Phyre2

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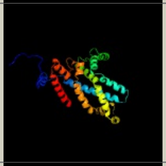
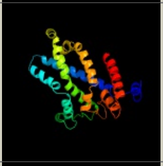
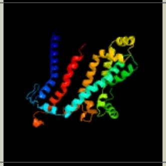
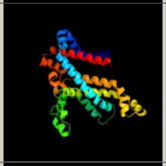
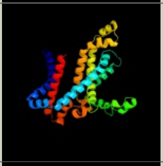
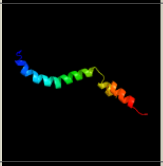
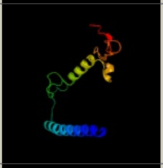
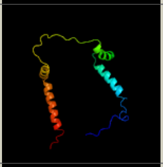
Description	RVBD2835c_(ugpA)_3141321_3142232
Date	Wed Aug 7 12:50:50 BST 2019
Unique Job ID	70fcc171d093ec04

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fh6F_	Alignment		100.0	25	**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	c4tqvI_	Alignment		100.0	21	**PDB header:**transport protein **Chain:** I: **PDB Molecule:**algm1; **PDBTitle:** crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
3	c2r6gF_	Alignment		100.0	27	**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
4	d2r6gg1	Alignment		100.0	19	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
5	d2r6gf2	Alignment		100.0	27	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
6	c4tqvJ_	Alignment		100.0	15	**PDB header:**transport protein **Chain:** J: **PDB Molecule:**algm2; **PDBTitle:** crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
7	c2onkC_	Alignment		100.0	20	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
8	d2onkc1	Alignment		100.0	20	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
9	d3d31c1	Alignment		100.0	19	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	c3d31D_	Alignment		100.0	19	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease protein; **PDBTitle:** modbc from methanosarcina acetivorans
11	c4ymuC_	Alignment		100.0	15	**PDB header:**protein binding/transport protein **Chain:** C: **PDB Molecule:**abc-type amino acid transport system, permease component; **PDBTitle:** crystal structure of an amino acid abc transporter complex with2 arginines and atps

12	d3dhwa1	Alignment		99.9	18	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
13	d2r6gf1	Alignment		95.9	21	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
14	c5kbuA_	Alignment		61.5	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glutamate receptor 2,voltage-dependent calcium channel **PDBTitle:** cryo-em structure of glua2-2xstz complex at 7.8 angstrom resolution
15	c4l5eA_	Alignment		33.8	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of a. aeolicus ntrc1 dna binding domain
16	c2m8gX_	Alignment		31.3	19	**PDB header:**transcription **Chain:** X: **PDB Molecule:**transcriptional regulator; **PDBTitle:** structure, function, and tethering of dna-binding domains in 542 transcriptional activators
17	c1umqA_	Alignment		28.4	16	**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
18	d1umqa_	Alignment		28.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
19	c6gcs6_	Alignment		26.2	8	**PDB header:**oxidoreductase **Chain:** 6: **PDB Molecule:**nd6 subunit (nu6m); **PDBTitle:** cryo-em structure of respiratory complex i from yarrowia lipolytica
20	d1fipa_	Alignment		25.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
21	d1ntca_	Alignment	not modelled	24.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
22	c2hx6A_	Alignment	not modelled	21.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb
23	d1etob_	Alignment	not modelled	20.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
24	d1etxa_	Alignment	not modelled	20.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
25	c3e7lD_	Alignment	not modelled	19.9	23	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
26	c1g2hA_	Alignment	not modelled	16.7	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein tyrr homolog; **PDBTitle:** solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
27	d1g2ha_	Alignment	not modelled	16.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
28	c1ojlD_	Alignment	not modelled	14.4	29	**PDB header:**response regulator **Chain:** D: **PDB Molecule:**transcriptional regulatory protein zrar; **PDBTitle:** crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding

29	c5m7nA_	Alignment	not modelled	14.0	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nitrogen assimilation regulatory protein; **PDBTitle:** crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
30	c6c14A_	Alignment	not modelled	8.9	13	**PDB header:**membrane protein, metal transport **Chain:** A: **PDB Molecule:**protocadherin-15; **PDBTitle:** cryoem structure of mouse pcdh15-1ec-lhfpl5 complex
31	c2cw1A_	Alignment	not modelled	7.3	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein
32	c3ipdB_	Alignment	not modelled	5.4	3	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
33	c2w6jH_	Alignment	not modelled	5.3	45	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**f1-atpase delta subunit; **PDBTitle:** low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 5.
34	c2kogA_	Alignment	not modelled	5.1	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** lipid-bound synaptobrevin solution nmr structure
35	c3wg7T_	Alignment	not modelled	5.0	15	**PDB header:**oxidoreductase **Chain:** T: **PDB Molecule:**cytochrome c oxidase subunit 6a2, mitochondrial; **PDBTitle:** a 1.9 angstrom radiation damage free x-ray structure of large (420kda)2 protein by femtosecond crystallography