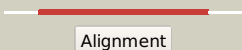
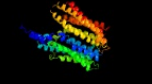
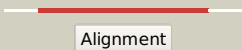

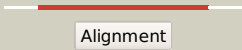









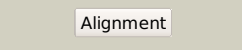



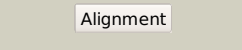

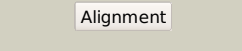




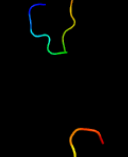
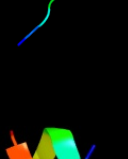


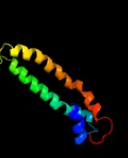
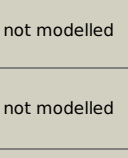


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1510_(-)_1701301_1702599
Date	Fri Aug 2 13:30:09 BST 2019
Unique Job ID	8ffd688fc34ac3ff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6cc4A_	 Alignment		100.0	10	PDB header: transport protein Chain: A: PDB Molecule: soluble cytochrome b562, lipid ii flippase murj chimera; PDBTitle: structure of murj from escherichia coli
2	c6idrA_	 Alignment		100.0	10	PDB header: transport protein Chain: A: PDB Molecule: mate family efflux transporter; PDBTitle: crystal structure of vibrio cholerae mate transporter vcmn in the bent2 form
3	c5y50A_	 Alignment		100.0	9	PDB header: membrane protein Chain: A: PDB Molecule: protein detoxification 14; PDBTitle: crystal structure of eukaryotic mate transporter atdtx14
4	c5xjiA_	 Alignment		100.0	11	PDB header: transport protein Chain: A: PDB Molecule: multi drug efflux transporter; PDBTitle: crystal structure of a mate family protein
5	c5t77A_	 Alignment		100.0	8	PDB header: transport protein Chain: A: PDB Molecule: putative lipid ii flippase murj; PDBTitle: crystal structure of the mop flippase murj
6	c4lz9A_	 Alignment		100.0	12	PDB header: transport protein Chain: A: PDB Molecule: bh2163 protein; PDBTitle: structure of mate multidrug transporter dinf-bh in complex with r6g
7	c6fv6A_	 Alignment		100.0	10	PDB header: membrane protein Chain: A: PDB Molecule: aq128; PDBTitle: monomer structure of the mate family multidrug resistance transporter2 aq_128 from aquifex aeolicus in the outward-facing state
8	c4z3pA_	 Alignment		100.0	10	PDB header: transport protein Chain: A: PDB Molecule: putative drug/sodium antiporter; PDBTitle: mate transporter clbm in complex with rb+
9	c3vvpA_	 Alignment		100.0	14	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of mate in complex with br-nrf
10	c3mkuB_	 Alignment		99.9	10	PDB header: transport protein Chain: B: PDB Molecule: multi antimicrobial extrusion protein (na+)/drug PDBTitle: structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
11	c3mkuA_	 Alignment		99.9	10	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

