

Table 6. Observed no. of three-residue motifs in protein sequences

Motif*	Nonredundant protein sequences (884,894) [†]			TrEMBL (1,036,258) [†]			Swiss-Prot and TrEMBL (847,587) [†]			Swiss-Prot (122,214) [†]		
	O _X	R _{O(ADW)} [‡]	R _{O(VIS)} [‡]	O _X	R _{O(ADW)} [‡]	R _{O(VIS)} [‡]	O _X	R _{O(ADW)} [‡]	R _{O(VIS)} [‡]	O _X	R _{O(ADW)} [‡]	R _{O(VIS)} [‡]
VII	37,473	2.716	0.526	37,410	2.301	0.436	37,423	2.825	0.540	9,332	4.510	0.705
LEF	45,588	3.304	0.640	53,657	3.300	0.625	43,936	3.317	0.634	7,924	3.830	0.598
WEF	7,230	0.524	0.102	5,955	0.366	0.069	6,887	0.520	0.099	937	0.453	0.071
LNF	56,977	4.130	0.801	67,098	4.127	0.782	55,386	4.181	0.799	6,925	3.347	0.523
ADW	13,796	—	0.194	16,260	—	0.189	13,247	—	0.191	2,069	—	0.156
VIS	71,178	5.159	—	85,836	5.279	—	69,300	5.231	—	13,245	6.402	—

Motif*	Nonredundant protein sequences (1,026,709) [†]			TrEMBL (1,087,429) [†]			Swiss-Prot and TrEMBL (988,484) [†]			Swiss-Prot (125,236) [†]		
	O _X	R _{O(ADW)} [‡]	R _{O(VIS)} [‡]	O _X	R _{O(ADW)} [‡]	R _{O(VIS)} [‡]	O _X	R _{O(ADW)} [‡]	R _{O(VIS)} [‡]	O _X	R _{O(ADW)} [‡]	R _{O(VIS)} [‡]
VIV	80,645	4.933	0.955	86,306	4.968	0.952	78,620	4.989	0.955	12,350	5.809	0.904
ADW	16,349	—	0.194	17,373	—	0.192	15,760	—	0.191	2,126	—	0.156
VIS	84,411	5.163	—	90,703	5.221	—	82,318	5.231	—	13,659	6.425	—

*Motif database scanning has been carried by out using PATTINPROT (1).

[†]Total number of proteins on the database.

[‡]R_O is the ratio between the number of hits found on the database for a given motif X and a control amino acid sequence C (ADW or VIS)

1. Combet, C., Blanchet, C., Geourjon, C. & Deleage, G. (2000) *Trends Biochem. Sci.* **25**, 147-150.