



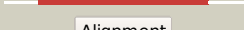

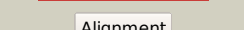







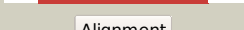

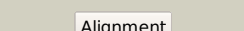

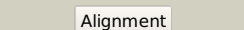


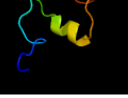


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0143c (-) _168702_170180
Date	Tue Jul 23 14:50:18 BST 2019
Unique Job ID	4e85f9d3a7d2c276

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1otsa_	 Alignment		100.0	23	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
2	c2ht2B_	 Alignment		100.0	23	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
3	d1kpla_	 Alignment		100.0	25	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
4	c3nd0A_	 Alignment		100.0	23	PDB header: transport protein Chain: A; PDB Molecule: sl0855 protein; PDBTitle: x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
5	c6coyB_	 Alignment		100.0	19	PDB header: transport protein Chain: B; PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, transmembrane domain
6	c6qvcB_	 Alignment		100.0	18	PDB header: membrane protein Chain: B; PDB Molecule: chloride channel protein 1; PDBTitle: cryoem structure of the human clc-1 chloride channel, cbs state 1
7	c5tr1A_	 Alignment		100.0	18	PDB header: transport protein Chain: A; PDB Molecule: chloride channel protein; PDBTitle: cryo-electron microscopy structure of a bovine clc-k chloride channel,2 alternate (class 2) conformation
8	c3orgB_	 Alignment		100.0	22	PDB header: transport protein Chain: B; PDB Molecule: cmclc; PDBTitle: crystal structure of a eukaryotic clc transporter
9	c6d0nA_	 Alignment		100.0	23	PDB header: transport protein Chain: A; PDB Molecule: clc-type fluoride/proton antiporter; PDBTitle: crystal structure of a clc-type fluoride/proton antiporter, v319g2 mutant
10	c3qe7A_	 Alignment		24.4	13	PDB header: transport protein Chain: A; PDB Molecule: uracil permease; PDBTitle: crystal structure of uracil transporter--uraa
11	c2inpE_	 Alignment		15.9	15	PDB header: oxidoreductase Chain: E; PDB Molecule: phenol hydroxylase component pho; PDBTitle: structure of the phenol hydroxylase-regulatory protein2 complex

