



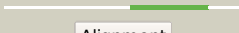







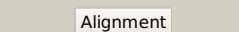


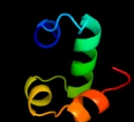





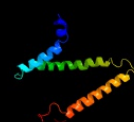

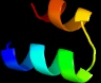
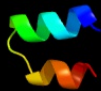








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2387_(-)_2680775_2682028
Date	Mon Aug 5 13:25:54 BST 2019
Unique Job ID	2827b829edbd4051

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4cz8A_	 Alignment		55.4	13	PDB header: membrane protein Chain: A: PDB Molecule: na+/h+ antiporter, putative; PDBTitle: structure of the sodium proton antiporter panhap from2 pyrococcus abyssii at ph 8.
2	c4bwzA_	 Alignment		55.1	14	PDB header: transport protein Chain: A: PDB Molecule: na(+)/h(+) antiporter; PDBTitle: crystal structure of the sodium proton antiporter, napa
3	c5bz3A_	 Alignment		55.1	14	PDB header: transport protein Chain: A: PDB Molecule: na(+)/h(+) antiporter; PDBTitle: crystal structure of sodium proton antiporter napa in outward-facing2 conformation.
4	d1kpla_	 Alignment		44.7	22	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
5	c4czbB_	 Alignment		41.9	17	PDB header: membrane protein Chain: B: PDB Molecule: na(+)/h(+) antiporter 1; PDBTitle: structure of the sodium proton antiporter mjnhap1 from2 methanocaldococcus jannaschii at ph 8.
6	d2bgwa1	 Alignment		36.0	13	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
7	c2ht2B_	 Alignment		30.8	22	PDB header: membrane protein Chain: B: PDB Molecule: h(+)/cl(-) exchange transporter clca; PDBTitle: structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
8	c2mutA_	 Alignment		28.3	17	PDB header: hydrolase Chain: A: PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region
9	d2a1jb1	 Alignment		27.7	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
10	c6hu9r_	 Alignment		26.7	33	PDB header: oxidoreductase/electron transport Chain: R: PDB Molecule: cytochrome b-c1 complex subunit 7; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
11	c6gctA_	 Alignment		26.1	18	PDB header: membrane protein Chain: A: PDB Molecule: neutral amino acid transporter b(0); PDBTitle: cryo-em structure of the human neutral amino acid transporter asct2

12	d1x2ia1	Alignment		25.6	12	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
13	d1v54e_	Alignment		25.5	33	Fold: alpha-alpha superhelix Superfamily: Cytochrome c oxidase subunit E Family: Cytochrome c oxidase subunit E
14	c2y69R_	Alignment		25.3	33	PDB header: electron transport Chain: R; PDB Molecule: cytochrome c oxidase subunit 5a; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
15	d1otsa_	Alignment		23.6	22	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
16	c5a40C_	Alignment		23.4	16	PDB header: transport protein Chain: C; PDB Molecule: putative fluoride ion transporter crcb; PDBTitle: crystal structure of a dual topology fluoride ion channel.
17	d2fyma2	Alignment		17.7	39	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
18	c3c1zA_	Alignment		16.8	14	PDB header: dna binding protein Chain: A; PDB Molecule: dna integrity scanning protein disa; PDBTitle: structure of the ligand-free form of a bacterial dna damage sensor2 protein
19	d2a1a2	Alignment		14.1	25	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
20	c2lyhA_	Alignment		13.3	12	PDB header: dna binding protein Chain: A; PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: structure of faap24 residues 141-215
21	d2akza2	Alignment	not modelled	12.1	32	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
22	c4r1iB_	Alignment	not modelled	12.0	18	PDB header: membrane protein Chain: B; PDB Molecule: aminobenzoyl-glutamate transporter; PDBTitle: structure and function of neisseria gonorrhoeae mtrf illuminates a2 class of antimetabolite efflux pumps
23	c6c62D_	Alignment	not modelled	11.8	43	PDB header: hydrolase Chain: D; PDB Molecule: atzg; PDBTitle: an unexpected vestigial protein complex reveals the evolutionary2 origins of an s-triazine catabolic enzyme.
24	c4bxoA_	Alignment	not modelled	11.5	4	PDB header: hydrolase/dna Chain: A; PDB Molecule: fanconi anemia group m protein; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex
25	c4n7wA_	Alignment	not modelled	11.0	10	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
26	c6humC_	Alignment	not modelled	10.7	16	PDB header: proton transport Chain: C; PDB Molecule: nad(p)h-quinone oxidoreductase subunit 3; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
27	c5a43B_	Alignment	not modelled	10.6	21	PDB header: transport protein Chain: B; PDB Molecule: putative fluoride ion transporter crcb; PDBTitle: crystal structure of a dual topology fluoride ion channel.
28	d2dy1a3	Alignment	not modelled	9.4	31	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components

29	d1nkza_	Alignment	not modelled	8.7	21	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
30	d1pdza2	Alignment	not modelled	8.1	38	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
31	c2m46A_	Alignment	not modelled	8.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase, putative; PDBTitle: solution nmr structure of saci0876 from staphylococcus aureus col,2 nesg target zr353 and csgid target idp00841
32	c4kt5C_	Alignment	not modelled	8.0	38	PDB header: transcription regulator Chain: C: PDB Molecule: gria; PDBTitle: structure of gria-gria complex
33	c4bxoB_	Alignment	not modelled	7.3	7	PDB header: hydrolase/dna Chain: B: PDB Molecule: fanconi anemia-associated protein of 24 kda; PDBTitle: architecture and dna recognition elements of the fanconi anemia fancm-2 faap24 complex
34	d1ijda_	Alignment	not modelled	7.3	21	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
35	c6c6IN_	Alignment	not modelled	7.2	6	PDB header: membrane protein Chain: N: PDB Molecule: v0 assembly protein 1; PDBTitle: yeast vacuolar atpase vo in lipid nanodisc
36	c2ka1B_	Alignment	not modelled	6.8	31	PDB header: membrane protein Chain: B: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles
37	c2ka2A_	Alignment	not modelled	6.8	31	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
38	c2ka2B_	Alignment	not modelled	6.8	31	PDB header: membrane protein Chain: B: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
39	c2ka1A_	Alignment	not modelled	6.8	31	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnp3 transmembrane peptide dimer2 in detergent micelles
40	c2momC_	Alignment	not modelled	6.7	24	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
41	c2momB_	Alignment	not modelled	6.7	24	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
42	c4ky0B_	Alignment	not modelled	6.3	23	PDB header: transport protein, membrane protein Chain: B: PDB Molecule: proton/glutamate symporter, sdf family; PDBTitle: crystal structure of a substrate-free glutamate transporter homologue2 from thermococcus kodakarensis
43	c2ecfA_	Alignment	not modelled	6.2	31	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
44	c6oitG_	Alignment	not modelled	6.0	50	PDB header: plant protein Chain: G: PDB Molecule: protein chromatin remodeling 35; PDBTitle: cryoem structure of arabidopsis ddr' complex (drd1 peptide-dms3-rdm1)
45	c2j5dA_	Alignment	not modelled	5.6	30	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting protein 3; PDBTitle: nmr structure of bnp3 transmembrane domain in lipid bicelles
46	c3f0iA_	Alignment	not modelled	5.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: arsenate reductase from vibrio cholerae.
47	c6a69A_	Alignment	not modelled	5.4	10	PDB header: structural protein Chain: A: PDB Molecule: plasma membrane calcium-transporting atpase 1; PDBTitle: cryo-em structure of a p-type atpase
48	d2aq0a1	Alignment	not modelled	5.2	7	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like