

Supplementary Information – Krisp et al.

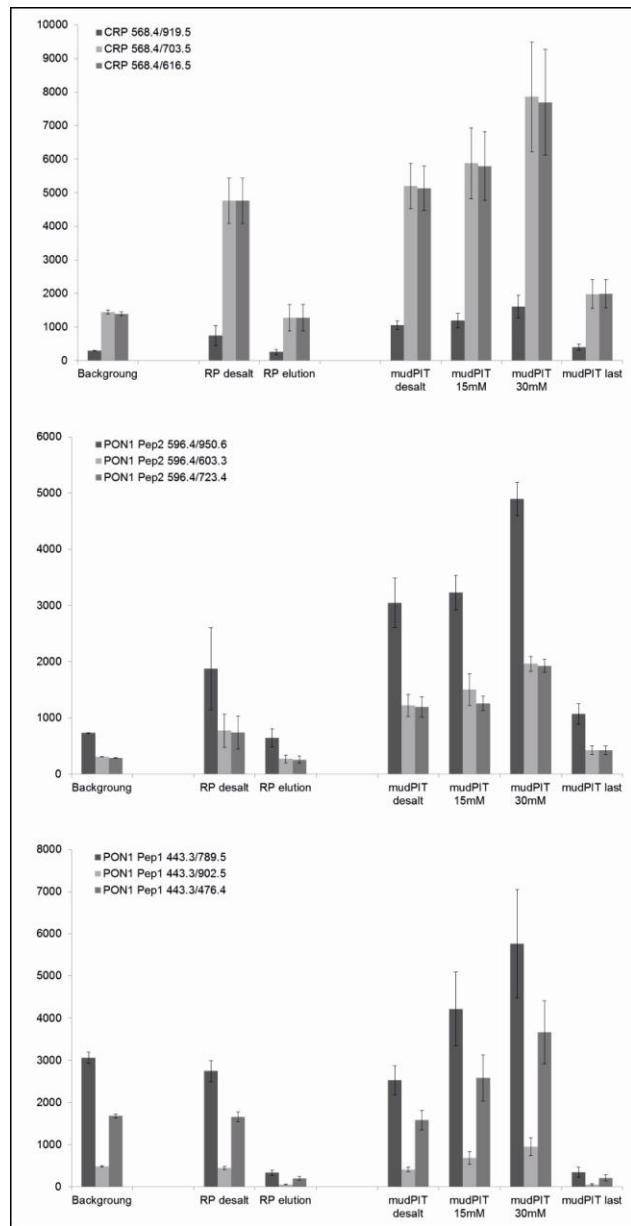


Figure S-1. Ionization efficiency response of reference peptides continuously infused into the elution pathway of the chromatographic background, RP-SRM analysis of a complex sample and mudPIT-SRM analysis of a complex sample

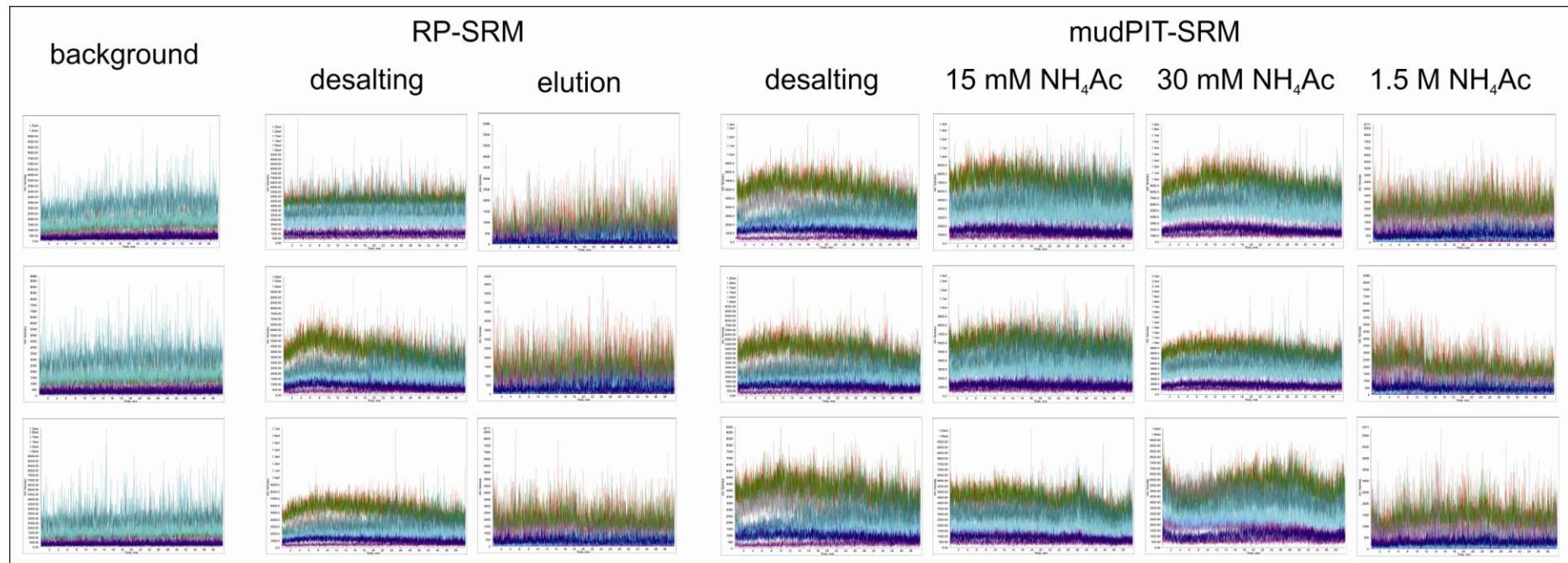
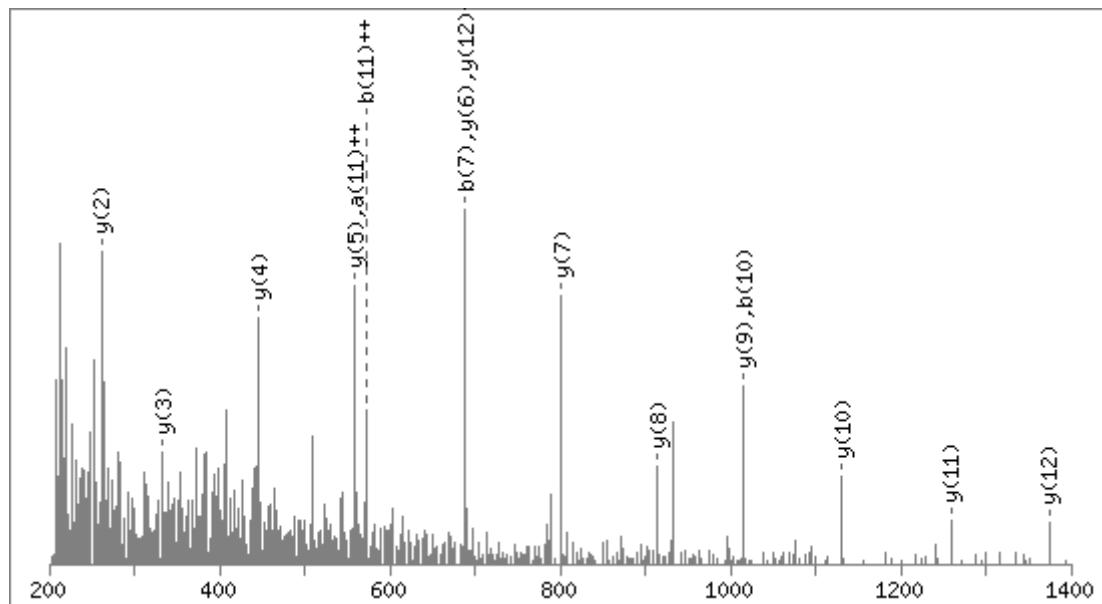
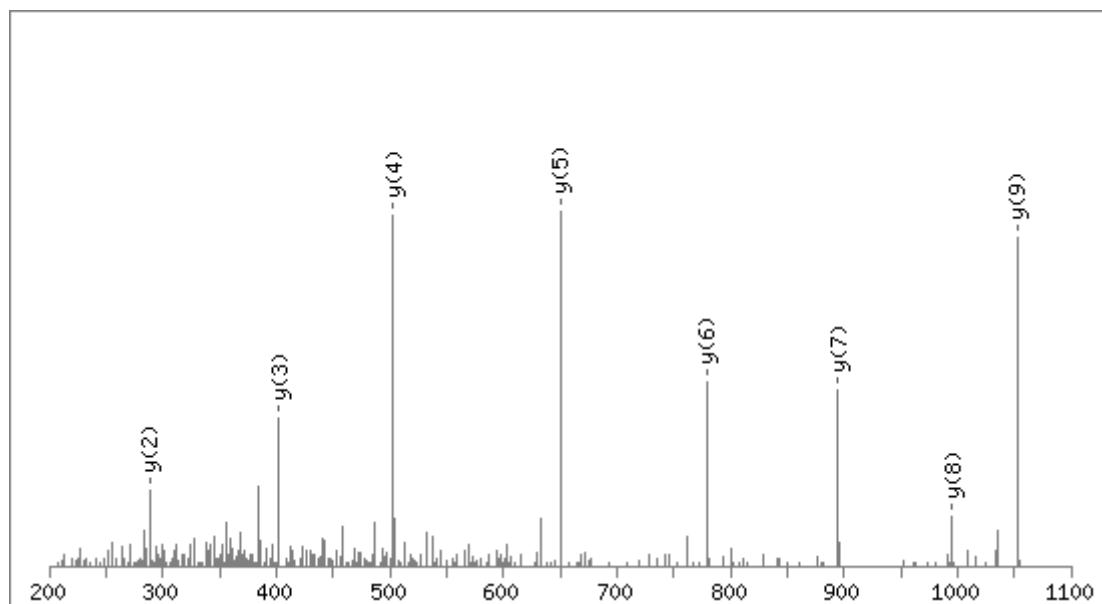


