

Table 12. Expected vs. actual frequency of the three-residue amyloidogenic motif WEF surrounded by amyloid breakers in protein sequences

Database*	WEF P [†]		P – WEF [†]		WEF P + [†]	
	O _{WEFP} [§]	E _{WEFP} [¶]	O _{P-WEF} [§]	E _{P-WEF} [¶]	O _{WEFP+} [§]	E _{WEFP+} [¶]
Nonredundant (NR)	551	318.12	1,124	36.90	160	35.63
TrEMBL (Tr)	440	262.02	967	30.39	117	29.35
Swiss-Prot and TrEMBL (SP + Tr)	537	303.03	991	35.15	153	33.94
Swiss-Prot (SP)	97	41.01	24	4.76	36	4.59
P _{WEFXX} (P _{XXWEF}) [‡]	1.486e ⁻⁶		1.724e ⁻⁷		1.664e ⁻⁷	
Mean difference	175.206		749.699		90.623	
df	3		3		3	
t value	4.1883		3.0504		4.2473	
t probability	0.02481		0.05541		0.02391	

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

[†]Only motifs where the difference between the number of observed and expected hits is statistically significant at a confidence level $\geq 5\%$.

[‡]Motif probabilities have been calculated as the product of the expected individual amino acid frequencies (see *Methods* in the main text).

[§]O_{WEFXX} (O_{XXWEF}) is the number of hits of an amyloid breaker motif that have been found on the database.

[¶]E_{WEFXX} (E_{XXWEF}) is the expected number of hits of a given amyloid breaker motif based on the average composition of proteins (see *Methods* in the main text) and the total number of WEF hits found in the database [O_{WEF} (NR) = 7,230; O_{WEF} (Tr) 5,955; O_{WEF} (SP + Tr) = 6,887; O_{WEF} (SP) = 932].

^{||}Student's test of significance.

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