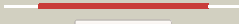
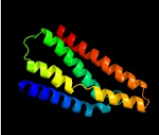


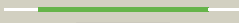






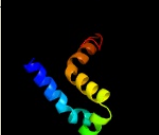





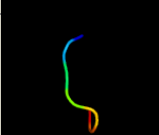

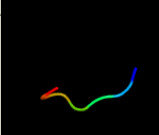


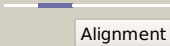

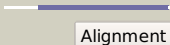

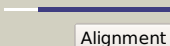
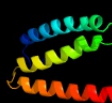
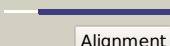

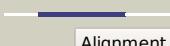

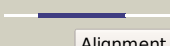

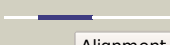


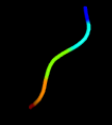

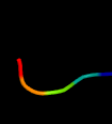
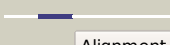
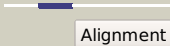
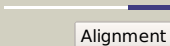
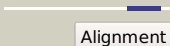
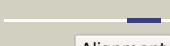

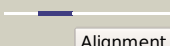


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3069_(ccrB)_3433689_3434087
 Date Thu Aug 8 16:20:24 BST 2019
 Unique Job ID 707c4be2c4e726f0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5a43B_	 Alignment		100.0	27	PDB header: transport protein Chain: B: PDB Molecule: putative fluoride ion transporter ccrb; PDBTitle: crystal structure of a dual topology fluoride ion channel.
2	c5a40C_	 Alignment		100.0	35	PDB header: transport protein Chain: C: PDB Molecule: putative fluoride ion transporter ccrb; PDBTitle: crystal structure of a dual topology fluoride ion channel.
3	c4hzuS_	 Alignment		56.1	10	PDB header: hydrolase, transport protein Chain: S: PDB Molecule: predicted membrane protein; PDBTitle: structure of a bacterial energy-coupling factor transporter
4	c3hd6A_	 Alignment		42.1	11	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: ammonium transporter rh type c; PDBTitle: crystal structure of the human rhesus glycoprotein rhcg
5	c5egiB_	 Alignment		18.0	15	PDB header: membrane protein Chain: B: PDB Molecule: uncharacterized protein y57a10a.10; PDBTitle: structure of a trimeric intracellular cation channel from c. elegans2 with bound ca2+
6	c5eikA_	 Alignment		17.6	18	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein y57a10a.28; PDBTitle: structure of a trimeric intracellular cation channel from c. elegans2 in the absence of ca2+
7	c5ediA_	 Alignment		14.6	14	PDB header: transport protein Chain: A: PDB Molecule: putative hmp/thiamine permease protein ykoe; PDBTitle: crystal structure of an s-component of ecf transporter
8	c2d10F_	 Alignment		13.4	29	PDB header: cell adhesion Chain: F: PDB Molecule: ezrin-radixin-moesin binding phosphoprotein 50; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide
9	c2d10H_	 Alignment		13.4	29	PDB header: cell adhesion Chain: H: PDB Molecule: ezrin-radixin-moesin binding phosphoprotein 50; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide
10	c2d10G_	 Alignment		13.4	29	PDB header: cell adhesion Chain: G: PDB Molecule: ezrin-radixin-moesin binding phosphoprotein 50; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide
11	c2d10E_	 Alignment		13.4	29	PDB header: cell adhesion Chain: E: PDB Molecule: ezrin-radixin-moesin binding phosphoprotein 50; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide

12	c1sgbB_	 Alignment		11.7	29	PDB header: structural protein Chain: B; PDB Molecule: ezrin-radixin-moesin binding phosphoprotein 50; PDBTitle: moesin ferm domain bound to ebp50 c-terminal peptide
13	c5aezA_	 Alignment		10.9	13	PDB header: membrane protein Chain: A; PDB Molecule: mep2; PDBTitle: crystal structure of candida albicans mep2
14	c5aexJ_	 Alignment		9.8	11	PDB header: membrane protein Chain: J; PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2
15	c3orgB_	 Alignment		9.2	13	PDB header: transport protein Chain: B; PDB Molecule: cmclc; PDBTitle: crystal structure of a eukaryotic clc transporter
16	c5ws4A_	 Alignment		8.8	20	PDB header: membrane protein Chain: A; PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
17	c5lj7B_	 Alignment		8.7	15	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)
18	c5xvjB_	 Alignment		7.9	29	PDB header: gene regulation Chain: B; PDB Molecule: phd finger protein alfin-like 7; PDBTitle: crystal structure of al7 pal domain
19	c2d11G_	 Alignment		7.5	40	PDB header: cell adhesion Chain: G; PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf2; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide
20	c2d11H_	 Alignment		7.5	40	PDB header: cell adhesion Chain: H; PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf2; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide
21	c2d11F_	 Alignment	not modelled	7.5	40	PDB header: cell adhesion Chain: F; PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf2; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide
22	c2d11E_	 Alignment	not modelled	7.5	40	PDB header: cell adhesion Chain: E; PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf2; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide
23	c4m48A_	 Alignment	not modelled	7.5	10	PDB header: transport protein Chain: A; PDB Molecule: transporter; PDBTitle: x-ray structure of dopamine transporter elucidates antidepressant2 mechanism
24	c2xokG_	 Alignment	not modelled	7.4	50	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: refined structure of yeast f1c10 atpase complex to 3 a resolution
25	c2w6hG_	 Alignment	not modelled	6.0	50	PDB header: hydrolase Chain: G; PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 4a.
26	c3gn8C_	 Alignment	not modelled	5.9	44	PDB header: hormone/hormone activator Chain: C; PDB Molecule: nuclear receptor coactivator 2; PDBTitle: x-ray crystal structure of ancgr2 in complex with2 dexamethasone
27	c3gn8E_	 Alignment	not modelled	5.7	44	PDB header: hormone/hormone activator Chain: E; PDB Molecule: nuclear receptor coactivator 2; PDBTitle: x-ray crystal structure of ancgr2 in complex with2 dexamethasone

28	c2qe7G_	Alignment	not modelled	5.3	38	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase subunit gamma; PDBTitle: crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
29	d2jdg1	Alignment	not modelled	5.3	50	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
30	d1fs0g_	Alignment	not modelled	5.2	75	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit