Table S2. TM-scores of *B. cereus*, Tupanvirus and PBCV-1 target sequences compared to their templates from SWISS-MODEL and/or RoseTTAFold

Template/Target	SWISS-MODEL			RoseTTAFold			
	PDB ID: 6IGY	PDB ID: 5GQB	PDB ID: 6BT9	PDB ID: 6IGY	PDB ID: 5GQB	PDB ID: 6BT9	RoseTTA/ SWISS
B. cereus	0.1324	0.1418	**0.656**	0.1328	0.14	**0.63**	0.9893
Tupanvirus	0.1501	**0.1978**	0.168	0.1357	**0.1861**	0.181	0.7283
PBCV-1	**0.3295**	0.1557	0.1805	**0.2568**	0.1649	0.183	0.9034

6IGY: chitinase B *Aspergillus niger*; 5GQB: chitinase H *Ostrinia furnacalis*; 6BT9: chitinase *Bacillus thuringiensis*; TM-scores > 0.17: not randomly chosen unrelated proteins; TM-scores > 0.5: in about the same fold in protein structures. Selected best hit (scored) models/templates were highlighted in bold.