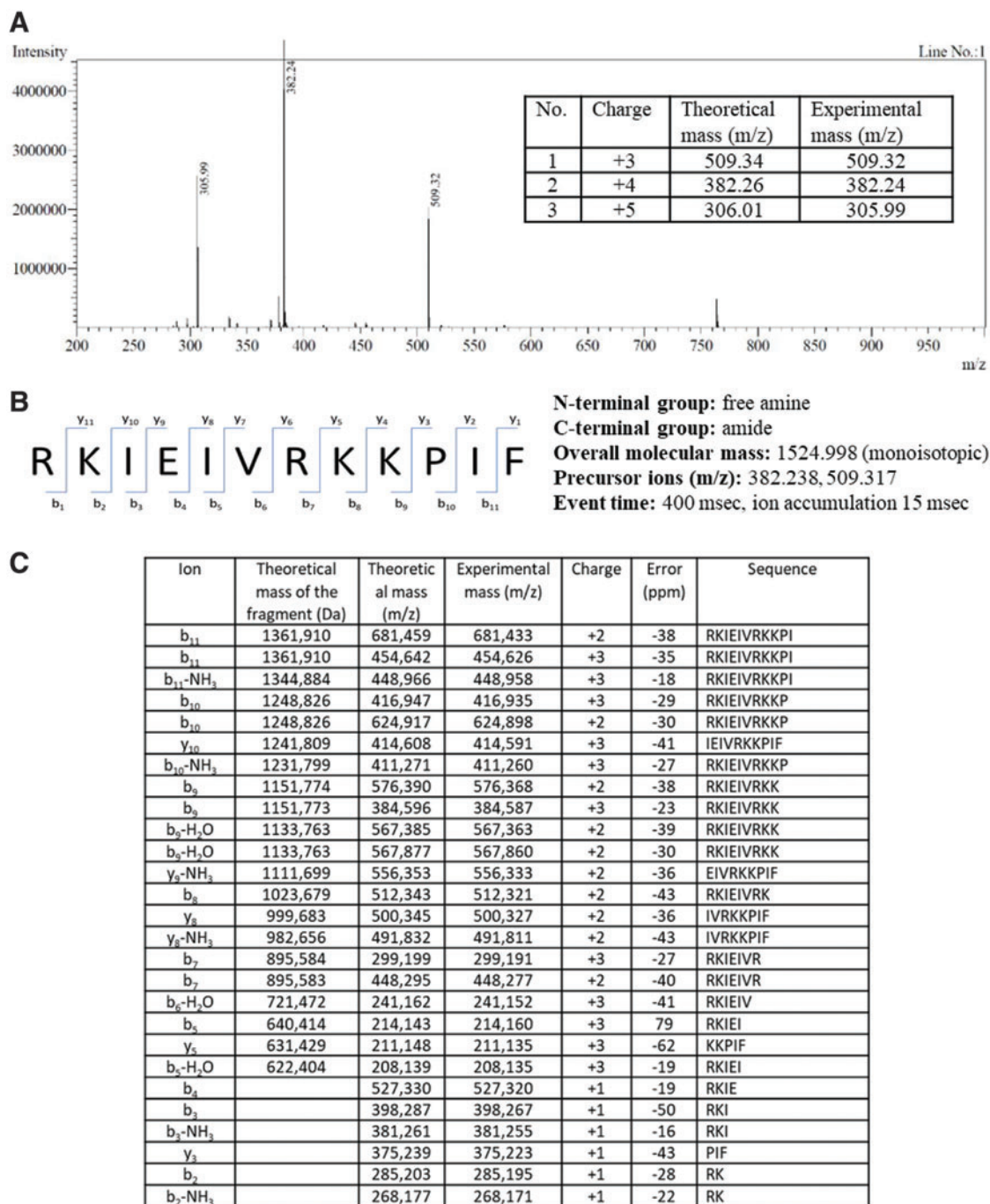


Supplementary Data



Supplementary Figure S1. Mass spectrometry analysis of PDGF1 peptide: **(A)** ESI chromatogram of detected ions, **(B)** theoretical fragments of PDGF1 generated by CID, and **(C)** fragments detected during the MS/MS experiment. Identification of PDGF1 was performed using tandem Shimadzu LC-MS IT-TOF. Pure peptide was loaded on column packed with Kromasil C8, 100 Å, 5 µm 250 × 1.0 mm and separated by linear gradient using 0.2% formic acid in water as starting and 100% acetonitrile as ending solvent (0.08 mL/min). Following MS² analysis, b and y ions of peptide were detected. The following experimental parameters were used: ion spray voltage was set at 1.7 kV, nebulizing gas flow at 1.5 L/min, and an interface heater temperature setting of 200°C. MS/MS switch criteria included precursor ions according to peptide. Data were analyzed with Shimadzu LCMS solution v3.8 software. A cutoff of 10% of intensity was applied, and the filtered data set was further analyzed manually. The following protein search parameters were used: MS tolerance 10 ppm, MS/MS tolerance 100 ppm, charge state +2–5. CID, collision-induced dissociation; ESI, electrospray ionization; LC-MS IT-TOF, liquid chromatography mass spectrometry ion trap time-of-flight.