

Unveiling a VEGF-mimetic peptide sequence in IQGAP1 protein

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Table S1: ^1H chemical shift assignment of the IQ peptide

Residue	δNH	δH_α	δH_β	δH_γ	δH_δ	δothers
Leu 1	8.24	4.33	1.55		0.82	
Thr 2	8.35	4.30	4.35	1.18		
Tyr 3	8.43	4.52	3.01; 2.94		7.08	6.79
Gln 4	8.19	4.11	1.91	2.17		
Asp 5	8.06	4.41	2.69			
Leu 6	7.98	4.07	1.62	1.51	0.84; 0.83	
Leu 7	7.88	4.13	1.65	1.51		
Gln 8	8.04	4.17	1.66	1.92		
Leu 9	8.09	4.16	1.63	1.5	0.81	
Gln 10	7.92	4.13	1.62 ; 1.55	2.11; 1.98		7.37; 6.83
Tyr 11	8.09	4.44	2.95		7.1	6.82
(D)Arg 12	8.12	4.29	1.49	1.16	2.96	7.11 ; 7.45

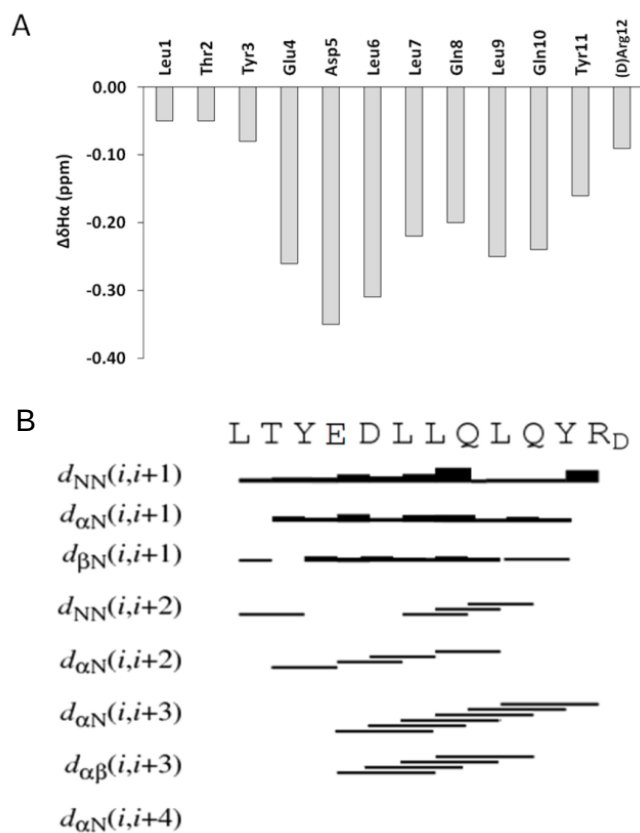


Figure S1. A) $H\alpha$ chemical shift differences ($\Delta\delta H\alpha$) plotted for the 12 residues of IQ. Value of $\Delta\delta H\alpha \geq -0.10$ ppm are indicative of a helical conformation. B) Sequential and medium-range NOE connectivities for the IQ peptide. Thin bars are indicative of weak NOE intensities. R_D indicates a (D)Arg.

Table S2: Amino acid sequence of the synthesized peptides

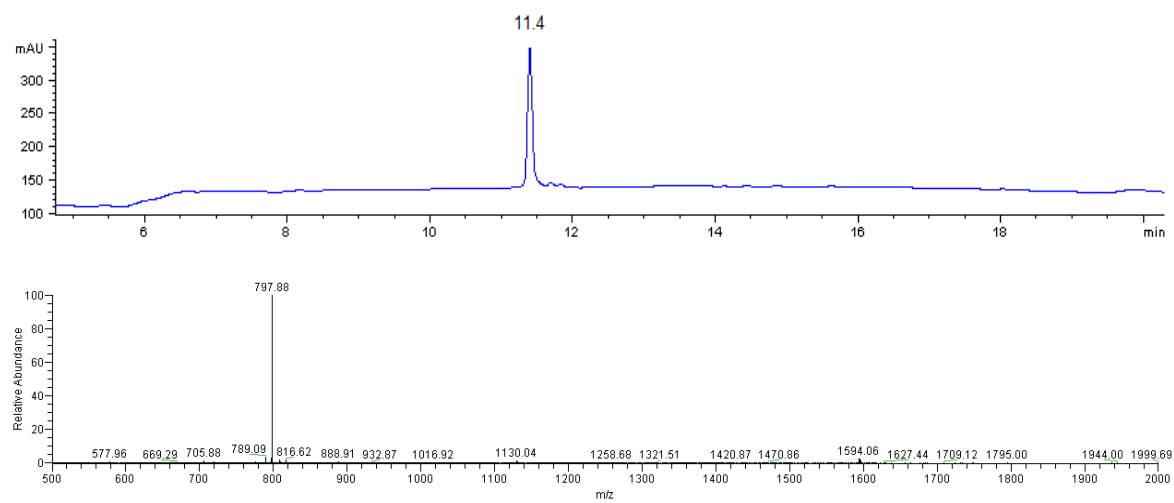
Peptide	Sequence ^a
IQ	<i>Acetyl</i> -L-T-Y-Q-D-L-L-Q-L-Q-Y-r ^b -NH ₂
IQsc	<i>Acetyl</i> -r ^b -L-Q-Y-T-L-D-Y-Q-L-L-Q-NH ₂
IQ biot	<i>Biotin</i> - L-T-Y-Q-D-L-L-Q-L-Q-Y-r ^b -NH ₂
QK	<i>Acetyl</i> - K-L-T-W-Q-E-L-Y-Q-L-K-Y-K-G-I- NH ₂

^aamino acids are indicated using the one letter code; ^b r denotes (D)Arg

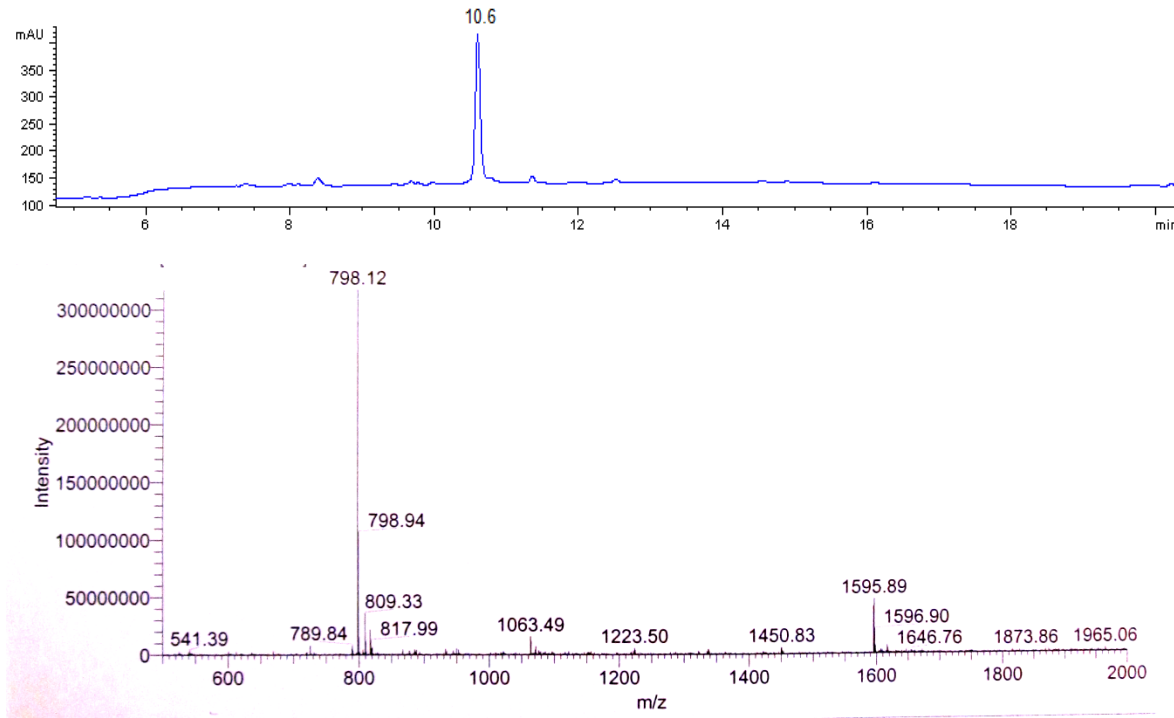
Table S3: Peptides analytical characterization

