Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P33226
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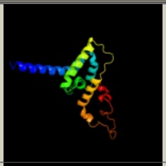
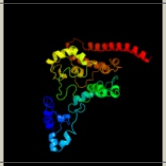
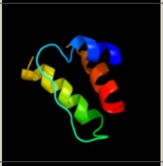
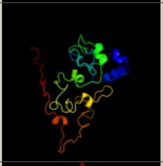
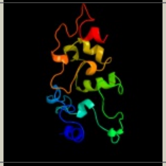
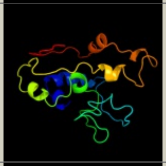
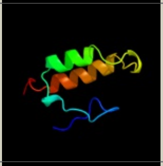
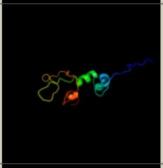
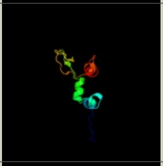
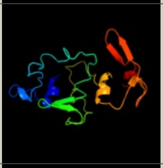
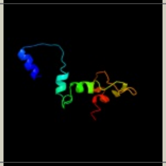
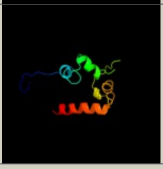
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j7aC_	Alignment		99.9	29	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**cytochrome c quinol dehydrogenase nrfh; **PDBTitle:** crystal structure of cytochrome c nitrite reductase nrfha2 complex from desulfovibrio vulgaris
2	d1fgja_	Alignment		99.7	18	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
3	c1fgjA_	Alignment		99.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxylamine oxidoreductase; **PDBTitle:** x-ray structure of hydroxylamine oxidoreductase
4	c2bpbB_	Alignment		98.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit b; **PDBTitle:** sulfite dehydrogenase from starkeya novella
5	d1sp3a_	Alignment		98.5	16	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
6	c2p0bA_	Alignment		98.3	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c-type protein nrfb; **PDBTitle:** crystal structure of chemically-reduced e.coli nrfb
7	d1ft5a_	Alignment		98.3	20	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
8	d2rdza1	Alignment		98.2	26	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
9	d1fs7a_	Alignment		98.1	20	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
10	c1fs9A_	Alignment		98.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c nitrite reductase; **PDBTitle:** cytochrome c nitrite reductase from wolinella succinogenes-azide2 complex
11	d1pbya1	Alignment		98.0	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2

12	d1jmxa1	Alignment		97.8	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
13	c2fwtA_	Alignment		97.7	30	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**dhc, diheme cytochrome c; **PDBTitle:** crystal structure of dhc purified from rhodobacter2 sphaeroides
14	c2vr0A_	Alignment		97.7	34	**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
15	c3f29A_	Alignment		97.6	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**eight-heme nitrite reductase; **PDBTitle:** structure of the thioalkalivibrio nitratireducens2 cytochrome c nitrite reductase in complex with sulfite
16	c2j7aE_	Alignment		97.6	34	**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
17	c3pmqA_	Alignment		97.6	25	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**decaheme cytochrome c mtrf; **PDBTitle:** crystal structure of the outer membrane decaheme cytochrome mtrf
18	d1qdba_	Alignment		97.5	27	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
19	d1oaha_	Alignment		97.5	29	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
20	c1oahA_	Alignment		97.5	29	**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).
21	c1kb0A_	Alignment	not modelled	97.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein alcohol dehydrogenase; **PDBTitle:** crystal structure of quinohemoprotein alcohol dehydrogenase from2 comamonas testosteroni
22	c3oueA_	Alignment	not modelled	96.9	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** structure of c-terminal hexaheme fragment of gsu1996
23	c2a3mA_	Alignment	not modelled	96.7	26	**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)
24	c1pbyA_	Alignment	not modelled	96.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein amine dehydrogenase 60 kda **PDBTitle:** structure of the phenylhydrazine adduct of the2 quinohemoprotein amine dehydrogenase from paracoccus3 denitrificans at 1.7 a resolution
25	d1mz4a_	Alignment	not modelled	96.6	11	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
26	d1h9xa1	Alignment	not modelled	96.5	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
27	c3cp5A_	Alignment	not modelled	96.5	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** cytochrome c from rhodothermus marinus
						Fold: Cytochrome c

