Phyre2

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Description	P14176
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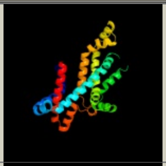
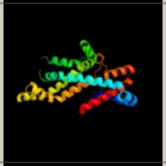
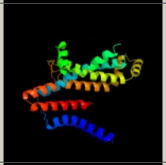
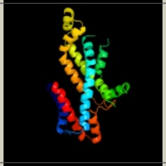
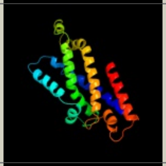
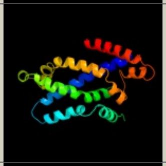
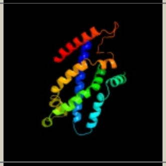
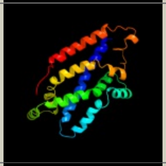
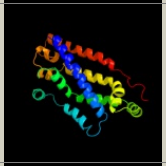
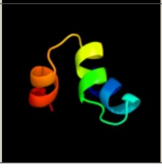
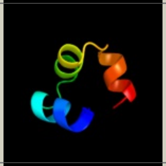
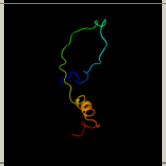
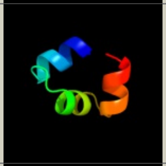
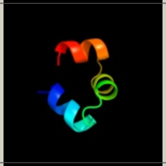
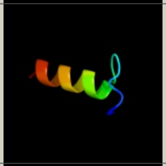
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2onkC_	Alignment		99.9	19	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
2	d2onkc1	Alignment		99.9	19	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
3	c3d31D_	Alignment		99.9	20	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
4	d3d31c1	Alignment		99.9	20	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
5	d3dhwa1	Alignment		99.9	27	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
6	c2r6gF_	Alignment		99.9	25	**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
7	d2r6gf2	Alignment		99.9	24	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
8	c3fh6F_	Alignment		99.9	24	**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		99.8	19	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	d1ntca_	Alignment		36.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
11	d1umqa_	Alignment		29.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like

12	c1umqA_	Alignment		29.5	10	**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	d1fipa_	Alignment		18.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
14	d2gqba1	Alignment		17.7	11	**Fold:**RPA2825-like **Superfamily:**RPA2825-like **Family:**RPA2825-like
15	d1etob_	Alignment		17.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
16	c3e7lD_	Alignment		15.6	13	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
17	d1etxa_	Alignment		14.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
18	c3hzqA_	Alignment		12.6	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** structure of a tetrameric mscl in an expanded intermediate2 state
19	c3bjrA_	Alignment		11.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative carboxylesterase; **PDBTitle:** crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcfs1 at 2.09 a resolution
20	c3a0bk_	Alignment		9.8	27	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
21	c3a0bK_	Alignment	not modelled	9.8	27	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
22	c2jwaA_	Alignment	not modelled	9.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
23	d1g2ha_	Alignment	not modelled	9.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
24	c3k3gA_	Alignment	not modelled	8.7	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**urea transporter; **PDBTitle:** crystal structure of the urea transporter from desulfovibrio vulgaris2 bound to 1,3-dimethylurea
25	c3a0hk_	Alignment	not modelled	8.4	27	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
26	d2axtk1	Alignment	not modelled	6.6	25	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein K, PsbK **Family:**PsbK-like
27	c2ka1B_	Alignment	not modelled	6.5	32	**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
28	c2ka1A_	Alignment	not modelled	6.5	32	**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

29	c2ka2A_	Alignment	not modelled	6.5	32	**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
30	c2ka2B_	Alignment	not modelled	6.5	32	**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
31	c2x7lP_	Alignment	not modelled	6.2	33	**PDB header:**immune system **Chain:** P: **PDB Molecule:**hiv rev; **PDBTitle:** implications of the hiv-1 rev dimer structure at 3.2a2 resolution for multimeric binding to the rev response3 element
32	d1iwga8	Alignment	not modelled	5.9	14	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
33	c1p58C_	Alignment	not modelled	5.6	16	**PDB header:**virus **Chain:** C: **PDB Molecule:**major envelope protein e; **PDBTitle:** complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
34	c2j5dA_	Alignment	not modelled	5.4	32	**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