Phyre2

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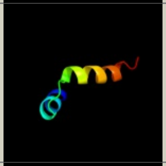
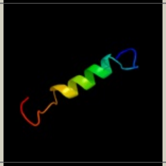
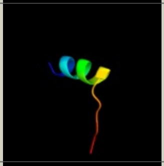
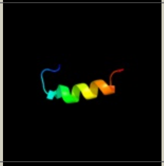
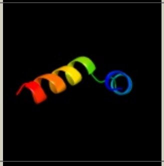
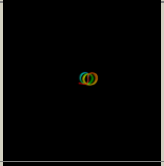
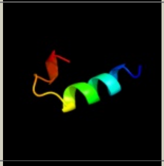
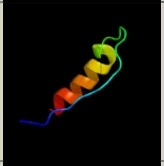
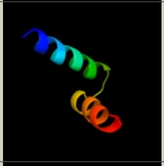
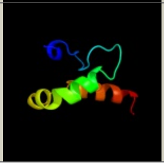
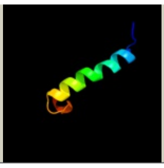
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1o98a1	Alignment		17.9	18	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
2	c2k5eA_	Alignment		17.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
3	c2qnfB_	Alignment		17.1	18	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**recombination endonuclease vii; **PDBTitle:** crystal structure of t4 endonuclease vii h43n mutant in2 complex with heteroduplex dna containing base mismatches
4	d2bbya_	Alignment		16.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding domain from rap30
5	c2iqcA_	Alignment		15.0	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fanconi anemia group f protein; **PDBTitle:** crystal structure of human fancf protein that functions in2 the assembly of a dna damage signaling complex
6	c2k53A_	Alignment		13.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**a3dk08 protein; **PDBTitle:** nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
7	d2ebfx2	Alignment		10.5	23	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**PMT domain-like
8	d5mdha1	Alignment		10.2	5	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
9	c2khzB_	Alignment		8.6	19	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**c-myc-responsive protein rcl; **PDBTitle:** solution structure of rcl
10	c3crcB_	Alignment		7.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein mazg; **PDBTitle:** crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response
11	c3s9vD_	Alignment		6.5	18	**PDB header:**lyase, isomerase **Chain:** D: **PDB Molecule:**abietadiene synthase, chloroplastic; **PDBTitle:** abietadiene synthase from abies grandis

12	c2auhB_	Alignment		5.8	39	**PDB header:**transferase/signaling protein **Chain:** B: **PDB Molecule:**growth factor receptor-bound protein 14; **PDBTitle:** crystal structure of the grb14 bps region in complex with2 the insulin receptor tyrosine kinase

13	c2vy2A_	Alignment		5.7	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein leafy; **PDBTitle:** structure of leafy transcription factor from arabidopsis2 thaliana in complex with dna from ag-i promoter