Phyre^2

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Description	P0AB55
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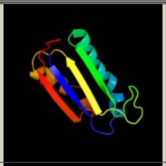
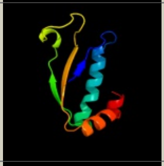
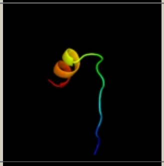
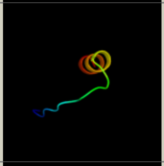
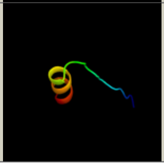
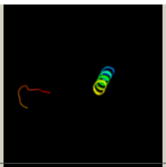
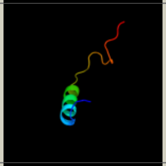
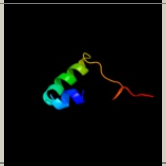
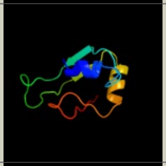
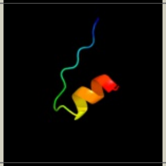
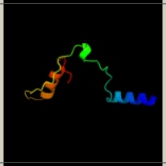
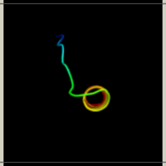
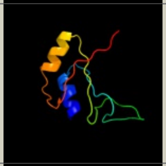
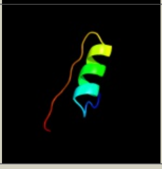
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mwqa_	Alignment		100.0	67	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YciI-like
2	d1s7ia_	Alignment		99.0	18	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**DGPF domain (Pfam 04946)
3	d1mlia_	Alignment		95.8	19	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Muconalactone isomerase, MLI
4	c3lo3E_	Alignment		58.9	23	**PDB header:**structure genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown2 protein from colwellia psychrerythraea 34h.
5	d2fiua1	Alignment		49.8	19	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Atu0297-like
6	c3dcaC_	Alignment		23.8	16	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**rpa0582; **PDBTitle:** crystal structure of the rpa0582- protein of unknown2 function from rhodopseudomonas palustris- a structural3 genomics target
7	d2f06a1	Alignment		23.2	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
8	c2dtcB_	Alignment		11.4	21	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**ral guanine nucleotide exchange factor ralgps1a; **PDBTitle:** crystal structure of ms0666
9	c2ayaA_	Alignment		10.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii subunit tau; **PDBTitle:** solution structure of the c-terminal 14 kda domain of the2 tau subunit from escherichia coli dna polymerase iii
10	d1btna_	Alignment		9.6	19	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
11	c2p0fA_	Alignment		8.3	20	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**rho gtpase-activating protein 9; **PDBTitle:** arhgap9 ph domain in complex with ins(1,3,5)p3

12	d2gp4a2	Alignment		8.3	21	**Fold:**IlvD/EDD N-terminal domain-like **Superfamily:**IlvD/EDD N-terminal domain-like **Family:**IvD/EDD N-terminal domain-like
13	c1o7dA_	Alignment		8.1	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysosomal alpha-mannosidase; **PDBTitle:** the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
14	c2wyhA_	Alignment		7.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase; **PDBTitle:** structure of the streptococcus pyogenes family gh38 alpha-2 mannosidase
15	c2dhxA_	Alignment		7.0	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase family, member 10 **PDBTitle:** solution structure of the rrm domain in the human poly (adp-2 ribose) polymerase family, member 10 variant
16	d1droa_	Alignment		6.2	10	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
17	c2e7xA_	Alignment		6.1	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**150aa long hypothetical transcriptional regulator; **PDBTitle:** structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
18	d1wjma_	Alignment		6.1	10	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
19	c2hfuB_	Alignment		6.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mevalonate kinase, putative; **PDBTitle:** crystal structure of l. major mevalonate kinase in complex2 with r-mevalonate
20	c2l4cA_	Alignment		6.0	15	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**endoplasmic reticulum resident protein 27; **PDBTitle:** solution structure of the b domain of human erp27
21	c2z0rA_	Alignment	not modelled	5.6	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0547; **PDBTitle:** crystal structure of hypothetical protein ttha0547
22	c3bsuF_	Alignment	not modelled	5.4	23	**PDB header:**hydrolase/rna/dna **Chain:** F: **PDB Molecule:**ribonuclease h1; **PDBTitle:** hybrid-binding domain of human rnase h1 in complex with 12-2 mer rna/dna
23	d1ueka2	Alignment	not modelled	5.3	25	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
24	d2coca1	Alignment	not modelled	5.3	20	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
25	c2hjdA_	Alignment	not modelled	5.2	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**quorum-sensing antiactivator; **PDBTitle:** crystal structure of a second quorum sensing antiactivator tram2 from2 a. tumefaciens strain a6
26	d1d6za3	Alignment	not modelled	5.0	18	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region