  ISQEVRGDVF  PSYTCTCLKG  YAGNHCETKC  VEPLGMENGN
IANSQIAASS  VRVTFLGLQH  WVPELARLNR  AGMVNAWTPS  SNDDNPWIQV  NLLRRMWVTG  VVTQGASRLA  SHEYLKAFKV
AYSLNGHEFD  FIHDVNKKHK  EFVGNWNKNA  VHVNLFETPV  EAQYVRLYPT  SCHTACTLRF  ELLGCELNGC  ANPLGLKNNS
IPDKQITASS  SYKTWGLHLF  SWNPSYARLD  KQGNFNAWVA  GSYGNDQWLQ  VDLGSSKEVT  GIITQGARNF  GSVQFVASYK
VAYSNDSANW  TEYQDPRTGS  SKIFPGNWDN  HSHKKNLFET  PILARYVRIL  PVAWHNRIAL  RLELLGC
```



**TSN8_HUMAN (100%), 26,045.0 Da**
**(P19075) Tetraspanin-8 (Tspan-8) (Transmembrane 4 superfamily member 3) (Tumor-associated antigen CO-029)**
**4 unique peptides, 6 unique spectra, 66 total spectra, 55/237 amino acids (23% coverage)**

```
MAGVSACIKY SMFTFNFLFW LCGILILALA IWVRVSNDSQ AIFGSEDVGS SSYVAVDILI AVGAIIMILG FLGCCGAIKE
SRCMLLLFFI GLLLILLLQV ATGILGAVFK SKSDRIVNET LYENTKLLSA TGESEKQFQE AIIVFQEEFK CCGLVNGAAD
WGNNFQHYPE LCACLDKQRP CQSYNGKQVY KETCISFIKD FLAKNLIIVI GISFGLAVIE ILGLVFSMVL YCQIGNK
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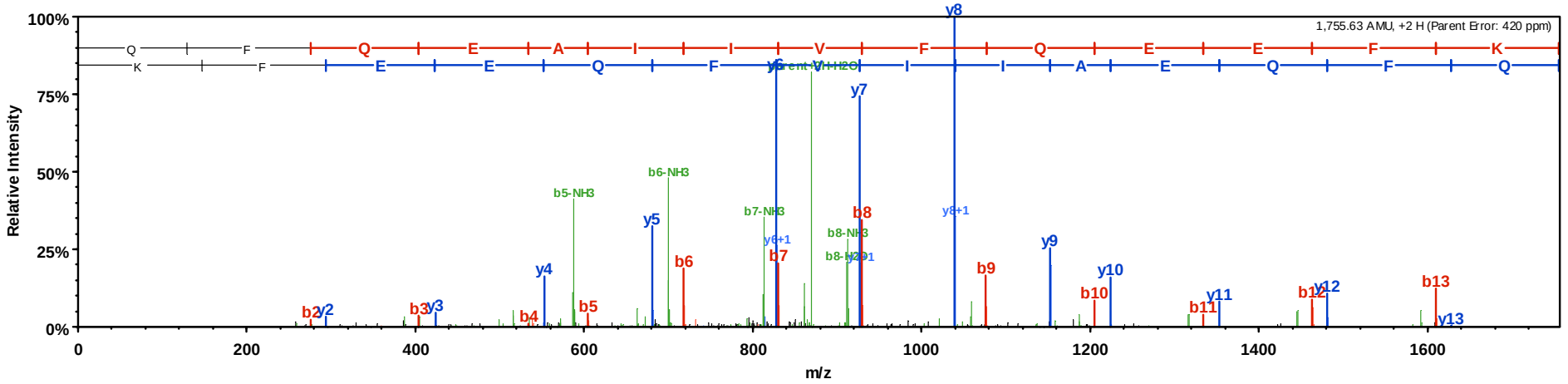


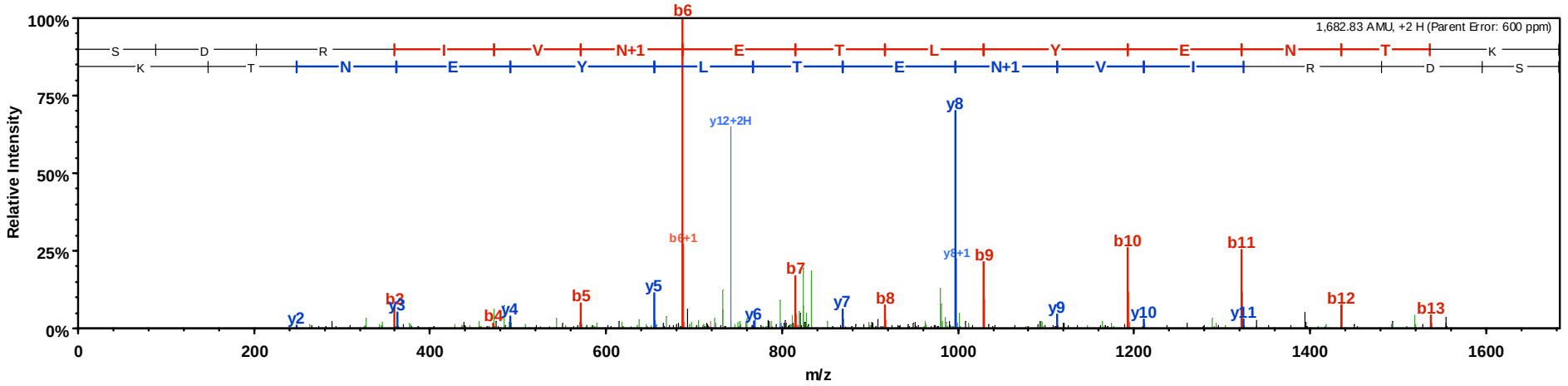

**TACD1_HUMAN (100%), 34,920.2 Da**

**(P16422) Tumor-associated calcium signal transducer 1 precursor (Major gastrointestinal tumor-associated protein GA733-2) (Epithelial cell surface antigen) (Epithelial glycoprotein) (EGP) (Adenocarcinoma-associated ant**

**10 unique peptides, 14 unique spectra, 97 total spectra, 148/314 amino acids (47% coverage)**

```
MAPPQVLAFG  LLLAAATATF  AAAQEECVCE  NYKLAVNCFV  NNNRQCQCTS  VGAQNTVICS  KLAAKCLVMK  AEMNGSKLGR
RAKPEGALQN  NDGLYDPDCD  ESGLFKAKQC  NGTSTCWCVN  TAGVRRTDKD  TEITCSERVR  TYWIIIELKH  KARFKPYDSK
SLRTALQKEI  TTRYQLDPKF  ITSILYENNV  ITIDLVQNSS  QKTQNDVDIA  DVAYYFEKDV  KGESLFHSKK  MDLTVNGEQL
DLDPGQTLIY  YVDEKAPEFS  MQGLKAGVIA  VIVVVVMAVV  AGIVVLVISR  KKRMAKYEKA  EIKEMGEMHR  ELNA
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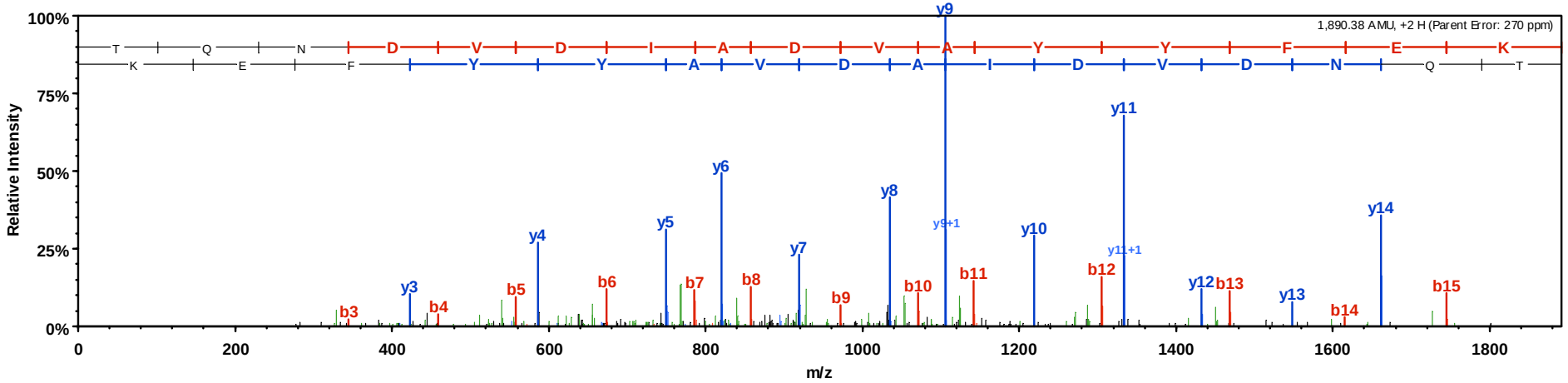


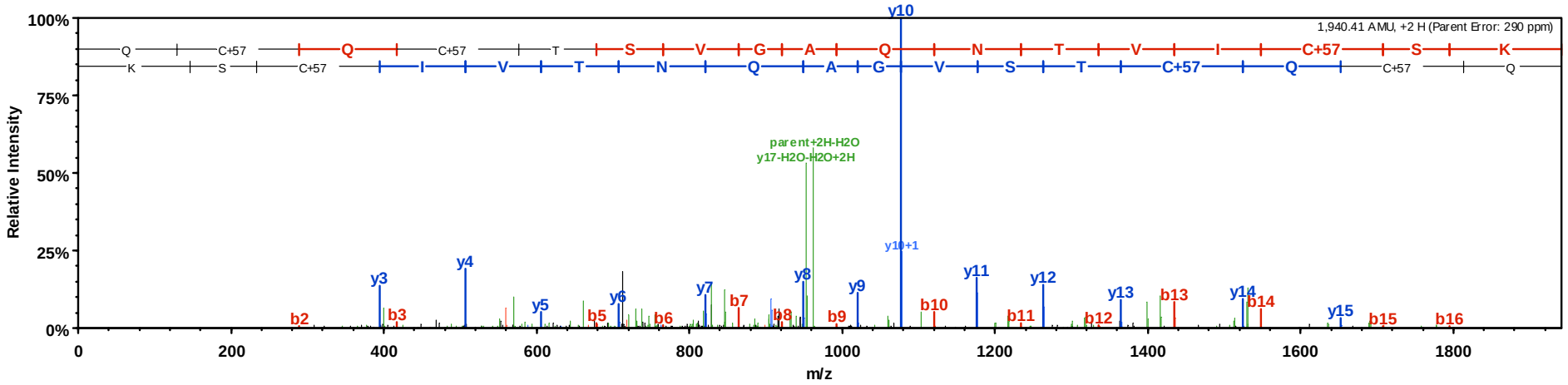

**EPHB3_HUMAN (100%), 110,330.7 Da**
**(P54753) Ephrin type-B receptor 3 precursor (EC 2.7.10.1) (Tyrosine-protein kinase receptor HEK-2)**
**8 unique peptides, 9 unique spectra, 14 total spectra, 156/998 amino acids (16% coverage)**

