

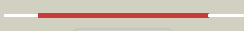
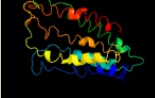

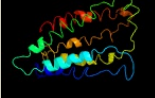




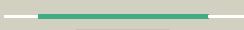

















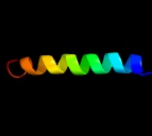

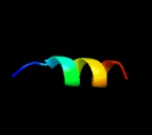


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3271c_(-)_3652676_3653344
Date	Thu Aug 8 16:20:47 BST 2019
Unique Job ID	f2bacfa3cde907c8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3j1zP_	 Alignment		100.0	19	PDB header: metal transport Chain: P: PDB Molecule: cation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy
2	c2qfiB_	 Alignment		100.0	19	PDB header: transport protein Chain: B: PDB Molecule: ferrous-iron efflux pump fief; PDBTitle: structure of the zinc transporter yiiip
3	d2qfia2	 Alignment		100.0	19	Fold: Cation efflux protein transmembrane domain-like Superfamily: Cation efflux protein transmembrane domain-like Family: Cation efflux protein transmembrane domain-like
4	c4x9zA_	 Alignment		60.8	88	PDB header: toxin Chain: A: PDB Molecule: alphad-conotoxin gexxa from the venom of conus generalis; PDBTitle: dimeric conotoxin alphad-gexxa
5	c3rkoN_	 Alignment		45.7	8	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-quinone oxidoreductase subunit n; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
6	c6humB_	 Alignment		42.7	10	PDB header: proton transport Chain: B: PDB Molecule: nad(p)h-quinone oxidoreductase subunit 2; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
7	c5m87A_	 Alignment		37.2	12	PDB header: transport protein Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of eremococcus coleocola manganese transporter
8	c4x9zB_	 Alignment		35.4	86	PDB header: toxin Chain: B: PDB Molecule: alphad-conotoxin gexxa from the venom of conus generalis; PDBTitle: dimeric conotoxin alphad-gexxa
9	c4k1cB_	 Alignment		28.8	7	PDB header: membrane protein/metal transport Chain: B: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
10	c5d92B_	 Alignment		28.4	12	PDB header: membrane protein Chain: B: PDB Molecule: af2299 protein,phosphatidylinositol synthase; PDBTitle: structure of a phosphatidylinositolphosphate (pip) synthase from2 renibacterium salmoninarum
11	c4he8M_	 Alignment		24.8	12	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-quinone oxidoreductase subunit 13; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus

12	c2l1aA_	Alignment		24.1	38	PDB header: actin binding protein Chain: A; PDB Molecule: formin-c; PDBTitle: solution nmr structure of the n-terminal gtpase-like domain of f2 dictyostelium discoideum fomin c
13	c4o6mA_	Alignment		18.9	13	PDB header: transferase Chain: A; PDB Molecule: af2299, a cdp-alcohol phosphotransferase; PDBTitle: structure of af2299, a cdp-alcohol phosphotransferase (cmp-bound)
14	c2jo1A_	Alignment		17.1	40	PDB header: hydrolase regulator Chain: A; PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
15	c2mkvA_	Alignment		15.7	24	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
16	d2gc4d1	Alignment		14.5	20	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
17	c5tsaA_	Alignment		14.3	10	PDB header: metal binding protein Chain: A; PDB Molecule: membrane protein; PDBTitle: crystal structure of the zrt-/irt-like protein from bordetella2 bronchiseptica with bound zn2+
18	c2jp3A_	Alignment		13.5	28	PDB header: transcription Chain: A; PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
19	c5ir6B_	Alignment		13.3	13	PDB header: oxidoreductase Chain: B; PDB Molecule: bd-type quinol oxidase subunit ii; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
20	c4fd dB_	Alignment		12.4	33	PDB header: transport protein Chain: B; PDB Molecule: rna-binding protein fus; PDBTitle: crystal structure of kap beta2-py-nls
21	c4fq3B_	Alignment	not modelled	12.2	33	PDB header: protein binding Chain: B; PDB Molecule: fusion (involved in t(12;16) in malignant liposarcoma); PDBTitle: crystal structure of transportin/fus-nls
22	c5yv hB_	Alignment	not modelled	12.2	33	PDB header: protein transport/rna binding protein Chain: B; PDB Molecule: rna-binding protein fus; PDBTitle: crystal structure of karyopherin beta2 in complex with fus(371-526)
23	c5yviB_	Alignment	not modelled	12.2	33	PDB header: protein transport/rna binding protein Chain: B; PDB Molecule: rna-binding protein fus; PDBTitle: crystal structure of karyopherin beta2 in complex with fus(456-526)
24	c6humD_	Alignment	not modelled	10.8	12	PDB header: proton transport Chain: D; PDB Molecule: nad(p)h-quinone oxidoreductase chain 4 1; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
25	c6h59B_	Alignment	not modelled	8.5	12	PDB header: transferase Chain: B; PDB Molecule: cdp-diacylglycerol--inositol 3-phosphatidyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis phosphatidylinositol2 phosphate synthase (pgsa1) with cdp-dag bound
26	c6humE_	Alignment	not modelled	8.1	10	PDB header: proton transport Chain: E; PDB Molecule: nad(p)h-quinone oxidoreductase subunit 4i; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
27	c2kdtA_	Alignment	not modelled	6.7	50	PDB header: protein transport Chain: A; PDB Molecule: neuroendocrine convertase 1; PDBTitle: pc1/3 dcs g sorting domain structure in dpc

28	c6f0fB_	Alignment	not modelled	6.3	38	PDB header: chaperone Chain: B: PDB Molecule: ip2_s; PDBTitle: crystal structure asf1-ip2_s
29	c4ljiA_	Alignment	not modelled	5.8	20	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c-550-like protein; PDBTitle: crystal structure at 1.5 angstrom resolution of the psbv2 cytochrome2 from the cyanobacterium thermosynechococcus elongatus
30	c1w9nA_	Alignment	not modelled	5.8	71	PDB header: antibiotic Chain: A: PDB Molecule: epilancin 15x; PDBTitle: isolation and characterization of epilancin 15x, a novel antibiotic2 from a clinical strain of staphylococcus epidermidis
31	c1wnkA_	Alignment	not modelled	5.1	38	PDB header: transcription Chain: A: PDB Molecule: fibroin-modulator-binding-protein-1; PDBTitle: nmr structure of fmbp-1 tandem repeat 3 in 30%(v/v) tfe2 solution