12	c5xyie_	Alignment		12.2	10	PDB header: ribosome Chain: E; PDB Molecule: 40s ribosomal protein s4; PDBTitle: small subunit of trichomonas vaginalis ribosome
13	c3m9hB_	Alignment		10.9	38	PDB header: chaperone Chain: B; PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain of the2 mycobacterium tuberculosis proteasomal atpase mpa
14	c3d9sB_	Alignment		10.4	18	PDB header: membrane protein Chain: B; PDB Molecule: aquaporin-5; PDBTitle: human aquaporin 5 (aqp5) - high resolution x-ray structure
15	c2kjfA_	Alignment		9.4	24	PDB header: antimicrobial protein Chain: A; PDB Molecule: carnocyclin-a; PDBTitle: the solution structure of the circular bacteriocin2 carnocyclin a (ccla)
16	c6m97A_	Alignment		9.2	13	PDB header: transport protein Chain: A; PDB Molecule: chimera protein of high affinity copper uptake protein 1 PDBTitle: crystal structure of the high-affinity copper transporter ctr1
17	c2kncA_	Alignment		9.1	14	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
18	c5cehA_	Alignment		8.1	40	PDB header: oxidoreductase/inhibitor Chain: A; PDB Molecule: lysine-specific demethylase 5a; PDBTitle: structure of histone lysine demethylase kdm5a in complex with2 selective inhibitor
19	d1j4na_	Alignment		7.8	19	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
20	c2mgyA_	Alignment		7.8	11	PDB header: membrane protein Chain: A; PDB Molecule: translocator protein; PDBTitle: solution structure of the mitochondrial translocator protein (tspo) in2 complex with its high-affinity ligand pk11195
21	c3fhkF_	Alignment	not modelled	7.4	38	PDB header: structural genomics, unknown function Chain: F; PDB Molecule: upf0403 protein yphp; PDBTitle: crystal structure of apc1446, b.subtilis yphp disulfide isomerase
22	c4iqpA_	Alignment	not modelled	7.1	40	PDB header: structural protein Chain: A; PDB Molecule: os05g0196500 protein; PDBTitle: histone h3 lysine 4 demethylating rice jmj703 apo enzyme
23	c3opwA_	Alignment	not modelled	7.0	30	PDB header: oxidoreductase Chain: A; PDB Molecule: dna damage-responsive transcriptional repressor rph1; PDBTitle: crystal structure of the rph1 catalytic core
24	c5ykna_	Alignment	not modelled	6.7	40	PDB header: gene regulation Chain: A; PDB Molecule: probable lysine-specific demethylase jmj14; PDBTitle: crystal structure of arabidopsis thaliana jmj14 catalytic domain
25	d2qtva4	Alignment	not modelled	6.7	11	Fold: Gelsolin-like Superfamily: C-terminal, gelsolin-like domain of Sec23/24 Family: C-terminal, gelsolin-like domain of Sec23/24
26	c5a1fa_	Alignment	not modelled	6.6	40	PDB header: oxidoreductase Chain: A; PDB Molecule: lysine-specific demethylase 5b, lysine-specific PDBTitle: crystal structure of the catalytic domain of plu1 in complex with2 n-oxalylglycine.
27	c6ip4A_	Alignment	not modelled	6.5	50	PDB header: gene regulation Chain: A; PDB Molecule: arabidopsis jmj13; PDBTitle: crystal structure of arabidopsis thaliana jmj13 catalytic domain in2 complex with nog and an h3k27me3 peptide
28	c5a1sB_	Alignment	not modelled	6.5	16	PDB header: transport protein Chain: B; PDB Molecule: citrate-sodium symporter; PDBTitle: crystal structure of the sodium-dependent citrate

						symporter secits2 form salmonella enterica.
29	c4k1cB_	Alignment	not modelled	6.4	20	PDB header: membrane protein/metal transport Chain: B: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
30	c3twkB_	Alignment	not modelled	6.4	25	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
31	c2w2iC_	Alignment	not modelled	6.3	40	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate oxygenase; PDBTitle: crystal structure of the human 2-oxoglutarate oxygenase2 loc390245
32	c4k1cA_	Alignment	not modelled	6.1	19	PDB header: membrane protein/metal transport Chain: A: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
33	c5sv9B_	Alignment	not modelled	5.9	15	PDB header: transport protein Chain: B: PDB Molecule: bor1p boron transporter; PDBTitle: structure of the slc4 transporter bor1p in an inward-facing2 conformation
34	c2os2A_	Alignment	not modelled	5.5	40	PDB header: oxidoreductase Chain: A: PDB Molecule: jmjc domain-containing histone demethylation protein 3a; PDBTitle: crystal structure of jmjd2a complexed with histone h3 peptide2 trimethylated at lys36
35	c3iz6Z_	Alignment	not modelled	5.3	14	PDB header: ribosome Chain: Z: PDB Molecule: 40s ribosomal protein s30 (s30e); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
36	c2q8eB_	Alignment	not modelled	5.3	40	PDB header: oxidoreductase Chain: B: PDB Molecule: jmjc domain-containing histone demethylation protein 3a; PDBTitle: specificity and mechanism of jmjd2a, a trimethyllysine-specific2 histone demethylase
37	c6hu9I_	Alignment	not modelled	5.1	25	PDB header: oxidoreductase/electron transport Chain: L: PDB Molecule: cytochrome b-c1 complex subunit 1, mitochondrial; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
38	c6hu9x_	Alignment	not modelled	5.1	25	PDB header: oxidoreductase/electron transport Chain: X: PDB Molecule: PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
39	c5x1gC_	Alignment	not modelled	5.0	6	PDB header: structural protein Chain: C: PDB Molecule: wasp homolog-associated protein with actin, membranes and PDBTitle: whamm's microtubule binding motif