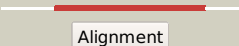



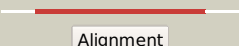





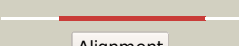











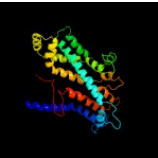

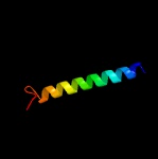
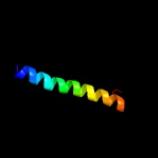
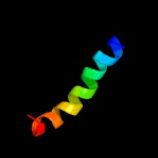



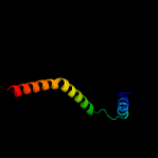




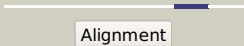
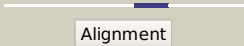
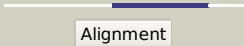

Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1282c_oppC_1435274_1436149
 Date Wed Jul 31 22:05:37 BST 2019
 Unique Job ID 77e3b86447d25203

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ymuC_	 Alignment		99.9	7	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
2	c4tqvI_	 Alignment		99.9	10	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	c3fh6F_	 Alignment		99.9	10	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
4	c2onkC_	 Alignment		99.9	15	PDB header: membrane protein Chain: C; PDB Molecule: solybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
5	d2onkc1	 Alignment		99.9	15	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
6	d3dhwa1	 Alignment		99.9	17	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
7	d3d31c1	 Alignment		99.9	17	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
8	c3d31D_	 Alignment		99.9	17	PDB header: transport protein Chain: D; PDB Molecule: sulfate/molybdate abc transporter, permease protein; PDBTitle: modbc from methanosarcina acetivorans
9	d2r6gf2	 Alignment		99.9	13	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	c4tqvI_	 Alignment		99.9	11	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	c2r6gF_	 Alignment		99.9	13	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

12	d2r6gg1	Alignment		99.9	12	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
13	c5kbuA	Alignment		96.3	18	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	c2jwaA	Alignment		24.6	9	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: erbB2 transmembrane segment dimer spatial structure
15	c2ks1A	Alignment		24.6	9	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
16	c2nd4A	Alignment		21.6	25	PDB header: hydrolase receptor Chain: A: PDB Molecule: amylase-binding protein abpa; PDBTitle: a distinct sortase srtB anchors and processes a streptococcal adhesin2 abpa with a novel structural property
17	c6o7xa	Alignment		16.3	10	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
18	c5gasN	Alignment		13.5	16	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
19	c3k07A	Alignment		10.9	15	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
20	c6b8hb	Alignment		10.7	10	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit alpha, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer
21	c2b9sB	Alignment	not modelled	10.4	23	PDB header: isomerase/dna Chain: B: PDB Molecule: dna topoisomerase i-like protein; PDBTitle: crystal structure of heterodimeric l. donovani topoisomerase i-2 vanadate-dna complex
22	c1umqA	Alignment	not modelled	10.1	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
23	d1umqa	Alignment	not modelled	10.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
24	c2lonA	Alignment	not modelled	9.8	9	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1b; PDBTitle: backbone structure of human membrane protein higd1b
25	c2m8gX	Alignment	not modelled	9.3	15	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
26	c4l5eA	Alignment	not modelled	8.7	9	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
27	c2lomA	Alignment	not modelled	7.5	6	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1a; PDBTitle: backbone structure of human membrane protein higd1a
28	d1ntca	Alignment	not modelled	7.2	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like

29	c1g2hA_	 Alignment	not modelled	7.2	29	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
30	d1g2ha_	 Alignment	not modelled	7.2	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
31	c6g3bA_	 Alignment	not modelled	6.6	22	PDB header: hydrolase Chain: A: PDB Molecule: type ii site-specific deoxyribonuclease; PDBTitle: avaii restriction endonuclease in complex with an rna/dna hybrid
32	d1fipa_	 Alignment	not modelled	6.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
33	c5xu1M_	 Alignment	not modelled	6.3	14	PDB header: transport protein Chain: M: PDB Molecule: abc transporter permeae; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
34	c1wz4A_	 Alignment	not modelled	5.5	63	PDB header: gene regulation Chain: A: PDB Molecule: major surface antigen; PDBTitle: solution conformation of adr subtype hbv pre-s2 epitope