Phyre^2

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Description	P0AEB0
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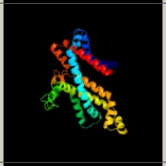
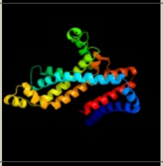
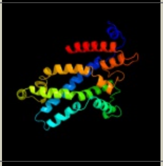
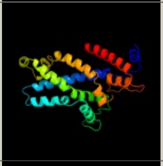
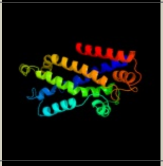
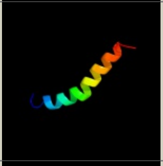
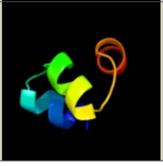
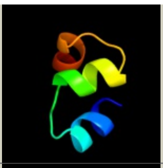
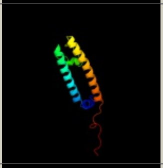
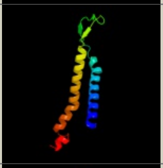
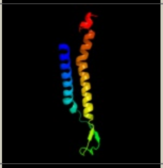
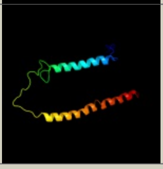
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fh6F_	Alignment		100.0	15	**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
2	c2onkC_	Alignment		100.0	24	**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		100.0	24	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
4	d3d31c1	Alignment		100.0	27	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
5	c3d31D_	Alignment		100.0	27	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
6	c2r6gF_	Alignment		100.0	20	**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	d2r6gg1	Alignment		100.0	22	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
8	d2r6gf2	Alignment		100.0	19	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
9	d3dhwa1	Alignment		99.9	14	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	d2r6gf1	Alignment		75.9	24	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
11	c1umqA_	Alignment		38.8	13	**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

12	d1umqa_	Alignment		38.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
13	d1ntca_	Alignment		35.3	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
14	c2qksA_	Alignment		31.7	8	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**kir3.1-prokaryotic kir channel chimera; **PDBTitle:** crystal structure of a kir3.1-prokaryotic kir channel chimera
15	d1fipa_	Alignment		30.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
16	c2oarA_	Alignment		27.5	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
17	d2oara1	Alignment		26.1	10	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
18	d1etob_	Alignment		25.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
19	d1etxa_	Alignment		23.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
20	d1pf4a2	Alignment		19.3	14	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
21	c3rkoF_	Alignment	not modelled	18.1	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nadh-quinone oxidoreductase subunit j; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
22	c2hx6A_	Alignment	not modelled	16.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb
23	c3e7lD_	Alignment	not modelled	15.4	9	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
24	d1g2ha_	Alignment	not modelled	14.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
25	d1fftb2	Alignment	not modelled	13.8	17	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
26	c2jwaA_	Alignment	not modelled	12.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
27	c3qnqD_	Alignment	not modelled	9.0	14	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
						PDB header:metal transport **Chain:** B: **PDB Molecule:**integral membrane channel and cytosolic

28	c1p7bB_	Alignment	not modelled	8.0	7	domains; **PDBTitle:** crystal structure of an inward rectifier potassium channel
29	c2kncA_	Alignment	not modelled	6.3	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
30	c2cw1A_	Alignment	not modelled	5.7	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein
31	c1ztoA_	Alignment	not modelled	5.7	33	**PDB header:**potassium channel **Chain:** A: **PDB Molecule:**potassium channel protein rck4; **PDBTitle:** inactivation gate of potassium channel rck4, nmr, 82 structures