Phyre^2

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Description	P39317
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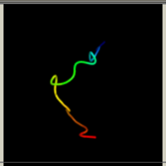
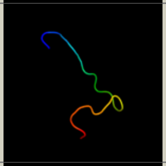
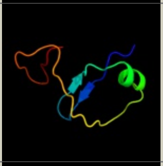
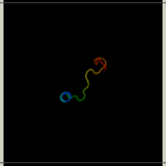
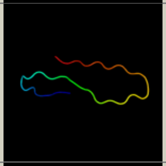
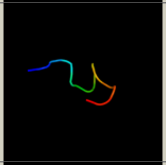
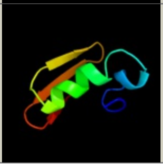
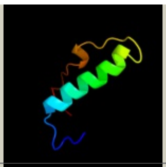
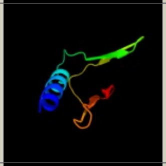
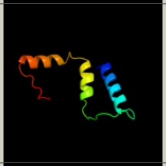
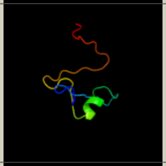
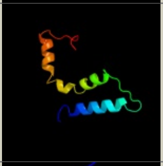
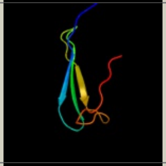
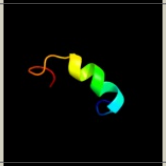
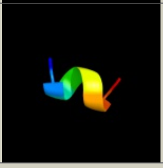
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2enga_	Alignment		44.9	53	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**Eng V-like
2	d1l8fa_	Alignment		42.4	50	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**Eng V-like
3	d1miua3	Alignment		37.0	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
4	d1iyjb3	Alignment		36.2	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
5	d1j6xa_	Alignment		34.2	35	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
6	d1vjea_	Alignment		29.7	42	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
7	d1i5pa1	Alignment		25.6	38	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain
8	d1j98a_	Alignment		24.0	38	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
9	d1j6wa_	Alignment		22.6	46	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
10	c2qqpD_	Alignment		22.4	48	**PDB header:**virus **Chain:** D: **PDB Molecule:**small capsid protein; **PDBTitle:** crystal structure of authentic providence virus
11	d1wy5a2	Alignment		21.3	24	**Fold:**MesJ substrate recognition domain-like **Superfamily:**MesJ substrate recognition domain-like **Family:**MesJ substrate recognition domain-like

12	d1cfra_	Alignment		16.8	23	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Cfr10I/Bse634I
13	c3na2C_	Alignment		14.0	30	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function from mine drainage2 metagenome leptospirillum rubarum
14	d1tbfa_	Alignment		13.4	27	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**PDEase
15	c2fvuA_	Alignment		13.2	41	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein sir3; **PDBTitle:** structure of the yeast sir3 bah domain
16	c1xozA_	Alignment		13.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** catalytic domain of human phosphodiesterase 5a in complex2 with tadalafil
17	d1qmja_	Alignment		12.4	27	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Galectin (animal S-lectin)
18	c2cosA_	Alignment		11.7	88	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine protein kinase lats2; **PDBTitle:** solution structure of rsgi ruh-038, a uba domain from mouse2 lats2 (large tumor suppressor homolog 2)
19	c2vy8A_	Alignment		11.1	40	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polymerase basic protein 2; **PDBTitle:** the 627-domain from influenza a virus polymerase pb22 subunit with glu-627
20	d1z0kb1	Alignment		9.9	50	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
21	c1mjeA_	Alignment	not modelled	9.8	23	**PDB header:**gene regulation/antitumor protein/dna **Chain:** A: **PDB Molecule:**breast cancer 2; **PDBTitle:** structure of a brca2-dss1-ssdna complex
22	d1ddba_	Alignment	not modelled	9.6	30	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
23	d1yzma1	Alignment	not modelled	9.5	50	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
24	c3cw4A_	Alignment	not modelled	9.2	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polymerase basic protein 2; **PDBTitle:** large c-terminal domain of influenza a virus rna-dependent polymerase2 pb2
25	c1x50A_	Alignment	not modelled	9.0	16	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**galectin-4; **PDBTitle:** solution structure of the c-terminal gal-bind lectin domain2 from human galectin-4
26	c2q2kA_	Alignment	not modelled	9.0	58	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of nucleic-acid binding protein
27	c3c8lB_	Alignment	not modelled	8.8	29	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**ftsz-like protein of unknown function; **PDBTitle:** crystal structure of a ftsz-like protein of unknown function2 (npun_r1471) from nostoc punctiforme pcc 73102 at 1.22 a resolution
28	c2wg6L_	Alignment	not modelled	8.4	24	**PDB header:**transcription,hydrolase **Chain:** L: **PDB Molecule:**general control protein gcn4, **PDBTitle:** proteasome-activating nucleotidase (pan) n-domain (57-134)2 from archaeoglobus fulgidus fused to gcn4, p61a mutant