```
MARARPPPPP SPPPGLLPLL PPLLLLPLLL LPAGCRALEE TLMDTKWVTS ELAWTSHPES GWEEVSGYDE AMNPIRTYQV
CNVRESSQNN WLRTGFIWRR DVQRVYVELK FTVRDCNSIP NIPGSCKETF NLFYYEADSD VASASSPFWM ENPYVKVDTI
APDESFSRLD AGRVNTKVRS FGPLSKAGFY LAFQDQGACM SLISVRAFYK KCASTTAGFA LFPETLTGAE PTSLVIAPGT
CIPNAVEVSV PLKLYCNGDG EWMVPVGACT CATGHEPAAK ESQCRPCPPG SYKAKQGEGP CLPCPPNSRT TSPAASICTC
HNNFYRADSD SADSACTTVP SPPRGVISNV NETSLILEWS EPRDLGGRDD LLYNVICKKC HGAGGASACS RCDDNVEFVP
RQLGLTERRV HISHLLAHTR YTFEVQAVNG VSGKSPLPPR YAAVNITTNQ AAPSEVPTLR LHSSSGSSLT LSWAPPERPN
GVILDYEMKY FEKSEGIAST VTSQMNSVQL DGLRPDARYV VQVRARTVAG YGQYSRPAEF ETTSERGSGA QQLQEQLPLI
VGSATAGLVF VVAVVVIAIV CLRKQRHGSD SEYTEKLQQY IAPGMKVYID PFTYEDPNEA VREFAKEIDV SCVKIEEVIG
AGEFGEVCRG RLKQPGRREV FVAIKTLKVG YTERQRRDFL SEASIMGQFD HPNIIRLEGV VTKSRPVMIL TEFMENCALD
SFLRLNDGQF TVIQLVGMLR GIAAGMKYLS EMNYVHRDLA ARNILVNSNL VCKVSDFGLS RFLEDDPSDP TYTSSLGGKI
PIRWTAPEAI AYRKFTSASD VWSYGIVMWE VMSYGERPYW DMSNQDVINA VEQDYRLPPP MDCPTALHQL MLDCWVRDRN
LRPKFSQIVN TLDKLIRNAA SLKVIASAQS GMSQPLLDRT VPDYTTFTTV GDWLDAIKMG RYKESFVSAG FASFDLVAQM
TAEDLLRIGV TLAGHQKKIL SSIQDMRLQM NQTLPVQV
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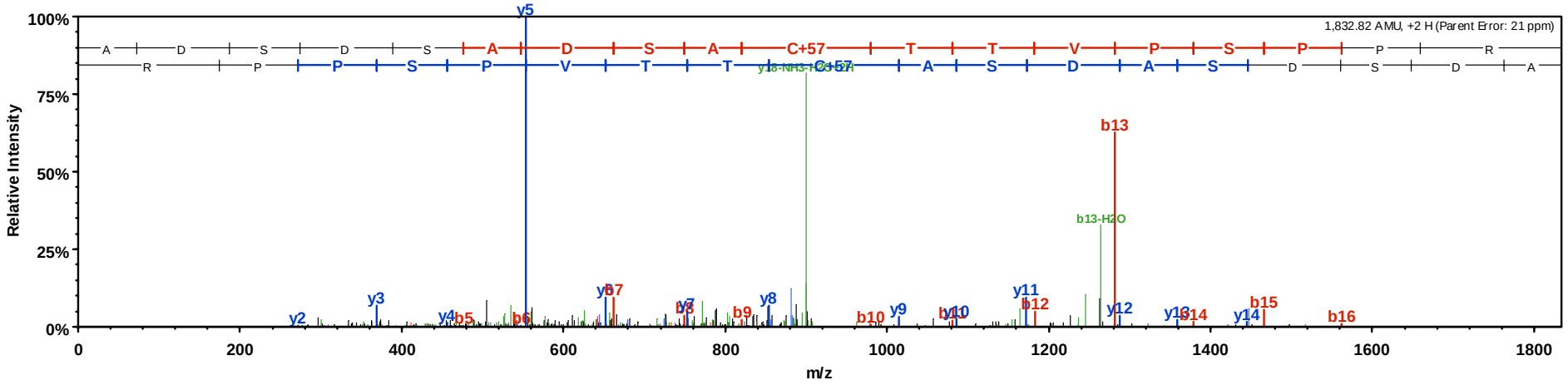
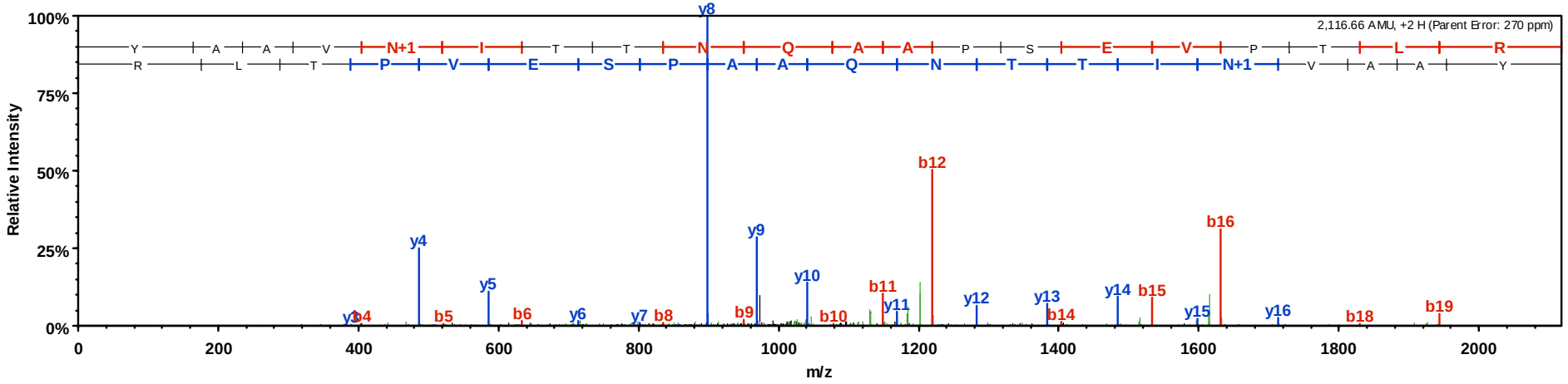
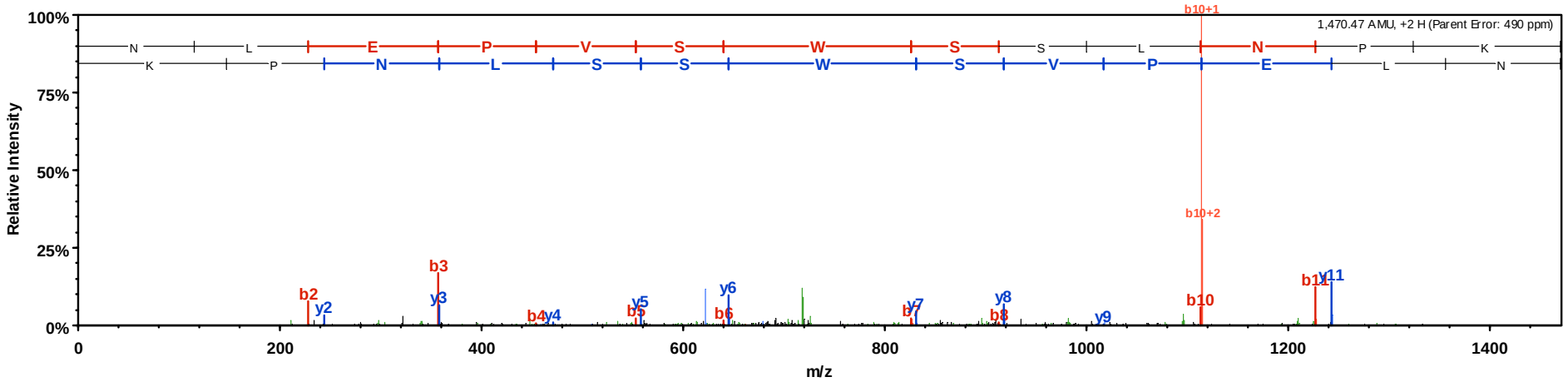
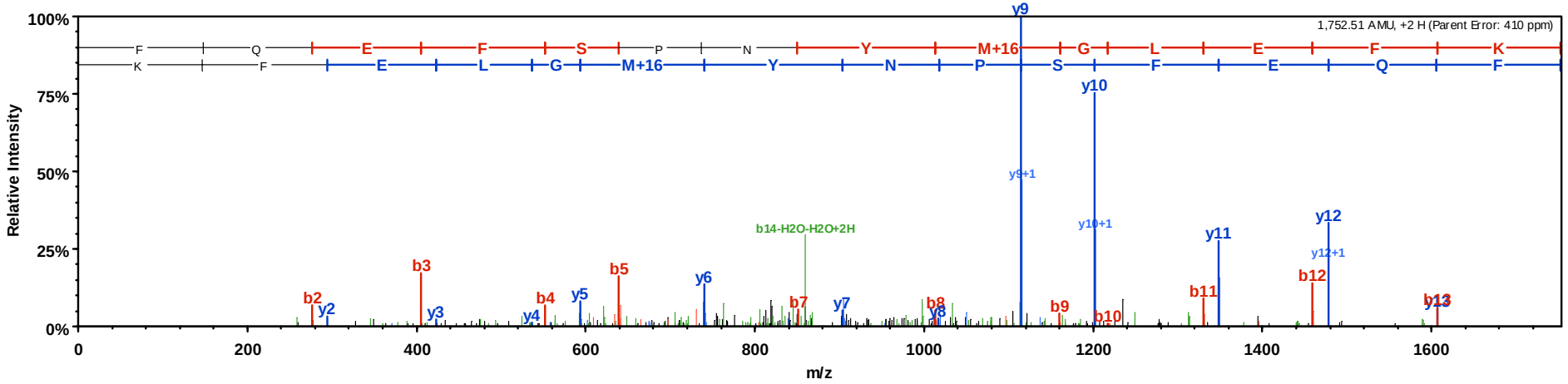


