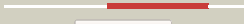

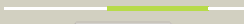

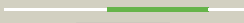





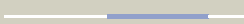
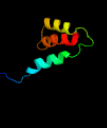


















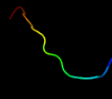


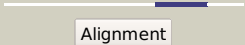


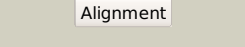
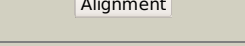
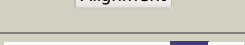

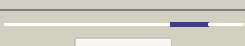
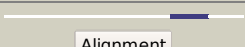

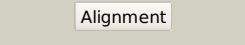
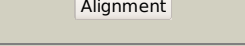
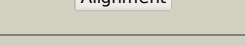


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1615_(-)_1815260_1815700
Date	Fri Aug 2 13:30:20 BST 2019
Unique Job ID	09c5a55374337caf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6o7ua_	 Alignment		91.9	21	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
2	c5gasN_	 Alignment		66.7	20	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
3	c5i1mV_	 Alignment		54.4	17	PDB header: membrane protein Chain: V: PDB Molecule: v-type proton atpase subunit a, vacuolar isoform; PDBTitle: yeast v-atpase average of densities, a subunit segment
4	d1kf6d_	 Alignment		52.4	25	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
5	c6o7xa_	 Alignment		43.4	28	PDB header: membrane protein Chain: A: PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
6	c5voxb_	 Alignment		25.7	16	PDB header: hydrolase Chain: B: PDB Molecule: v-type proton atpase subunit b; PDBTitle: yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
7	c2aklA_	 Alignment		25.5	42	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phna-like protein pa0128; PDBTitle: solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
8	d1epwa2	 Alignment		24.9	33	Fold: beta-Trefoil Superfamily: STI-like Family: Clostridium neurotoxins, C-terminal domain
9	c1erfA_	 Alignment		24.0	42	PDB header: viral protein Chain: A: PDB Molecule: transmembrane glycoprotein; PDBTitle: conformational mapping of the n-terminal fusion peptide of2 hiv-1 gp41 using 13c-enhanced fourier transform infrared3 spectroscopy (ftir)
10	c2pjvA_	 Alignment		17.9	42	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: solution structure of hiv-1 gp41 fusion domain bound to dpc micelle
11	c5xvjB_	 Alignment		15.6	21	PDB header: gene regulation Chain: B: PDB Molecule: phd finger protein alfin-like 7; PDBTitle: crystal structure of al7 pal domain

12	c5tj5A_	Alignment		15.5	18	PDB header: motor protein Chain: A: PDB Molecule: v-type proton atpase subunit a; PDBTitle: atomic model for the membrane-embedded motor of a eukaryotic v-atpase
13	c5nwuA_	Alignment		14.8	44	PDB header: viral protein Chain: A: PDB Molecule: wtfp-tag, gp41; PDBTitle: nmr assignment and structure of a peptide derived from the fusion2 peptide of hiv-1 gp41 in the presence of hexafluoroisopropanol
14	c6cfwB_	Alignment		13.7	27	PDB header: membrane protein Chain: B: PDB Molecule: monovalent cation/h+ antiporter subunit f; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
15	c2jxfA_	Alignment		11.9	23	PDB header: viral protein, membrane protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: the solution structure of hcv ns4b(40-69)
16	c2ariaA_	Alignment		8.8	22	PDB header: viral protein Chain: A: PDB Molecule: envelope polyprotein gp160; PDBTitle: solution structure of micelle-bound fusion domain of hiv-12 gp41
17	c4nl6C_	Alignment		8.0	12	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
18	c1p5aA_	Alignment		7.5	42	PDB header: viral protein Chain: A: PDB Molecule: envelope polyprotein gp160; PDBTitle: conformational mapping of the n-terminal peptide of hiv-12 gp41 in lipid detergent and aqueous environments using 13c-3 enhanced fourier transform infrared spectroscopy
19	c5xtdo_	Alignment		7.5	16	PDB header: oxidoreductase/electron transport Chain: O: PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 2, PDBTitle: cryo-em structure of human respiratory complex i
20	c1s0bA_	Alignment		7.4	33	PDB header: toxin, hydrolase Chain: A: PDB Molecule: botulinum neurotoxin type b; PDBTitle: crystal structure of botulinum neurotoxin type b at ph 4.0
21	c4pv1E_	Alignment	not modelled	7.2	12	PDB header: electron transport/inhibitor Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: cytochrome b6f structure from m. lamosus with the quinone analog2 inhibitor stigmatellin
22	c4i7zE_	Alignment	not modelled	7.2	12	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of cytochrome b6f in dopg, with disordered rieske2 iron-sulfur protein soluble domain
23	c5vf3Z_	Alignment	not modelled	6.4	31	PDB header: virus Chain: Z: PDB Molecule: highly immunogenic outer capsid protein; PDBTitle: bacteriophage t4 isometric capsid
24	c5ldwg_	Alignment	not modelled	6.4	18	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class1
25	c6b4iD_	Alignment	not modelled	6.3	20	PDB header: transport protein Chain: D: PDB Molecule: nucleoporin like 2; PDBTitle: crystal structure of human gle1 ctd-nup42 gbm-ddx19b(adp) complex
26	d3btaa2	Alignment	not modelled	6.3	17	Fold: beta-Trefoil Superfamily: STI-like Family: Clostridium neurotoxins, C-terminal domain
27	c6hu9t_	Alignment	not modelled	6.2	23	PDB header: oxidoreductase/electron transport Chain: T: PDB Molecule: cytochrome b-c1 complex subunit 9; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
28	c3jcuw_	Alignment	not modelled	6.1	20	PDB header: membrane protein Chain: W: PDB Molecule: photosystem ii reaction center w protein, chloroplastic; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution

29	d1kf6c_	 Alignment	not modelled	6.0	9	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
30	c6b4jD_	 Alignment	not modelled	5.9	20	PDB header: transport protein Chain: D: PDB Molecule: nucleoporin like 2; PDBTitle: crystal structure of human gle1 ctd-nup42 gbm-ddx19b(amppnp) complex
31	d3pcca_	 Alignment	not modelled	5.9	35	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
32	c2e74E_	 Alignment	not modelled	5.7	12	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex from m.laminosus
33	c4h13E_	 Alignment	not modelled	5.7	12	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex from mastigocladus2 laminosus with tds
34	c2e76E_	 Alignment	not modelled	5.7	12	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
35	d2e74e1	 Alignment	not modelled	5.7	12	Fold: Single transmembrane helix Superfamily: PetL subunit of the cytochrome b6f complex Family: PetL subunit of the cytochrome b6f complex
36	c2e75E_	 Alignment	not modelled	5.7	12	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
37	c4h0IE_	 Alignment	not modelled	5.7	12	PDB header: photosynthesis Chain: E: PDB Molecule: cytochrome b6-f complex subunit 6; PDBTitle: cytochrome b6f complex crystal structure from mastigocladus laminosus2 with n-side inhibitor nqno
38	c1vf5R_	 Alignment	not modelled	5.7	12	PDB header: photosynthesis Chain: R: PDB Molecule: protein pet l; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
39	d2burb1	 Alignment	not modelled	5.6	35	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
40	d3pccm_	 Alignment	not modelled	5.5	29	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
41	c4l6uB_	 Alignment	not modelled	5.5	33	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of af1868: cmr1 subunit of the cmr rna silencing2 complex
42	d2j8c1l	 Alignment	not modelled	5.4	30	Fold: Bacterial photosystem II reaction centre, L and M subunits Superfamily: Bacterial photosystem II reaction centre, L and M subunits Family: Bacterial photosystem II reaction centre, L and M subunits
43	c2boyC_	 Alignment	not modelled	5.4	47	PDB header: oxidoreductase Chain: C: PDB Molecule: 3-chlorocatechol 1,2-dioxygenase; PDBTitle: crystal structure of 3-chlorocatechol 1,2-dioxygenase from rhodococcus2 opacus 1cp