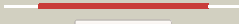



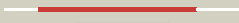


















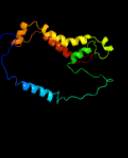



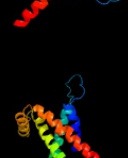

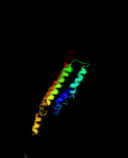
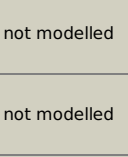


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2196_(qcrB)_2459686_2461335
Date	Mon Aug 5 13:25:32 BST 2019
Unique Job ID	00c4330076072f7e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6hwhb_	 Alignment		100.0	83	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
2	c2qjkM_	 Alignment		100.0	22	PDB header: electron transport Chain: M: PDB Molecule: cytochrome b; PDBTitle: crystal structure analysis of mutant rhodobacter2 sphaeroides bc1 with stigmatellin and antimycin
3	c3cx5N_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: N: PDB Molecule: cytochrome b; PDBTitle: structure of complex iii with bound cytochrome c in reduced state and2 definition of a minimal core interface for electron transfer.
4	c3cwbC_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome b; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
5	d3cx5c2	 Alignment		100.0	22	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
6	d1bcc3	 Alignment		100.0	21	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
7	d1ppjc2	 Alignment		100.0	24	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
8	d1q90b_	 Alignment		100.0	27	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
9	d2e74a1	 Alignment		100.0	31	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
10	d2e74b1	 Alignment		100.0	19	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
11	d1q90d_	 Alignment		99.9	18	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)

12	d3cx5c1	Alignment		99.9	14	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
13	d1vfb5b	Alignment		99.9	19	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
14	d1ppjc1	Alignment		99.9	14	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
15	d1bccc2	Alignment		99.9	16	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
16	d1kqfc	Alignment		97.4	11	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Formate dehydrogenase N, cytochrome (gamma) subunit
17	c4gd3A	Alignment		96.0	17	PDB header: oxidoreductase/electron transport Chain: A: PDB Molecule: ni/fe-hydrogenase 1 b-type cytochrome subunit; PDBTitle: structure of e. coli hydrogenase-1 in complex with cytochrome b
18	c4gd3B	Alignment		96.0	17	PDB header: oxidoreductase/electron transport Chain: B: PDB Molecule: ni/fe-hydrogenase 1 b-type cytochrome subunit; PDBTitle: structure of e. coli hydrogenase-1 in complex with cytochrome b
19	c5oc0A	Alignment		86.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b561; PDBTitle: structure of e. coli superoxide oxidase
20	c4aq5B	Alignment		69.4	15	PDB header: membrane protein Chain: B: PDB Molecule: acetylcholine receptor beta subunit; PDBTitle: gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)
21	c3aygA	Alignment	not modelled	62.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric oxide reductase; PDBTitle: crystal structure of nitric oxide reductase complex with hqno
22	c2bg9B	Alignment	not modelled	61.1	15	PDB header: ion channel/receptor Chain: B: PDB Molecule: acetylcholine receptor protein, beta chain; PDBTitle: refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
23	c5xmjG	Alignment	not modelled	52.6	13	PDB header: electron transport Chain: G: PDB Molecule: fumarate reductase respiratory complex; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
24	c4hydA	Alignment	not modelled	49.4	20	PDB header: membrane protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a presenilin family intramembrane aspartate protease in2 c2221 space group
25	c6rdi8	Alignment	not modelled	44.1	23	PDB header: proton transport Chain: 8: PDB Molecule: mitochondrial atp synthase subunit asa8; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1a,2 monomer-masked refinement
26	c6rdr8	Alignment	not modelled	44.1	23	PDB header: proton transport Chain: 8: PDB Molecule: mitochondrial atp synthase subunit asa8; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1d,2 monomer-masked refinement
27	d1z9ha1	Alignment	not modelled	39.4	23	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
28	c5o0tA	Alignment	not modelled	28.3	17	PDB header: membrane protein Chain: A: PDB Molecule: putative ferric reductase; PDBTitle: crystal structure of trans-membrane domain of cylindrospermum stagnale2 nadph-oxidase 5 (nox5) PDB header: photoreceptor

