Phyre^2

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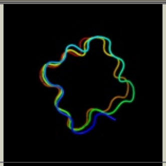
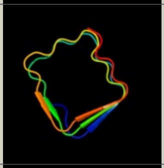
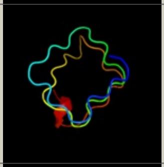
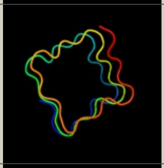
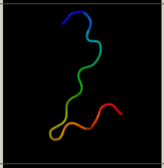
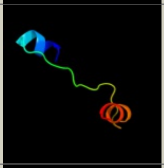
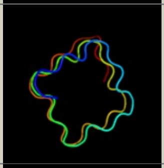
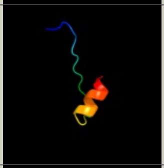
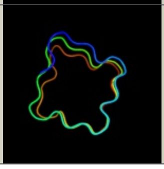
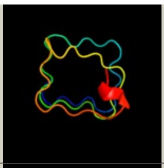
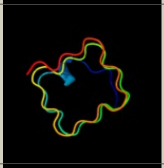
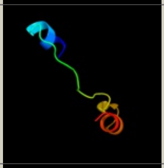
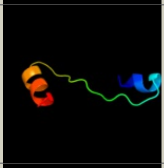
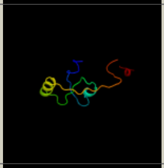
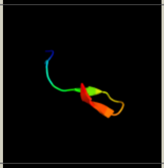
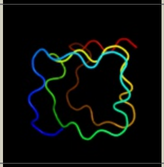
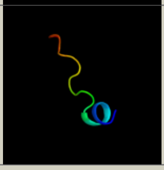
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nb2B_	Alignment		31.4	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**secreted effector protein; **PDBTitle:** crystal structure of e. coli o157:h7 effector protein nleI
2	c2w7zB_	Alignment		29.1	15	**PDB header:**inhibitor **Chain:** B: **PDB Molecule:**pentapeptide repeat family protein; **PDBTitle:** structure of the pentapeptide repeat protein efsqnr, a dna2 gyrase inhibitor. free amines modified by cyclic3 pentylation with glutaraldehyde.
3	c2xt4B_	Alignment		28.4	15	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mcbg-like protein; **PDBTitle:** structure of the pentapeptide repeat protein albg, a2 resistance factor for the topoisomerase poison albicidin.
4	c2g0yA_	Alignment		15.4	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**pentapeptide repeat protein; **PDBTitle:** crystal structure of a lumenal pentapeptide repeat protein from2 cyanothece sp 51142 at 2.3 angstrom resolution. tetragonal crystal3 form
5	c3sxuB_	Alignment		14.3	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii subunit psi; **PDBTitle:** structure of the e. coli ssb-dna polymerase iii interface
6	c3du1X_	Alignment		14.2	20	**PDB header:**structural protein **Chain:** X: **PDB Molecule:**all3740 protein; **PDBTitle:** the 2.0 angstrom resolution crystal structure of hetl, a pentapeptide2 repeat protein involved in heterocyst differentiation regulation from3 the cyanobacterium nostoc sp. strain pcc 7120
7	d1kz1a_	Alignment		13.3	20	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
8	c2o6wA_	Alignment		12.5	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**repeat five residue (rfr) protein or **PDBTitle:** crystal structure of a pentapeptide repeat protein (rfr23)2 from the cyanobacterium cyanothece 51142
9	c3r2cJ_	Alignment		12.4	23	**PDB header:**transcription/rna **Chain:** J: **PDB Molecule:**30s ribosomal protein s10; **PDBTitle:** crystal structure of antitermination factors nusb and nuse in complex2 with boxa rna
10	d1nbwb_	Alignment		9.6	20	**Fold:**Anticodon-binding domain-like **Superfamily:**B12-dependent dehydatase associated subunit **Family:**Dehydratase-reactivating factor beta subunit
11	d2f3la1	Alignment		9.6	26	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats

12	c2xt4A_	Alignment		9.2	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**mcbg-like protein; **PDBTitle:** structure of the pentapeptide repeat protein albg, a2 resistance factor for the topoisomerase poison albicidin.
13	c3n90A_	Alignment		9.2	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**thylakoid lumenal 15 kda protein 1, chloroplastic; **PDBTitle:** the 1.7 angstrom resolution crystal structure of at2g44920, a2 pentapeptide repeat protein from arabidopsis thaliana thylakoid3 lumen.
14	c1w19E_	Alignment		9.0	34	**PDB header:**transferase **Chain:** E: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase; **PDBTitle:** lumazine synthase from mycobacterium tuberculosis bound to2 3-(1,3,7-trihydro-9-d-ribityl-2,6,8-purinetrione-7-yl)3 propane 1-phosphate
15	d1ejba_	Alignment		8.9	23	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
16	c2x0dA_	Alignment		8.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
17	d1r0va1	Alignment		8.5	64	**Fold:**Restriction endonuclease-like **Superfamily:**tRNA-intron endonuclease catalytic domain-like **Family:**tRNA-intron endonuclease catalytic domain-like
18	c3be3A_	Alignment		8.4	53	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein belonging to pfam duf16532 from bordetella bronchiseptica
19	c3pssB_	Alignment		7.9	19	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**qnr; **PDBTitle:** crystal structure of ahqnr, the qnr protein from aeromonas hydrophila2 (p21 crystal form)
20	d1h9ea_	Alignment		7.9	42	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
21	c2f59B_	Alignment	not modelled	7.6	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
22	c1y7xA_	Alignment	not modelled	7.5	41	**PDB header:**structural protein, protein binding **Chain:** A: **PDB Molecule:**major vault protein; **PDBTitle:** solution structure of a two-repeat fragment of major vault2 protein
23	d1nqua_	Alignment	not modelled	7.4	43	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
24	d1em8b_	Alignment	not modelled	7.4	33	**Fold:**DNA polymerase III psi subunit **Superfamily:**DNA polymerase III psi subunit **Family:**DNA polymerase III psi subunit
25	c3b1bA_	Alignment	not modelled	6.8	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase 1; **PDBTitle:** the unique structure of wild type carbonic anhydrase alpha-ca1 from2 chlamydomonas reinhardtii
26	c3etbJ_	Alignment	not modelled	6.7	33	**PDB header:**immune system/toxin **Chain:** J: **PDB Molecule:**anthrax protective antigen; **PDBTitle:** crystal structure of the engineered neutralizing antibody2 m18 complexed with anthrax protective antigen domain 4
27	c3rkiB_	Alignment	not modelled	6.6	45	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structural basis for immunization with post-fusion rsv f to elicit2 high neutralizing antibody titers
28	d1u0la1	Alignment	not modelled	6.3	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

29	c2j8iB_	Alignment	not modelled	6.3	22	**PDB header:**toxin **Chain:** B: **PDB Molecule:**np275; **PDBTitle:** structure of np275, a pentapeptide repeat protein from2 nostoc punctiforme
30	d1di0a_	Alignment	not modelled	6.3	17	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
31	d2igta1	Alignment	not modelled	5.8	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**hypothetical RNA methyltransferase
32	d2j8ia1	Alignment	not modelled	5.7	23	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pentapeptide repeat-like **Family:**Pentapeptide repeats
33	d1zvpa2	Alignment	not modelled	5.7	24	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**VC0802-like
34	c2xtwB_	Alignment	not modelled	5.4	22	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**qnrb1; **PDBTitle:** structure of qnrb1 (full length), a plasmid-mediated2 fluoroquinolone resistance protein
35	d1t6la2	Alignment	not modelled	5.3	34	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
36	d1zhva2	Alignment	not modelled	5.3	28	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
37	c1y7wB_	Alignment	not modelled	5.1	33	**PDB header:**lyase **Chain:** B: **PDB Molecule:**halotolerant alpha-type carbonic anhydrase (dca ii); **PDBTitle:** crystal structure of a halotolerant carbonic anhydrase from dunaliella2 salina
38	c2k0nA_	Alignment	not modelled	5.1	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mediator of rna polymerase ii transcription **PDBTitle:** solution structure of yeast gal11p kix domain