Table 1: Protein fractionation, peptide separation and mass spectrometric identification strategies for enhancement of proteome identification coverage explored in this study.

Steps	*Procedures*
(A) Protein fractionation	(1) SDS-PAGE slicing (2) Serial ultrafiltration (3) No protein fractionation
(B) Tryptic digestion	(1) In-solution digestion (2) In-gel digestion
(C) Peptide chromatography	(1) Strong cation exchange chromatograhpy (2) Strong anion exchange chromatograhpy (3) C18 ion pair chromatograhpy (4) PSDVB with NH_4OH, using StageTip (5) No peptide chromatography
(D) Parent ion selection in LC-MS	(1) Simple repetition (2) Sequential static exclusion (3) Different ion pair reagents in subsequent runs (4) Subdivided scan range (5) Shallow gradient elution
(E) CID for MS/MS	(1) Quadrupole-TOF (2) Linear ion trap

Abbreviations: SDS-PAGE, sodium dodecylsulfate polyacrylamide gel electrophoresis; PSDVB, poly(styrene-divinylbenzene) copolymer; TOF: time-of-flight.