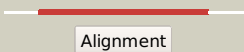

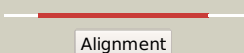

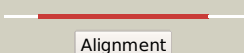

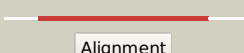





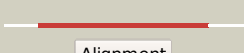

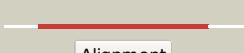
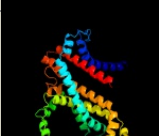

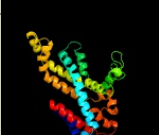



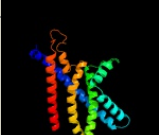











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2316_(uspA)_2588848_2589720
Date	Mon Aug 5 13:25:46 BST 2019
Unique Job ID	82ef472e8d9734cd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fh6F_	 Alignment		100.0	26	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	c4tqv1_	 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	30	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	17	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
5	c4tqv1_	 Alignment		100.0	17	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
6	d2r6gf2	 Alignment		100.0	30	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
7	d2onkc1	 Alignment		100.0	20	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
8	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
9	d3d31c1	 Alignment		100.0	17	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	c3d31D_	 Alignment		100.0	17	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	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
13	d2r6gf1	Alignment		94.7	22	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
14	c5kbuA	Alignment		79.2	11	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	c2hx6A	Alignment		39.0	23	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb
16	c2m8gX	Alignment		20.4	23	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
17	c4l5eA	Alignment		20.2	13	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
18	d1umqa	Alignment		18.5	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
19	c1umqA	Alignment		18.5	6	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
20	d1fipa	Alignment		16.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
21	d1ntca	Alignment	not modelled	14.5	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
22	d1etob	Alignment	not modelled	14.4	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
23	d1etxa	Alignment	not modelled	13.0	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
24	c3e7ID	Alignment	not modelled	11.3	19	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
25	c1g2hA	Alignment	not modelled	10.9	10	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
26	d1g2ha	Alignment	not modelled	10.9	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
27	c6gcs6	Alignment	not modelled	9.4	10	PDB header: oxidoreductase Chain: 6: PDB Molecule: nd6 subunit (nu6m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
28	c1ojID	Alignment	not modelled	9.3	23	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	c3wg7T_	Alignment	not modelled	7.8	15	<p>PDB header:oxidoreductase</p> <p>Chain: T; PDB Molecule:cytochrome c oxidase subunit 6a2, mitochondrial;</p> <p>PDBTitle: a 1.9 angstrom radiation damage free x-ray structure of large (420kda)2 protein by femtosecond crystallography</p>
30	c5m7nA_	Alignment	not modelled	7.6	13	<p>PDB header:signaling protein</p> <p>Chain: A; PDB Molecule:nitrogen assimilation regulatory protein;</p> <p>PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology</p>
31	d1v54g_	Alignment	not modelled	6.9	15	<p>Fold:Single transmembrane helix</p> <p>Superfamily:Mitochondrial cytochrome c oxidase subunit VIa</p> <p>Family:Mitochondrial cytochrome c oxidase subunit VIa</p>
32	d1brwa3	Alignment	not modelled	6.6	25	<p>Fold:alpha/beta-Hammerhead</p> <p>Superfamily:Pyrimidine nucleoside phosphorylase C-terminal domain</p> <p>Family:Pyrimidine nucleoside phosphorylase C-terminal domain</p>