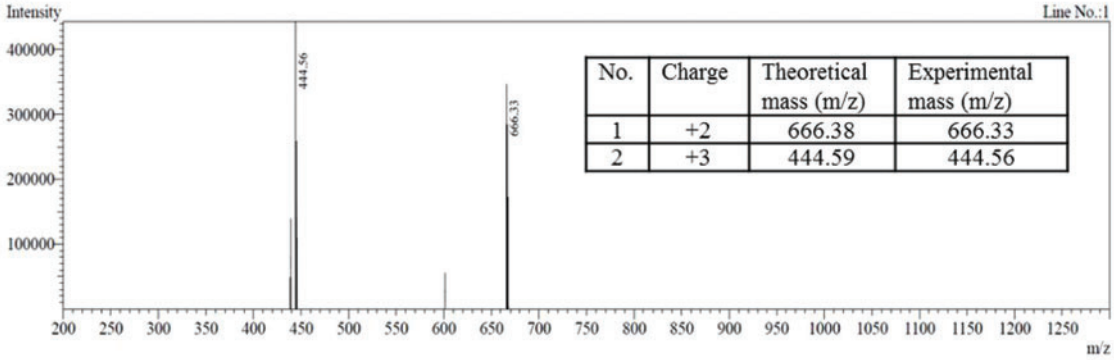
A



No.	Charge	Theoretical mass (m/z)	Experimental mass (m/z)
1	+2	666.38	666.33
2	+3	444.59	444.56

B

N-terminal group: free amine
C-terminal group: amide
Overall molecular mass: 1330.747 (monoisotopic)
Precursor ions (m/z): 444.590, 666.381
Event time: 400 msec, ion accumulation 15 msec

C

Ion	Theoretical mass of the fragment (Da)	Theoretical mass (m/z)	Experimental mass (m/z)	Charge	Error (ppm)	Sequence
$MH\text{-}NH_3$	1314,728	657,868	657,853	+2	-23	RLIDRTNANFL
b_{10}	1201,644	601,326	601,306	+2	-33	RLIDRTNANF
$b_{10}\text{-}NH_3$	1184,617	592,812	592,792	+2	-34	RLIDRTNANF
$y_{10}\text{-}H_2O$	1157,643	579,325	579,296	+2	-50	LIDRTNANFL
b_9	1054,575	527,791	527,773	+2	-34	RLIDRTNAN
$b_9\text{-}NH_3$	1039,549	519,278	519,260	+2	-35	RLIDRTNAN
b_7	869,495	435,251	435,236	+2	-34	RLIDRTN
y_7		834,458	834,426	+1	-38	RTNANFL
$y_7\text{-}NH_3$		817,432	817,400	+1	-39	RTNANFL
b_4		498,304	498,286	+1	-36	RLID
$b_4\text{-}NH_3$		481,277	481,258	+1	-39	RLID
b_3		383,277	383,262	+1	-39	RLI
$b_2\text{-}NH_3$		253,166	253,157	+1	-36	RL

Supplementary Figure S2. Mass spectrometry analysis of PDGF2 peptide: **(A)** ESI chromatogram of detected ions, **(B)** theoretical fragments of PDGF2 generated by CID, and **(C)** fragments detected during the MS/MS experiment. Identification of PDGF2 was performed using tandem Shimadzu LC-MS IT-TOF. Pure peptide was loaded on column packed with Kromasil C8, 100 Å, 5 μm 250 $\times$ 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 MS^2 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.