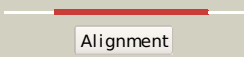

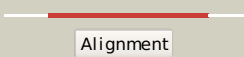

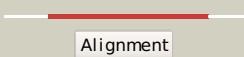

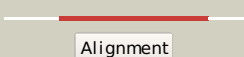

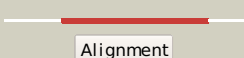

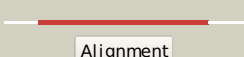

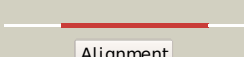

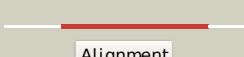

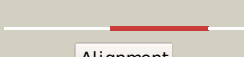

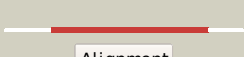



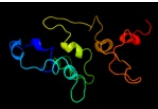



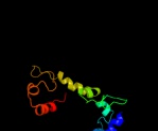






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2p0bA_	 Alignment		99.8	100	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c-type protein nrfb; PDBTitle: crystal structure of chemically-reduced e.coli nrfb
2	c1oahA_	 Alignment		99.3	26	PDB header: reductase Chain: A: PDB Molecule: cytochrome c nitrite reductase; PDBTitle: cytochrome c nitrite reductase from desulfovibrio2 desulfuricans atcc 27774: the relevance of the two3 calcium sites in the structure of the catalytic subunit4 (nrfa).
3	d1oaha_	 Alignment		99.3	26	Fold: Multi-heme cytochromes Superfamily: Multi-heme cytochromes Family: Di-heme elbow motif
4	d2rdza1	 Alignment		99.1	23	Fold: Multi-heme cytochromes Superfamily: Multi-heme cytochromes Family: Di-heme elbow motif
5	d1fs7a_	 Alignment		99.1	29	Fold: Multi-heme cytochromes Superfamily: Multi-heme cytochromes Family: Di-heme elbow motif
6	c2j7aC_	 Alignment		99.1	15	PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome c quinol dehydrogenase nrhf; PDBTitle: crystal structure of cytochrome c nitrite reductase nrfa2 complex from desulfovibrio vulgaris
7	c1fs9A_	 Alignment		99.1	29	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c nitrite reductase; PDBTitle: cytochrome c nitrite reductase from wolinetella succinogenes-azide2 complex
8	d1qdba_	 Alignment		99.0	21	Fold: Multi-heme cytochromes Superfamily: Multi-heme cytochromes Family: Di-heme elbow motif
9	d1m1qa_	 Alignment		99.0	30	Fold: Multi-heme cytochromes Superfamily: Multi-heme cytochromes Family: Di-heme elbow motif
10	c3pmqA_	 Alignment		98.9	19	PDB header: electron transport Chain: A: PDB Molecule: decaheme cytochrome c mtrf; PDBTitle: crystal structure of the outer membrane decaheme cytochrome mtrf
11	c2k3vA_	 Alignment		98.8	36	PDB header: electron transport Chain: A: PDB Molecule: tetraheme cytochrome c-type; PDBTitle: solution structure of a tetrahaem cytochrome from2 shewanella frigidimarina

12	c2vr0A_	Alignment		98.7	25	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c nitrite reductase, catalytic subunit nfrA; PDBTitle: crystal structure of cytochrome c nitrite reductase nrfha2 complex bound to the hqno inhibitor
13	c2j7aE_	Alignment		98.7	23	PDB header: oxidoreductase Chain: E: PDB Molecule: cytochrome c nitrite reductase nrfA; PDBTitle: crystal structure of cytochrome c nitrite reductase nrfha2 complex from desulfovibrio vulgaris
14	c2cvcA_	Alignment		98.7	17	PDB header: electron transport Chain: A: PDB Molecule: high-molecular-weight cytochrome c precursor; PDBTitle: crystal structure of high-molecular weight cytochrome c2 from desulfovibrio vulgaris (hildenborough)
15	d1y0pa1	Alignment		98.6	29	Fold: Multi-heme cytochromes Superfamily: Multi-heme cytochromes Family: Di-heme elbow motif
16	c1fgjA_	Alignment		98.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxylamine oxidoreductase; PDBTitle: x-ray structure of hydroxylamine oxidoreductase
17	d1fgja_	Alignment		98.6	24	Fold: Multi-heme cytochromes Superfamily: Multi-heme cytochromes Family: Di-heme elbow motif
18	c2e84A_	Alignment		98.6	17	PDB header: electron transport Chain: A: PDB Molecule: high-molecular-weight cytochrome c; PDBTitle: crystal structure of high-molecular weight cytochrome c2 from desulfovibrio vulgaris (miyazaki f) in the presence3 of zinc ion
19	c3f29A_	Alignment		98.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: eight-heme nitrite reductase; PDBTitle: structure of the thioalkalivibrio nitratreducens2 cytochrome c nitrite reductase in complex with sulfite
20	c3oueA_	Alignment		98.5	25	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: structure of c-terminal hexaheme fragment of gsu1996
21	d1d4ca1	Alignment	not modelled	98.5	26	Fold: Multi-heme cytochromes Superfamily: Multi-heme cytochromes Family: Di-heme elbow motif
22	d1sp3a_	Alignment	not modelled	98.5	18	Fold: Multi-heme cytochromes Superfamily: Multi-heme cytochromes Family: Di-heme elbow motif
23	d1qo8a1	Alignment	not modelled	98.5	30	Fold: Multi-heme cytochromes Superfamily: Multi-heme cytochromes Family: Di-heme elbow motif
24	c1qo8A_	Alignment	not modelled	98.3	32	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
25	d2cvca1	Alignment	not modelled	98.3	18	Fold: Multi-heme cytochromes Superfamily: Multi-heme cytochromes Family: Cytochrome c3-like
26	c3ouqa_	Alignment	not modelled	98.3	20	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: structure of n-terminal hexaheme fragment of gsu1996
27	d1ft5a_	Alignment	not modelled	98.3	20	Fold: Multi-heme cytochromes Superfamily: Multi-heme cytochromes Family: Di-heme elbow motif
28	c1jrxA_	Alignment	not modelled	98.2	34	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
29	c3ov0A_	Alignment	not modelled	97.8	26	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: structure of dodecaheme cytochrome c gsu1996

