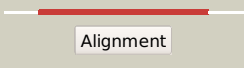

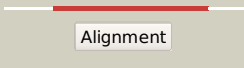

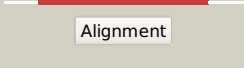

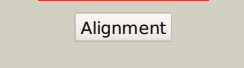

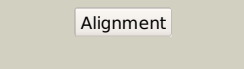

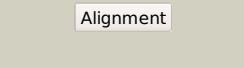

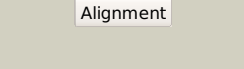

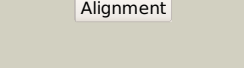

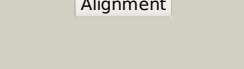
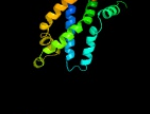
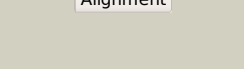

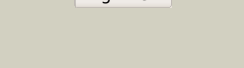



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3664c_dppC_4103853_4104716
Date	Fri Aug 9 18:20:35 BST 2019
Unique Job ID	521eebcb78c06234

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4tqv1_			99.9	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	c4ymuC_			99.9	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
3	d2onkc1			99.9	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
4	c2onkC_			99.9	16	PDB header: membrane protein Chain: C; PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
5	c3fh6F_			99.9	14	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	d3d31c1			99.9	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
7	c3d31D_			99.9	16	PDB header: transport protein Chain: D; PDB Molecule: sulfate/molybdate abc transporter, permease protein; PDBTitle: modbc from methanosarcina acetivorans
8	c4tqv1_			99.9	10	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
9	d2r6gf2			99.9	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
10	d3dhwa1			99.9	16	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
11	d2r6gg1			99.9	13	Fold: MetI-like Superfamily: MetI-like Family: MetI-like

12	c2r6gF_	Alignment		99.9	14	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
13	c5kbuA_	Alignment		95.8	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
14	c2nd4A_	Alignment		38.0	38	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
15	c2voyB_	Alignment		26.8	15	PDB header: hydrolase Chain: B: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
16	d1p7ba2	Alignment		21.9	15	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
17	c2qksA_	Alignment		18.0	13	PDB header: metal transport Chain: A: PDB Molecule: kir3.1-prokaryotic kir channel chimera; PDBTitle: crystal structure of a kir3.1-prokaryotic kir channel chimera
18	c3lgeG_	Alignment		14.8	11	PDB header: lyase/protein binding Chain: G: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of rabbit muscle aldolase-snx9 lc4 complex
19	c3lgeF_	Alignment		14.8	11	PDB header: lyase/protein binding Chain: F: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of rabbit muscle aldolase-snx9 lc4 complex
20	c2jwaA_	Alignment		14.3	24	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
21	c2ks1A_	Alignment	not modelled	14.3	24	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
22	d2pofa1	Alignment	not modelled	13.7	25	Fold: HIT-like Superfamily: HIT-like Family: CDH-like
23	c1p7bB_	Alignment	not modelled	10.4	15	PDB header: metal transport Chain: B: PDB Molecule: integral membrane channel and cytosolic domains; PDBTitle: crystal structure of an inward rectifier potassium channel
24	c2lomA_	Alignment	not modelled	9.9	11	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1a; PDBTitle: backbone structure of human membrane protein higd1a
25	c1xl6B_	Alignment	not modelled	9.7	16	PDB header: metal transport Chain: B: PDB Molecule: inward rectifier potassium channel; PDBTitle: intermediate gating structure 2 of the inwardly rectifying k+ channel2 kirbac3.1
26	c2b9sB_	Alignment	not modelled	7.9	29	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
27	c2lonA_	Alignment	not modelled	7.7	14	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1b; PDBTitle: backbone structure of human membrane protein higd1b
28	c5nf8A_	Alignment	not modelled	7.0	18	PDB header: membrane protein Chain: A: PDB Molecule: respiratory supercomplex factor 1, mitochondrial; PDBTitle: solution structure of detergent-solubilized rcf1, a yeast2 mitochondrial inner membrane protein involved in respiratory

						complex3 iii/iv supercomplex formation
29	c1wz4A_	Alignment	not modelled	6.6	57	PDB header: gene regulation Chain: A: PDB Molecule: major surface antigen; PDBTitle: solution conformation of adr subtype hbv pre-s2 epitope
30	c2hx6A_	Alignment	not modelled	6.2	21	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease; PDBTitle: solution structure analysis of the phage t42 endoribonuclease regb
31	c6o7xa_	Alignment	not modelled	6.2	8	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
32	c2cw1A_	Alignment	not modelled	5.8	43	PDB header: de novo protein Chain: A: PDB Molecule: sn4m; PDBTitle: solution structure of the de novo-designed lambda cro fold2 protein
33	c2d7dB_	Alignment	not modelled	5.7	42	PDB header: hydrolase/dna Chain: B: PDB Molecule: 40-mer from uvrabc system protein b; PDBTitle: structural insights into the cryptic dna dependent atp-ase2 activity of uvrbc
34	c3d0wD_	Alignment	not modelled	5.7	24	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: yflh protein; PDBTitle: crystal structure of yflh protein from bacillus subtilis. northeast2 structural genomics consortium target sr326
35	d1xl4a2_	Alignment	not modelled	5.4	15	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
36	c4p6vB_	Alignment	not modelled	5.3	8	PDB header: oxidoreductase Chain: B: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit b; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
37	c6g3bA_	Alignment	not modelled	5.2	17	PDB header: hydrolase Chain: A: PDB Molecule: type ii site-specific deoxyribonuclease; PDBTitle: avaii restriction endonuclease in complex with an rna/dna hybrid