






















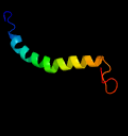









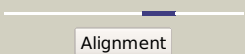
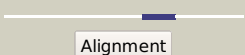
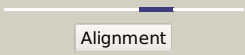
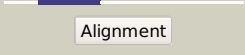
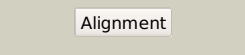
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1236_(sugA)_1378933_1379856
Date	Wed Jul 31 22:05:32 BST 2019
Unique Job ID	94237a3450e9e2a4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fh6F_	 Alignment		100.0	20	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	22	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	d2r6gg1	 Alignment		100.0	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
4	c2r6gF_	 Alignment		100.0	23	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
5	c4tqvI_	 Alignment		100.0	18	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	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
7	d2onkc1	 Alignment		100.0	20	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
8	d2r6gf2	 Alignment		100.0	23	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
9	d3d31c1	 Alignment		100.0	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	c3d31D_	 Alignment		100.0	16	PDB header: transport protein Chain: D; PDB Molecule: sulfate/molybdate abc transporter, permease protein; PDBTitle: modbc from methanosarcina acetivorans
11	c4ymuC_	 Alignment		100.0	16	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		100.0	20	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
13	d2r6gf1	Alignment		96.6	11	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
14	c5kbuA	Alignment		67.2	12	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	c5iwsA	Alignment		52.7	15	PDB header: transferase Chain: A: PDB Molecule: protein-n(pi)-phosphohistidine-sugar phosphotransferase PDBTitle: crystal structure of the transporter malt, the eic domain from the2 maltose-specific phosphotransferase system
16	c2m8gX	Alignment		41.1	16	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		33.4	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		31.4	3	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
19	c1umqA	Alignment		31.4	3	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	d1ntca	Alignment		27.7	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
21	c2hx6A	Alignment	not modelled	21.4	12	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb
22	d1fipa	Alignment	not modelled	21.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
23	d1etob	Alignment	not modelled	18.9	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
24	c3e7lD	Alignment	not modelled	16.9	23	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
25	d1etxa	Alignment	not modelled	16.7	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
26	c1g2hA	Alignment	not modelled	11.0	27	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	11.0	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
28	c6gcs6	Alignment	not modelled	9.6	12	PDB header: oxidoreductase Chain: 6: PDB Molecule: nd6 subunit (nu6m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica

29	c1ojlD_	 Alignment	not modelled	8.1	26	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
30	c5m7nA_	 Alignment	not modelled	7.9	19	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
31	c2cw1A_	 Alignment	not modelled	7.4	27	PDB header: de novo protein Chain: A; PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein
32	c6iiuA_	 Alignment	not modelled	5.7	11	PDB header: signaling protein Chain: A; PDB Molecule: soluble cytochrome b562,thromboxane a2 receptor,rubredoxin, PDBTitle: crystal structure of the human thromboxane a2 receptor bound to2 ramatroban
33	c2oarA_	 Alignment	not modelled	5.2	8	PDB header: membrane protein Chain: A; PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: mechanosensitive channel of large conductance (mscl)