Peptide	Theoretical Mass(Da)	[M+H] ⁺ found	[M+2H] ²⁺ found	HPLC elution times (min)
IQ	1595.19	1594.1	797.9	11.4
IQsc	1595.19	1595.9	798.1	10.6
IQ biot	1891.67	1892.6	946.7	15.6

IQ



IQsc



IQ biot

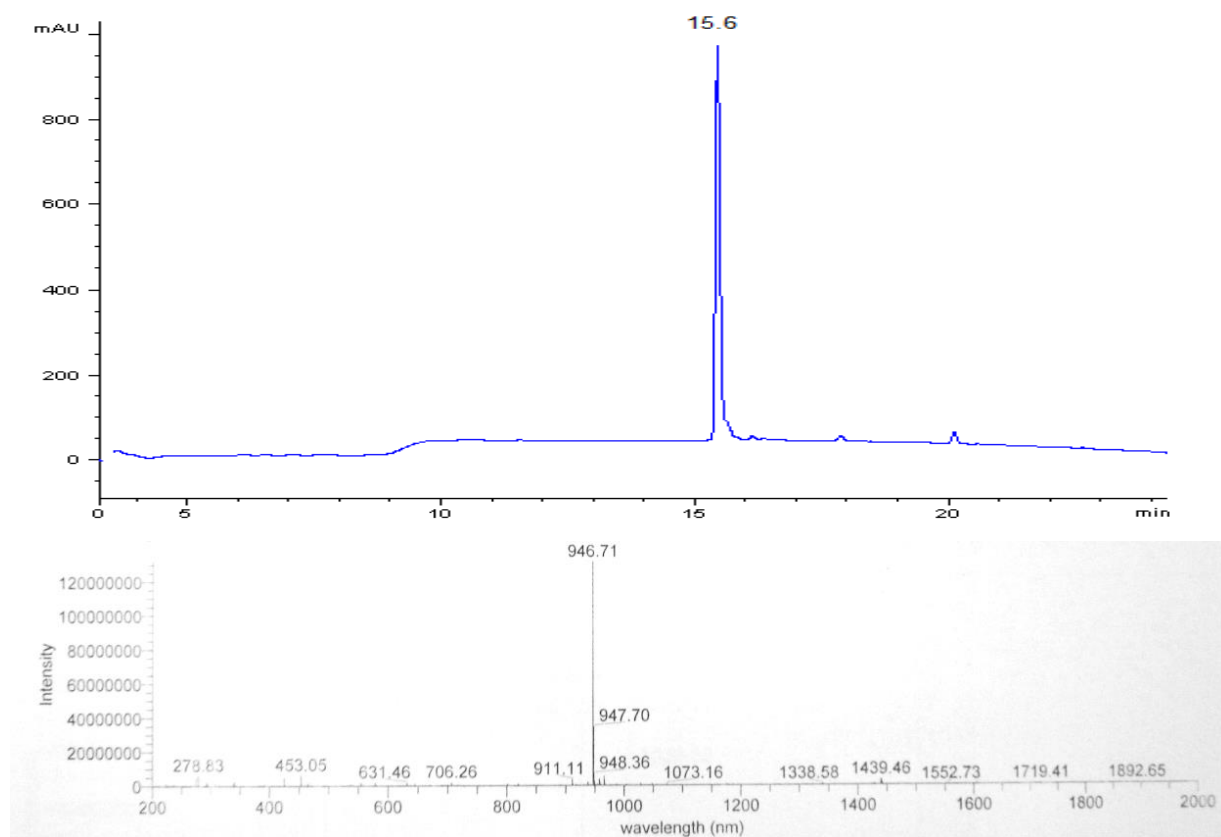


Figure S3. Chromatographic profiles revealed at 210 nm and ESI-MS spectra of IQ, IQsc and IQbiot peptides.