Phyre2

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Description	P45795
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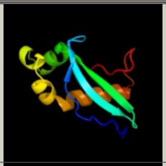
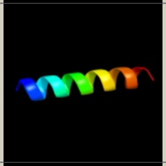
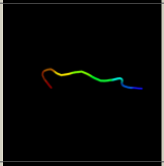
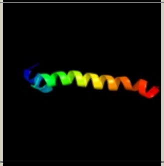
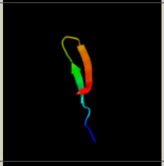
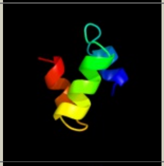
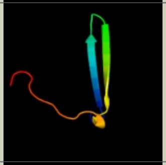
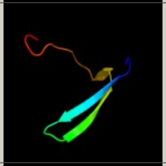
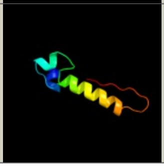
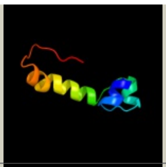
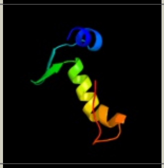
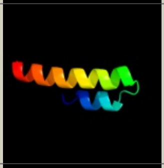
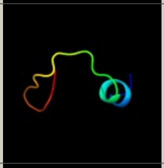
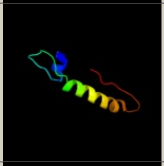
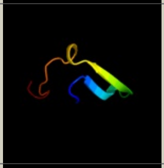
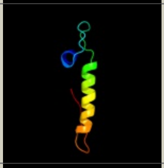
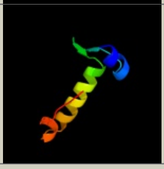
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gpia1	Alignment		100.0	33	**Fold:**Shew3726-like **Superfamily:**Shew3726-like **Family:**Shew3726-like
2	d1pd3a_	Alignment		17.6	38	**Fold:**ROP-like **Superfamily:**Nonstructural protein ns2, Nep, M1-binding domain **Family:**Nonstructural protein ns2, Nep, M1-binding domain
3	c3fhkF_	Alignment		17.0	18	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**upf0403 protein yphp; **PDBTitle:** crystal structure of apc1446, b.subtilis yphp disulfide2 isomerase
4	c2rnmC_	Alignment		16.4	22	**PDB header:**protein fibril **Chain:** C: **PDB Molecule:**small s protein; **PDBTitle:** structure of the het-s(218-289) prion in its amyloid form2 obtained by solid-state nmr
5	d3c07a1	Alignment		13.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
6	d3ctaa2	Alignment		12.4	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
7	d1ou8a_	Alignment		11.9	12	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**Stringent starvation protein B, SspB
8	c2dhyA_	Alignment		10.9	11	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cue domain-containing protein 1; **PDBTitle:** solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)
9	d1zszc1	Alignment		10.1	9	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**Stringent starvation protein B, SspB
10	d1yfna1	Alignment		9.6	12	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**Stringent starvation protein B, SspB
11	d1y67a2	Alignment		9.0	27	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain

12	d1b06a2	Alignment		8.8	24	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
13	d1wb8a2	Alignment		8.3	24	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
14	d2gyqa1	Alignment		8.0	15	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**YciF-like
15	d1s6la1	Alignment		7.8	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
16	c1p7gL_	Alignment		7.5	27	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**superoxide dismutase; **PDBTitle:** crystal structure of superoxide dismutase from pyrobaculum2 aerophilum
17	d1ou9a_	Alignment		7.1	11	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**Stringent starvation protein B, SspB
18	d1jr9a2	Alignment		6.6	21	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
19	d1q1la_	Alignment		6.0	19	**Fold:**Chorismate synthase, AroC **Superfamily:**Chorismate synthase, AroC **Family:**Chorismate synthase, AroC
20	c1gv3B_	Alignment		6.0	24	**PDB header:**manganese superoxide dismutase **Chain:** B: **PDB Molecule:**manganese superoxide dismutase; **PDBTitle:** the 2.0 angstrom resolution structure of the catalytic2 portion of a cyanobacterial membrane-bound manganese3 superoxide dismutase
21	c1ztbA_	Alignment	not modelled	5.9	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**chorismate synthase; **PDBTitle:** crystal structure of chorismate synthase from mycobacterium2 tuberculosis
22	c2cw3A_	Alignment	not modelled	5.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron superoxide dismutase; **PDBTitle:** x-ray structure of pmsod2, superoxide dismutase from2 perkinsus marinus
23	c1mngA_	Alignment	not modelled	5.4	27	**PDB header:**oxidoreductase(superoxide acceptor) **Chain:** A: **PDB Molecule:**manganese superoxide dismutase; **PDBTitle:** structure-function in e. coli iron superoxide dismutase: comparisons2 with the manganese enzyme from t. thermophilus
24	d1wgla_	Alignment	not modelled	5.3	14	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
25	d2g3qa1	Alignment	not modelled	5.1	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
26	d2bgca1	Alignment	not modelled	5.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like