








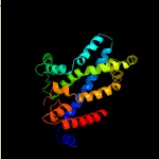








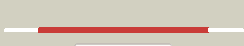














Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2040c (-)_2285636_2286538
Date	Mon Aug 5 13:25:15 BST 2019
Unique Job ID	65ce84d39521c586

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fh6F_	 Alignment		100.0	28	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	c4tqvl_	 Alignment		100.0	21	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	29	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	d2r6gg1	 Alignment		100.0	15	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
5	d2r6gf2	 Alignment		100.0	30	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
6	c4tqvl_	 Alignment		100.0	17	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
7	d2onkc1	 Alignment		100.0	20	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
8	c2onkC	 Alignment		100.0	20	PDB header: membrane protein Chain: C; PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
9	d3d31c1	 Alignment		100.0	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	c3d31D_	 Alignment		100.0	16	PDB header: transport protein Chain: D; PDB Molecule: sulfate/molybdate abc transporter, permease protein; PDBTitle: modbc from methanosarcina acetivorans
11	c4ymuC_	 Alignment		100.0	15	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	d2r6gf1	Alignment		95.0	27	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
14	c5kbuA	Alignment		88.3	15	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		40.3	16	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
16	c4l5eA	Alignment		39.2	13	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
17	c1umqA	Alignment		36.7	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	d1umqa	Alignment		36.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
19	d1fipa	Alignment		30.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
20	d1ntca	Alignment		30.1	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
21	d1etxa	Alignment	not modelled	29.0	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
22	d1etob	Alignment	not modelled	27.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
23	c3e7lD	Alignment	not modelled	27.7	10	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
24	c2hx6A	Alignment	not modelled	23.9	12	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb
25	d1g2ha	Alignment	not modelled	21.9	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
26	c1g2hA	Alignment	not modelled	21.9	17	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	c1ojlD	Alignment	not modelled	15.6	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
28	c5m7nA	Alignment	not modelled	14.7	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
29	c6gcs6_	Alignment	not modelled	13.3	5	PDB header: oxidoreductase Chain: 6: PDB Molecule: nd6 subunit (nu6m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
30	c2cw1A_	Alignment	not modelled	11.6	29	PDB header: de novo protein Chain: A: PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein
31	c5a1sB_	Alignment	not modelled	11.1	13	PDB header: transport protein Chain: B: PDB Molecule: citrate-sodium symporter; PDBTitle: crystal structure of the sodium-dependent citrate symporter secits2 form salmonella enterica.
32	c4j2nB_	Alignment	not modelled	5.8	15	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
33	c4j2nA_	Alignment	not modelled	5.8	15	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
34	c1pyuD_	Alignment	not modelled	5.7	23	PDB header: lyase Chain: D: PDB Molecule: aspartate 1-decarboxylase alfa chain; PDBTitle: processed aspartate decarboxylase mutant with ser25 mutated to cys
35	c3hd7A_	Alignment	not modelled	5.7	7	PDB header: exocytosis Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
36	c2n2aA_	Alignment	not modelled	5.6	12	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 juxtamembrane domains
37	c3wg7T_	Alignment	not modelled	5.4	24	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
38	c5u4jw_	Alignment	not modelled	5.3	20	PDB header: ribosome Chain: W: PDB Molecule: PDBTitle: structural basis of co-translational quality control by arfa and rf22 bound to ribosome
39	d1cf7a_	Alignment	not modelled	5.3	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Cell cycle transcription factor e2f-dp