Table 13. Expected vs. actual frequency of the three-residue amyloidogenic motif LNF surrounded by amyloid breakers in protein sequences

Database*	LNF P[†]	
	O_{LNFP}[§]	E_{LNFP}[¶]
Nonredundant (NR)	12,793	2,507.00
TrEMBL (Tr)	13,885	2,952.30
Swiss-Prot + TrEMBL (SP + Tr)	12,739	2,437.00
Swiss-Prot (SP)	115	93.18
P_{LNFXX} (P_{XXLNF})[‡]	$9.029e^{-7}$	
Mean difference[‖]	7885.63	
df[‖]	3	
t value[‖]	3.0034	
t probability[‖]	0.05751	

*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 ≥5%

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

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

[¶]E_{LNFXX} (E_{XXLNF}) 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 LNF hits found in database [O_{LNF} (NR) 56,977; O_{LNF} (Tr) = 67,098; O_{LNF} (SP + Tr) = 55,386; O_{LNF} (SP) = 6,925].

[‖]Student's test of significance.

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