



С

lon	Theoretical	Theoretic	Experimental	Charge	Error	Sequence
	mass of the	al mass	mass (m/z)	~	(ppm)	
	fragment (Da)	(m/z)				
b <sub>11</sub>	1361,910	681,459	681,433	+2	-38	RKIEIVRKKPI
b <sub>11</sub>	1361,910	454,642	454,626	+3	-35	RKIEIVRKKPI
b <sub>11</sub> -NH <sub>3</sub>	1344,884	448,966	448,958	+3	-18	RKIEIVRKKPI
b <sub>10</sub>	1248,826	416,947	416,935	+3	-29	RKIEIVRKKP
b <sub>10</sub>	1248,826	624,917	624,898	+2	-30	RKIEIVRKKP
Y10	1241,809	414,608	414,591	+3	-41	IEIVRKKPIF
b10-NH3	1231,799	411,271	411,260	+3	-27	RKIEIVRKKP
b <sub>9</sub>	1151,774	576,390	576,368	+2	-38	RKIEIVRKK
bg	1151,773	384,596	384,587	+3	-23	RKIEIVRKK
b <sub>9</sub> -H <sub>2</sub> O	1133,763	567,385	567,363	+2	-39	RKIEIVRKK
b <sub>9</sub> -H <sub>2</sub> O	1133,763	567,877	567,860	+2	-30	RKIEIVRKK
y <sub>9</sub> -NH <sub>3</sub>	1111,699	556,353	556,333	+2	-36	EIVRKKPIF
b <sub>8</sub>	1023,679	512,343	512,321	+2	-43	RKIEIVRK
Y <sub>8</sub>	999,683	500,345	500,327	+2	-36	IVRKKPIF
y8-NH3	982,656	491,832	491,811	+2	-43	IVRKKPIF
b <sub>7</sub>	895,584	299,199	299,191	+3	-27	RKIEIVR
b <sub>7</sub>	895,583	448,295	448,277	+2	-40	RKIEIVR
b <sub>6</sub> -H <sub>2</sub> O	721,472	241,162	241,152	+3	-41	RKIEIV
bs	640,414	214,143	214,160	+3	79	RKIEI
y <sub>s</sub>	631,429	211,148	211,135	+3	-62	KKPIF
b <sub>5</sub> -H <sub>2</sub> O	622,404	208,139	208,135	+3	-19	RKIEI
b <sub>4</sub>		527,330	527,320	+1	-19	RKIE
b <sub>3</sub>		398,287	398,267	+1	-50	RKI
b <sub>3</sub> -NH <sub>3</sub>		381,261	381,255	+1	-16	RKI
<b>Y</b> <sub>3</sub>		375,239	375,223	+1	-43	PIF
b <sub>2</sub>		285,203	285,195	+1	-28	RK
b <sub>2</sub> -NH <sub>2</sub>		268,177	268,171	+1	-22	RK

**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,  $5 \mu m 250 \times 1.0 \text{ mm}$  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<sup>2</sup> 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.