Phyre2

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Description	P0AFH2
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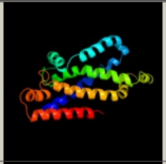
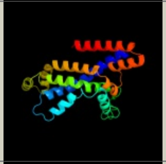
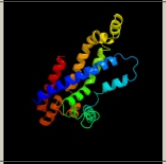
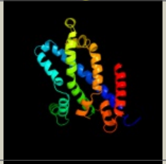
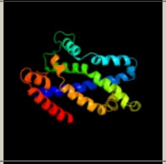
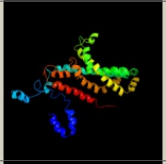
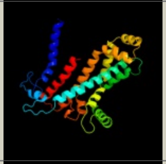
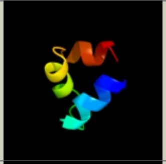
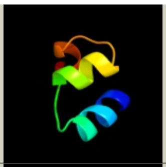
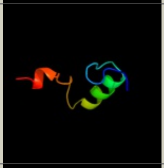
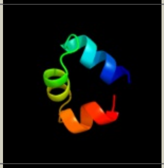
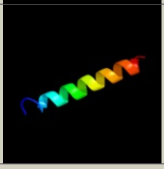
Unique Job ID	902dc12a6339784c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3dhwa1	Alignment		99.9	17	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
2	c3d31D_	Alignment		99.9	18	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
3	d3d31c1	Alignment		99.9	18	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
4	d2onkc1	Alignment		99.9	15	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
5	c2onkC_	Alignment		99.9	15	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
6	d2r6gf2	Alignment		99.8	13	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
7	c2r6gF_	Alignment		99.7	12	**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
8	c3fh6F_	Alignment		99.7	12	**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
9	d2r6gg1	Alignment		99.5	15	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	d1ntca_	Alignment		24.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
11	c1wz4A_	Alignment		23.7	44	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**major surface antigen; **PDBTitle:** solution conformation of adr subtype hbv pre-s2 epitope

12	c1umqA_	Alignment		17.7	19	**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
13	d1umqa_	Alignment		17.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
14	d1n0ua5	Alignment		17.3	11	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
15	d1fipa_	Alignment		13.9	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
16	d1etob_	Alignment		13.8	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
17	c2cw1A_	Alignment		11.0	39	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein
18	c3e7lD_	Alignment		10.7	15	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
19	c2ka1A_	Alignment		9.8	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
20	c2ka2B_	Alignment		9.8	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
21	c2ka1B_	Alignment	not modelled	9.8	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
22	c2ka2A_	Alignment	not modelled	9.8	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
23	d1wpga4	Alignment	not modelled	9.4	22	**Fold:**Calcium ATPase, transmembrane domain M **Superfamily:**Calcium ATPase, transmembrane domain M **Family:**Calcium ATPase, transmembrane domain M
24	c2jwaA_	Alignment	not modelled	8.5	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
25	d1g2ha_	Alignment	not modelled	8.1	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
26	d1etxa_	Alignment	not modelled	7.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
27	c2j5dA_	Alignment	not modelled	7.7	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** nmr structure of bnip3 transmembrane domain in lipid2 bicelles
						PDB header:transmembrane protein

28	c1ciiA_	Alignment	not modelled	7.0	15	**Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
29	d1tdpa_	Alignment	not modelled	6.9	5	**Fold:**Bromodomain-like **Superfamily:**Bacteriocin immunity protein-like **Family:**Carnobacteriocin B2 immunity protein