12	c4hunA	Alignment		99.4	10	PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux protein; PDBTitle: mate transporter norm-ng in complex with r6g and monobody
13	c4n7wA	Alignment		63.3	11	PDB header: transport protein Chain: A: PDB Molecule: transporter, sodium/bile acid symporter family; PDBTitle: crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
14	c3wdoA	Alignment		39.4	11	PDB header: transport protein Chain: A: PDB Molecule: mfs transporter; PDBTitle: structure of e. coli yajr transporter
15	c3epsB	Alignment		15.7	25	PDB header: transferase, hydrolase Chain: B: PDB Molecule: isocitrate dehydrogenase kinase/phosphatase; PDBTitle: the crystal structure of isocitrate dehydrogenase kinase/phosphatase2 from e. coli
16	c3ukzC	Alignment		15.4	44	PDB header: protein transport/protein binding Chain: C: PDB Molecule: nuclear cap-binding protein subunit 1; PDBTitle: mouse importin alpha: mouse cbp80 cnls complex
17	c3dxeB	Alignment		14.3	50	PDB header: protein binding Chain: B: PDB Molecule: amyloid beta a4 protein; PDBTitle: crystal structure of the intracellular domain of human app (t668a2 mutant) in complex with fe65-ptb2
18	c1l4aE	Alignment		12.6	50	PDB header: endocytosis/exocytosis Chain: E: PDB Molecule: synaphin a; PDBTitle: x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
19	c3efdK	Alignment		12.0	33	PDB header: immune system Chain: K: PDB Molecule: kcsa; PDBTitle: the crystal structure of the cytoplasmic domain of kcsa
20	c5mg3D	Alignment		11.7	10	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secD; PDBTitle: em fitted model of bacterial holo-translocon
21	d2crba1	Alignment	not modelled	9.9	38	Fold: Spectrin repeat-like Superfamily: MIT domain-like Family: MIT domain
22	c2n90A	Alignment	not modelled	9.8	16	PDB header: transferase Chain: A: PDB Molecule: high affinity nerve growth factor receptor; PDBTitle: trka transmembrane domain nmr structure in dpc micelles
23	c2n90B	Alignment	not modelled	9.8	16	PDB header: transferase Chain: B: PDB Molecule: high affinity nerve growth factor receptor; PDBTitle: trka transmembrane domain nmr structure in dpc micelles
24	c6g9xB	Alignment	not modelled	9.5	11	PDB header: membrane protein Chain: B: PDB Molecule: major facilitator superfamily mfs_1; PDBTitle: crystal structure of a mfs transporter at 2.54 angstrom resolution
25	d1rfya	Alignment	not modelled	8.8	31	Fold: Long alpha-hairpin Superfamily: Transcriptional repressor TraM Family: Transcriptional repressor TraM
26	d1sb0a	Alignment	not modelled	8.5	22	Fold: Kix domain of CBP (creb binding protein) Superfamily: Kix domain of CBP (creb binding protein) Family: Kix domain of CBP (creb binding protein)
27	c3cguB	Alignment	not modelled	8.4	20	PDB header: hormone/signaling protein Chain: B: PDB Molecule: protein giant-lens; PDBTitle: crystal structure of unliganded argos
28	d1upgb	Alignment	not modelled	8.1	31	Fold: Long alpha-hairpin Superfamily: Transcriptional repressor TraM Family: Transcriptional repressor TraM
						PDB header: membrane protein

29	c2ko2A_	Alignment	not modelled	8.1	18	Chain: A: PDB Molecule: reticulon-4; PDBTitle: nogo66
30	c4wriA_	Alignment	not modelled	7.8	83	PDB header: toxin/toxin inhibitor Chain: A: PDB Molecule: okadaic acid binding protein 2-alpha; PDBTitle: crystal structure of okadaic acid binding protein 2.1
31	c6j9lE_	Alignment	not modelled	7.5	60	PDB header: hydrolase inhibitor/hydrolase Chain: E: PDB Molecule: hnh endonuclease family protein; PDBTitle: fnohb+acriic2
32	c2hjdA_	Alignment	not modelled	7.3	23	PDB header: signaling protein Chain: A: PDB Molecule: quorum-sensing antiactivator; PDBTitle: crystal structure of a second quorum sensing antiactivator tram2 from2 a. tumefaciens strain a6
33	c5ogeE_	Alignment	not modelled	7.1	7	PDB header: membrane protein Chain: E: PDB Molecule: gdp-mannose transporter 1; PDBTitle: crystal structure of a nucleotide sugar transporter
34	c2bx9l_	Alignment	not modelled	6.9	31	PDB header: transcription regulation Chain: J: PDB Molecule: tryptophan rna-binding attenuator protein-inhibitory PDBTitle: crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
35	c5wljD_	Alignment	not modelled	6.8	40	PDB header: de novo protein Chain: D: PDB Molecule: de novo metal binding helical bundle; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh1
36	c5wljA_	Alignment	not modelled	6.8	40	PDB header: de novo protein Chain: A: PDB Molecule: de novo metal binding helical bundle; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh1
37	c5wljC_	Alignment	not modelled	6.8	40	PDB header: de novo protein Chain: C: PDB Molecule: de novo metal binding helical bundle; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh1
38	c5wljB_	Alignment	not modelled	6.8	40	PDB header: de novo protein Chain: B: PDB Molecule: de novo metal binding helical bundle; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh1
39	c6oitG_	Alignment	not modelled	6.7	10	PDB header: plant protein Chain: G: PDB Molecule: protein chromatin remodeling 35; PDBTitle: cryoem structure of arabidopsis ddr' complex (drd1 peptide-dms3-rdm1)
40	c2jv5A_	Alignment	not modelled	6.7	19	PDB header: protein binding Chain: A: PDB Molecule: reticulon-4; PDBTitle: nogo54
41	d2p7tc1	Alignment	not modelled	6.5	9	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
42	c5tpjA_	Alignment	not modelled	6.4	19	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
43	c2z3xC_	Alignment	not modelled	6.3	14	PDB header: dna binding protein/dna Chain: C: PDB Molecule: small, acid-soluble spore protein c; PDBTitle: structure of a protein-dna complex essential for dna protection in2 spore of bacillus species
44	c2ks1B_	Alignment	not modelled	6.3	14	PDB header: transferase Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
45	c2vckC_	Alignment	not modelled	6.3	13	PDB header: oxidoreductase Chain: C: PDB Molecule: cyanobacterial phycoerythrobilin; PDBTitle: structure of phycoerythrobilin synthase pebs from the cyanophage p-2 ssm2 in complex with the bound substrate biliverdin ixa
46	c2f9jP_	Alignment	not modelled	6.3	29	PDB header: rna binding protein Chain: P: PDB Molecule: splicing factor 3b subunit 1; PDBTitle: 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
47	c5ldwo_	Alignment	not modelled	6.2	38	PDB header: oxidoreductase Chain: O: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: structure of mammalian respiratory complex i, class1
48	c4wybP_	Alignment	not modelled	6.2	23	PDB header: contractile protein/protein binding Chain: P: PDB Molecule: bud site selection protein 6; PDBTitle: structure of the bud6 flank domain in complex with actin
49	c2yvxD_	Alignment	not modelled	6.0	11	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
50	c5z62N_	Alignment	not modelled	5.9	30	PDB header: electron transport Chain: N: PDB Molecule: cytochrome c oxidase subunit ndufa4; PDBTitle: structure of human cytochrome c oxidase
51	d1pw4a_	Alignment	not modelled	5.9	10	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
52	c4gkgA_	Alignment	not modelled	5.9	28	PDB header: signaling protein Chain: A: PDB Molecule: c4-dicarboxylate transport sensor protein dctb; PDBTitle: crystal structure of the s-helix linker
53	c2bbjB_	Alignment	not modelled	5.9	9	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
54	d2i76a1	Alignment	not modelled	5.8	24	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like PDB header: protein binding

