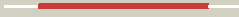











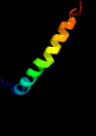






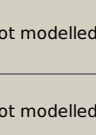


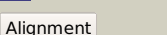
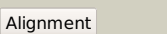
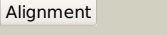
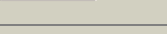




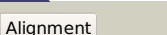
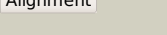
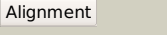
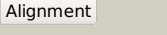
Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0936_(pstA2)_1044321_1045226
 Date Fri Jul 26 01:50:53 BST 2019
 Unique Job ID e0c297881acf681d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4tqv1_	 Alignment		100.0	12	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	c3fh6F_	 Alignment		100.0	11	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
3	c2r6gF_	 Alignment		100.0	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
4	c4tqv1_	 Alignment		100.0	9	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
5	d2r6gf2	 Alignment		100.0	13	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
6	c2onkC_	 Alignment		100.0	17	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	17	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
8	d2r6gg1	 Alignment		100.0	13	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
9	c4ymuC_	 Alignment		100.0	17	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
10	c3d31D_	 Alignment		100.0	18	PDB header: transport protein Chain: D; PDB Molecule: sulfate/molybdate abc transporter, permease protein; PDBTitle: modbc from methanosarcina acetivorans
11	d3d31c1	 Alignment		100.0	18	Fold: MetI-like Superfamily: MetI-like Family: MetI-like

12	d3dhwa1	Alignment		99.9	23	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
13	d2r6gf1	Alignment		50.4	8	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
14	c5kbuA	Alignment		38.2	17	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	c2m8gX	Alignment		32.4	23	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
16	d1umqa	Alignment		28.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
17	c1umqA	Alignment		28.4	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
18	c2hx6A	Alignment		28.4	31	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb
19	d1ntca	Alignment		27.7	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
20	c4l5eA	Alignment		25.6	22	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
21	c2jpwA	Alignment	not modelled	24.1	39	PDB header: contractile protein Chain: A: PDB Molecule: troponin i, cardiac muscle; PDBTitle: solution structure of the bisphosphorylated cardiac2 specific n-extension of cardiac troponin i
22	d1fipa	Alignment	not modelled	18.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
23	d1etob	Alignment	not modelled	18.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
24	c3e7lD	Alignment	not modelled	14.8	26	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	13.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
26	c6e59A	Alignment	not modelled	11.3	10	PDB header: signaling protein Chain: A: PDB Molecule: substance-p receptor, glga glycogen synthase, substance-p PDBTitle: crystal structure of the human nk1 tachykinin receptor
27	c1g2hA	Alignment	not modelled	10.2	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
28	d1g2ha	Alignment	not modelled	10.2	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like

29	c2momB_	 Alignment	not modelled	9.2	21	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
30	c2momC_	 Alignment	not modelled	9.2	21	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
31	c2n2aA_	 Alignment	not modelled	9.2	17	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: spatial structure of her2/erbB2 dimeric transmembrane domain in the presence of cytoplasmic juxtamembrane domains
32	c4qiwT_	 Alignment	not modelled	9.0	29	PDB header: transcription Chain: T: PDB Molecule: dna-directed rna polymerase subunit k; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
33	c2ks1A_	 Alignment	not modelled	8.4	19	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
34	c2jwaA_	 Alignment	not modelled	8.4	19	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: erbB2 transmembrane segment dimer spatial structure
35	c2wwbA_	 Alignment	not modelled	7.9	17	PDB header: ribosome Chain: A: PDB Molecule: protein transport protein sec61 subunit alpha isoform 1; PDBTitle: cryo-em structure of the mammalian sec61 complex bound to the actively translating wheat germ 80s ribosome
36	c2l2tA_	 Alignment	not modelled	7.9	7	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-4; PDBTitle: solution nmr structure of the erbB4 dimeric membrane domain
37	c2lxB_	 Alignment	not modelled	7.9	7	PDB header: transferase Chain: B: PDB Molecule: receptor tyrosine-protein kinase erbB-4; PDBTitle: spatial structure of the erbB4 dimeric tm domain
38	c1twcF_	 Alignment	not modelled	7.7	36	PDB header: transcription Chain: F: PDB Molecule: dna-directed rna polymerases i, ii, and iii 23 PDBTitle: rna polymerase ii complexed with gtp
39	c3mkuA_	 Alignment	not modelled	7.7	11	PDB header: transport protein Chain: A: PDB Molecule: multi antimicrobial extrusion protein (na(+))/drug PDBTitle: structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
40	d1twff_	 Alignment	not modelled	7.6	36	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RPB6
41	c2wwaA_	 Alignment	not modelled	7.5	17	PDB header: ribosome Chain: A: PDB Molecule: sec sixty-one protein homolog; PDBTitle: cryo-em structure of idle yeast ssh1 complex bound to the yeast 80s2 ribosome
42	c2pmzW_	 Alignment	not modelled	7.4	21	PDB header: translation, transferase Chain: W: PDB Molecule: dna-directed rna polymerase subunit k; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
43	d1j8ca_	 Alignment	not modelled	7.0	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
44	c3twfB_	 Alignment	not modelled	6.5	11	PDB header: unknown function Chain: B: PDB Molecule: alpha4f3a; PDBTitle: crystal structure of the de novo designed fluorinated peptide2 alpha4f3a
45	c5ws4A_	 Alignment	not modelled	6.4	10	PDB header: membrane protein Chain: A: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
46	c5a40C_	 Alignment	not modelled	6.2	10	PDB header: transport protein Chain: C: PDB Molecule: putative fluoride ion transporter crcb; PDBTitle: crystal structure of a dual topology fluoride ion channel.
47	d1qkla_	 Alignment	not modelled	6.2	36	Fold: RPB6/omega subunit-like Superfamily: RPB6/omega subunit-like Family: RPB6
48	c2m20B_	 Alignment	not modelled	6.1	20	PDB header: signaling protein Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
49	c1ojjD_	 Alignment	not modelled	6.1	29	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
50	c5m7nA_	 Alignment	not modelled	6.0	16	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
51	c1wlpA_	 Alignment	not modelled	5.9	45	PDB header: oxidoreductase/signaling protein Chain: A: PDB Molecule: cytochrome b-245 light chain; PDBTitle: solution structure of the p22phox-p47phox complex
52	c3h0gF_	 Alignment	not modelled	5.3	36	PDB header: transcription Chain: F: PDB Molecule: dna-directed rna polymerases i, ii, and iii subunit rpabc2; PDBTitle: rna polymerase ii from schizosaccharomyces pombe