Phyre2

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Description	P08370
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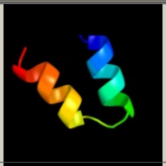
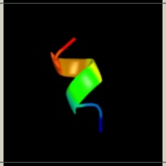
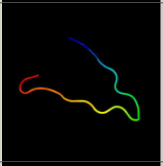
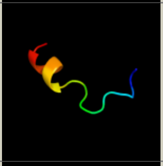
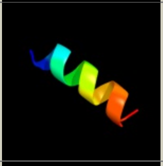
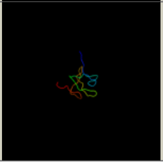
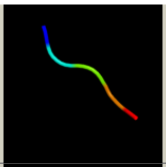
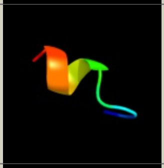
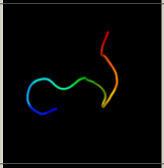
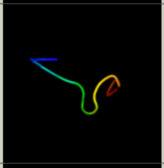
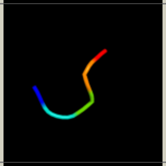
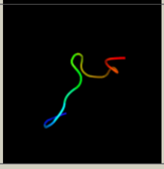
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vxgB_	Alignment		34.1	13	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**cg6181-pa, isoform a; **PDBTitle:** crystal structure of the conserved c-terminal region of ge-2 1
2	c1v06A_	Alignment		21.3	33	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**hmg box-containing protein 1; **PDBTitle:** axh domain of the transcription factor hbp1 from m.musculus
3	c2px2B_	Alignment		12.3	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**genome polyprotein [contains: capsid protein c **PDBTitle:** crystal structure of the murray valley encephalitis virus2 ns5 2'-o methyltransferase domain in complex with sah3 (monoclinic form 1)
4	c3gczA_	Alignment		11.3	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyprotein; **PDBTitle:** yokose virus methyltransferase in complex with adomet
5	c2yu1A_	Alignment		10.3	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**jmjc domain-containing histone demethylation protein 1a; **PDBTitle:** crystal structure of hjhdm1a complexed with a-ketoglutarate
6	c2ds2A_	Alignment		10.3	19	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**sweet protein mabinlin-2 chain a; **PDBTitle:** crystal structure of mabinlin ii
7	c2kixD_	Alignment		10.2	21	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**bm2 protein; **PDBTitle:** channel domain of bm2 protein from influenza b virus
8	c3n9mC_	Alignment		10.2	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** cekdm7a from c.elegans, alone
9	d1yela1	Alignment		10.0	13	**Fold:**DNA-binding pseudobarrel domain **Superfamily:**DNA-binding pseudobarrel domain **Family:**B3 DNA binding domain
10	c3evaA_	Alignment		9.6	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna-directed rna polymerase ns5; **PDBTitle:** crystal structure of yellow fever virus methyltransferase complexed2 with s-adenosyl-l-homocysteine
11	d1i94l_	Alignment		9.4	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

12	c1wazA_	Alignment		8.8	40	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** nmr structure determination of the bacterial mercury2 transporter, merf, in micelles
13	c3lkzB_	Alignment		8.8	20	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**non-structural protein 5; **PDBTitle:** structural and functional analyses of a conserved hydrophobic pocket2 of flavivirus methyltransferase
14	d2p41a1	Alignment		8.5	40	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap methylase
15	c2jo1A_	Alignment		7.5	25	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
16	c2jp3A_	Alignment		7.3	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
17	d1s3ga2	Alignment		7.0	21	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
18	d1zina2	Alignment		6.7	21	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
19	c2h3oA_	Alignment		6.6	40	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** structure of merft, a membrane protein with two trans-2 membrane helices
20	d1p3ja2	Alignment		6.5	29	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
21	d2uubl1	Alignment	not modelled	6.1	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
22	d1t1ra3	Alignment	not modelled	6.1	75	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
23	c3pu3A_	Alignment	not modelled	5.7	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 2; **PDBTitle:** phf2 jumonji domain-nog complex
24	d1xvha1	Alignment	not modelled	5.7	22	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**GA module, an albumin-binding domain
25	d2qall1	Alignment	not modelled	5.6	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
26	c3pesA_	Alignment	not modelled	5.5	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein gp49; **PDBTitle:** crystal structure of uncharacterized protein from pseudomonas phage2 yua
27	c1ujlA_	Alignment	not modelled	5.5	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily h **PDBTitle:** solution structure of the herg k+ channel s5-p2 extracellular linker
28	c2p3qA_	Alignment	not modelled	5.3	50	**PDB header:**viral protein,transferase **Chain:** A: **PDB Molecule:**type ii methyltransferase; **PDBTitle:** crystal structure of dengue methyltransferase in complex with gpppg2 and s-adenosyl-l-homocysteine

29	d1akya2	Alignment	not modelled	5.2	29	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
30	c3kv5D_	Alignment	not modelled	5.2	33	**PDB header:**h3k4me3 binding protein, transferase **Chain:** D: **PDB Molecule:**jmjc domain-containing histone demethylation **PDBTitle:** structure of kiaa1718, human jumonji demethylase, in complex2 with n-oxalylglycine
31	c3alrA_	Alignment	not modelled	5.1	33	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**nanos protein; **PDBTitle:** crystal structure of nanos