**EFNB1_HUMAN (100%), 38,007.4 Da**
**(P98172) Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2) (LERK-2) (ELK ligand) (ELK-L)**
**5 unique peptides, 6 unique spectra, 20 total spectra, 91/346 amino acids (26% coverage)**

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| M A R P G Q R W L G | K W L V A M V V W A | L C R L A T P L A K | **N L E P V S W S S L** | **N P K** F L S G K G L | V I Y P K **I G D K L** | **D I I C P R** A E A G | R P Y E Y Y K **L Y L** |
| **V R P E Q A A A C S** | **T V L D P N V L V T** | **C N R P E Q E I R** F | T I K **F Q E F S P N** | **Y M G L E F K K H H** | **D Y Y I T S T S N G** | **S L E G L E N R** E G | G V C R T R T M K I |
| I M K V G Q D P N A | V T P E Q L T T S R | P S K E A D N T V K | M A T Q A P G S R G | S L G D S D G K H E | T V N Q E E K S G P | G A S G G S S G D P | D G F F N S K V A L |
| F A A V G A G C V I | F L L I I I F L T V | L L L K L R K R H R | K H T Q Q R A A A L | S L S T L A S P K G | G S G T A G T E P S | D I I I P L R T T E | N N Y C P H Y E K V |
| S G D Y G H P V Y I | V Q E M P P Q S P A | N I Y Y K V | | | | | |



**HPLN1_HUMAN (100%), 40,166.2 Da**

**(P10915) Hyaluronan and proteoglycan link protein 1 precursor (Proteoglycan link protein) (Cartilage link protein) (LP)**

**13 unique peptides, 17 unique spectra, 124 total spectra, 182/354 amino acids (51% coverage)**

```
MKSLLLLVLI SICWADHLSD NYTLDHDRAI HIQAENGPHL LVEAEQAKVF SHRGGNVTLP CKFYRDPTAF GSGIHKIRIK
WTKLTSDYLK EVDVFVSMGY HKKTYGGYQG RVFLKGGSDS DASLVITDLT LEDYGRYKCE VIEGLEDDTV VVALDLQGVV
FPYFPRLGRY NLNFHEAQQA CLDQDAVIAS FDQLYDAWRG GLDWCNAGWL SDGSVQYPIT KPREPCGGQN TVPGVRNYGF
WDKDKSRYDV FCFTSNFNGR FYYLIHPTKL TYDEAVQACL NDGAQIAKVG QIFAAWKILG YDRCDAGWLA DGSVRYPISR
PRRRCSPTEA AVRFVGFPDK KHKLYGVYCF RAYN
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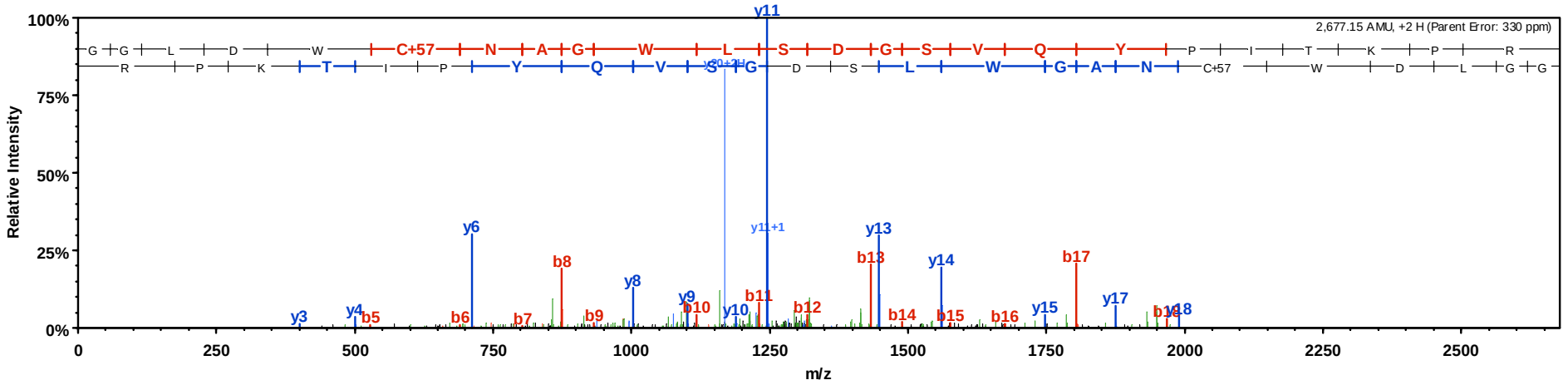


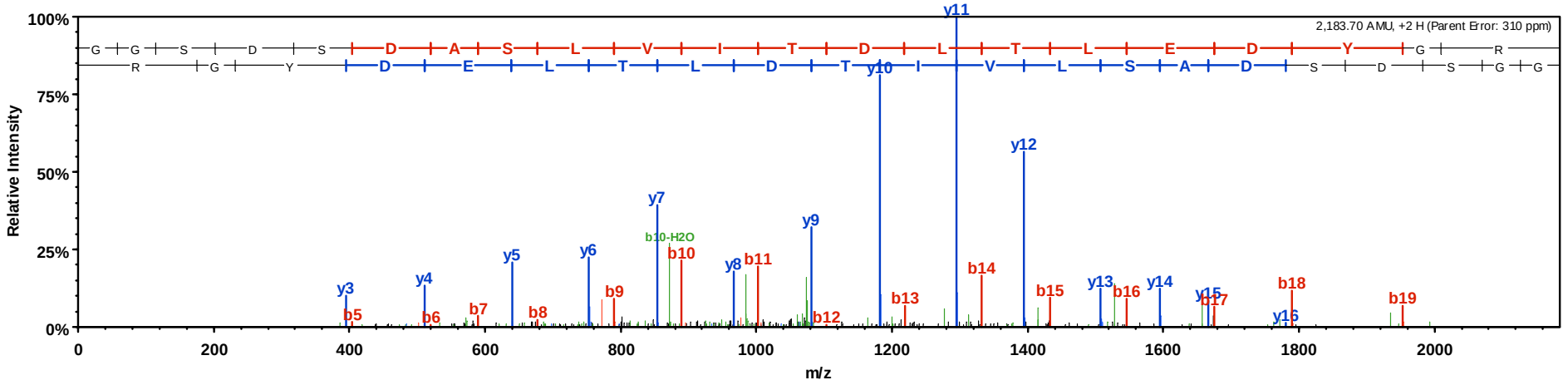

**EMIL1_HUMAN (100%), 106,694.7 Da**
**(Q9Y6C2) EMILIN-1 precursor (Elastin microfibril interface-located protein 1) (Elastin microfibril interfacer 1)**
**19 unique peptides, 23 unique spectra, 66 total spectra, 287/1016 amino acids (28% coverage)**

```
MAPRTLWSCY LCCLLTAAAG AASYPPRGFS LYTGSSGALS PGGPQAQIAP RPASRHRNWC AYVVTRTVSC VLEDGVETYV
KYQPCAWGQP QCPQSIMYRR FLRPRYRVAY KTVTDMEWRC CQGYGGDDCA ESPAPALGPA SSTPRPLARP ARPNLSGSSA
GSPLSGLGGE GPGESEKVQQ LEEQVQSLTK ELQGLRGVLQ GLSGRLAEDV QRAVETAFNG RQQPADAAAR PGVHETLNEI
QHQLQLLDTR VSTHDQELGH LNNHHGGSSS SGGSRAPAPA SAPPGPSEEL LRQLEQRLQE SCSVCLAGLD GFRRQQQEDR
ERLRAMEKLL ASVEERQRHL AGLAVGRRPP QECCSPELGR RLAELERRLD VVAGSVTVLS GRRGTELGGA AGQGGHPPGY
TSLASRLSRL EDRFNSTLGP SEEQEESWPG APGGLSHWLP AARGRLEQLG GLLANVSGEL GGRLDLLEEQ VAGAMQACGQ
LCSGAPGEQD SQVSEILSAL ERRVLDSEGQ LRLVGSGLHT VEAAGEARQA TLEGLQEVVG RLQDRVDAQD ETAAEFTLRL
NLTAARLGQL EGLLQAHGDE GCGACGGVQE ELGRLRDGVE RCSCPLLPPR GPGAGPGVGG PSRGPLDGFS VFGGSSGSAL
QALQGELSEV ILSFSSLNDS LNELQTTVEG QGADLADLGA TKDRIISEIN RLQQEATEHA TESEERFRGL EEGQAQAGQC
PSLEGRLGRL EGVCERLDTV AGGLQGLREG LSRHVAGLWA GLRETNTTSQ MQAALLEKLV GGQAGLGRRL GALNSSLQLL
EDRLHQLSLK DLTGPAGEAG PPGPPGLQGP PGPAGPPGSP GKDGQEGPIG PPGPQGEQGV EGAPAAPVPQ VAFSAALSLP
RSEPGTVPFD RVLLNDGGYY DPETGVFTAP LAGRYLLSAV LTGHRHEKVE AVLSRSNQGV ARVDSGGYEP EGLENKPVAE
SQPSPGTLGV FSLILPLQAG DTVCVDLVMG QLAHSEEPLT IFSGALLYGD PELEHA
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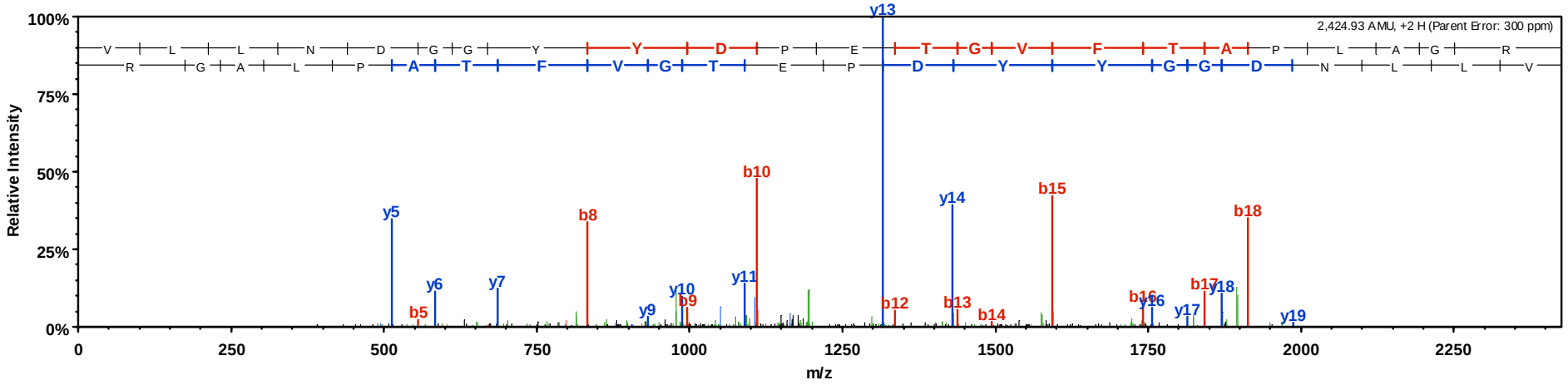
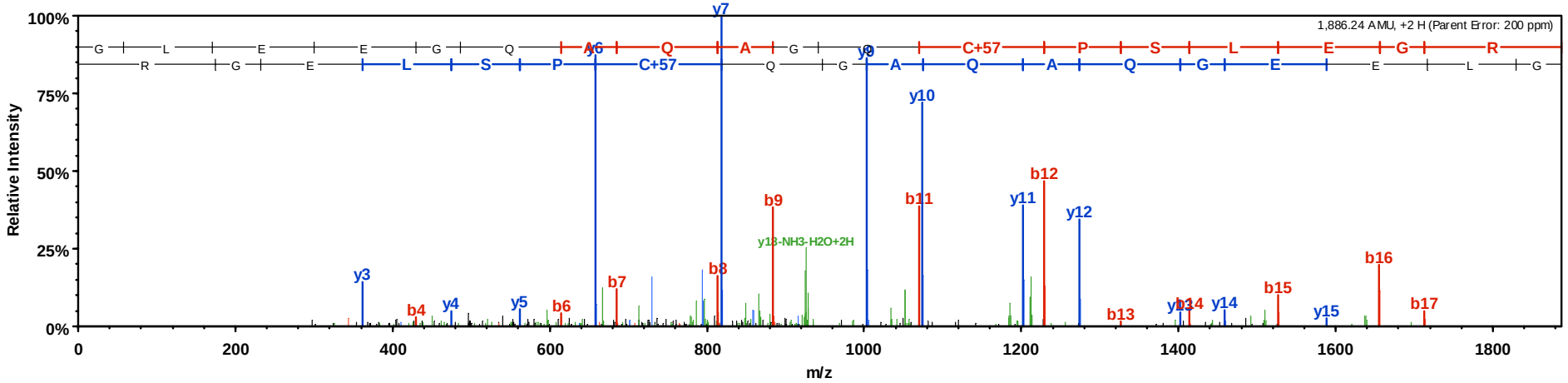
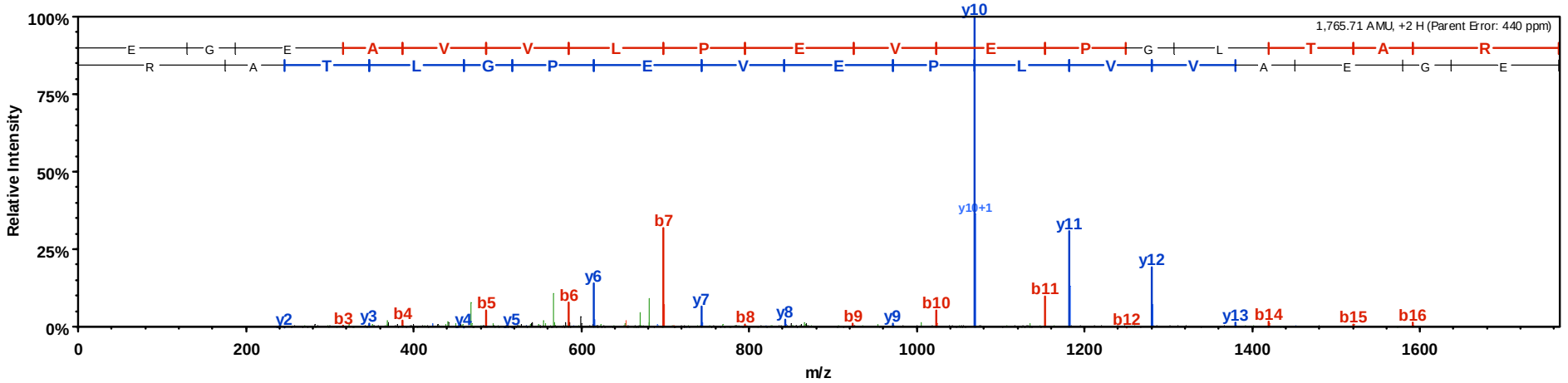
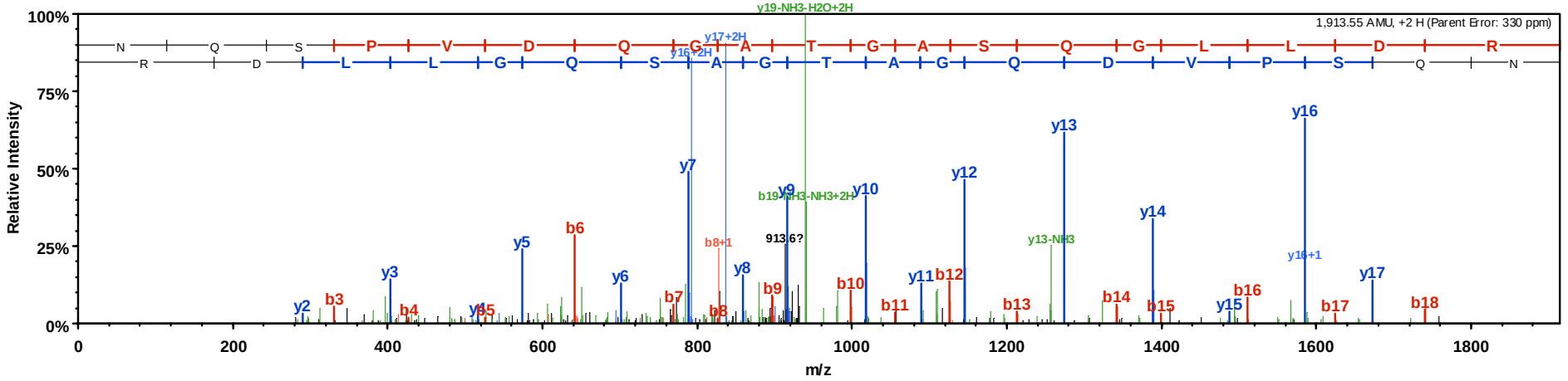