29	d1hlca_	Alignment	not modelled	8.4	21	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Galectin (animal S-lectin)
30	c3duiB_	Alignment	not modelled	7.5	20	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**beta-galactoside-binding lectin; **PDBTitle:** crystal structure of the oxidized cg-1b: an adhesion/growth-2 regulatory lectin from chicken
31	d2cosa1	Alignment	not modelled	7.4	88	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
32	d1ok7a2	Alignment	not modelled	7.2	17	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase III, beta subunit
33	c3h6nA_	Alignment	not modelled	6.7	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**plexin-d1; **PDBTitle:** crystal structure of the ubiquitin-like domain of plexin d1
34	c3bjcA_	Alignment	not modelled	6.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of the pde5a catalytic domain in complex2 with a novel inhibitor
35	c1iyjB_	Alignment	not modelled	6.5	22	**PDB header:**gene regulation/antitumor protein **Chain:** B: **PDB Molecule:**breast cancer susceptibility; **PDBTitle:** structure of a brca2-dss1 complex
36	c3najA_	Alignment	not modelled	6.3	18	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**galectin-8; **PDBTitle:** crystal structure of a protease-resistant mutant form of human2 galectin-8
37	c3zwfA_	Alignment	not modelled	6.3	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc phosphodiesterase elac protein 1; **PDBTitle:** crystal structure of human trnase z, short form (elac1).
38	c3bg4D_	Alignment	not modelled	6.2	30	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**guamerin; **PDBTitle:** the crystal structure of guamerin in complex with2 chymotrypsin and the development of an elastase-specific3 inhibitor
39	d1f3va_	Alignment	not modelled	6.0	44	**Fold:**Ferredoxin-like **Superfamily:**TRADD, N-terminal domain **Family:**TRADD, N-terminal domain
40	c2l6pA_	Alignment	not modelled	6.0	19	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**phac1, phac2 and phad genes; **PDBTitle:** nmr solution structure of the protein np_253742.1
41	c4a0kB_	Alignment	not modelled	5.9	83	**PDB header:**ligase/dna-binding protein/dna **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase rbx1; **PDBTitle:** structure of ddb1-ddb2-cul4a-rbx1 bound to a 12 bp abasic2 site containing dna-duplex
42	c3phfX_	Alignment	not modelled	5.8	23	**PDB header:**viral protein **Chain:** X: **PDB Molecule:**envelope glycoprotein l; **PDBTitle:** crystal structure of the epstein-barr virus gh and gl complex
43	c1gl9B_	Alignment	not modelled	5.7	22	**PDB header:**topoisomerase **Chain:** B: **PDB Molecule:**reverse gyrase; **PDBTitle:** archaeoglobus fulgidus reverse gyrase complexed with adpnp
44	c2jphA_	Alignment	not modelled	5.7	21	**PDB header:**signaling protein, protein binding **Chain:** A: **PDB Molecule:**plexin-b1; **PDBTitle:** nmr solution structure of the rho gtpase binding domain of2 human plexin-b1
45	c1xtcC_	Alignment	not modelled	5.6	47	**PDB header:**toxin **Chain:** C: **PDB Molecule:**cholera toxin; **PDBTitle:** cholera toxin
46	c3h43F_	Alignment	not modelled	5.6	19	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** n-terminal domain of the proteasome-activating nucleotidase2 of methanocaldococcus jannaschii
47	c2ounA_	Alignment	not modelled	5.2	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**camp and camp-inhibited cgmp 3',5'-cyclic **PDBTitle:** crystal structure of pde10a2 in complex with amp