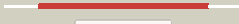
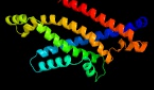


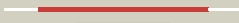


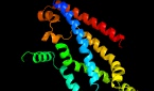























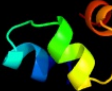








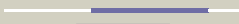


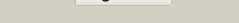
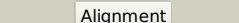


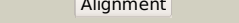


Phyre2


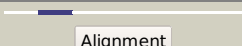

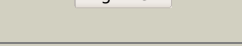
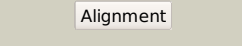
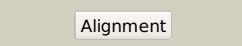

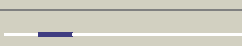
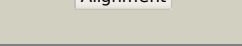

Email	mdejesus@rockefeller.edu
Description	RVBD3756c_(proZ)_420272_4202791
Date	Fri Aug 9 18:20:46 BST 2019
Unique Job ID	bd2baa3597bb8a2a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ymuC_	 Alignment		99.9	21	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 with 2 arginines and atps
2	d2onkc1	 Alignment		99.9	15	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
3	c2onkC_	 Alignment		99.9	15	PDB header: membrane protein Chain: C; PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
4	c4tqvI_	 Alignment		99.9	15	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
5	c3d31D_	 Alignment		99.8	18	PDB header: transport protein Chain: D; PDB Molecule: sulfate/molybdate abc transporter, permease protein; PDBTitle: modbc from methanosarcina acetivorans
6	d3d31c1	 Alignment		99.8	18	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
7	d3dhwa1	 Alignment		99.8	22	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
8	c2r6gF_	 Alignment		99.8	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
9	d2r6gf2	 Alignment		99.8	17	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	c4tqvJ_	 Alignment		99.8	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	c3fh6F_	 Alignment		99.8	15	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

12	d2r6gg1	 Alignment		99.7	15	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
13	c5kbuA	 Alignment		76.7	14	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		18.6	19	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
15	d1ntca	 Alignment		15.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
16	d1umqa	 Alignment		15.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
17	c1umqA	 Alignment		15.5	16	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	c4l5eA	 Alignment		14.6	13	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
19	c5lj7B	 Alignment		14.3	11	PDB header: transport protein Chain: B: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
20	c5nikK	 Alignment		12.7	15	PDB header: transport protein Chain: K: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump
21	c5xu1M	 Alignment	not modelled	11.4	16	PDB header: transport protein Chain: M: PDB Molecule: abc transporter permeae; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
22	c2jwaA	 Alignment	not modelled	11.4	17	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erb2-2; PDBTitle: erb22 transmembrane segment dimer spatial structure
23	c2ks1A	 Alignment	not modelled	10.5	19	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erb2-2; PDBTitle: heterodimeric association of transmembrane domains of erb1 and erb22 receptors enabling kinase activation
24	d2jdid1	 Alignment	not modelled	10.4	33	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
25	c2mkvA	 Alignment	not modelled	8.8	20	PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
26	d1etob	 Alignment	not modelled	8.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
27	d1fipa	 Alignment	not modelled	8.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
28	c3e7ID	 Alignment	not modelled	7.8	13	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna

						binding2 domain
29	c5ws4A_	Alignment	not modelled	7.6	12	PDB header: membrane protein Chain: A: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from <i>Acinetobacter baumannii</i>
30	d1etxa_	Alignment	not modelled	7.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
31	c2ka1B_	Alignment	not modelled	7.5	30	PDB header: membrane protein Chain: B: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles
32	c2ka2B_	Alignment	not modelled	7.5	30	PDB header: membrane protein Chain: B: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
33	c2ka1A_	Alignment	not modelled	7.5	30	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles
34	c2ka2A_	Alignment	not modelled	7.5	30	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
35	d1g2ha_	Alignment	not modelled	7.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
36	c1g2hA_	Alignment	not modelled	7.1	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 <i>Haemophilus influenzae</i>
37	d1skye1	Alignment	not modelled	7.1	33	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
38	c2jo1A_	Alignment	not modelled	6.8	15	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in 2 micelles
39	d2auwa1	Alignment	not modelled	6.7	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
40	c2j5dA_	Alignment	not modelled	6.7	30	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting protein 3; PDBTitle: nmr structure of bnp3 transmembrane domain in lipid bicelles
41	d2phcb1	Alignment	not modelled	6.7	16	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like
42	c2lhuA_	Alignment	not modelled	6.6	19	PDB header: structural protein Chain: A: PDB Molecule: mybpc3 protein; PDBTitle: structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
43	c2k11B_	Alignment	not modelled	6.3	39	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the e2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
44	c2k1kA_	Alignment	not modelled	6.3	39	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the e2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
45	c2k11A_	Alignment	not modelled	6.3	39	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the e2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
46	c2k1kB_	Alignment	not modelled	6.3	39	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the e2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
47	c2zp2B_	Alignment	not modelled	6.0	12	PDB header: transferase inhibitor Chain: B: PDB Molecule: kinase a inhibitor; PDBTitle: c-terminal domain of kipi from <i>Bacillus subtilis</i>
48	d1fx0b1	Alignment	not modelled	5.9	33	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
49	c5m87A_	Alignment	not modelled	5.8	13	PDB header: transport protein Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of <i>Eremococcus coleocola</i> manganese transporter
50	c3mmlD_	Alignment	not modelled	5.7	22	PDB header: hydrolase Chain: D: PDB Molecule: allophanate hydrolase subunit 1; PDBTitle: allophanate hydrolase complex from <i>Mycobacterium smegmatis</i> , msmeg0435-2 msmeg0436
51	c1oj1D_	Alignment	not modelled	5.7	23	PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for 2 the conformational switch necessary for sigma54 binding

52	c2m1aA_	 Alignment	not modelled	5.5	22	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 rev arginine-rich motif (arm); PDBTitle: hiv-1 rev arm peptide (residues t34-r50)
53	c1ciiA_	 Alignment	not modelled	5.4	25	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
54	c5m7nA_	 Alignment	not modelled	5.4	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
55	d2ns0a1	 Alignment	not modelled	5.4	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
56	c2cw1A_	 Alignment	not modelled	5.4	33	PDB header: de novo protein Chain: A: PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein
57	c3rkoF_	 Alignment	not modelled	5.4	7	PDB header: oxidoreductase Chain: F: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
58	c2momB_	 Alignment	not modelled	5.4	29	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
59	c2momC_	 Alignment	not modelled	5.4	29	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
60	c1etgB_	 Alignment	not modelled	5.3	21	PDB header: viral protein/rna Chain: B: PDB Molecule: rev peptide; PDBTitle: rev response element (rre) rna complexed with rev peptide,2 nmr, 19 structures
61	c1etfB_	 Alignment	not modelled	5.3	21	PDB header: viral protein/rna Chain: B: PDB Molecule: rev peptide; PDBTitle: rev response element (rre) rna complexed with rev peptide,2 nmr, minimized average structure