55	c6et8B_	Alignment	not modelled	5.7	18	Chain: B: PDB Molecule: albicidin resistance protein; PDBTitle: crystal structure of alba in complex with albicidin
56	c2l37A_	Alignment	not modelled	5.6	24	PDB header: hydrolase Chain: A: PDB Molecule: ribosome-inactivating protein luffin p1; PDBTitle: 3d solution structure of arginine/glutamate-rich polypeptide luffin p12 from the seeds of sponge gourd (luffa cylindrical)
57	d1azta1	Alignment	not modelled	5.6	43	Fold: Transducin (alpha subunit), insertion domain Superfamily: Transducin (alpha subunit), insertion domain Family: Transducin (alpha subunit), insertion domain
58	d2j0111	Alignment	not modelled	5.5	17	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L28
59	c5bs7F_	Alignment	not modelled	5.5	20	PDB header: transcription regulator Chain: F: PDB Molecule: protein spt2 homolog; PDBTitle: structure of histone h3/h4 in complex with spt2
60	c2momB_	Alignment	not modelled	5.4	12	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
61	c2momC_	Alignment	not modelled	5.4	12	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
62	d3ehbb2	Alignment	not modelled	5.4	6	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
63	c4wybj_	Alignment	not modelled	5.4	23	PDB header: contractile protein/protein binding Chain: J: PDB Molecule: bud site selection protein 6; PDBTitle: structure of the bud6 flank domain in complex with actin
64	c6o3sA_	Alignment	not modelled	5.4	24	PDB header: plant protein, hydrolase Chain: A: PDB Molecule: ribosome-inactivating protein luffin p1; PDBTitle: nmr solution structure of vicilin-buried peptide-8 (vbp-8)
65	d1jo5a_	Alignment	not modelled	5.2	16	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
66	c2d7dB_	Alignment	not modelled	5.2	44	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 uvrb
67	c3hlsE_	Alignment	not modelled	5.2	25	PDB header: signaling protein Chain: E: PDB Molecule: guanylate cyclase soluble subunit beta-1; PDBTitle: crystal structure of the signaling helix coiled-coil domain2 of the beta-1 subunit of the soluble guanylyl cyclase
68	c3j47O_	Alignment	not modelled	5.1	50	PDB header: protein binding Chain: O: PDB Molecule: 26s proteasome regulatory subunit rpn9; PDBTitle: formation of an intricate helical bundle dictates the assembly of the2 26s proteasome lid
69	c5vnyA_	Alignment	not modelled	5.1	10	PDB header: endocytosis, protein binding Chain: A: PDB Molecule: lethal (2) giant discs 1, isoform b; PDBTitle: crystal structure of dm14-3 domain of lgd