30	d1ofwa_	Alignment	not modelled	97.8	15	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
31	c2a3mA_	Alignment	not modelled	97.7	20	PDB header: electron transport Chain: A: PDB Molecule: cog3005: nitrate/tmao reductases, membrane-bound tetraheme PDBTitle: structure of desulfovibrio desulfuricans g20 tetraheme cytochrome2 (oxidized form)
32	c1z1nX_	Alignment	not modelled	97.7	18	PDB header: electron transport Chain: X: PDB Molecule: sixteen heme cytochrome; PDBTitle: crystal structure of the sixteen heme cytochrome from desulfovibrio2 gigas
33	d19hca_	Alignment	not modelled	97.5	22	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
34	d1duwa_	Alignment	not modelled	97.1	18	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
35	d1i77a_	Alignment	not modelled	97.0	18	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
36	d1j0pa_	Alignment	not modelled	96.9	21	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
37	c2bq4A_	Alignment	not modelled	96.6	18	PDB header: electron transport Chain: A: PDB Molecule: basic cytochrome c3; PDBTitle: crystal structure of type i cytochrome c3 from2 desulfovibrio africanus
38	d1aqea_	Alignment	not modelled	96.5	26	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
39	d3caoa_	Alignment	not modelled	96.2	23	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
40	d1up9a_	Alignment	not modelled	96.2	20	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
41	d2cy3a_	Alignment	not modelled	96.2	22	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
42	c1d4cB_	Alignment	not modelled	96.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: flavocytochrome c fumarate reductase; PDBTitle: crystal structure of the uncomplexed form of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1
43	d2ctha_	Alignment	not modelled	95.7	21	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
44	d1gyoa_	Alignment	not modelled	95.6	16	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
45	c3h34A_	Alignment	not modelled	94.6	24	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c7; PDBTitle: ppce, a cytochrome c7 from geobacter sulfurreducens
46	c3h4nB_	Alignment	not modelled	94.6	18	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c7; PDBTitle: ppcd, a cytochrome c7 from geobacter sulfurreducens
47	d1wada_	Alignment	not modelled	94.1	14	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
48	d1rwja_	Alignment	not modelled	93.7	23	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
49	c3h33A_	Alignment	not modelled	92.8	23	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c7; PDBTitle: ppcc, a cytochrome c7 from geobacter sulfurreducens
50	d1hh5a_	Alignment	not modelled	92.5	20	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
51	d1os6a_	Alignment	not modelled	92.1	23	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Cytochrome c3-like
52	d1ogyb_	Alignment	not modelled	90.8	17	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif
53	d2i5nc1	Alignment	not modelled	88.5	13	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Photosynthetic reaction centre (cytochrome subunit)
54	c2jblC_	Alignment	not modelled	88.5	13	PDB header: electron transport Chain: C: PDB Molecule: photosynthetic reaction center cytochrome c PDBTitle: photosynthetic reaction center from blastochloris viridis
55	d1h21a_	Alignment	not modelled	82.5	27	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif
56	c1jniA_	Alignment	not modelled	76.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: di heme cytochrome c napb; PDBTitle: structure of the napb subunit of the periplasmic nitrate2 reductase from haemophilus influenzae.

57	d1jnia_	Alignment	not modelled	76.6	22	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif
58	c3o5aB_	Alignment	not modelled	64.7	27	PDB header: oxidoreductase Chain: B: PDB Molecule: di-heme cytochrome c napb; PDBTitle: crystal structure of partially reduced periplasmic nitrate reductase2 from cupriavidus necator using ionic liquids
59	c3o0rC_	Alignment	not modelled	57.8	10	PDB header: immune system/oxidoreductase Chain: C: PDB Molecule: nitric oxide reductase subunit c; PDBTitle: crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
60	d1pbya2	Alignment	not modelled	47.3	31	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
61	d1iqca1	Alignment	not modelled	44.4	29	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
62	d1jmx2	Alignment	not modelled	44.1	38	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
63	d1nmla1	Alignment	not modelled	42.1	19	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
64	d1eb7a1	Alignment	not modelled	40.7	17	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
65	d1bbha_	Alignment	not modelled	36.6	31	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
66	c2czsB_	Alignment	not modelled	35.5	18	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c, putative; PDBTitle: crystal structure analysis of the di-heme c-type cytochrome dhc2
67	d1mqva_	Alignment	not modelled	33.5	38	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
68	d1eysc_	Alignment	not modelled	32.5	36	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Photosynthetic reaction centre (cytochrome subunit)
69	c1eysC_	Alignment	not modelled	32.5	36	PDB header: electron transport Chain: C: PDB Molecule: photosynthetic reaction center; PDBTitle: crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
70	c3l4oB_	Alignment	not modelled	30.5	36	PDB header: oxidoreductase/electron transport Chain: B: PDB Molecule: methylamine utilization protein maug; PDBTitle: crystal structure of the maug/pre-methylamine dehydrogenase complex2 after treatment with hydrogen peroxide
71	d1gqaa_	Alignment	not modelled	30.3	38	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
72	c1nmlA_	Alignment	not modelled	28.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: di-haem cytochrome c peroxidase; PDBTitle: di-haemic cytochrome c peroxidase from pseudomonas nautica 617, form2 in (ph 4.0)
73	c2c1uB_	Alignment	not modelled	28.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: di-haem cytochrome c peroxidase; PDBTitle: crystal structure of the di-haem cytochrome c peroxidase2 from paracoccus pantotrophus - oxidised form
74	d2j8wa1	Alignment	not modelled	28.8	25	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
75	d1fcdc2	Alignment	not modelled	28.8	25	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
76	d1e85a_	Alignment	not modelled	28.1	33	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
77	d1s05a_	Alignment	not modelled	27.7	38	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
78	c3hq7A_	Alignment	not modelled	25.1	27	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c551 peroxidase; PDBTitle: ccpa from g. sulfurreducens, g94k/k97q/r100i variant
79	c3o5cA_	Alignment	not modelled	25.1	24	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c551 peroxidase; PDBTitle: cytochrome c peroxidase bccp of shewanella oneidensis
80	d1cpqa_	Alignment	not modelled	24.8	45	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
81	d2ccya_	Alignment	not modelled	24.3	36	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
82	c2vhdB_	Alignment	not modelled	23.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c551 peroxidase; PDBTitle: crystal structure of the di-haem cytochrome c peroxidase2 from pseudomonas aeruginosa - mixed valence form
83	d1h32a1	Alignment	not modelled	23.1	29	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c SoxA

84	d1wejf_	Alignment	not modelled	23.0	17	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
85	c3oa8B_	Alignment	not modelled	22.7	38	PDB header: heme-binding protein/heme-binding protei Chain: B: PDB Molecule: soxx; PDBTitle: diheme soxax
86	c1w2lA_	Alignment	not modelled	22.6	50	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome oxidase subunit ii; PDBTitle: cytochrome c domain of caa3 oxygen oxidoreductase
87	c1iqcB_	Alignment	not modelled	21.7	29	PDB header: oxidoreductase Chain: B: PDB Molecule: di-heme peroxidase; PDBTitle: crystal structure of di-heme peroxidase from nitrosomonas europaea
88	c2zxyA_	Alignment	not modelled	21.5	33	PDB header: oxygen binding, transport protein Chain: A: PDB Molecule: cytochrome c552; PDBTitle: crystal structure of cytochrome c555 from aquifex aeolicus
89	d1c53a_	Alignment	not modelled	21.1	36	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
90	c2d0sA_	Alignment	not modelled	20.9	19	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c; PDBTitle: crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
91	d1h32a2	Alignment	not modelled	20.8	26	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c SoxA
92	d1nmla2	Alignment	not modelled	20.2	33	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
93	d1m70a2	Alignment	not modelled	20.0	17	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
94	c3oa8A_	Alignment	not modelled	19.8	20	PDB header: heme-binding protein/heme-binding protei Chain: A: PDB Molecule: soxa; PDBTitle: diheme soxax
95	d1h32b_	Alignment	not modelled	19.4	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
96	d1gu2a_	Alignment	not modelled	19.0	27	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
97	c1zzhA_	Alignment	not modelled	19.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c peroxidase; PDBTitle: structure of the fully oxidized di-heme cytochrome c2 peroxidase from r. capsulatus
98	d3c2ca_	Alignment	not modelled	18.5	19	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
99	c2c1dB_	Alignment	not modelled	18.4	24	PDB header: oxidoreductase Chain: B: PDB Molecule: soxx; PDBTitle: crystal structure of soxxa from p. pantotrophus