Figure S-2. Real time ionization efficiency profiles of the reference peptides CRP and PON1 (2 peptides) directly infused into the flow path of the chromatographic background and during the elution of a complex sample analysed with RP- and mudPIT-SRM.

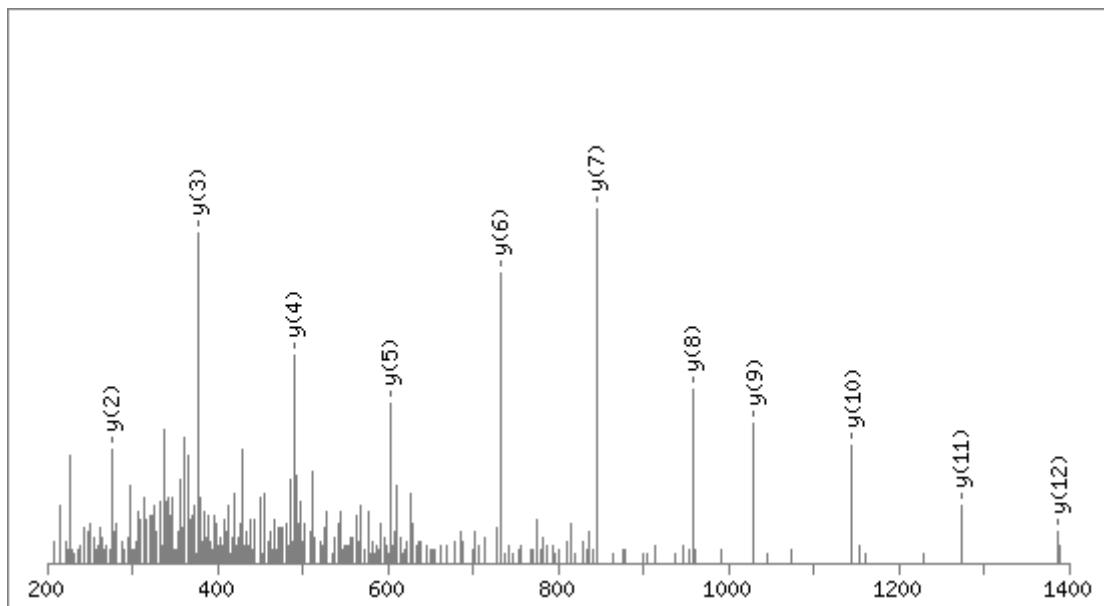
Figure S-3. SRM triggered MS/MS spectra of targeted peptides of proteins from human wound fluid samples.



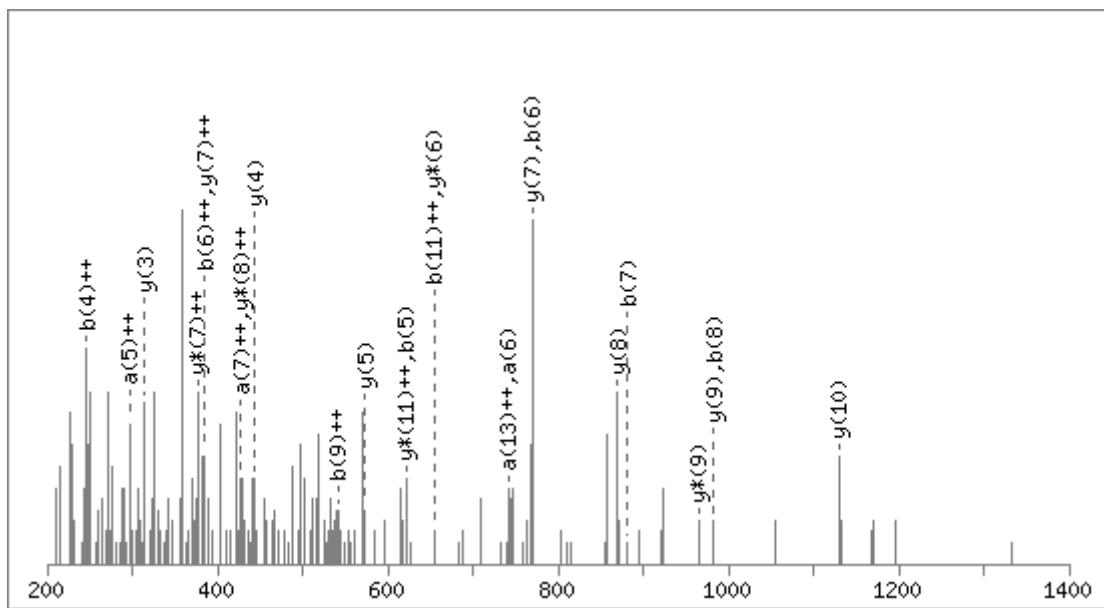
MS/MS spectrum of the peptide GLGTDEDTLIEILASR from Annexin A1 (ANXA1; Swiss Prot accession code: P04083); targeted precursor mass 851.946 m/z (2+), corresponding $[M+H]^+$ mass 1701.877, Mascot Score: 71



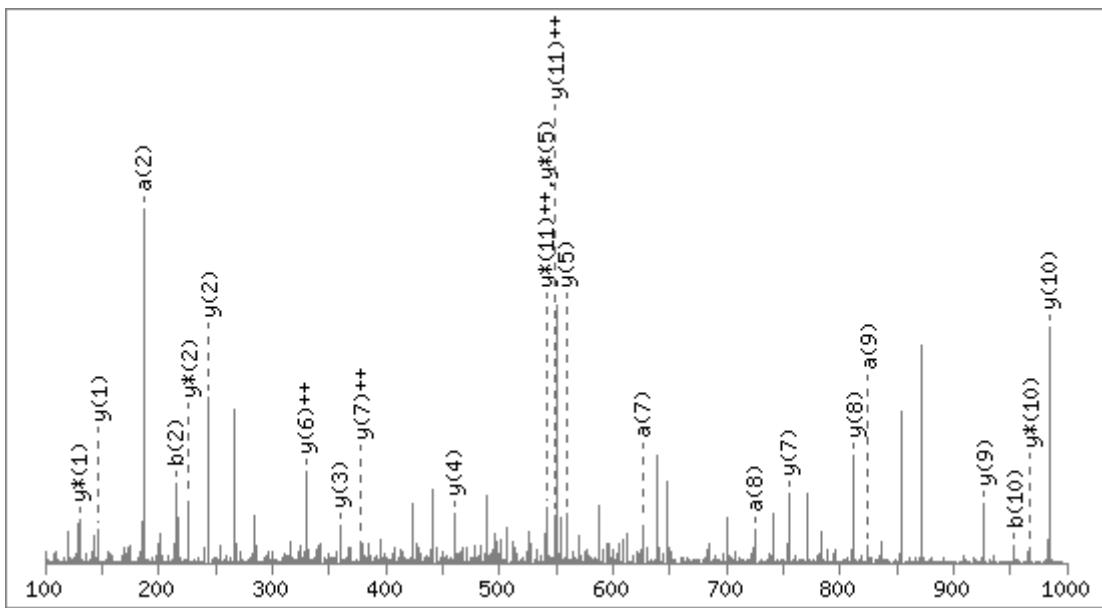
MS/MS spectrum of the peptide GIGTDEFTLNR from Annexin A3 (P12429); targeted precursor mass 611.806 m/z (2+), corresponding $[M+H]^+$ mass 1221.598, Mascot Score: 80



