Phyre2

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Description	P62395
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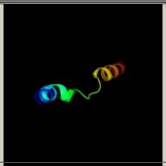
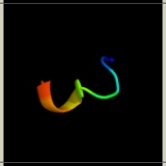
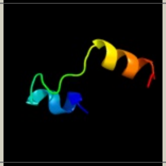
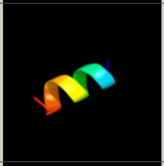
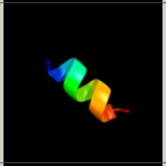
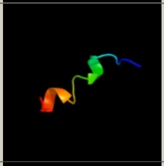
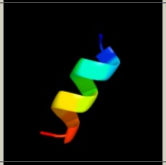
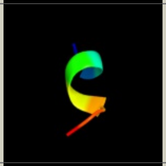
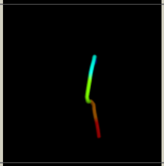
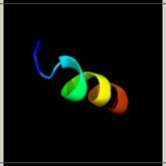
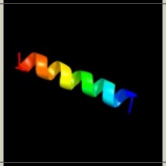
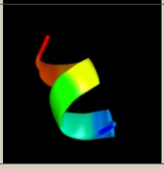
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ibpA_	Alignment		24.8	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**chromosome partition protein mukb; **PDBTitle:** the crystal structure of the dimerization domain of escherichia coli2 structural maintenance of chromosomes protein mukb
2	c3ostA_	Alignment		20.8	44	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase kcc4; **PDBTitle:** structure of the kinase associated-1 (ka1) from kcc4p
3	d1wdka2	Alignment		12.8	15	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
4	c1jb0X_	Alignment		12.4	55	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i subunit psax; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
5	d1jb0x_	Alignment		12.4	55	**Fold:**Single transmembrane helix **Superfamily:**Subunit PsaX of photosystem I reaction centre **Family:**Subunit PsaX of photosystem I reaction centre
6	c3pcqX_	Alignment		11.6	55	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i 4.8k protein; **PDBTitle:** femtosecond x-ray protein nanocrystallography
7	d1zmba1	Alignment		11.0	67	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Putative acetylxylan esterase-like
8	d1ylea1	Alignment		10.3	25	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**AstA-like
9	c2ks1B_	Alignment		9.5	58	**PDB header:**transferase **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
10	d2fiqa1	Alignment		9.4	63	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
11	d2izva1	Alignment		9.2	50	**Fold:**SOCS box-like **Superfamily:**SOCS box-like **Family:**SOCS box-like

12	c3nnqA_	Alignment		8.2	6	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**n-terminal domain of moloney murine leukemia virus **PDBTitle:** crystal structure of the n-terminal domain of moloney murine leukemia2 virus integrase, northeast structural genomics consortium target or3
13	d1hlya_	Alignment		7.9	100	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
14	d1g3nc2	Alignment		7.8	40	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
15	d1vf5g_	Alignment		7.0	64	**Fold:**Single transmembrane helix **Superfamily:**PetG subunit of the cytochrome b6f complex **Family:**PetG subunit of the cytochrome b6f complex
16	c1vf5G_	Alignment		7.0	64	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**protein pet g; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
17	d2e74g1	Alignment		6.9	64	**Fold:**Single transmembrane helix **Superfamily:**PetG subunit of the cytochrome b6f complex **Family:**PetG subunit of the cytochrome b6f complex
18	c2e76D_	Alignment		6.7	30	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
19	c2qdoC_	Alignment		6.5	67	**PDB header:**photosynthesis **Chain:** C: **PDB Molecule:**nbla protein; **PDBTitle:** nbla protein from t. vulcanus
20	c3d7vB_	Alignment		6.2	38	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** crystal structure of mcl-1 in complex with an mcl-12 selective bh3 ligand
21	c2kfdA_	Alignment	not modelled	6.1	50	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**pre-mrna-processing protein prp40; **PDBTitle:** prp40 ff4 domain
22	c1bm4A_	Alignment	not modelled	6.0	40	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (moloney murine leukemia virus capsid); **PDBTitle:** momlv capsid protein major homology region peptide analog
23	c2vy8A_	Alignment	not modelled	6.0	43	**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
24	c3io9B_	Alignment	not modelled	6.0	38	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** biml12y in complex with mcl-1
25	c3kj2B_	Alignment	not modelled	6.0	38	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** mcl-1 in complex with bim bh3 mutant f4ae
26	c2nl9B_	Alignment	not modelled	5.9	38	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** crystal structure of the mcl-1:bim bh3 complex
27	d2nysa1	Alignment	not modelled	5.9	54	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**AGR C 3712p-like
28	c2nysA_	Alignment	not modelled	5.9	54	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**agr_c_3712p; **PDBTitle:** x-ray crystal structure of protein agr_c_3712 from2 agrobacterium tumefaciens. northeast structural genomics3 consortium target atr88.

29	c3rfrI_	Alignment	not modelled	5.6	35	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
30	c2qazC_	Alignment	not modelled	5.3	31	**PDB header:**hydrolase activator **Chain:** C: **PDB Molecule:**sspb protein; **PDBTitle:** structure of c. crescentus sspb ortholog
31	d2e74b1	Alignment	not modelled	5.1	36	**Fold:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Superfamily:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)