Supplemental information

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

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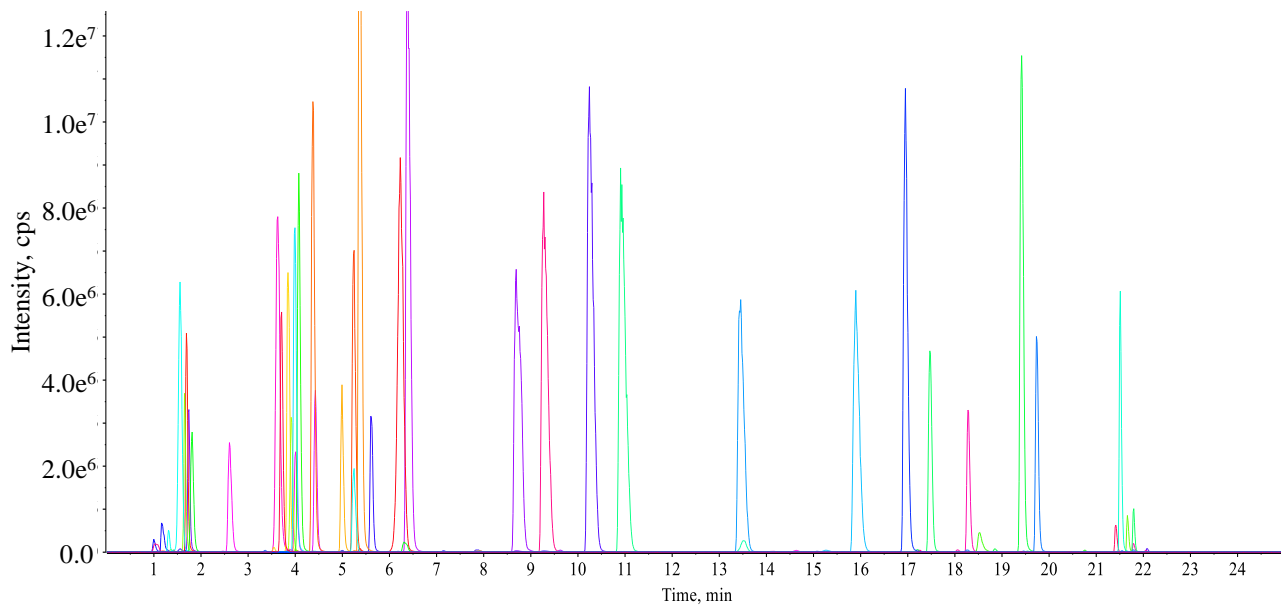[#] These two authors contributed equally to this article.

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.

DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPE
VDVMCTAFHDNEETFLKKYLYEIARHPYFYAPELLFFAKRYKAAFTECCQAADKAACL
LPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDL
TKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEM
PADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEARRHPDYSVVLLLRLAKTYETTLE
KCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQ
VSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKC
CTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKP
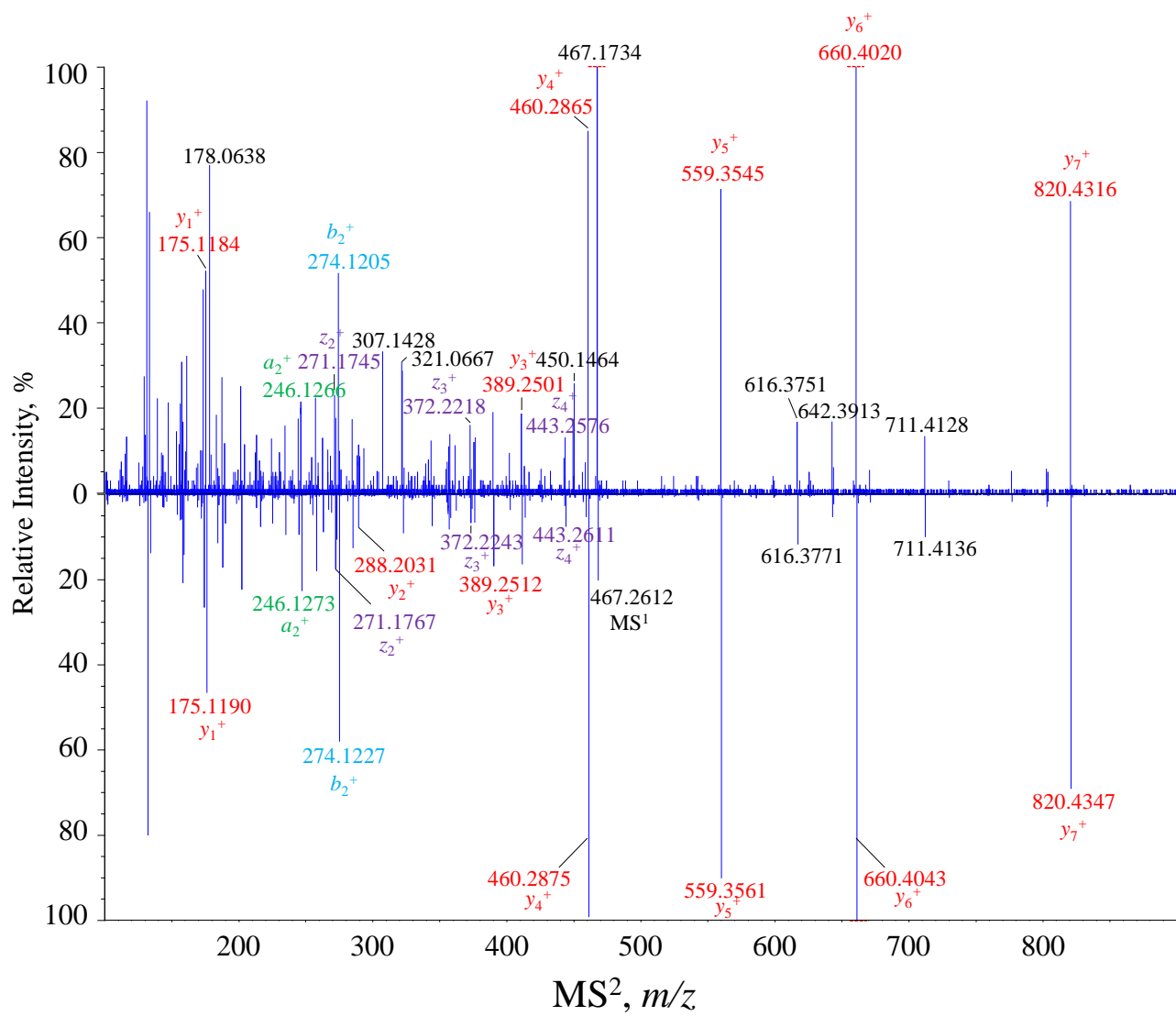KATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL

Fig. S1

Fig. S2

Fig. S3