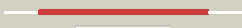










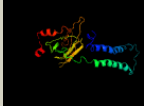












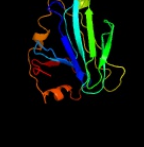



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2200c_(ctaC)_2463668_2464759
 Date Mon Aug 5 13:25:32 BST 2019
 Unique Job ID c7c937da3c8d3145

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6hwhL_	 Alignment		100.0	78	PDB header: electron transport Chain: L; PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of a functional obligate respiratory supercomplex from <i>Mycobacterium smegmatis</i>
2	c1m57H_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: H; PDB Molecule: cytochrome c oxidase; PDBTitle: structure of a functional obligate respiratory supercomplex from <i>Rhodospirillum rubrum</i> (eq(i-286) mutant)
3	clar1B_	 Alignment		100.0	25	PDB header: complex (oxidoreductase/antibody) Chain: B; PDB Molecule: cytochrome c oxidase; PDBTitle: structure at 2.7 angstrom resolution of the <i>Paracoccus denitrificans</i> two-subunit cytochrome c oxidase complexed with an antibody Fv fragment
4	c1qleB_	 Alignment		100.0	25	PDB header: oxidoreductase/immune system Chain: B; PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: cryo-structure of the <i>Paracoccus denitrificans</i> four-subunit cytochrome c oxidase in the completely oxidized state complexed with an antibody Fv fragment
5	c6hu9n_	 Alignment		100.0	22	PDB header: oxidoreductase/electron transport Chain: N; PDB Molecule: cytochrome b; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from <i>Saccharomyces cerevisiae</i>
6	c1fftG_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: G; PDB Molecule: ubiquinol oxidase; PDBTitle: the structure of ubiquinol oxidase from <i>Escherichia coli</i>
7	c1v55B_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: B; PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: bovine heart cytochrome c oxidase at the fully reduced state
8	c2yevB_	 Alignment		100.0	28	PDB header: electron transport Chain: B; PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of caa3-type cytochrome oxidase
9	d3ehbb1	 Alignment		100.0	28	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
10	d3dtub1	 Alignment		100.0	27	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
11	c4txvB_	 Alignment		100.0	27	PDB header: protein binding Chain: B; PDB Molecule: cytochrome c oxidase subunit ii; PDBTitle: crystal structure of the mixed disulfide intermediate between thioredoxin-like tlpas(c110s) and subunit ii of cytochrome c oxidase3 cox3cpd (c233s)

12	d1v54b1	Alignment		100.0	26	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
13	d1cyxa_	Alignment		100.0	23	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
14	c1cyxA_	Alignment		100.0	23	PDB header: electron transport Chain: A; PDB Molecule: cyoa; PDBTitle: quinol oxidase (periplasmic fragment of subunit ii with2 engineered cu-a binding site)(cyoa)
15	d1fftb1	Alignment		100.0	19	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
16	c1xmeB_	Alignment		100.0	18	PDB header: oxidoreductase Chain: B; PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: structure of recombinant cytochrome ba3 oxidase from thermus2 thermophilus
17	d2cuab_	Alignment		99.9	28	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
18	d2cuaa_	Alignment		99.9	28	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
19	d1fftb2	Alignment		99.8	21	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
20	d3ehbb2	Alignment		99.8	20	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
21	d3dtub2	Alignment	not modelled	99.8	23	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
22	d1fwxa1	Alignment	not modelled	99.8	20	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Nitrosocyanin
23	d1qnia1	Alignment	not modelled	99.7	24	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Nitrosocyanin
24	c3mk7F_	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: F; PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
25	d1libya_	Alignment	not modelled	99.6	23	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Nitrosocyanin
26	d1v54b2	Alignment	not modelled	99.5	11	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
27	c4f2fA_	Alignment	not modelled	99.2	17	PDB header: metal binding protein Chain: A; PDB Molecule: cation-transporting atpase, e1-e2 family protein; PDBTitle: crystal structure of the metal binding domain (mbd) of the2 streptococcus pneumoniae d39 cu(i) exporting p-type atpase copa with3 cu(i)
28	c2iwkB_	Alignment	not modelled	99.0	17	PDB header: oxidoreductase Chain: B; PDB Molecule: nitrous oxide reductase; PDBTitle: inhibitor-bound form of nitrous oxide reductase from2

