Phyre^2

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Description	P77308
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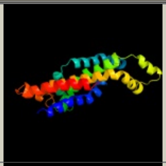
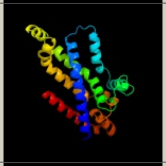
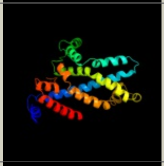
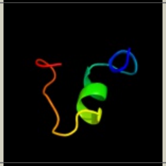
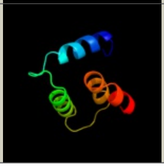
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3dhwa1	Alignment		99.9	22	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
2	c2onkC_	Alignment		99.8	14	**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		99.8	14	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
4	d3d31c1	Alignment		99.8	18	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
5	c3d31D_	Alignment		99.8	18	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
6	d2r6gf2	Alignment		99.7	14	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
7	c3fh6F_	Alignment		99.7	14	**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
8	c2r6gF_	Alignment		99.6	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
9	d2r6gg1	Alignment		99.3	13	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	c2cw1A_	Alignment		27.6	36	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein
11	c1ciiA_	Alignment		24.0	11	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia

12	c2ka2A_	Alignment		19.1	36	**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
13	c2ka1B_	Alignment		19.1	36	**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
14	c2ka1A_	Alignment		19.1	36	**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
15	c2ka2B_	Alignment		19.1	36	**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
16	d1a9xa1	Alignment		14.6	14	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
17	c1wz4A_	Alignment		14.3	33	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**major surface antigen; **PDBTitle:** solution conformation of adr subtype hbv pre-s2 epitope
18	c2j5dA_	Alignment		13.1	36	**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
19	c1y66D_	Alignment		10.8	33	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**engrailed homeodomain; **PDBTitle:** dioxane contributes to the altered conformation and2 oligomerization state of a designed engrailed homeodomain3 variant
20	c2b9sB_	Alignment		9.2	63	**PDB header:**isomerase/dna **Chain:** B: **PDB Molecule:**dna topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
21	c2l6pA_	Alignment	not modelled	8.4	15	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**phac1, phac2 and phad genes; **PDBTitle:** nmr solution structure of the protein np_253742.1
22	d1g2ha_	Alignment	not modelled	7.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
23	d1umqa_	Alignment	not modelled	6.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
24	c1umqA_	Alignment	not modelled	6.8	15	**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
25	c2l6nA_	Alignment	not modelled	6.7	15	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yp_001092504.1; **PDBTitle:** nmr solution structure of the protein yp_001092504.1
26	d1etob_	Alignment	not modelled	6.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
27	d1fipa_	Alignment	not modelled	5.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
28	d1tc3c_	Alignment	not modelled	5.6	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain