

Table S3 Hps5I76N 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%	1.9E-7	0.478	-3.36	~ -3	~ -180
73-189	17.4%	2.6E-6	0.418	-3.78	~ +2	~ -150
30-358	14.5%	3.2E-6	0.284	-7.82	~ +4	~ -40