Supplemental information

Rapid tryptic peptide mapping of human serum albumin using DI–MS/MS^ALL

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Figure legends

Fig. S1 The canonical sequence of HSA (ID: P02768) obtained from UniProt, and the peptides captured by DI–MS/MS^ALL and LC–MS/MS, including 4 ones (blue characters) solely found by LC–MS/MS, 47 ones (red characters) found by either DI–MS/MS^ALL or LC–MS/MS, and four ones (black characters) found by neither DI–MS/MS^ALL nor LC–MS/MS.

Fig. S2 Overlaid extract ion current chromatogram of tryptic peptide pool of HSA acquired by LC-MS/MS.

Fig. S3 Representative MS^2 spectral comparison of LC*TVATLR between DI–MS/MS^ALL (upper) and LC–MS/MS (downer) and the assignment of primary fragment ions to the fragments.

DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESA
ENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRP
EVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAAC
LLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVT
DLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVEND
EMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEARRHPDYSVVLLLRLAKTYET
TLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKK
VPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRV
TKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVK
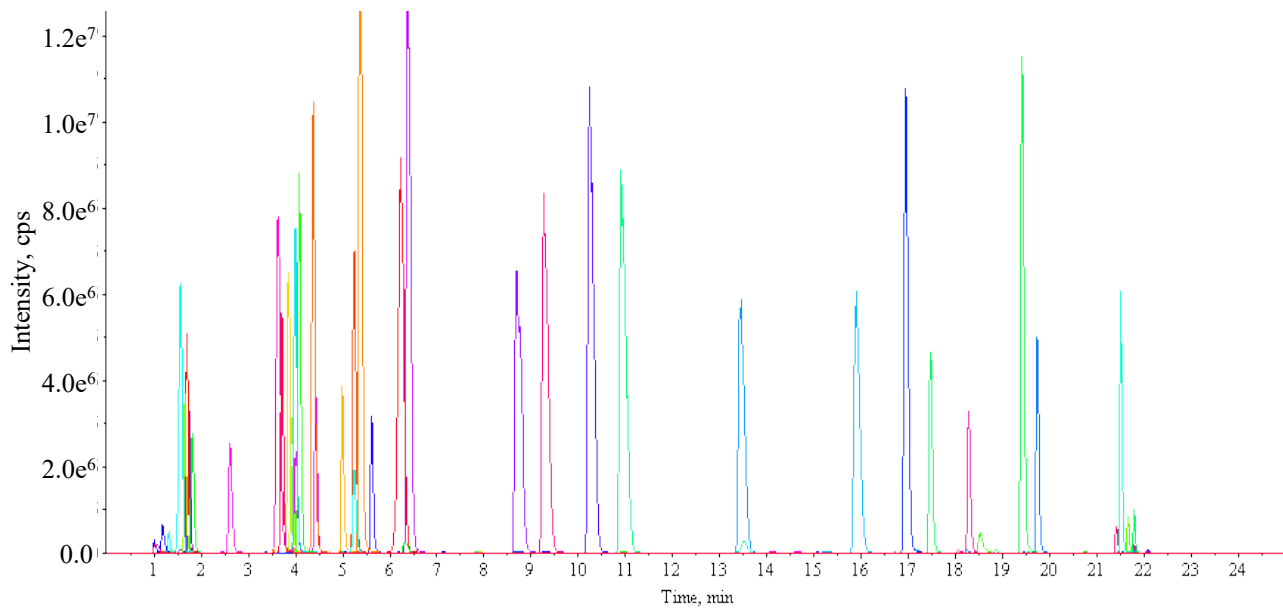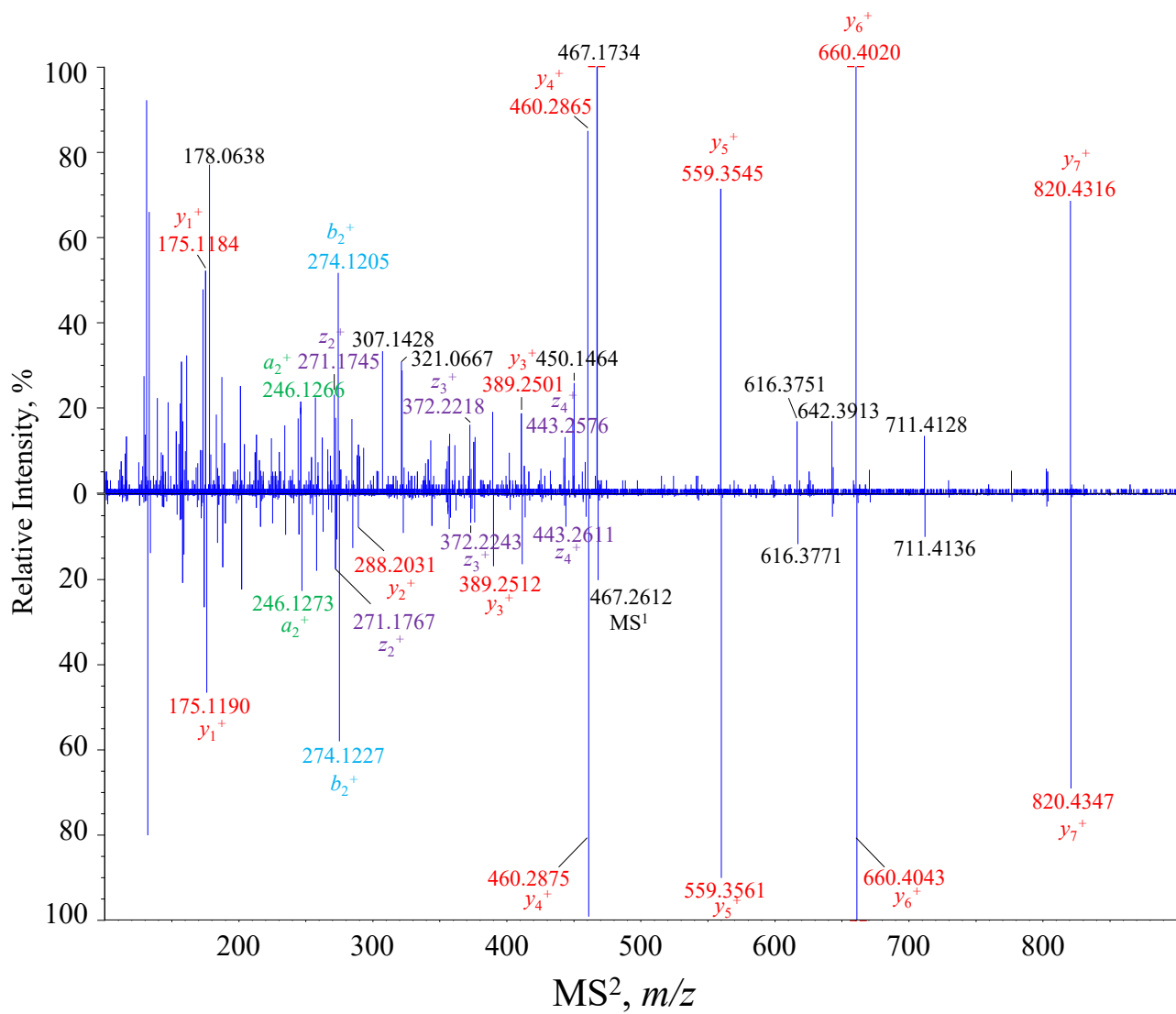HKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL

Fig. S1

Fig. S2

Fig. S3