Phyre^2

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Description	P75884
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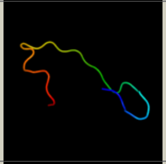
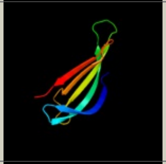
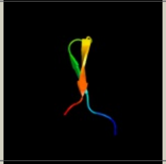
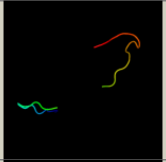
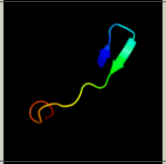
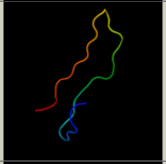
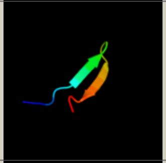
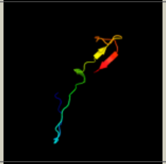
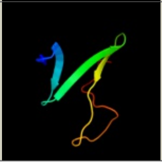
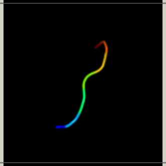
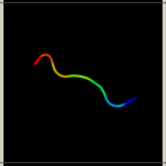
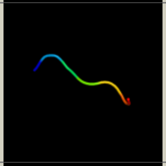
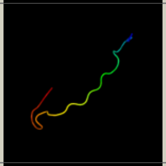
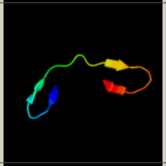
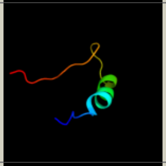
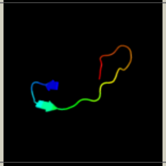
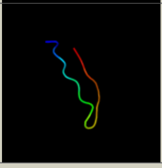
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2in5a1	Alignment		100.0	96	**Fold:**YmcC-like **Superfamily:**YmcC-like **Family:**YmcC-like
2	d1bmlc3	Alignment		44.1	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
3	d2byoa1	Alignment		41.3	16	**Fold:**LolA-like prokaryotic lipoproteins and lipoprotein localization factors **Superfamily:**Prokaryotic lipoproteins and lipoprotein localization factors **Family:**LppX-like
4	c3jslA_	Alignment		22.1	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of the adenylation domain of nad+-2 dependent dna ligase from staphylococcus aureus
5	c2x6vB_	Alignment		18.5	28	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**t-box transcription factor tbx5; **PDBTitle:** crystal structure of human tbx5 in the dna-bound and dna-2 free form
6	d1a0ia1	Alignment		18.4	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
7	c3o0lB_	Alignment		15.6	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution
8	c3fzxA_	Alignment		12.6	12	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of a putative exported protein with ymcc-like fold2 (bf2203) from bacteroides fragilis nctc 9343 at 2.22 a resolution
9	d1v9pa3	Alignment		12.5	24	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
10	d1ogmx1	Alignment		12.4	16	**Fold:**Dextranase, N-terminal domain **Superfamily:**Dextranase, N-terminal domain **Family:**Dextranase, N-terminal domain
11	c3kdvB_	Alignment		12.2	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna damage response b protein; **PDBTitle:** crystal structure of dna damage response b (ddrb) from deinococcus2 geothermalis

12	c2v43A_	Alignment		11.8	15	**PDB header:**regulator **Chain:** A: **PDB Molecule:**sigma-e factor regulatory protein rseb; **PDBTitle:** crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli
13	c2h8bA_	Alignment		11.3	57	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**insulin-like 3; **PDBTitle:** solution structure of insl3
14	c2k6tA_	Alignment		11.3	57	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin-like 3 a chain; **PDBTitle:** solution structure of the relaxin-like factor
15	c2k6uA_	Alignment		10.9	57	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin-like 3 a chain; **PDBTitle:** the solution structure of a conformationally restricted2 fully active derivative of the human relaxin-like factor3 (rlf)
16	d1h6fa_	Alignment		9.5	24	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**T-box
17	c3mlqE_	Alignment		9.1	19	**PDB header:**transferase/transcription **Chain:** E: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
18	d1zbsa2	Alignment		9.0	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
19	c3mlqH_	Alignment		7.7	19	**PDB header:**transferase/transcription **Chain:** H: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
20	d1dgsa3	Alignment		7.2	18	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
21	c3bacA_	Alignment	not modelled	6.8	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** structural basis for the inhibition of bacterial nad+2 dependent dna ligase
22	d1bhia_	Alignment	not modelled	6.8	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
23	d2f1la2	Alignment	not modelled	6.8	8	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**RimM N-terminal domain-like
24	d1b04a_	Alignment	not modelled	6.5	18	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
25	d1azwa_	Alignment	not modelled	5.9	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
26	d4tsva_	Alignment	not modelled	5.9	17	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
27	d1r57a_	Alignment	not modelled	5.8	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
28	c3o44G_	Alignment	not modelled	5.8	16	**PDB header:**toxin **Chain:** G: **PDB Molecule:**hemolysin; **PDBTitle:** crystal structure of the vibrio cholerae cytolysin (hlya) heptameric2 pore
29	c1c9lA	Alignment	not modelled	5.8	44	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**clathrin;

29	c1c9iA_	Alignment	not modelled	5.8	44	**PDBTitle:** peptide-in-groove interactions link target proteins to the2 b-propeller of clathrin
30	d2cupa3	Alignment	not modelled	5.8	44	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
31	d1a9xb1	Alignment	not modelled	5.7	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Carbamoyl phosphate synthetase, small subunit N-terminal domain **Family:**Carbamoyl phosphate synthetase, small subunit N-terminal domain
32	c2j8pA_	Alignment	not modelled	5.6	36	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**cleavage stimulation factor 64 kda subunit; **PDBTitle:** nmr structure of c-terminal domain of human cstf-64
33	d1utca2	Alignment	not modelled	5.5	44	**Fold:**7-bladed beta-propeller **Superfamily:**Clathrin heavy-chain terminal domain **Family:**Clathrin heavy-chain terminal domain
34	c3f6zB_	Alignment	not modelled	5.4	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of pseudomonas aeruginosa mlic in complex2 with hen egg white lysozyme
35	d3bl9a2	Alignment	not modelled	5.4	24	**Fold:**mRNA decapping enzyme DcpS N-terminal domain **Superfamily:**mRNA decapping enzyme DcpS N-terminal domain **Family:**mRNA decapping enzyme DcpS N-terminal domain
36	d1vlra2	Alignment	not modelled	5.3	18	**Fold:**mRNA decapping enzyme DcpS N-terminal domain **Superfamily:**mRNA decapping enzyme DcpS N-terminal domain **Family:**mRNA decapping enzyme DcpS N-terminal domain