29	c1bhba_	Alignment	not modelled	20.0	27	Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: three-dimensional structure of (1-71) bacterioopsin2 solubilized in methanol-chloroform and sds micelles3 determined by 15n-1h heteronuclear nmr spectroscopy
30	d1khba2	Alignment	not modelled	18.0	23	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
31	c2fahB_	Alignment	not modelled	16.2	16	PDB header: lyase Chain: B: PDB Molecule: phosphoenolpyruvate carboxykinase; PDBTitle: the structure of mitochondrial pepck, complex with mn and gdp
32	c6e8wC_	Alignment	not modelled	14.2	10	PDB header: viral protein Chain: C: PDB Molecule: envelope glycoprotein gp160; PDBTitle: mper-tm domain of hiv-1 envelope glycoprotein (env)
33	d1qlec_	Alignment	not modelled	12.0	13	Fold: Cytochrome c oxidase subunit III-like Superfamily: Cytochrome c oxidase subunit III-like Family: Cytochrome c oxidase subunit III-like
34	c2h3oA_	Alignment	not modelled	11.9	18	PDB header: membrane protein Chain: A: PDB Molecule: merf; PDBTitle: structure of merft, a membrane protein with two trans-2 membrane helices
35	d2bs2c1	Alignment	not modelled	11.2	12	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Fumarate reductase respiratory complex cytochrome b subunit, FrdC
36	c4lb6B_	Alignment	not modelled	9.8	39	PDB header: transferase/dna Chain: B: PDB Molecule: protein kinase containing z-dna binding domains; PDBTitle: crystal structure of pkz alpha in complex with ds(cg)6 (tetragonal2 form)
37	c5fshA_	Alignment	not modelled	9.7	14	PDB header: hydrolase Chain: A: PDB Molecule: csm6; PDBTitle: crystal structure of thermus thermophilus csm6
38	c2vpiA_	Alignment	not modelled	9.5	21	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
39	c2m67A_	Alignment	not modelled	9.1	14	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
40	d1pn2a1	Alignment	not modelled	8.6	37	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
41	c2mpnB_	Alignment	not modelled	8.4	20	PDB header: membrane protein Chain: B: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
42	d2e74g1	Alignment	not modelled	8.2	22	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
43	c2jh3C_	Alignment	not modelled	8.1	19	PDB header: ribosomal protein Chain: C: PDB Molecule: ribosomal protein s2-related protein; PDBTitle: the crystal structure of dr2241 from deinococcus2 radiodurans at 1.9 a resolution reveals a multi-domain3 protein with structural similarity to chelatases but also4 with two additional novel domains
44	d1s9ca2	Alignment	not modelled	8.1	37	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
45	c2zciD_	Alignment	not modelled	7.8	20	PDB header: signaling protein, lyase Chain: D: PDB Molecule: phosphoenolpyruvate carboxykinase [gtp]; PDBTitle: structure of a gtp-dependent bacterial pep-carboxykinase2 from corynebacterium glutamicum
46	d1m56c_	Alignment	not modelled	7.7	16	Fold: Cytochrome c oxidase subunit III-like Superfamily: Cytochrome c oxidase subunit III-like Family: Cytochrome c oxidase subunit III-like
47	c5jqfB_	Alignment	not modelled	7.7	70	PDB header: unknown function Chain: B: PDB Molecule: sphingopyxin i; PDBTitle: crystal structure of the lasso peptide sphingopyxin i (spi)
48	c5jqfA_	Alignment	not modelled	7.7	70	PDB header: unknown function Chain: A: PDB Molecule: sphingopyxin i; PDBTitle: crystal structure of the lasso peptide sphingopyxin i (spi)
49	c1y4eA_	Alignment	not modelled	7.4	22	PDB header: membrane protein Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: nmr structure of transmembrane segment iv of the nhe12 isoform of the na+/h+ exchanger
50	c2e76G_	Alignment	not modelled	7.2	21	PDB header: photosynthesis Chain: G: PDB Molecule: cytochrome b6-f complex subunit 5; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
51	c5zlgA_	Alignment	not modelled	7.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b reductase 1; PDBTitle: human duodenal cytochrome b (dcytb) in zinc ion and ascorbate bound2 form
52	c6elhA_	Alignment	not modelled	7.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide reductase; PDBTitle: low resolution structure of neisseria meningitidis qnor
53	d3byqa1	Alignment	not modelled	6.6	18	Fold: Bacillus chorismate mutase-like Superfamily: BB2672-like Family: BB2672-like
54	c5v2sA_	Alignment	not modelled	6.6	19	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex

						virus type i
55	c1gpmD_	Alignment	not modelled	6.5	17	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
56	d2gtaa1	Alignment	not modelled	6.5	16	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
57	c2kdrX_	Alignment	not modelled	6.4	23	PDB header: viral protein, membrane protein Chain: X: PDB Molecule: non-structural protein 4b; PDBTitle: solution structure of hcv ns4b(227-254)
58	c3omlA_	Alignment	not modelled	6.3	20	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: peroxisomal multifunctional enzyme type 2, cg3415; PDBTitle: structure of full-length peroxisomal multifunctional enzyme type 22 from drosophila melanogaster
59	c2micA_	Alignment	not modelled	6.1	27	PDB header: membrane protein Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
60	c2micB_	Alignment	not modelled	6.1	27	PDB header: membrane protein Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 16; PDBTitle: nmr structure of p75 transmembrane domain in dpc micelles
61	c2od8B_	Alignment	not modelled	6.1	15	PDB header: protein binding Chain: B: PDB Molecule: dna ligase i, mitochondrial precursor; PDBTitle: structure of a peptide derived from cdc9 bound to pcna
62	c1wa7B_	Alignment	not modelled	6.1	43	PDB header: sh3 domain Chain: B: PDB Molecule: hypothetical 28.7 kda protein in dhfr 3'region PDBTitle: sh3 domain of human lyn tyrosine kinase in complex with a2 herpesviral ligand
63	c1wazA_	Alignment	not modelled	6.0	21	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: nmr structure determination of the bacterial mercury transporter,2 merf, in micelles
64	c5tw7E_	Alignment	not modelled	5.9	17	PDB header: ligase Chain: E: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
65	d1gpm2	Alignment	not modelled	5.9	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
66	d1qdb_	Alignment	not modelled	5.8	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
67	c2j0bA_	Alignment	not modelled	5.7	50	PDB header: transferase Chain: A: PDB Molecule: beta-1,3-n-acetylglucosaminyltransferase manic fringe; PDBTitle: structure of the catalytic domain of mouse manic fringe in2 complex with udp and manganese
68	c5sy1A_	Alignment	not modelled	5.6	16	PDB header: membrane protein/calcium binding protein Chain: A: PDB Molecule: stra6; PDBTitle: structure of the stra6 receptor for retinol uptake in complex with2 calmodulin
69	c2n7iA_	Alignment	not modelled	5.6	35	PDB header: hormone receptor Chain: A: PDB Molecule: prolactin receptor; PDBTitle: nmr structure of the prolactin receptor transmembrane domain
70	c2n28A_	Alignment	not modelled	5.6	15	PDB header: viral protein Chain: A: PDB Molecule: protein vpu; PDBTitle: solid-state nmr structure of vpu
71	d2qj2a1	Alignment	not modelled	5.4	25	Fold: Hairpin loop containing domain-like Superfamily: Hairpin loop containing domain-like Family: Hairpin loop containing domain
72	d2zgw1	Alignment	not modelled	5.4	28	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: Biotin repressor (BirA)
73	c3msqC_	Alignment	not modelled	5.3	11	PDB header: biosynthetic protein Chain: C: PDB Molecule: putative ubiquinone biosynthesis protein; PDBTitle: crystal structure of a putative ubiquinone biosynthesis protein2 (npun02000094) from nostoc punctiforme pcc 73102 at 2.85 a resolution
74	d1k3ia1	Alignment	not modelled	5.2	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
75	c3jcuJ_	Alignment	not modelled	5.2	29	PDB header: membrane protein Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
76	c2kwvA_	Alignment	not modelled	5.2	44	PDB header: protein binding/signaling protein Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: solution structure of ubm1 of murine polymerase iota in complex with2 ubiquitin
77	d2p5ka1	Alignment	not modelled	5.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
78	c2xc7A_	Alignment	not modelled	5.2	11	PDB header: rna binding protein Chain: A: PDB Molecule: phosphorylated adapter rna export protein; PDBTitle: solution structure of phax-rbd in complex with srna
79	c6e1kA_	Alignment	not modelled	5.1	14	PDB header: membrane protein Chain: A: PDB Molecule: two pore calcium channel protein 1; PDBTitle: structure of attpc1(dde) reconstituted in saposin a with

				cat06 fab		
80	c6mk1V_	Alignment	not modelled	5.1	60	PDB header: protein fibril Chain: V: PDB Molecule: PDBTitle: cryo-em of self-assembly peptide filament heat_r1
81	d2d0oa3	Alignment	not modelled	5.1	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit