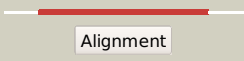

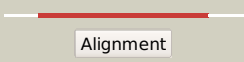

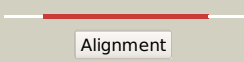

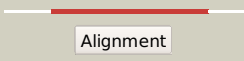

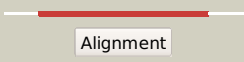

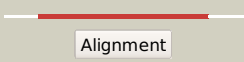

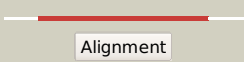

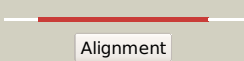

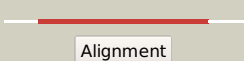

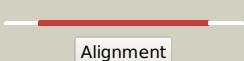

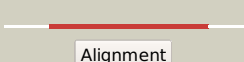
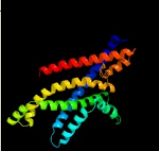


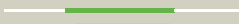








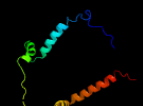





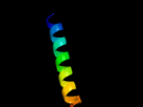

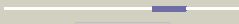

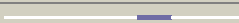


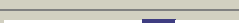



Phyre2

Email: mdejesus@rockefeller.edu
 Description: RVBD0929_(pstC2)_1036032_1037006
 Date: Fri Jul 26 01:50:52 BST 2019
 Unique Job ID: 6fa6d6c17d1f8aac

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fh6F_	 Alignment		100.0	12	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	13	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	15	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	d2r6gf2	 Alignment		100.0	13	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
5	c4tqvI_	 Alignment		100.0	14	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	d2r6gg1	 Alignment		100.0	14	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
7	c2onkC_	 Alignment		100.0	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
8	d2onkc1	 Alignment		100.0	19	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
9	d3d31c1	 Alignment		100.0	15	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	c3d31D_	 Alignment		100.0	15	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		99.9	23	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
13	c5kbuA	 Alignment		58.8	27	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
14	c2m8gX	 Alignment		28.1	23	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
15	c1umqA	 Alignment		22.1	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
16	d1umqa	 Alignment		22.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
17	c6gcs6	 Alignment		18.5	9	PDB header: oxidoreductase Chain: 6: PDB Molecule: nd6 subunit (nu6m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
18	c4l5eA	 Alignment		18.1	13	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
19	d1ntca	 Alignment		17.7	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
20	c2momB	 Alignment		14.8	18	PDB header: membrane protein Chain: B: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
21	c2momC	 Alignment	not modelled	14.8	18	PDB header: membrane protein Chain: C: PDB Molecule: lysosome-associated membrane glycoprotein 2; PDBTitle: structural insights of tm domain of lamp-2a in dpc micelles
22	c3wg7T	 Alignment	not modelled	14.7	12	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
23	d1v54g	 Alignment	not modelled	14.1	12	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIa Family: Mitochondrial cytochrome c oxidase subunit VIa
24	c2hx6A	 Alignment	not modelled	12.2	27	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb
25	d1fipa	 Alignment	not modelled	11.9	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
26	d1etob	 Alignment	not modelled	11.5	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
27	d1etxa	 Alignment	not modelled	9.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
28	c4qiWT	 Alignment	not modelled	8.8	29	PDB header: transcription Chain: T: PDB Molecule: dna-directed rna polymerase subunit k; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis

29	c3e7ID_	Alignment	not modelled	8.7	16	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
30	c1twcF_	Alignment	not modelled	8.0	29	PDB header: transcription Chain: F: PDB Molecule: dna-directed rna polymerases i, ii, and iii 23 PDBTitle: rna polymerase ii complexed with gtp
31	d1twff_	Alignment	not modelled	7.9	29	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RPB6
32	c2pmzW_	Alignment	not modelled	7.7	21	PDB header: translation, transferase Chain: W: PDB Molecule: dna-directed rna polymerase subunit k; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
33	c1g2hA_	Alignment	not modelled	6.6	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
34	d1g2ha_	Alignment	not modelled	6.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
35	d1qkla_	Alignment	not modelled	6.5	29	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RPB6
36	c4xnwC_	Alignment	not modelled	5.7	8	PDB header: transport protein Chain: C: PDB Molecule: p2y purinoceptor 1,rubredoxin,p2y purinoceptor 1; PDBTitle: the human p2y1 receptor in complex with mrs2500
37	d1cf7a_	Alignment	not modelled	5.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cell cycle transcription factor e2f-dp
38	c6hwhB_	Alignment	not modelled	5.5	18	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron- sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
39	c3h0gF_	Alignment	not modelled	5.4	29	PDB header: transcription Chain: F: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc2; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
40	d2ns0a1	Alignment	not modelled	5.2	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
41	c1pyuD_	Alignment	not modelled	5.1	23	PDB header: lyase Chain: D: PDB Molecule: aspartate 1-decarboxylase alfa chain; PDBTitle: processed aspartate decarboxylase mutant with ser25 mutated to cys