**SDC1_HUMAN (100%), 32,476.3 Da**
**(P18827) Syndecan-1 precursor (SYND1) (CD138 antigen)**
**2 unique peptides, 2 unique spectra, 3 total spectra, 36/310 amino acids (12% coverage)**

M R R A A L W L W L C A L A L S L Q P A L P Q I V A T N L P P E D Q D G S G D D S D N F S G S G A G A L Q D I T L S Q Q T P S T W K D T Q L L T A I P T S P E P
T G L E A T A A S T S T L P A G E G P K **E G E A V V L P E V** **E P G L T A R** E Q E A T P R P R E T T Q L P T T H Q A S T T T A T T A Q E P A T S H P H R D M Q P G
H H E T S T P A G P S Q A D L H T P H T E D G G P S A T E R A A E D G A S S Q L P A A E G S G E Q D F T F E T S G E N T A V V A V E P D R R **N Q S P V D Q G A T**
**G A S Q G L L D R** K E V L G G V I A G G L V G L I F A V C L V G F M L Y R M K K K D E G S Y S L E E P K Q A N G G A Y Q K P T K Q E E F Y A



**CAD13_HUMAN (100%), 78,287.6 Da**
**(P55290) Cadherin-13 precursor (Truncated-cadherin) (T-cadherin) (T-cad) (Heart-cadherin) (H-cadherin) (P105)**
**2 unique peptides, 2 unique spectra, 2 total spectra, 55/713 amino acids (8% coverage)**

```
M Q P R T P L V L C   V L L S Q V L L L T   S A E D L D C T P G   F Q Q K V F H I N Q   P A E F I E D Q S I   L N L T F S D C K G   N D K L R Y E V S S   P Y F K V N S D G G
L V A L R N I T A V   G K T L F V H A R T   P H A E D M A E L V   I V G G K D I Q G S   L Q D I F K F A R T   S P V P R Q K R S I   V V S P I L I P E N   Q R Q P F P R D V G
K V V D S D R P E R   S K F R L T G K G V   D Q E P K G I F R I   N E N T G S V S V T   R T L D R E V I A V   Y Q L F V E T T D V   N G K T L E G P V P   L E V I V I D Q N D
N R P I F R E G P Y   I G H V M E G S P T   G T T V M R M T A F   D A D D P A T D N A   L L R Y N I R Q Q T   P D K P S P N M F Y   I D P E K G D I V T   V V S P A L L D R E
T L E N P K Y E L I   I E A Q D M A G L D   V G L T G T A T A T   I M I D D K N D H S   P K F T K K E F Q A   T V E E G A V G V I   V N L T V E D K D D   P T T G A W R A A Y
T I I N G N P G Q S   F E I H T N P Q T N   E G M L S V V K P L   D Y E I S A F H T L   L I K V E N E D P L   V P D V S Y G P S S   T A T V H I T V L D   V N E G P V F Y P D
P M M V T R Q E D L   S V G S V L L T V N   A T D P D S L Q H Q   T I R Y S V Y K D P   A G W L N I N P I N   G T V D T T A V L D   R E S P F V D N S V   Y T A L F L A I D S
G N P P A T G T G T   L L I T L E D V N D   N A P F I Y P T V A   E V C D D A K N L S   V V I L G A S D K D   L H P N T D P F K F   E I H K Q A V P D K   V W K I S K I N N T
H A L V S L L Q N L   N K A N Y N L P I M   V T D S G K P P M T   N I T D L R V Q V C   S C R N S K V D C N   A A G A L R F S L P   S V L L L S L F S L   A C L
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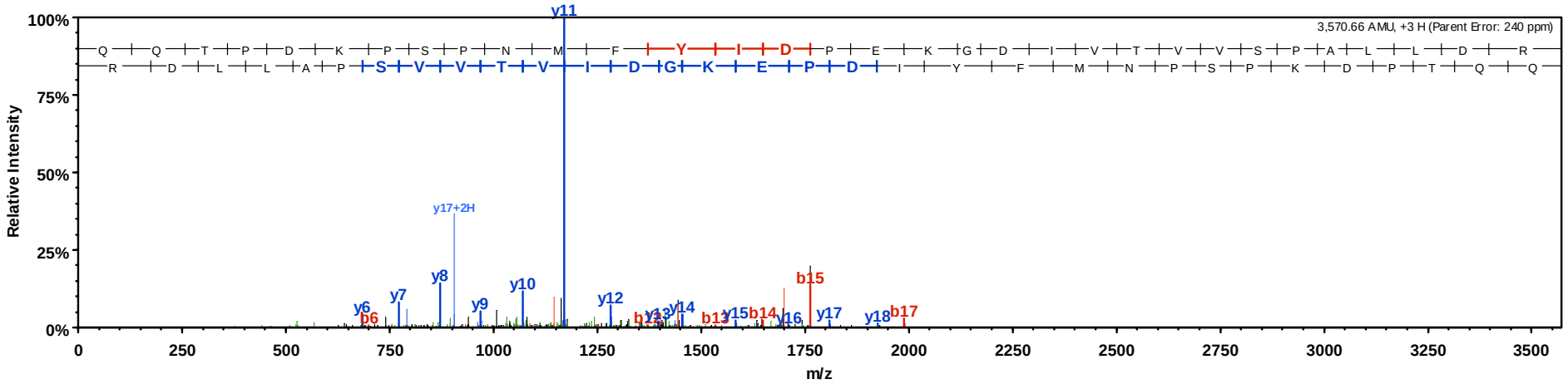


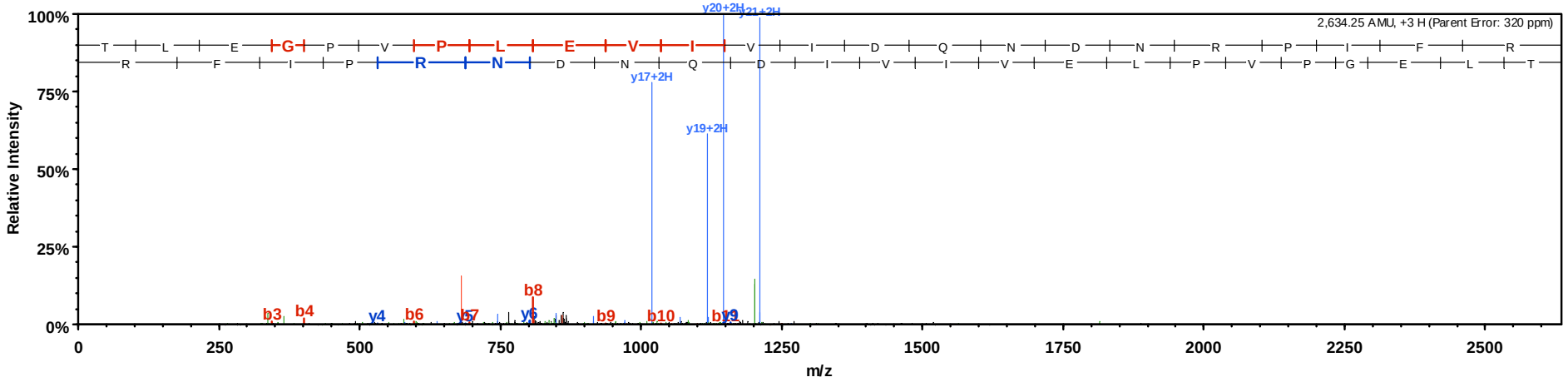

DKK3_HUMAN (100%), 38,290.3 Da

(Q9UBP4) Dickkopf-related protein 3 precursor (Dkk-3) (Dickkopf-3) (hDkk-3)

4 unique peptides, 4 unique spectra, 7 total spectra, 90/350 amino acids (26% coverage)

