

Table S1 Hps5^{WT} protein modeling parameters from SwissModel of entire protein (residues #1-1133)

Residues	Sequence identity	E-score	Q-MEAN4 raw score	Q-MEAN4 Z-score	ANOLEA score at #76	GROMOS score at #76
31-152	22.0%	2.0E-7	0.480	-3.34	~ +1	~ +20
73-189	17.4%	2.7E-6	0.407	-3.89	~ +4	~ +10
31-358	12.6%	1.4E-6	0.208	-8.99	~ +130	~ +10