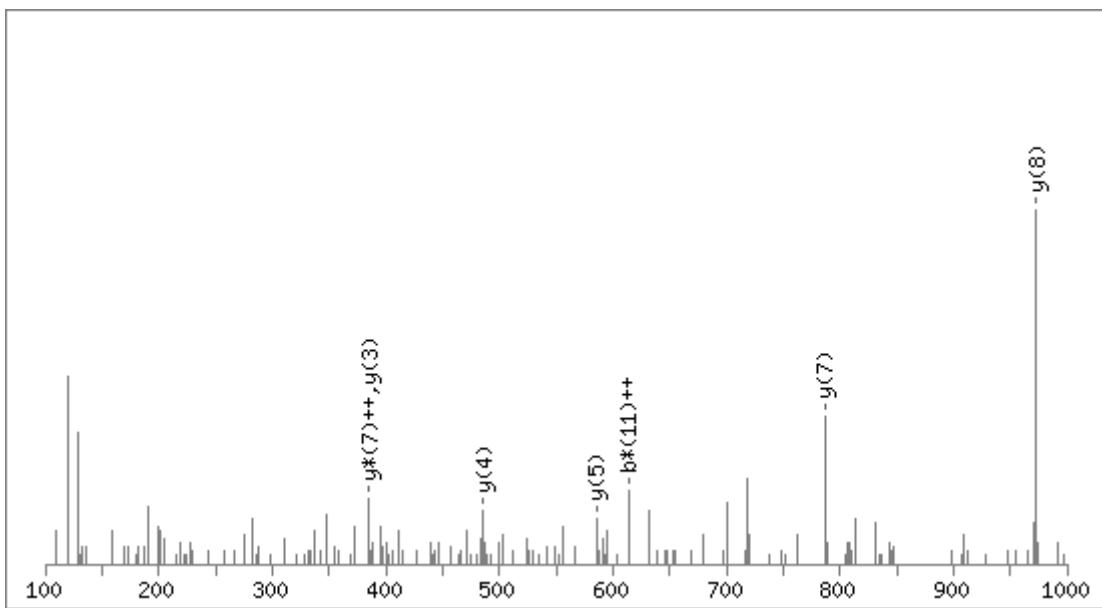
MS/MS spectrum of the peptide GAGTNEDALIEILTTR from Annexin A3 (P12429); targeted precursor mass 837.440 m/z (2+), corresponding $[M+H]^+$ mass 1672.865, Mascot Score: 118



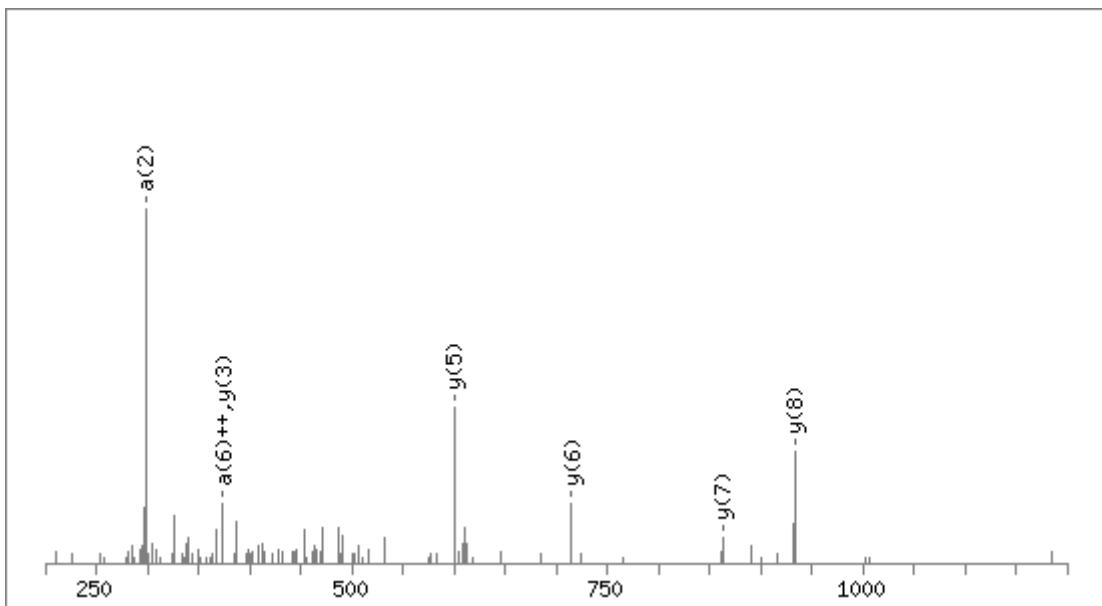
MS/MS spectrum of the peptide AEEYEFLTPVEEAPK from Rho GDP-dissociation inhibitor 1 (GDIR1; P52565); targeted precursor mass 876.420 m/z (2+), corresponding $[M+H]^+$ mass 1750.825, Mascot Score: 19



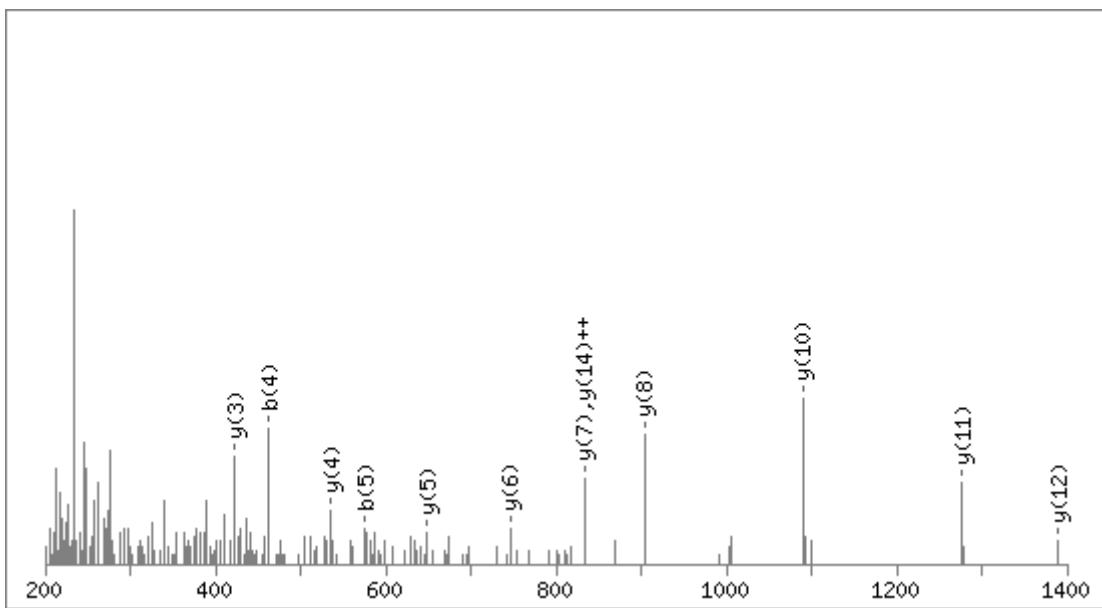
MS/MS spectrum of the peptide TLLGDGPVVTDPK Rho GDP-dissociation inhibitor 2 (GDIR2; P52566); targeted precursor mass 656.360 m/z (2+), corresponding $[M+H]^+$ mass 1310.705, Mascot Score: 50



MS/MS spectrum of the peptide AFQVWSDVTPLR from Matrix metalloproteinase 2 (MMP2; P08253); targeted precursor mass 709.880 m/z (2+), corresponding $[M+H]^+$ mass 1417.745, Mascot Score: 28