```
MQRLGATLLC LLLAAAVPTA PAPAPTATSA PVKPGPALSY PQEEATLNEM FREVEELMED TQHKLRSAVE EMEAEEAAAK ASSEVNLANL
PPSYHNETNT DTKVGNNTIH VHREIHKITN NQTGQMVFSE TVITSVGDEE GRRSHECIID EDCGPSMYCQ FASFQYTCQP CRGQRMLCTR
DSECCGDQLC VWGHCTKMAT RGSNGTICDN QRDCQPGLCC AFQRGLLFPV CTPLPVEGEL CHDPASRLLD LITWELEPDG ALDRCPCASG
LLCQPHSHSL VYVCKPTFVG SRDQDGEILL PREVPDEYEV GSFMEEVRQE LEDLERSLTE EMALGEPAAA AAALLGGEEI
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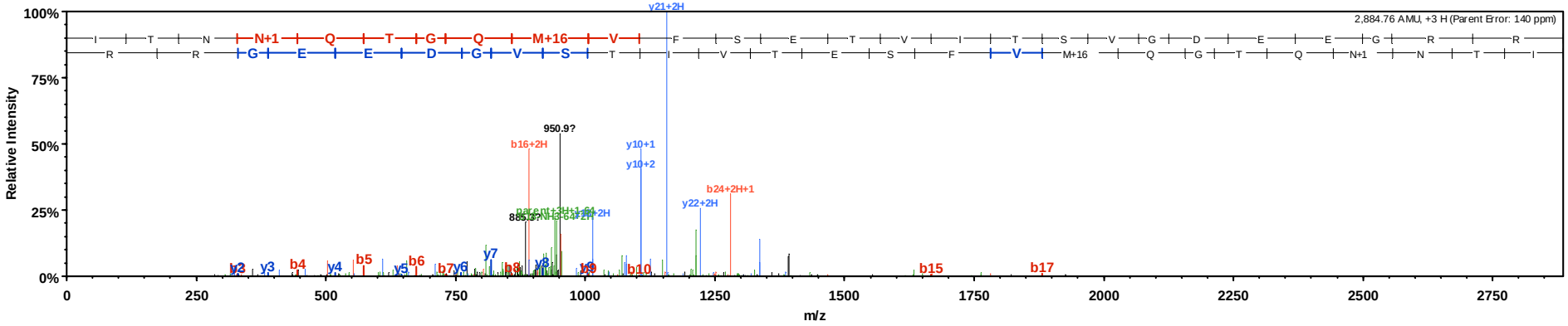


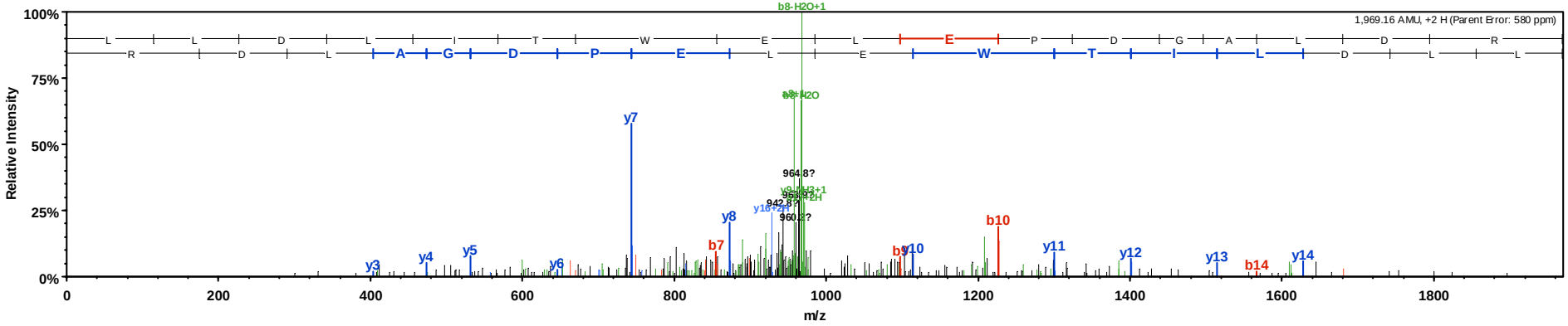

**FSTL1_HUMAN (100%), 34,985.3 Da**
**(Q12841) Follistatin-related protein 1 precursor (Follistatin-like 1)**
**7 unique peptides, 7 unique spectra, 27 total spectra, 74/308 amino acids (24% coverage)**

```
MWKRWLALAL  ALVAVAWVRA  EEELRSKSKI  CANVFCGAGR  ECAVTEKGEP  TCLCIEQCKP  HKRPVCGSNG  KTYLNHCELH
RDACLTGSKI  QVDYDGHCKE  KKSVSPSASP  VVCYQSNRDE  LRRRIIQWLE  AEIIPDGWFS  KGSNYSEILD  KYFKNFDNGD
SRLDSSEFLK  FVEQNETAIN  ITTYPDQENN  KLLRGLCVDA  LIELSDENAD  WKLSFQEFLK  CLNPSFNPPE  KKCALEDETY
ADGAETEVDC  NRCVCACGNW  VCTAMTCDGK  NQKGAQTQTE  EEMTRYVQEL  QKHQETAEKT  KRVSTKEI
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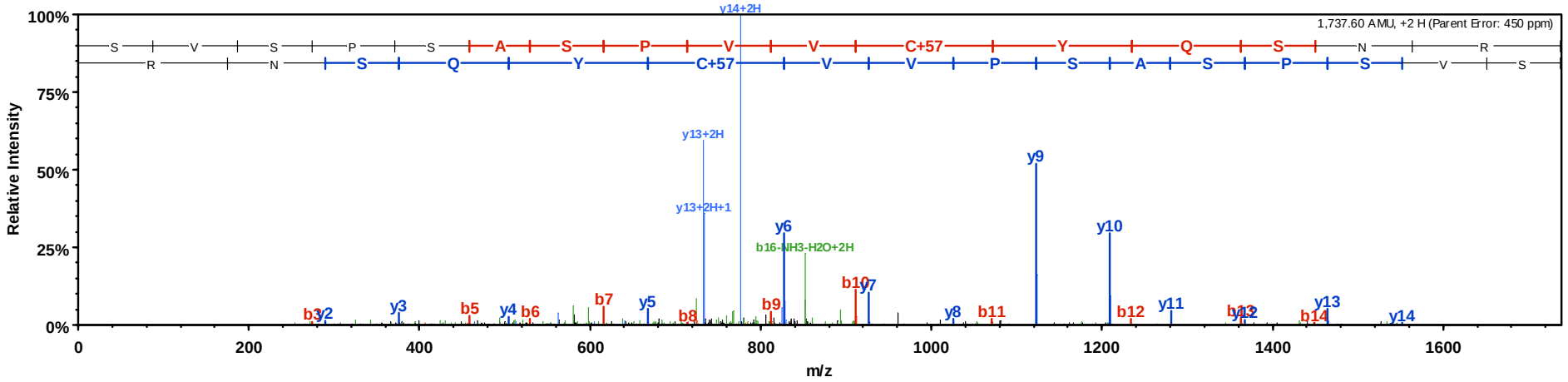


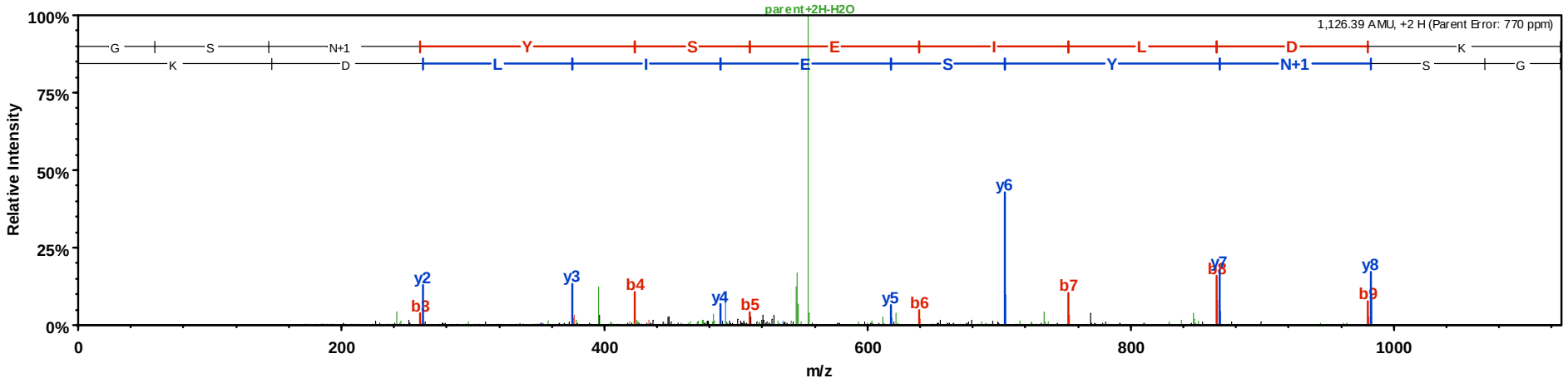

**PTPRM_HUMAN (100%), 163,633.8 Da**
**(P28827) Receptor-type tyrosine-protein phosphatase mu precursor (EC 3.1.3.48) (Protein-tyrosine phosphatase mu) (R-PTP-mu)**
**3 unique peptides, 3 unique spectra, 3 total spectra, 50/1452 amino acids (3% coverage)**

```
M R T L G T C L A T   L A G L L L T A A G   E T F S G G C L F D   E P Y S T C G Y S Q   S E G D D F N W E Q   V N T L T K P T S D   P W M P S G S L M L   V N A S G R P E G Q
R A H L L L P Q L K   E N D T H C I D F H   Y F V S S K S N S P   P G L L N V Y V K V   N N G P L G N P I W   N I S G D P T R T W   N R A E L A I S T F   W P N F Y Q V I F E
V I T S G H Q G Y L   A I D E V K V L G H   P C T R T P H F L R   I Q N V E V N A G Q   F A T F Q C S A I G   R T V A G D R L W L   Q G I D V R D A P L   K E I K V T S S R R
F I A S F N V V N T   T K R D A G K Y R C   M I R T E G G V G I   S N Y A E L V V K E   P P V P I A P P Q L   A S V G A T Y L W I   Q L N A N S I N G D   G P I V A R E V E Y
C T A S G S W N D R   Q P V D S T S Y K I   G H L D P D T E Y E   I S V L L T R P G E   G G T G S P G P A L   R T R T K C A D P M   R G P R K L E V V E   V K S R Q I T I R W
E P F G Y N V T R C   H S Y N L T V H Y C   Y Q V G G Q E Q V R   E E V S W D T E N S   H P Q H T I T N L S   P Y T N V S V K L I   L M N P E G R K E S   Q E L I V Q T D E D
L P G A V P T E S I   Q G S T F E E K I F   L Q W R E P T Q T Y   G V I T L Y E I T Y   K A V S S F D P E I   D L S N Q S G R V S   K L G N E T H F L F   F G L Y P G T T Y S
F T I R A S T A K G   F G P P A T N Q F T   T K I S A P S M P A   Y E L E T P L N Q T   D N T V T V M L K P   A H S R G A P V S V   Y Q I V V E E E R P   R R T K K T T E I L
K C Y P V P I H F Q   N A S L L N S Q Y Y   F A A E F P A D S L   Q A A Q P F T I G D   N K T Y N G Y W N T   P L L P Y K S Y R I   Y F Q A A S R A N G   E T K I D C V Q V A
T K G A A T P K P V   P E P E K Q T D H T   V K I A G V I A G I   L L F V I I F L G V   V L V M K K R K L A   K K R K E T M S S T   R Q E M T V M V N S   M D K S Y A E Q G T
N C D E A F S F M D   T H N L N G R S V S   S P S S F T M K T N   T L S T S V P N S Y   Y P D E T H T M A S   D T S S L V Q S H T   Y K K R E P A D V P   Y Q T G Q L H P A I
R V A D L L Q H I T   Q M K C A E G Y G F   K E E Y E S F F E G   Q S A P W D S A K K   D E N R M K N R Y G   N I I A Y D H S R V   R L Q T I E G D T N   S D Y I N G N Y I D
G Y H R P N H Y I A   T Q G P M Q E T I Y   D F W R M V W H E N   T A S I I M V T N L   V E V G R V K C C K   Y W P D D T E I Y K   D I K V T L I E T E   L L A E Y V I R T F
A V E K R G V H E I   R E I R Q F H F T G   W P D H G V P Y H A   T G L L G F V R Q V   K S K S P P S A G P   L V V H C S A G A G   R T G C F I V I D I   M L D M A E R E G V
V D I Y N C V R E L   R S R R V N M V Q T   E E Q Y V F I H D A   I L E A C L C G D T   S V P A S Q V R S L   Y Y D M N K L D P Q   T N S S Q I K E E F   R T L N M V T P T L
R V E D C S I A L L   P R N H E K N R C M   D I L P P D R C L P   F L I T I D G E S S   N Y I N A A L M D S   Y K Q P S A F I V T   Q H P L P N T V K D   F W R L V L D Y H C
T S V V M L N D V D   P A Q L C P Q Y W P   E N G V H R H G P I   Q V E F V S A D L E   E D I I S R I F R I   Y N A A R P Q D G Y   R M V Q Q F Q F L G   W P M Y R D T P V S
K R S F L K L I R Q   V D K W Q E E Y N G   G E G P T V V H C L   N G G G R S G T F C   A I S I V C E M L R   H Q R T V D V F H A   V K T L R N N K P N   M V D L L D Q Y K F
C Y E V A L E Y L N   S G
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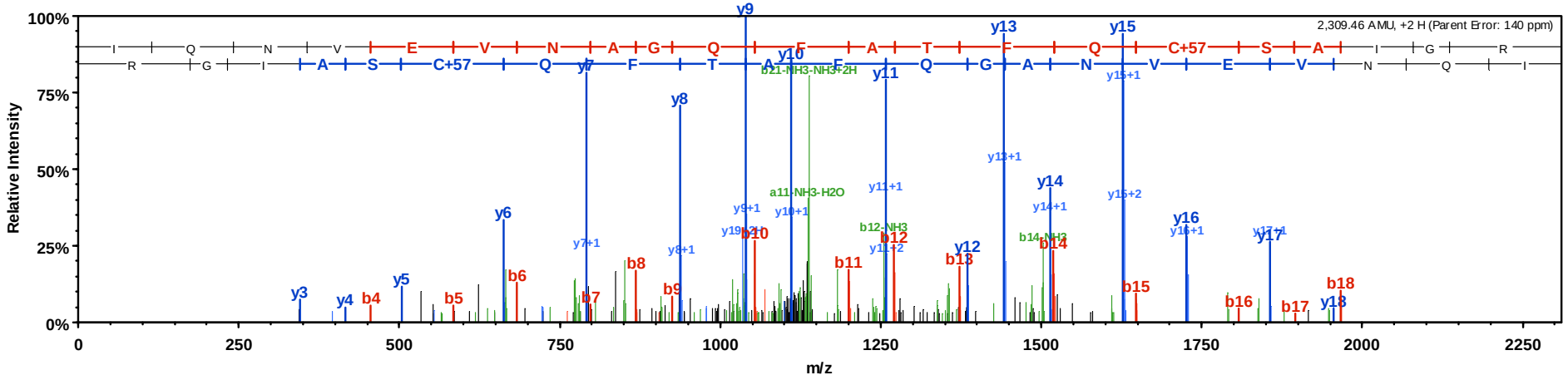


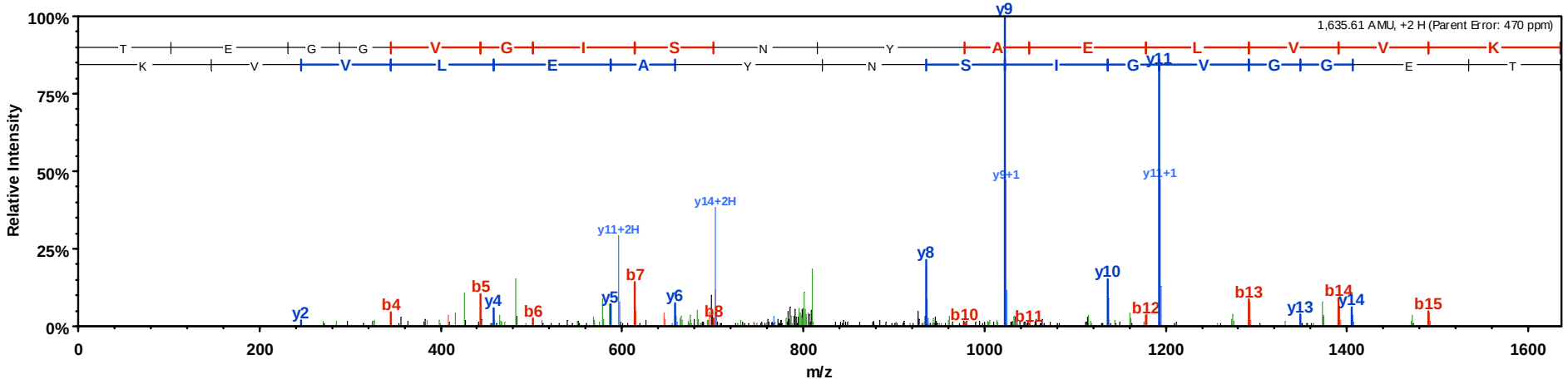

**BST1_HUMAN (100%), 35,739.4 Da**

**(Q10588) ADP-ribosyl cyclase 2 precursor (EC 3.2.2.5) (Cyclic ADP-ribose hydrolase 2) (cADPr hydrolase 2) (Bone marrow stromal antigen 1) (BST-1) (CD157 antigen)**

**8 unique peptides, 12 unique spectra, 22 total spectra, 146/318 amino acids (46% coverage)**

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MAAQGCAASR LLQLLLQLLL LLLLLAAGGA RARWRAEGTS AHLRDIFLGR CAEYRALLSP EQRNKNCTAI WEAFKVALDK
DPCSVLPSDY DLFINLSRHS IPRDKSLFWE NSHLLVNSFA DNTRRFMPLS DVLYGRVADF LSWCRQKNDS GLDYQSCPTS
EDCENNPVDS FWKRASIQYS KDSSGVIHVM LNGSEPTGAY PIKGFFADYE IPNLQKEKIT RIEIWVMHEI GGPNVESCGE
GSMKVLEKRL KDMGFQYSCI NDYRPVKLLQ CVDHSTHPDC ALKSAAAATQ RKAPSLYTEQ RAGLIIPLFL VLASRTQL
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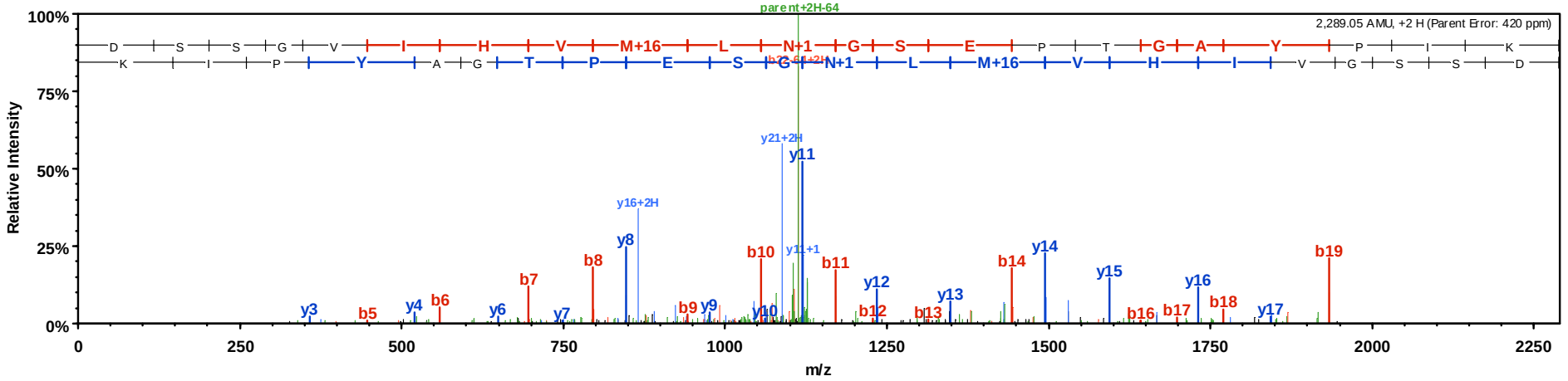


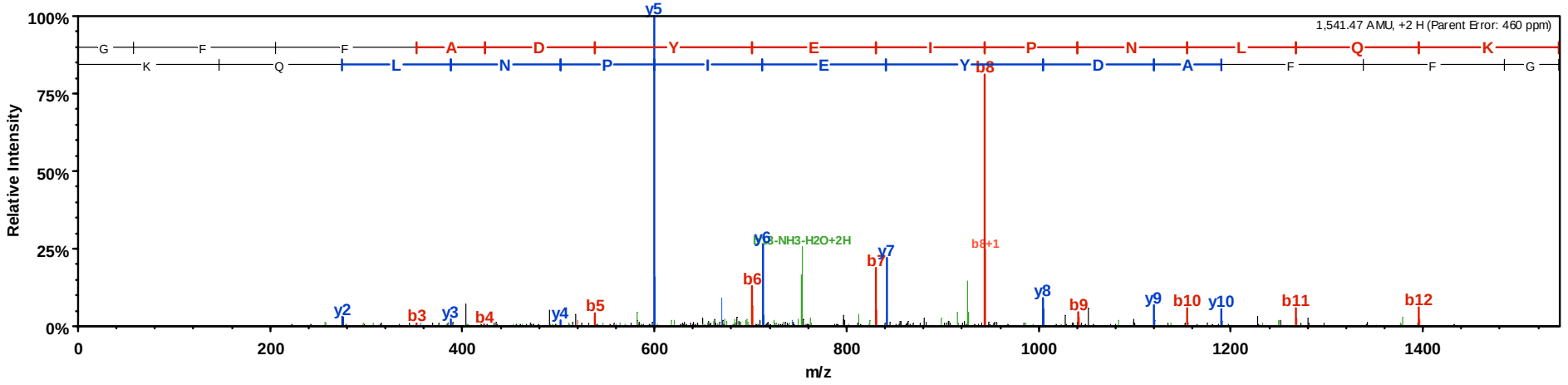

**GPR64_HUMAN (100%), 111,494.3 Da**
**(Q8IZP9) G-protein coupled receptor 64 precursor (Epididymis-specific protein 6) (He6 receptor)**
**5 unique peptides, 6 unique spectra, 12 total spectra, 80/1017 amino acids (8% coverage)**

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M V F S V R Q C G H   V G R T E E V L L T   F K I F L V I I C L   H V V L V T S L E E   D T D N S S L S P P   P A K L S V V S F A   P S S N G T P E V E   T T S L N D V T L S
L L P S N E T E K T   K I T I V K T F N A   S G V K P Q R N I C   N L S S I C N D S A   F F R G E I M F Q Y   D K E S T V P Q N Q   H I T N G T L T G V   L S L S E L K R S E
L N K T L Q T L S E   T Y F I M C A T A E   A Q S T L N C T F T   I K L N N T M N A C   A A I A A L E R V K   I R P M E H C C C S   V R I P C P S S P E   E L G K L Q C D L Q
D P I V C L A D H P   R G P P F S S S Q S   I P V V P R A T V L   S Q V P K A T S F A   E P P D Y S P V T H   N V P S P I G E I Q   P L S P Q P S A P I   A S S P A I D M P P
Q S E T I S S P M P   Q T H V S G T P P P   V K A S F S S P T V   S A P A N V N T T S   A P P V Q T D I V N   T S S I S D L E N Q   V L Q M E K A L S L   G S L E P N L A G E
M I N Q V S R L L H   S P P D M L A P L A   Q R L L K V V D D I   G L Q L N F S N T T   I S L T S P S L A L   A V I R V N A S S F   N T T T F V A Q D P   A N L Q V S L E T Q
A P E N S I G T I T   L P S S L M N N L P   A H D M E L A S R V   Q F N F F E T P A L   F Q D P S L E N L S   L I S Y V I S S S V   A N L T V R N L T R   N V T V T L K H I N
P S Q D E L T V R C   V F W D L G R N G G   R G G W S D N G C S   V K D R R L N E T I   C T C S H L T S F G   V L L D L S R T S V   L P A Q M M A L T F   I T Y I G C G L S S
I F L S V T L V T Y   I A F E K I R R D Y   P S K I L I Q L C A   A L L L L N L V F L   L D S W I A L Y K M   Q G L C I S V A V F   L H Y F L L V S F T   W M G L E A F H M Y
L A L V K V F N T Y   I R K Y I L K F C I   V G W G V P A V V V   T I I L T I S P D N   Y G L G S Y G K F P   N G S P D D F C W I   N N N A V F Y I T V   V G Y F C V I F L L
N V S M F I V V L V   Q L C R I K K K K Q   L G A Q R K T S I Q   D L R S I A G L T F   L L G I T W G F A F   F A W G P V N V T F   M Y L F A I F N T L   Q G F F I F I F Y C
V A K E N V R K Q W   R R Y L C C G K L R   L A E N S D W S K T   A T N G L K K Q T V   N Q G V S S S S N S   L Q S S S N S T N S   T T L L V N N D C S   V H A S G N G N A S
T E R N G V S F S V   Q N G D V C L H D F   T G K Q H M F N E K   E D S C N G K G R M   A L R R T S K R G S   L H F I E Q M
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