

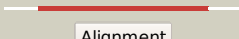

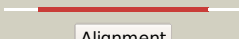
















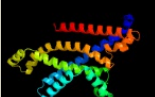
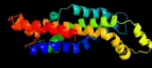

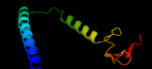








Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1858 (modB)_2105780_2106574
 Date Fri Aug 2 13:30:47 BST 2019
 Unique Job ID 44fcac2c68e14438

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	d3d31c1	 Alignment		100.0	30	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
3	c3d31D_	 Alignment		100.0	30	PDB header: transport protein Chain: D; PDB Molecule: sulfate/molybdate abc transporter, permease protein; PDBTitle: modbc from methanosarcina acetivorans
4	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
5	c3fh6F_	 Alignment		100.0	21	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
6	c2onkC_	 Alignment		100.0	30	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	30	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
8	d2r6gf2	 Alignment		100.0	18	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
9	d2r6gg1	 Alignment		100.0	22	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	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
11	c4ymuC_	 Alignment		100.0	14	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	15	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
13	c2m8gX	Alignment		57.9	19	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
14	c5kbuA	Alignment		57.9	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
15	c4l5eA	Alignment		57.7	13	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
16	d1umqa	Alignment		54.1	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
17	c1umqA	Alignment		54.1	10	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	d1fipa	Alignment		52.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
19	d1ntca	Alignment		51.7	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
20	d1etob	Alignment		48.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
21	c2jwaA	Alignment	not modelled	48.3	26	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: erbB2 transmembrane segment dimer spatial structure
22	c2ks1A	Alignment	not modelled	46.2	26	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: heterodimeric association of transmembrane domains of erbB1 and erbB2 receptors enabling kinase activation
23	d1etxa	Alignment	not modelled	41.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
24	c3e7ID	Alignment	not modelled	38.0	16	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
25	d1g2ha	Alignment	not modelled	27.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
26	c1g2hA	Alignment	not modelled	27.5	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	c5m7nA	Alignment	not modelled	24.1	13	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
28	c2hx6A	Alignment	not modelled	21.1	12	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42

					endoribonuclease regb
29	c1ojlD_	Alignment	not modelled	19.0	19 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	c2n2aA_	Alignment	not modelled	16.5	28 PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: spatial structure of her2/erbB2 dimeric transmembrane domain in the2 presence of cytoplasmic jxtamembrane domains
31	c2cw1A_	Alignment	not modelled	11.2	27 PDB header: de novo protein Chain: A: PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein
32	d2r6gf1	Alignment	not modelled	10.5	24 Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
33	c2momC_	Alignment	not modelled	7.5	19 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
34	c2momB_	Alignment	not modelled	7.5	19 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