					achromobacter cycloclastes at 1.7 angstrom resolution PDB header: oxidoreductase Chain: A: PDB Molecule: nitrous-oxide reductase; PDBTitle: shewanella denitrificans nitrous oxide reductase, app form
29	c5i5iA_	Alignment	not modelled	99.0	20
30	c3sbrF_	Alignment	not modelled	99.0	18
31	c4f2eA_	Alignment	not modelled	98.9	19
32	c4hcgA_	Alignment	not modelled	98.9	18
33	c1qniE_	Alignment	not modelled	98.9	18
34	c1fwxB_	Alignment	not modelled	98.7	14
35	d1paza_	Alignment	not modelled	97.1	16
36	d1qhqa_	Alignment	not modelled	97.0	18
37	d1bxua_	Alignment	not modelled	96.9	15
38	d1bqka_	Alignment	not modelled	96.8	18
39	c3ef4A_	Alignment	not modelled	96.7	19
40	c3ay2A_	Alignment	not modelled	96.6	13
41	d2ov0a1	Alignment	not modelled	96.5	20
42	d1cuoa_	Alignment	not modelled	96.4	16
43	d1iuza_	Alignment	not modelled	96.3	18
44	c3tu6A_	Alignment	not modelled	96.3	16
45	d1pmya_	Alignment	not modelled	96.3	16
46	d1e30a_	Alignment	not modelled	96.2	19
47	d1cc3a_	Alignment	not modelled	96.1	14
48	d1ag6a_	Alignment	not modelled	96.1	18
49	d1id2a_	Alignment	not modelled	96.1	17
50	c3c75B_	Alignment	not modelled	96.1	17
51	d1adwa_	Alignment	not modelled	96.1	21
52	c5fc9D_	Alignment	not modelled	96.1	19
53	c2aanA_	Alignment	not modelled	96.1	15
54	d1pcsa_	Alignment	not modelled	95.9	14
55	d2ccwa1	Alignment	not modelled	95.9	19

						Family: Plastocyanin/azurin-like
56	c2h47C_	Alignment	not modelled	95.8	10	PDB header: oxidoreductase/electron transport Chain: C: PDB Molecule: azurin; PDBTitle: crystal structure of an electron transfer complex between2 aromatic amine dehydrogenase and azurin from alcaligenes3 faecalis (form 1)
57	d1lazca_	Alignment	not modelled	95.7	18	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
58	d2plta_	Alignment	not modelled	95.7	23	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
59	d1nwpa_	Alignment	not modelled	95.7	11	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
60	d1plaa_	Alignment	not modelled	95.6	26	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
61	d7pcya_	Alignment	not modelled	95.5	19	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
62	d1mzya2	Alignment	not modelled	95.4	11	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
63	d1plca_	Alignment	not modelled	95.4	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
64	d1joia_	Alignment	not modelled	95.3	18	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
65	d2cj3a1	Alignment	not modelled	95.3	14	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
66	d9pcya_	Alignment	not modelled	95.2	22	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
67	d1rkra_	Alignment	not modelled	94.9	15	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
68	d1bypa_	Alignment	not modelled	94.8	24	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
69	d2jxma1	Alignment	not modelled	94.7	18	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
70	d1kdja_	Alignment	not modelled	94.6	17	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
71	d1jzga_	Alignment	not modelled	94.5	16	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
72	d2q5ba1	Alignment	not modelled	93.3	14	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
73	d1snra2	Alignment	not modelled	92.8	7	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
74	c4ax3A_	Alignment	not modelled	92.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: copper-containing nitrite reductase; PDBTitle: structure of three-domain heme-cu nitrite reductase from ralstonia2 pickettii at 1.6 a resolution
75	d1kbva1	Alignment	not modelled	91.9	14	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
76	d1kbva2	Alignment	not modelled	91.7	13	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
77	c3oa8B_	Alignment	not modelled	91.6	6	PDB header: heme-binding protein/heme-binding protei Chain: B: PDB Molecule: soxx; PDBTitle: diheme soxax
78	d2j5wa5	Alignment	not modelled	91.4	15	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
79	d1sddb2	Alignment	not modelled	91.3	12	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
80	d1kcwa2	Alignment	not modelled	90.0	13	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
81	c1kbwA_	Alignment	not modelled	89.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: major outer membrane protein pan 1; PDBTitle: crystal structure of the soluble domain of ania from2 neisseria gonorrhoeae
82	c1aq8B_	Alignment	not modelled	88.2	7	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrite reductase; PDBTitle: structure of alcaligenes faecalis nitrite reductase reduced2 with ascorbate

83	d2bw4a2	Alignment	not modelled	87.8	11	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
84	d1ndsA1	Alignment	not modelled	86.9	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
85	c1sddB_	Alignment	not modelled	86.5	12	PDB header: blood clotting Chain: B: PDB Molecule: coagulation factor v; PDBTitle: crystal structure of bovine factor vai
86	d1ndsA2	Alignment	not modelled	85.9	8	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
87	d1snra1	Alignment	not modelled	85.4	18	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
88	c1mzZC_	Alignment	not modelled	85.4	11	PDB header: oxidoreductase Chain: C: PDB Molecule: copper-containing nitrite reductase; PDBTitle: crystal structure of mutant (m182t)of nitrite reductase
89	c3cdzB_	Alignment	not modelled	84.2	21	PDB header: blood clotting Chain: B: PDB Molecule: coagulation factor viii light chain; PDBTitle: crystal structure of human factor viii
90	c2dv6F_	Alignment	not modelled	84.0	17	PDB header: oxidoreductase Chain: F: PDB Molecule: nitrite reductase; PDBTitle: crystal structure of nitrite reductase from hypomicrobium2 denitrificans
91	c1wa1X_	Alignment	not modelled	83.9	8	PDB header: reductase Chain: X: PDB Molecule: dissimilatory copper-containing nitrite reductase; PDBTitle: crystal structure of h313q mutant of alcaligenes xylooxidans nitrite2 reductase
92	c4knuB_	Alignment	not modelled	82.1	15	PDB header: oxidoreductase Chain: B: PDB Molecule: multicopper oxidase type 1; PDBTitle: copper nitrite reductase from nitrosomonas europaea at ph 6.5
93	c2kncA_	Alignment	not modelled	80.5	18	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
94	d2j5wa2	Alignment	not modelled	78.4	20	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
95	c3gdcC_	Alignment	not modelled	78.1	15	PDB header: oxidoreductase Chain: C: PDB Molecule: multicopper oxidase; PDBTitle: crystal structure of multicopper oxidase
96	c3kw8A_	Alignment	not modelled	77.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative copper oxidase; PDBTitle: two-domain laccase from streptomyces coelicolor at 2.3 a resolution
97	d1mzya1	Alignment	not modelled	75.6	20	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
98	c3t9wA_	Alignment	not modelled	74.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: small laccase, multi-copper oxidase; PDBTitle: small laccase from amycolatopsis sp. atcc 39116
99	d1aoza3	Alignment	not modelled	72.6	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
100	d2bw4a1	Alignment	not modelled	72.5	23	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
101	c2zooA_	Alignment	not modelled	72.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: probable nitrite reductase; PDBTitle: crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125
102	c4djiA_	Alignment	not modelled	72.1	12	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
103	c2k1aA_	Alignment	not modelled	71.3	17	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: bicelle-embedded integrin alpha(iiB) transmembrane segment
104	c5z1A_	Alignment	not modelled	65.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative copper-type nitrite reductase; PDBTitle: hexameric structure of copper-containing nitrite reductase of an2 anammox organism ksu-1
105	c2l8sA_	Alignment	not modelled	63.7	13	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
106	c6nd1E_	Alignment	not modelled	61.1	25	PDB header: protein transport Chain: E: PDB Molecule: translocation protein sec66; PDBTitle: cryoem structure of the sec complex from yeast
107	d1ws8a_	Alignment	not modelled	60.8	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
108	c3cg8B_	Alignment	not modelled	60.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: laccase; PDBTitle: laccase from streptomyces coelicolor
109	c3wkoA_	Alignment	not modelled	60.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: copper-containing nitrite reductase from thermophilic

					bacterium2_geobacillus_thermodenitrificans
110	c3tasC	Alignment	not modelled	58.8	22 PDB header: oxidoreductase Chain: C: PDB Molecule: small laccase, multi-copper oxidase; PDBTitle: small laccase from streptomyces viridosporus t7a
111	d2d7pa1	Alignment	not modelled	57.6	13 Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
112	c6c14A	Alignment	not modelled	57.4	10 PDB header: membrane protein, metal transport Chain: A: PDB Molecule: protocadherin-15; PDBTitle: cryoem structure of mouse pcdh15-1ec-lhfp15 complex
113	c1x9rA	Alignment	not modelled	56.6	21 PDB header: electron transport Chain: A: PDB Molecule: umecyanin; PDBTitle: umecyanin from horse raddish- crystal structure of the2 oxidised form
114	c6hbeA	Alignment	not modelled	53.4	31 PDB header: oxidoreductase Chain: A: PDB Molecule: copper-containing nitrite reductase; PDBTitle: cu-containing nitrite reductase (nirk) from thermus scotoductus sa-01
115	d2auwa1	Alignment	not modelled	51.9	16 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
116	c1kcwA	Alignment	not modelled	47.5	14 PDB header: oxidoreductase Chain: A: PDB Molecule: ceruloplasmin; PDBTitle: x-ray crystal structure of human ceruloplasmin at 3.0 angstroms
117	c2r7eB	Alignment	not modelled	46.1	24 PDB header: blood clotting Chain: B: PDB Molecule: coagulation factor viii; PDBTitle: crystal structure analysis of coagulation factor viii
118	d1hfua3	Alignment	not modelled	42.9	21 Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
119	c2icuB	Alignment	not modelled	40.1	21 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein yedk; PDBTitle: crystal structure of hypothetical protein yedk from escherichia coli
120	d1hfua1	Alignment	not modelled	40.0	14 Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins