Phyre^2

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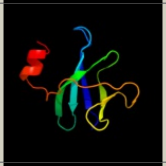
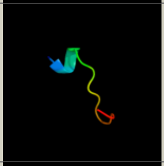
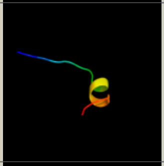
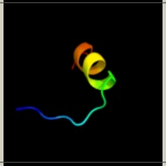
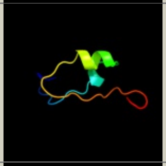
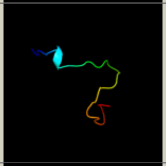
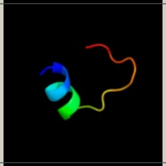
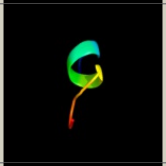
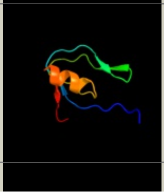
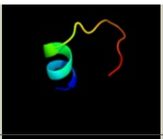
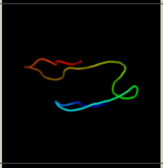
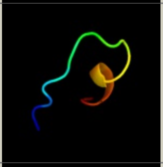
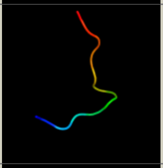
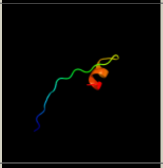
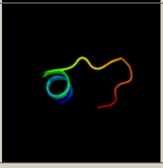
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jsoA_	Alignment		100.0	100	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**polymyxin resistance protein pmrd; **PDBTitle:** antimicrobial resistance protein
2	c2rqxA_	Alignment		100.0	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**polymyxin b resistance protein; **PDBTitle:** solution nmr structure of pmrd from klebsiella pneumoniae
3	d1lwha1	Alignment		28.7	23	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
4	c2l66B_	Alignment		22.8	47	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
5	d1v9ja_	Alignment		13.2	25	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**BolA-like **Family:**BolA-like
6	d1ny8a_	Alignment		12.1	42	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**BolA-like **Family:**BolA-like
7	d1vc4a_	Alignment		10.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
8	c3hcjB_	Alignment		9.5	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** structure of msrb from xanthomonas campestris (oxidized2 form)
9	d1hyoa2	Alignment		9.3	22	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
10	c2dhmA_	Alignment		9.0	36	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein bola; **PDBTitle:** solution structure of the bola protein from escherichia coli
11	c3anwA_	Alignment		8.7	13	**PDB header:**replication **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** a protein complex essential initiation of dna replication

12	c1hyoB_	Alignment		7.8	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fumarylacetoacetate hydrolase; **PDBTitle:** crystal structure of fumarylacetoacetate hydrolase2 complexed with 4-(hydroxymethylphosphinoyl)-3-oxo-butanoic3 acid
13	c1uijA_	Alignment		7.6	19	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**beta subunit of beta conglycinin; **PDBTitle:** crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
14	c3gdwA_	Alignment		7.5	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma-54 interaction domain protein; **PDBTitle:** crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
15	d1fx0b2	Alignment		7.5	18	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
16	c1g5vA_	Alignment		7.1	38	**PDB header:**translation **Chain:** A: **PDB Molecule:**survival motor neuron protein 1; **PDBTitle:** solution structure of the tudor domain of the human smn2 protein
17	d1m2sa_	Alignment		7.0	38	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
18	c3epsB_	Alignment		6.1	39	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase kinase/phosphatase; **PDBTitle:** the crystal structure of isocitrate dehydrogenase kinase/phosphatase2 from e. coli
19	c2vxaL_	Alignment		6.0	25	**PDB header:**flavoprotein **Chain:** L: **PDB Molecule:**dodecin; **PDBTitle:** h.halophila dodecin in complex with riboflavin
20	c3lzkC_	Alignment		6.0	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fumarylacetoacetate hydrolase family protein; **PDBTitle:** the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
21	c3o2eA_	Alignment	not modelled	5.9	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bola-like protein; **PDBTitle:** crystal structure of a bol-like protein from babesia bovis
22	d2cqaa1	Alignment	not modelled	5.8	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
23	c2kaoA_	Alignment	not modelled	5.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase b1; **PDBTitle:** structure of reduced mouse methionine sulfoxide reductase b12 (sec95cys mutant)
24	d2aw2a1	Alignment	not modelled	5.7	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
25	c1v60A_	Alignment	not modelled	5.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**riken cdna 1810037g04; **PDBTitle:** solution structure of bola1 protein from mus musculus