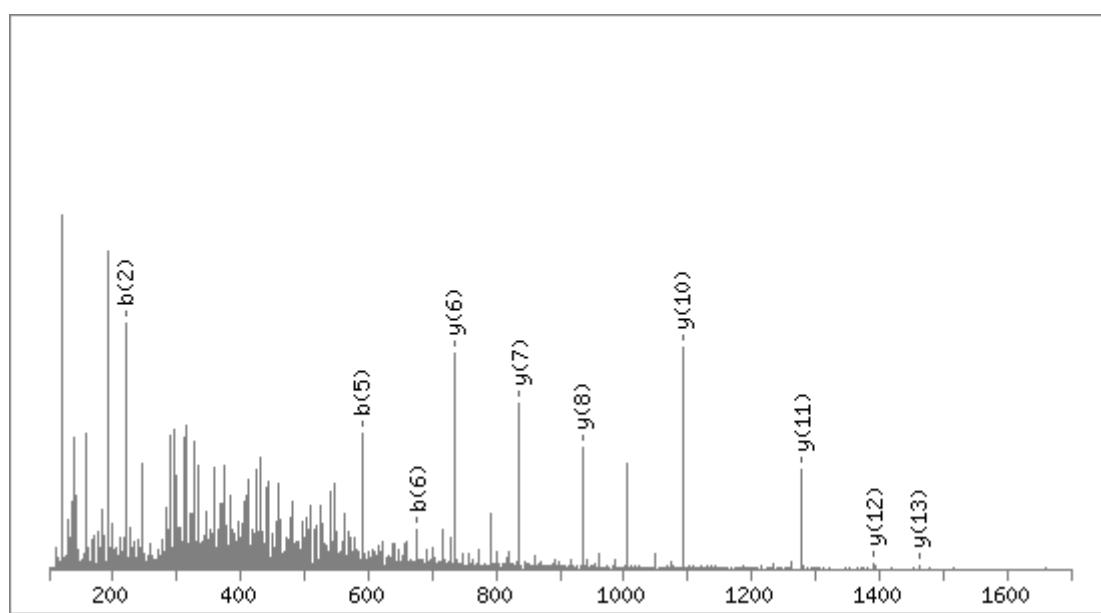
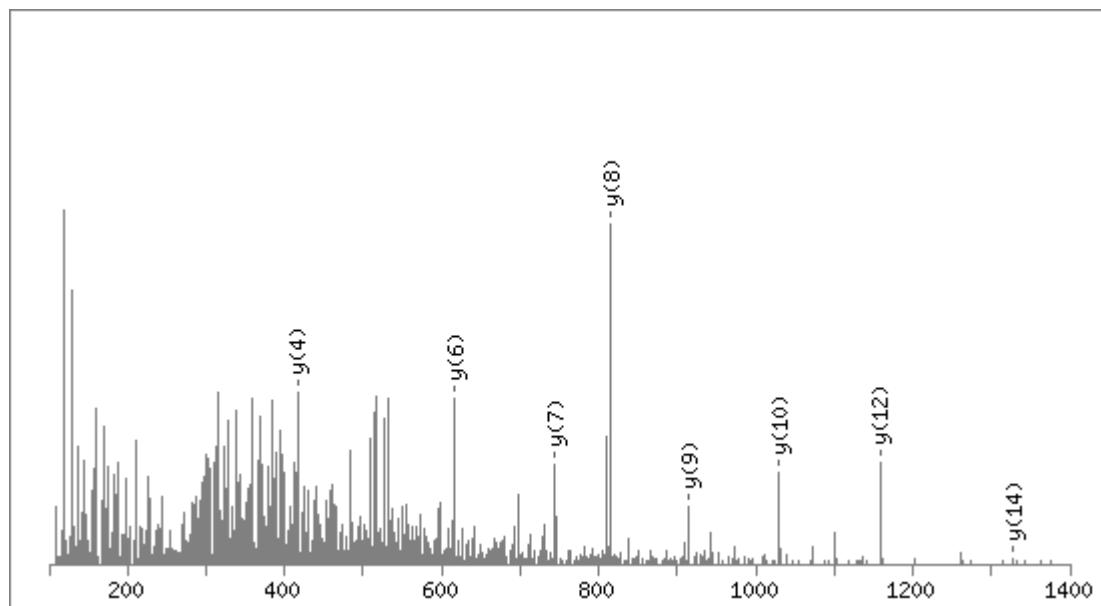


MS/MS spectrum of the peptide YYAFDLIAQR from Matrix metalloproteinase 8 (MMP8; P22894); targeted precursor mass 630.330 m/z (2+), corresponding [M+H]⁺ mass 1258.645, Mascot Score: 31

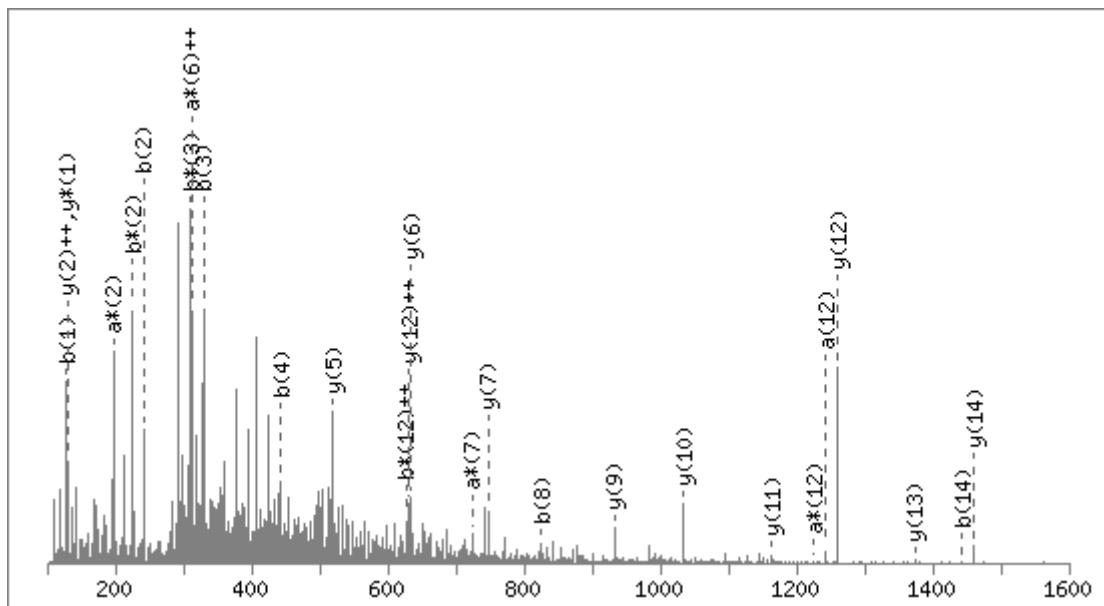


MS/MS spectrum of the peptide DAFELWSVASPLIFTR from Matrix metalloproteinase 8 (MMP8; P22894); targeted precursor mass 926.485 m/z (2+), corresponding [M+H]⁺ mass 1850.955, Mascot Score: 63

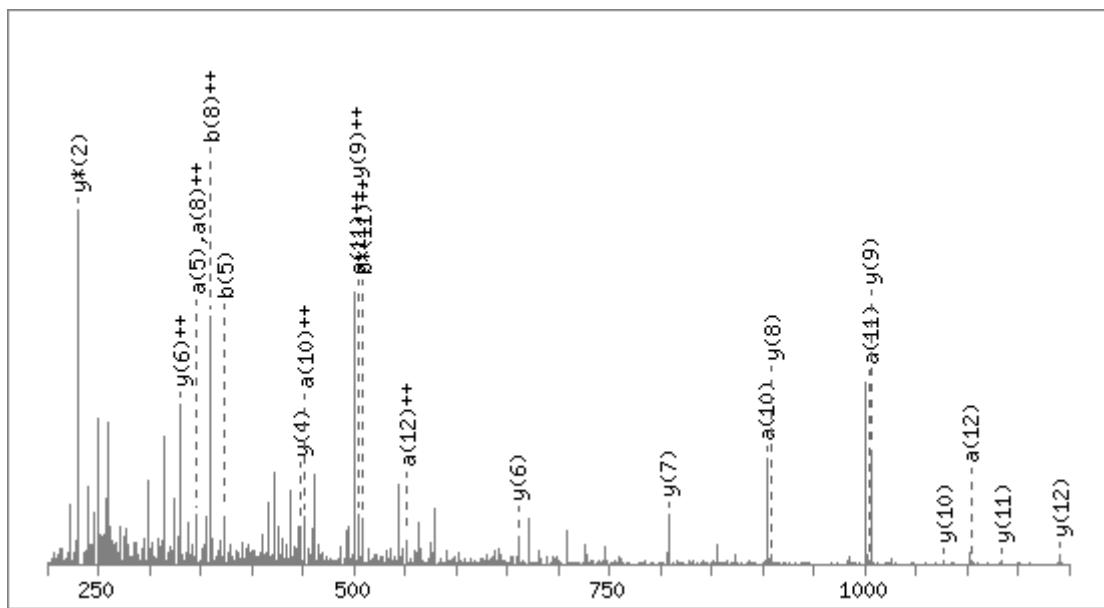
MS/MS spectrum of the peptide LGLGADVAQVTGALR from Matrix metalloproteinase 9 (MMP9; P14780); targeted precursor mass 720.910 m/z (2+), corresponding $[M+H]^+$ mass 1439.805, Mascot Score: 53



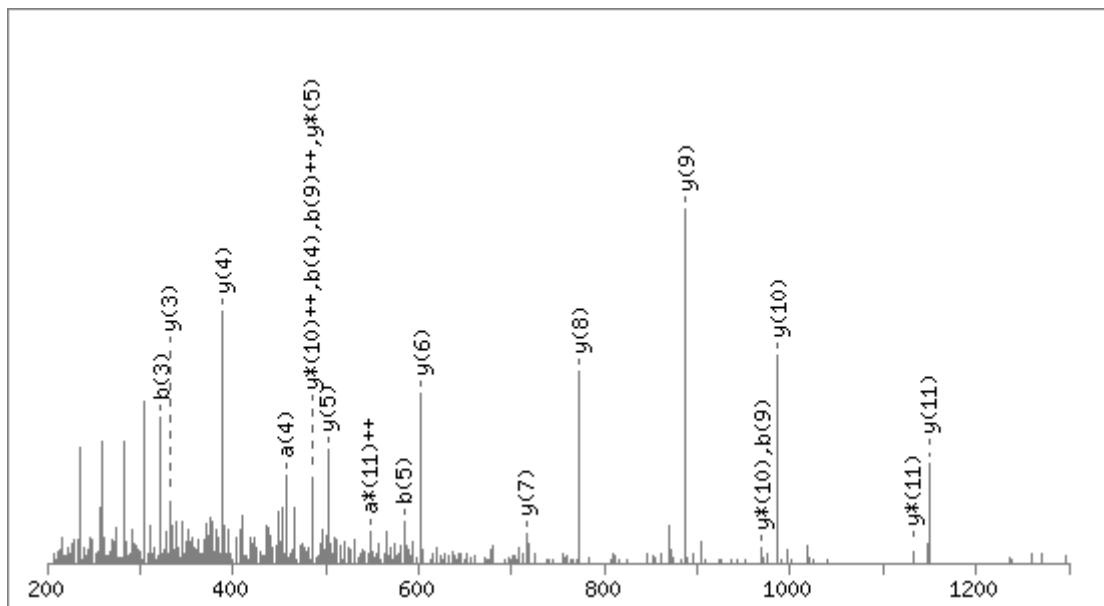
MS/MS spectrum of the peptide AFALWSAVTPLTFTR from Matrix metalloproteinase 9 (MMP9; P14780); targeted precursor mass 840.960 m/z (2+), corresponding $[M+H]^+$ mass 1679.905, Mascot Score: 42



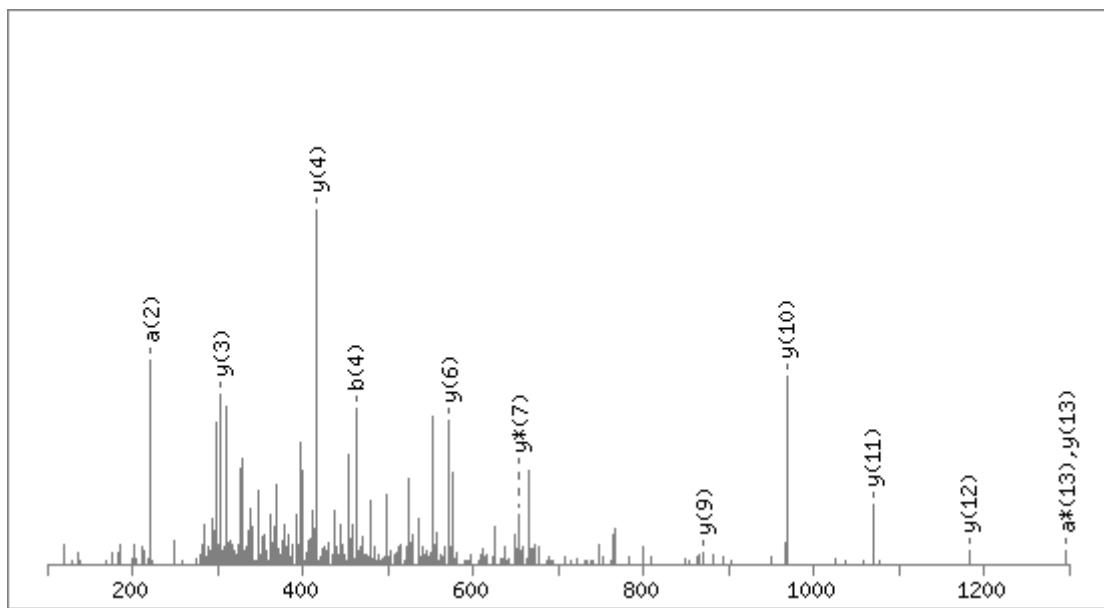
MS/MS spectrum of the peptide QLSPPETGELDSATLK from Matrix metalloproteinase 9 (MMP9; P14780); targeted precursor mass 851.450 m/z (2+), corresponding $[M+H]^+$ mass 1700.885, Mascot Score: 51



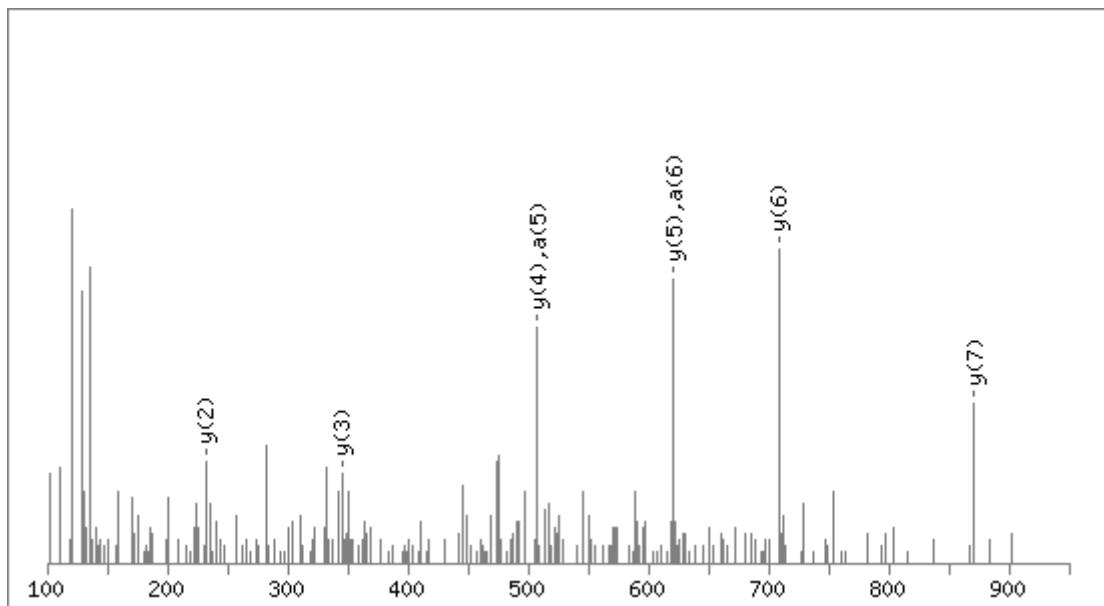
MS/MS spectrum of the peptide QLSPPETGELDSATLK from Profilin 1 (PROF1; P07737); targeted precursor mass 690.361 m/z (2+), corresponding $[M+H]^+$ mass 1378.707, Mascot Score: 25



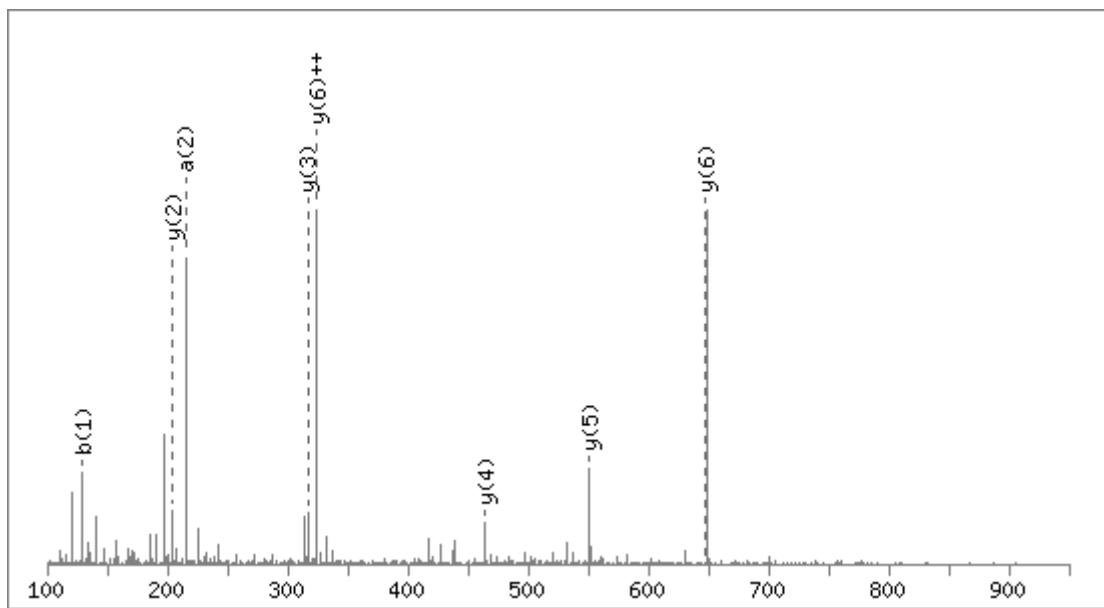
MS/MS spectrum of the peptide SSFYVNGLTLGGQK from Profilin 1 (PROF1; P07737); targeted precursor mass 735.880 m/z (2+), corresponding $[M+H]^+$ mass 1469.745, Mascot Score: 55



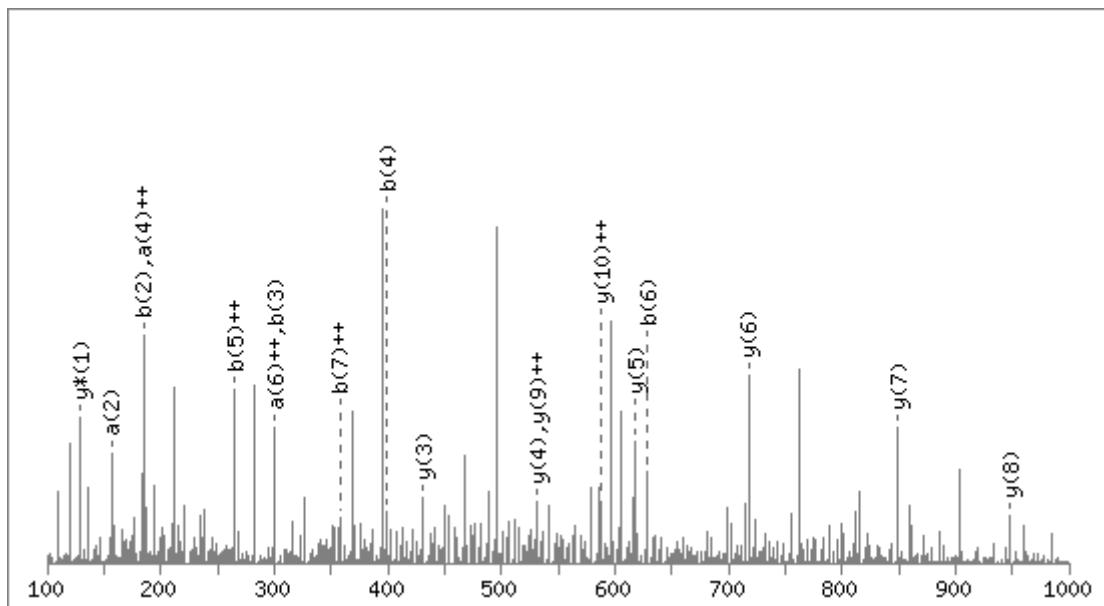
MS/MS spectrum of the peptide TFVNITPAEVGVLVGK from Profilin 1 (PROF1; P07737); targeted precursor mass 822.470 m/z (2+), corresponding $[M+H]^+$ mass 1642.925, Mascot Score: 40



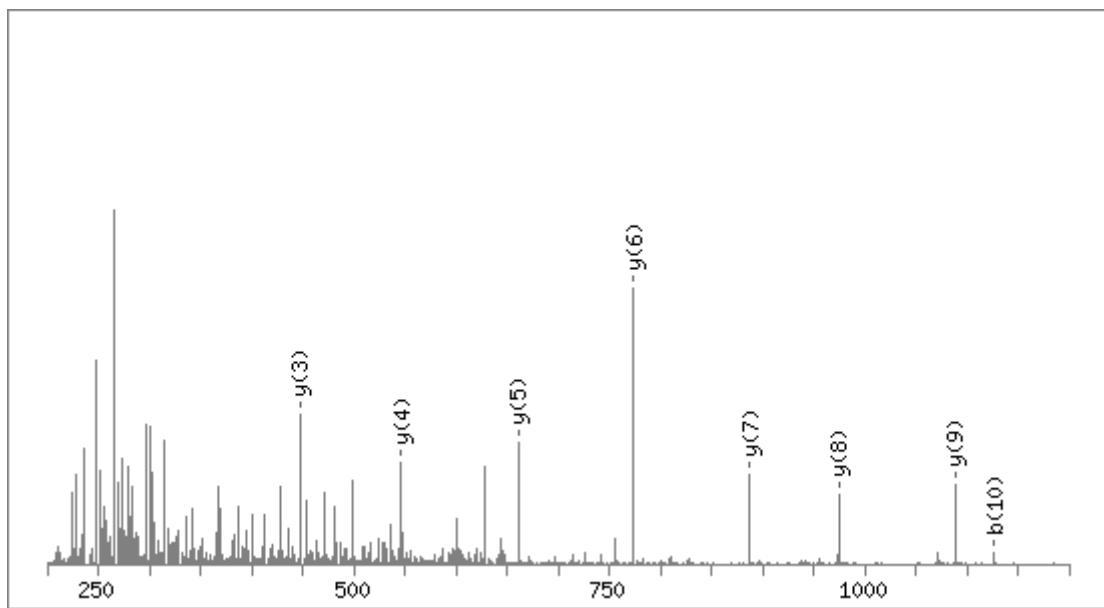
MS/MS spectrum of the peptide VGEYSLYIGR from serum amyloid component P (SAMP; P07737); targeted precursor mass 578.800 m/z (2+), corresponding $[M+H]^+$ mass 1155.585, Mascot Score: 31



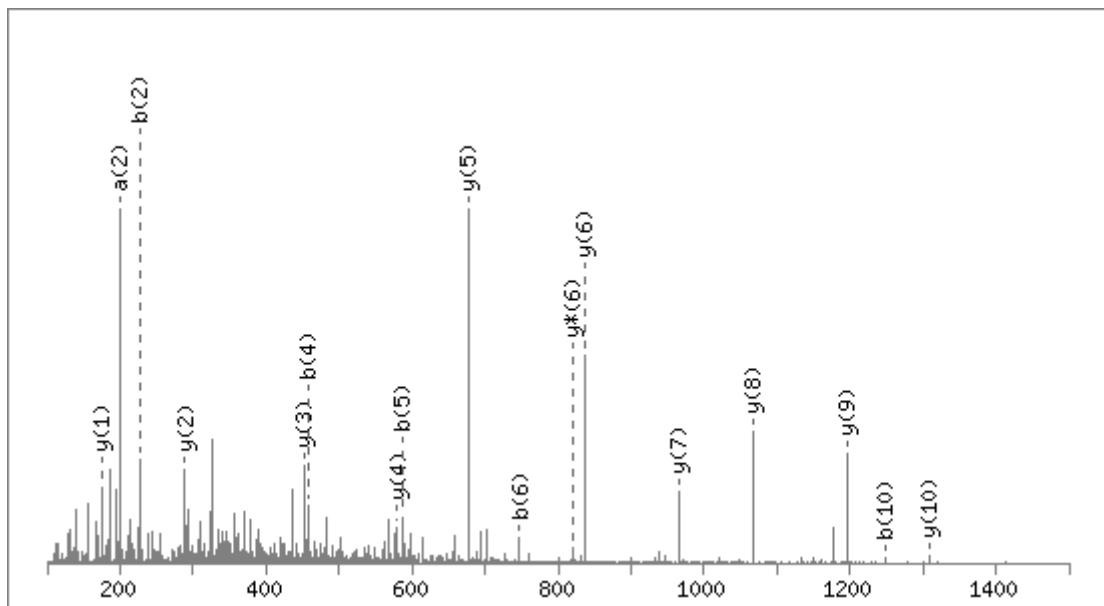
MS/MS spectrum of the peptide ELPSFLGK from S100 A4 (P26447); targeted precursor mass 445.752 m/z (2+), corresponding $[M+H]^+$ mass 889.489, Mascot Score: 23



