

Table S4. Results of HHpred analysis of selected Rpl1 phage proteins. The best and most relevant hits are shown, including the coordinates of the matching regions, PDB ID and chain identifier, and the HHpred probability (%) in the matched regions.

Predicted gene product	Protein length (aa)	Matching residues (aa)	HHpred best match	PDB ID	Probability (%)
Rpl59_054	374	22-159	Protein O-linked-mannose beta-1,2-N-acetylglucosaminyltransferase 1; glycosyltransferase, O-mannosylation, alpha-dystroglycan, TRANSFERASE, SUGAR BINDING PROTEIN; 2.49A { <i>Homo sapiens</i> }	5GGF_C	99.23
		19-177	Protein O-linked-mannose beta-1,2-N-acetylglucosaminyltransferase 1; glycosyltransferase, O-mannosylation, alpha-dystroglycan, SUGAR BINDING PROTEIN; HET: LEC; 1.211A { <i>Homo sapiens</i> }	5GGN_B	99.17
		224-320	ENDO-1,4-BETA-XYLANASE Y; CARBOHYDRATE-BINDING MODULE, XYLAN-BINDING, XYLANASE; HET: MSE; 2.1A { <i>CLOSTRIDIUM THERMOCELLUM</i> } SCOP: b.18.1.7	1DYO_B	95.49
		224-322	HYALURONATE LYASE; LYASE, HYALURONAN BINDING CARBOHYDRATE BINDING MODULE, CBM, PL FAMILY 8, PL8, HYL; HET: EDO; 1.2A { <i>STREPTOCOCCUS PNEUMONIAE TIGR4</i> }	1D0Q_A	95.12
		224-322	Endo-1,4-beta-xylanase C; Binding Site, Carbohydrates, Enzyme Stability, Substrate Specificity, Endo-1, 4-beta-xylanase, Xylan-binding domain, Thermophilic enzymes, Thermostabilizing Domains, Xylotetraose; HET: XYP; 1.67A { <i>Paenibacillus barcinonensis</i> }	4XUR_B	94.02
Rpl59_056	1328	1230-1328	L-SHAPED TAIL FIBER PROTEIN; VIRAL PROTEIN, BACTERIAL VIRUSES, CAUDOVIRALES, SIPHOVIRIDAE, INFECTION; HET: FLC; 2.52A { <i>ENTEROBACTERIA PHAGE T5</i> }	4UW8_H	98.80
		1231-1286	Endo-N-acetylneuraminidase; Chaperone, Glycosidase, Hydrolase; HET: TAM, PEG; 2.6A { <i>Enterobacteria phage K1F</i> }	3GW6_B	98.46
		1231-1386	Long tail fiber distal subunit; Bacteriophage, Helical sandwich, Tail fiber, polyglycine, VIRAL PROTEIN; HET: MRD, MPD, IMD; 1.70355818561A { <i>Salmonella phage vB_SenMS16</i> }	6F45_B	98.53
		1233-1321	Tail spike protein; bacteriophage, tailspike, <i>Acinetobacter baumannii</i> , gp42, VIRAL PROTEIN; HET: MSE; 1.794A { <i>Acinetobacter phage vB_AbaP_AS12</i> }	6EU4_B	97.92
		1233-1324	Neck appendage protein; 3-helix bundle, chaperon, CHAPERONE; HET: PEG; 2.2A { <i>Bacillus phage GA-1</i> }	3GUD_A	97.80
		1185-1328	Isoform 2 of Myelin regulatory factor; auto-catalytic protease, protein chaperone. trimeric protein, triple coiled-coil, membrane PROTEIN; HET: MSE; 2.4A { <i>Mus musculus</i> }	7DC3_A	97.69
Rpl59_262	1032	1-1028	Baseplate wedge protein gp7; T4, baseplate, complex, VIRAL PROTEIN; 3.8A { <i>Enterobacteria phage T4</i> }	5HX2_A	100.00
		178-448	Glycosyl hydrolase, BNR repeat; 7-bladed beta-propeller fold, structural genomics, Joint Center for Structural Genomics, JCSG, Protein Structure Initiative, PSI-2, hydrolase; HET: MSE, EDO; 2.2A { <i>Ralstonia eutropha</i> }	3B7F_A	70.14
		190-417	Exo-arabinanase; ARABINASE, GLYCOSYL HYDROLASE, HYDROLASE; HET: AHR; 1.04A { <i>Penicillium chrysogenum</i> }	3A72_A	67.31
		183-417	oligoxyloglucan reducing-end-specific cellobiohydrolase; BETA-PROPELLER, HYDROLASE; 2.2A { <i>Geotrichum sp. M128</i> } SCOP: b.69.13.1	1SQJ_B	66.14
		176-448	Cellulase; Glycoside Hydrolase Family 74, Xyloglucanase, Xyloglucan, HYDROLASE; HET: XYS, IOD, BGC, EDO; 1.95A { <i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)}	7KN8_B	65.60
Rpl59_134	121	5-117	ENDONUCLEASE II; GIY-YIG, NUCLEASE, HYDROLASE; HET: PEG, MSE; 1.9A { <i>ENTEROBACTERIA PHAGE T4</i> }	2WSH_A	99.53