Phyre^2

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Description	P0AFH6
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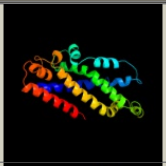
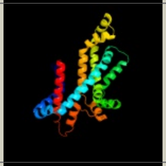
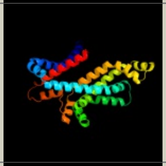
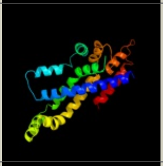
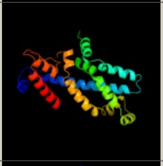
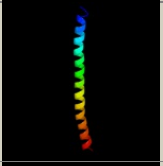
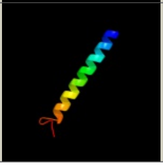
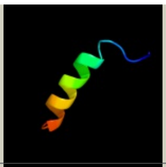
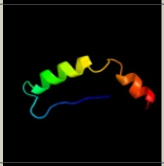
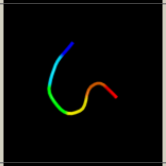
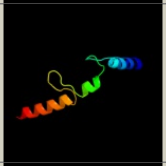
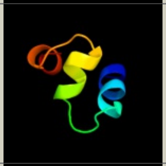
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3dhwa1	Alignment		99.9	18	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
2	c2onkC_	Alignment		99.9	16	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
3	d2onkc1	Alignment		99.9	16	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
4	d3d31c1	Alignment		99.8	19	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
5	c3d31D_	Alignment		99.8	19	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
6	c3fh6F_	Alignment		99.8	11	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** crystal structure of the resting state maltose transporter from e.2 coli
7	d2r6gf2	Alignment		99.8	12	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
8	d2r6gg1	Alignment		99.8	12	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
9	c2r6gF_	Alignment		99.8	13	**PDB header:**hydrolase/transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** the crystal structure of the e. coli maltose transporter
10	c3hd7A_	Alignment		44.2	12	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
11	c2jwaA_	Alignment		18.7	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure

12	c2kc8B_	Alignment		11.9	27	**PDB header:**toxin/toxin repressor **Chain:** B: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of e. coli toxin rele (r81a/r83a) mutant in2 complex with antitoxin relbc (k47-l79) peptide
13	d1pjqa3	Alignment		10.2	24	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
14	c1wz4A_	Alignment		9.4	67	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**major surface antigen; **PDBTitle:** solution conformation of adr subtype hbv pre-s2 epitope
15	c3k8pC_	Alignment		8.1	46	**PDB header:**transport protein/transport protein **Chain:** C: **PDB Molecule:**dsl1; **PDBTitle:** structural basis for vesicle tethering by the dsl1 complex
16	c1umqA_	Alignment		7.4	6	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein; **PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
17	d1umqa_	Alignment		7.4	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
18	c1zrtD_	Alignment		7.4	14	**PDB header:**oxidoreductase/metal transport **Chain:** D: **PDB Molecule:**cytochrome c1; **PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
19	d1ntca_	Alignment		6.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
20	c2pcoA_	Alignment		6.0	33	**PDB header:**toxin **Chain:** A: **PDB Molecule:**latarcin-1; **PDBTitle:** spatial structure and membrane permeabilization for2 latarcin-1, a spider antimicrobial peptide
21	d1g2ha_	Alignment	not modelled	6.0	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
22	d1fipa_	Alignment	not modelled	5.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
23	d2axtk1	Alignment	not modelled	5.1	16	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein K, PsbK **Family:**PsbK-like
24	d1q7ha2	Alignment	not modelled	5.1	17	**Fold:**Cystatin-like **Superfamily:**Pre-PUA domain **Family:**Hypothetical protein Ta1423, N-terminal domain
25	c3a0hk_	Alignment	not modelled	5.1	24	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of i-substituted photosystem ii complex