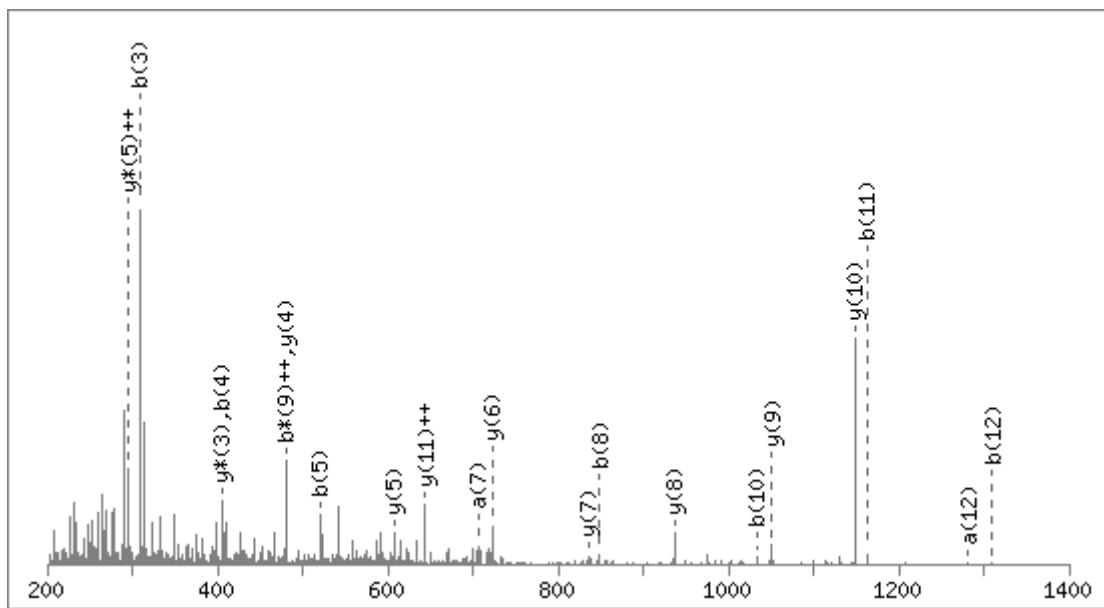
MS/MS spectrum of the peptide ALDVMVSTFHK from S100 A4 (P26447);
 targeted precursor mass 624.326 m/z (2+), corresponding $[M+H]^+$ mass
 1246.637, Mascot Score: 18



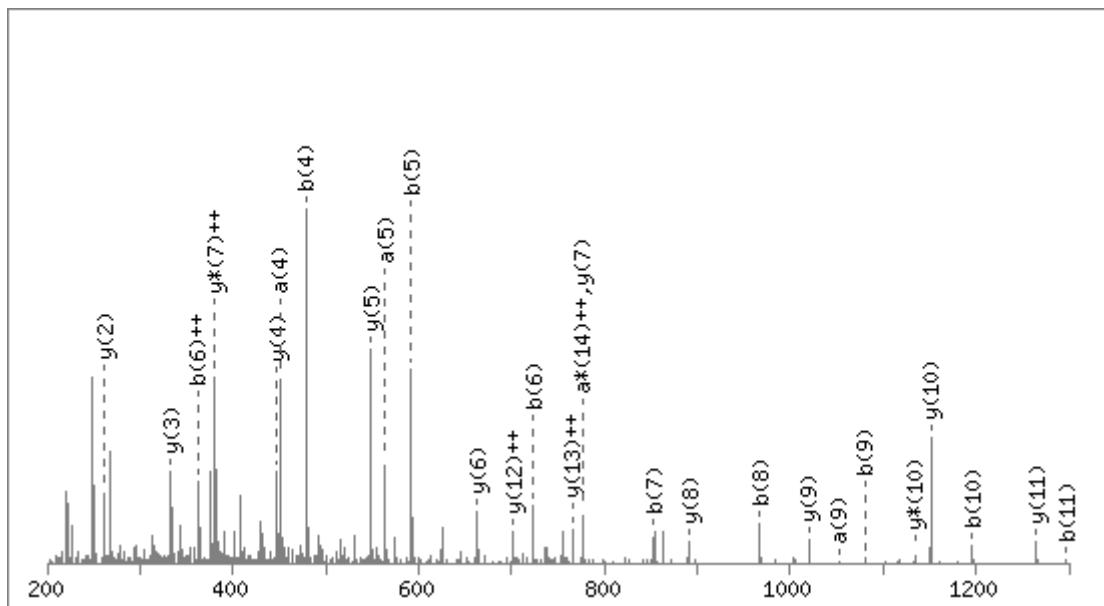
MS/MS spectrum of the peptide ALNSIIDVYHK from S100 A8 (P05109);
 targeted precursor mass 636.849 m/z (2+), corresponding $[M+H]^+$ mass
 1271.685, Mascot Score: 54



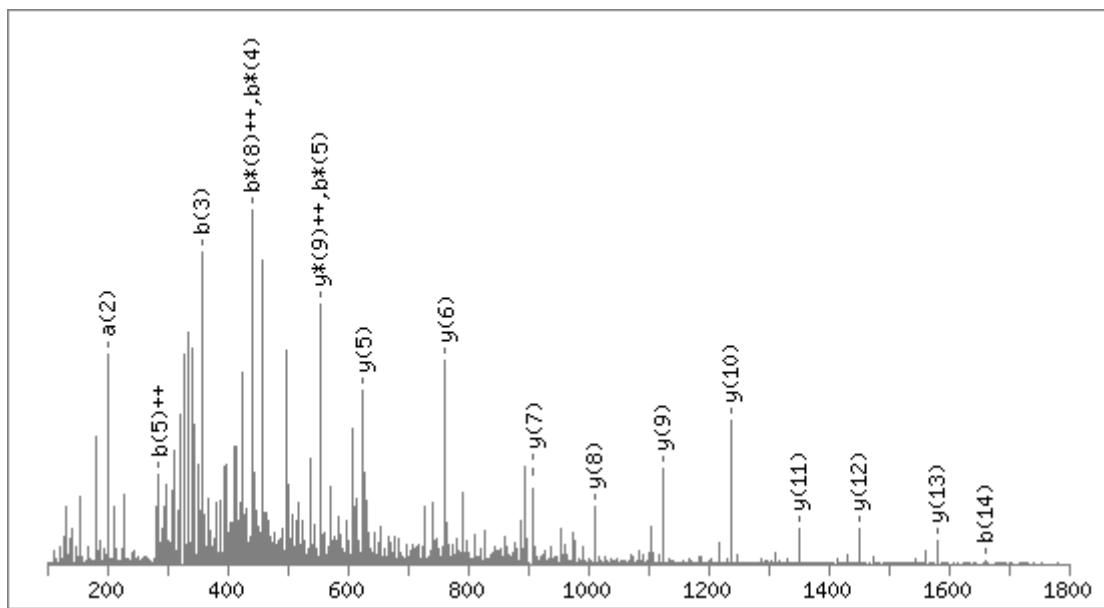
MS/MS spectrum of the peptide LLETEC*PQYIR from S100 A8 (P05109);
targeted precursor mass 711.358 m/z (2+), corresponding [M+H]⁺ mass
1420.701, Mascot Score: 57



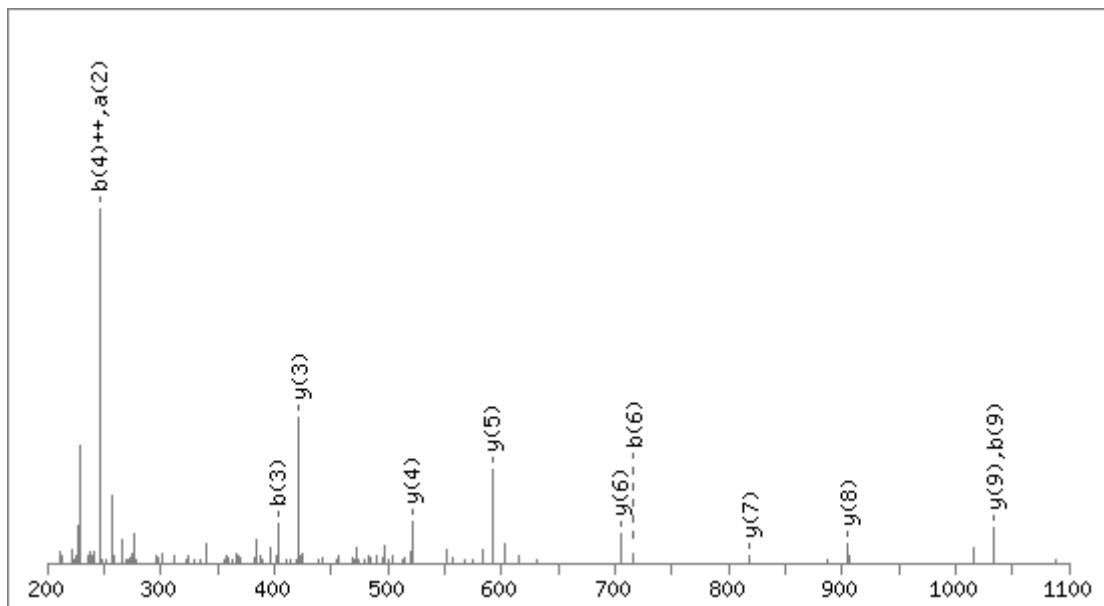
MS/MS spectrum of the peptide LGHPDTLNQGEFK from S100 A9 (P06702);
targeted precursor mass 728.370 m/z (2+), corresponding [M+H]⁺ mass
1454.725, Mascot Score: 59



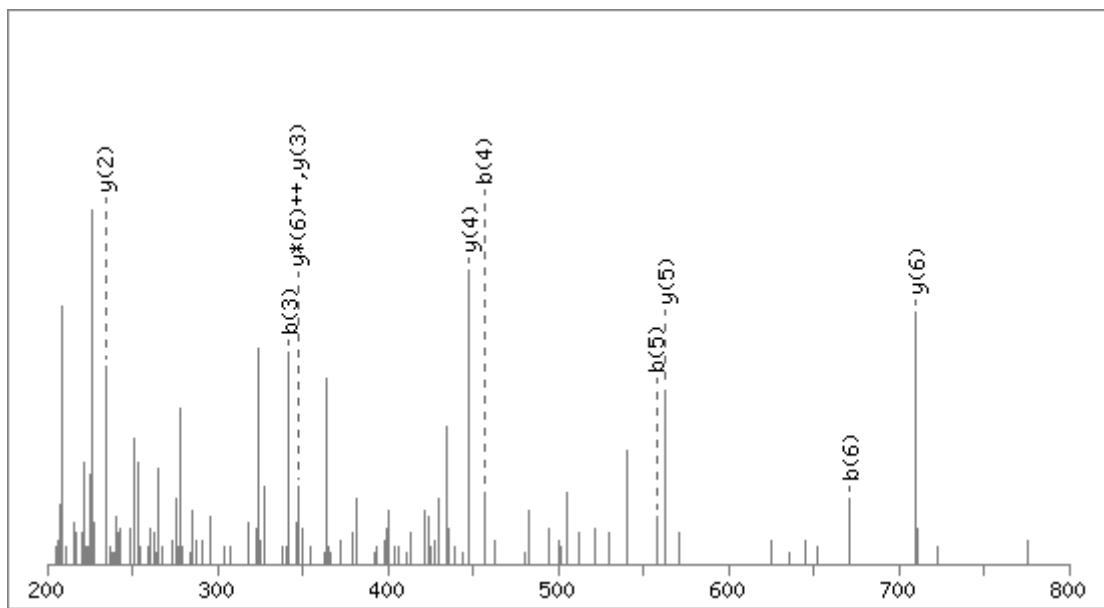
MS/MS spectrum of the peptide VIEHIMEDLDTNADK from S100 A9 (P06702); targeted precursor mass 871.920 m/z (2+), corresponding $[M+H]^+$ mass 1741.825 Da, Mascot Score: 58



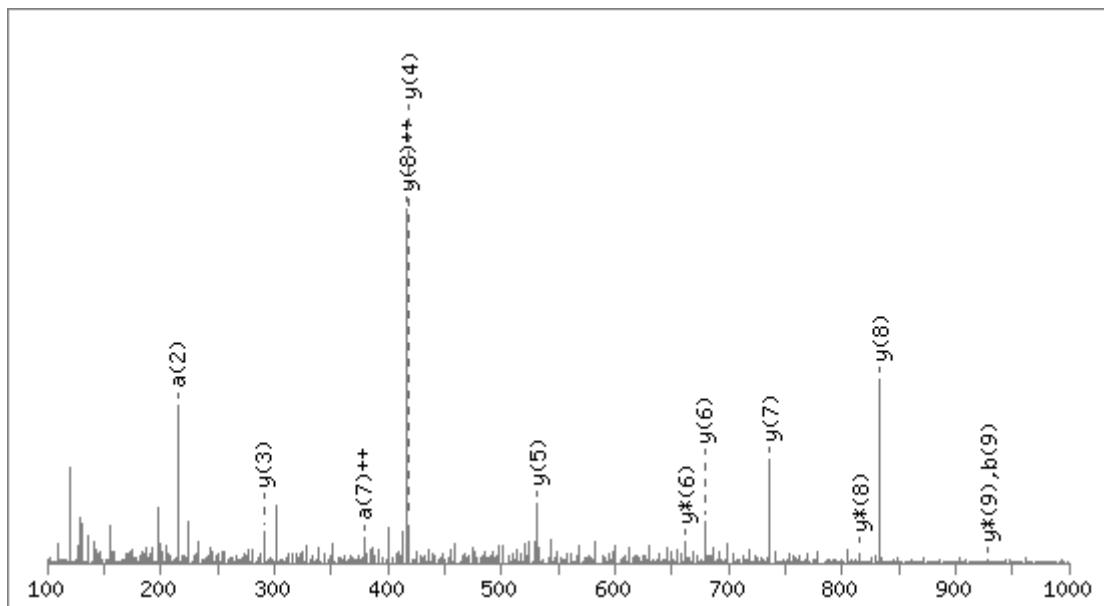
MS/MS spectrum of the peptide NIETIINTFHQYSVK from S100 A9 (P06702); targeted precursor mass 903.970 m/z (2+), corresponding $[M+H]^+$ mass 1805.925 Da, Mascot Score: 70



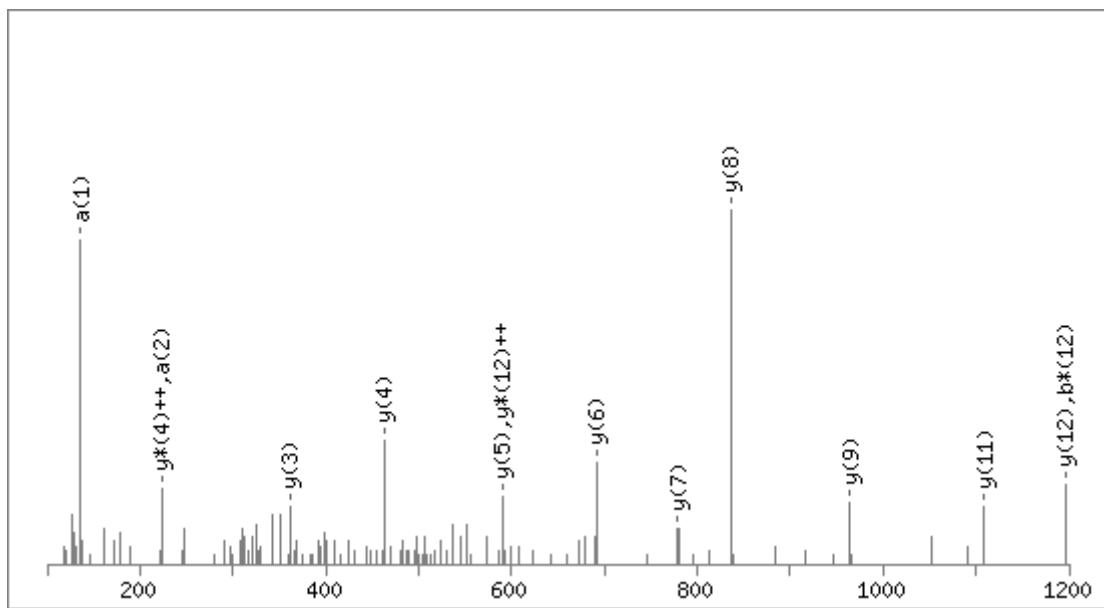
MS/MS spectrum of the peptide C*IESLIAVFQK from S100 A11 (P31949);
targeted precursor mass 654.355 m/z (2+), corresponding $[M+H]^+$ mass
1306.695 Da, Mascot Score: 53



MS/MS spectrum of the peptide GHFDTLSK from S100 A12 (P80511);
targeted precursor mass 452.730 m/z (2+), corresponding $[M+H]^+$ mass
903.445 Da, Mascot Score: 19



MS/MS spectrum of the peptide ELPGFLQSGK from S100 P (P25815);
targeted precursor mass 538.290 m/z (2+), corresponding $[M+H]^+$ mass
1074.565 Da, Mascot Score: 28



MS/MS spectrum of the peptide C*IESLIAVFQK from S100 P (P25815);
targeted precursor mass 679.830 m/z (2+), corresponding $[M+H]^+$ mass
1357.645 Da, Mascot Score: 98