

Table 2S. Data computed from the MSA containing 310 sequences of diverse TFPs.

Case	Residues	Conservation/Divergence/Similarity			Comments
1	L1, E2, C3, H4	0.65	0.51	0.54	β -strand 1 (F1)
2	T14, K15, T16, C17	0.64	0.51	0.55	β -strand 2 (F1)
3	C23, Y24, K25, K26, V27, W28, R29	0.54	0.56	0.42	β -strand 3 (F2)
4	I35, I36, E37, R38, G39, C40	0.60	0.50	0.40	β -strand 4 (F2)
5	K50, L51, N52, C53, C54	0.68	0.42	0.56	β -strand 5 (F3)
6	D57, K58, C59, N60, N61	0.74	0.32	0.53	C-terminal
7	C3	1.00			Cys-1 (Db1)
8	C17	0.99			Cys-1 (Db2)
9	C23	0.99			Cys-2 (Db1)
10	C40	0.98			Cys-2 (Db2)
11	C42	0.96			Cys-1 (Db3)
12	C53	0.95			Cys-2 (Db3)
13	C54	0.99			Cys-1 (Db4)
14	C59	1.00			Cys-2 (Db4)
15	C59, N60	0.98			C-terminal CN

The sequence conservation was calculated using the sequence of P01426 (short neurotoxin from *Naja nigricollis*) as reference and the Blosum30 matrix. Divergence and similarity scores were calculated using the AAC derived from the human genome database containing 28243 entries.