28	d1nira1	Alignment	not modelled	96.5	29	**Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
29	c3ouqA_	Alignment	not modelled	96.4	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** structure of n-terminal hexaheme fragment of gsu1996
30	d1i77a_	Alignment	not modelled	96.3	22	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
31	c1w5cT_	Alignment		96.3	15	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**cytochrome c-550; **PDBTitle:** photosystem ii from thermosynechococcus elongatus
32	c1jmxA_	Alignment	not modelled	96.2	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**amine dehydrogenase; **PDBTitle:** crystal structure of a quinohemoprotein amine dehydrogenase2 from pseudomonas putida
33	d1e29a_	Alignment	not modelled	96.2	15	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
34	c2zonG_	Alignment	not modelled	96.2	30	**PDB header:**oxidoreductase/electron transport **Chain:** G: **PDB Molecule:**cytochrome c551; **PDBTitle:** crystal structure of electron transfer complex of nitrite2 reductase with cytochrome c
35	d1e2rb1	Alignment	not modelled	96.2	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
36	d1f1ca_	Alignment	not modelled	96.1	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
37	d1y0pa1	Alignment	not modelled	96.1	27	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
38	c1jrxA_	Alignment	not modelled	96.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
39	c2xtsD_	Alignment	not modelled	96.0	25	**PDB header:**oxidoreductase/electron transport **Chain:** D: **PDB Molecule:**cytochrome; **PDBTitle:** crystal structure of the sulfane dehydrogenase soxcd from paracoccus2 pantotrophus
40	d1hzua1	Alignment	not modelled	96.0	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
41	c1kv9A_	Alignment	not modelled	95.9	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**type ii quinohemoprotein alcohol dehydrogenase; **PDBTitle:** structure at 1.9 a resolution of a quinohemoprotein alcohol2 dehydrogenase from pseudomonas putida hk5
42	d1ls9a_	Alignment	not modelled	95.9	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
43	d1kv9a1	Alignment	not modelled	95.9	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinoprotein alcohol dehydrogenase, C-terminal domain
44	d1ytca_	Alignment	not modelled	95.9	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
45	c2zxyA_	Alignment	not modelled	95.9	17	**PDB header:**oxygen binding, transport protein **Chain:** A: **PDB Molecule:**cytochrome c552; **PDBTitle:** crystal structure of cytochrome c555 from aquifex aeolicus
46	d1gyoa_	Alignment	not modelled	95.9	41	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
47	d1wvec1	Alignment	not modelled	95.9	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
48	d2gc4d1	Alignment	not modelled	95.8	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
49	d1d4ca1	Alignment	not modelled	95.8	26	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
50	c1nnoA_	Alignment	not modelled	95.7	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrite reductase; **PDBTitle:** conformational changes occurring upon no binding in nitrite2 reductase from pseudomonas aeruginosa
51	d1wada_	Alignment	not modelled	95.7	32	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
52	d2ctha_	Alignment	not modelled	95.7	25	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
53	d1j0pa_	Alignment	not modelled	95.7	34	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like

54	c1qo8A_	Alignment	not modelled	95.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c3 fumarate reductase; **PDBTitle:** the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
55	d1h1oa2	Alignment	not modelled	95.6	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
56	d1ccra_	Alignment	not modelled	95.6	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
57	d1lfma_	Alignment	not modelled	95.5	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
58	d1hj3a1	Alignment	not modelled	95.5	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
59	d1wejf_	Alignment	not modelled	95.5	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
60	d1yeba_	Alignment	not modelled	95.5	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
61	c2d0wA_	Alignment	not modelled	95.5	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome cl; **PDBTitle:** crystal structure of cytochrome cl from hyphomicrobium2 denitrificans
62	d1ycca_	Alignment	not modelled	95.5	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
63	d1fcdc1	Alignment	not modelled	95.4	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
64	d1kb0a1	Alignment	not modelled	95.4	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinoprotein alcohol dehydrogenase, C-terminal domain
65	d1c75a_	Alignment	not modelled	95.4	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
66	d1qo8a1	Alignment	not modelled	95.4	23	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
67	c2w9kA_	Alignment	not modelled	95.4	25	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crithidia fasciculata cytochrome c
68	c3dmiA_	Alignment	not modelled	95.4	23	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c6; **PDBTitle:** crystallization and structural analysis of cytochrome c62 from the diatom phaeodactylum tricornutum at 1.5 a3 resolution
69	d1qksa1	Alignment	not modelled	95.4	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
70	d1duwa_	Alignment	not modelled	95.3	29	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
71	c2l4dA_	Alignment	not modelled	95.3	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**sco1/senc family protein/cytochrome c; **PDBTitle:** cytochrome c domain of pp3183 protein from pseudomonas putida
72	d1c52a_	Alignment	not modelled	95.3	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
73	d1m70a1	Alignment	not modelled	95.3	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
74	d1ofwa_	Alignment	not modelled	95.2	27	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
75	c2e84A_	Alignment	not modelled	95.2	28	**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
76	c2zooA_	Alignment	not modelled	95.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nitrite reductase; **PDBTitle:** crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125
77	d1up9a_	Alignment	not modelled	95.2	20	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
78	d1j3sa_	Alignment	not modelled	95.2	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
79	c3dr0B_	Alignment	not modelled	95.2	19	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c6; **PDBTitle:** structure of reduced cytochrome c6 from synechococcus sp.2 pcc 7002
80	d1kx7a_	Alignment	not modelled	95.1	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c

81	d1dy7b1	Alignment	not modelled	95.1	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
82	d1cc5a_	Alignment	not modelled	95.1	23	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
83	d1cyja_	Alignment	not modelled	95.1	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
84	d1c53a_	Alignment	not modelled	95.1	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
85	d1f1fa_	Alignment	not modelled	95.0	26	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
86	c3a9fA_	Alignment	not modelled	95.0	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the c-terminal domain of cytochrome cz2 from chlorobium tepidum
87	c3cu4A_	Alignment	not modelled	95.0	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** omcf, outer membrance cytochrome f from geobacter2 sulfurreducens
88	d1m1qa_	Alignment	not modelled	94.9	22	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
89	d1fcdc2	Alignment	not modelled	94.9	12	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
90	d1hroa_	Alignment	not modelled	94.8	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
91	d1aqea_	Alignment	not modelled	94.8	20	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
92	d1cnoa_	Alignment	not modelled	94.7	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
93	d2c8sa1	Alignment	not modelled	94.7	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
94	c2v07A_	Alignment	not modelled	94.7	23	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**cytochrome c6; **PDBTitle:** structure of the arabidopsis thaliana cytochrome c6a v52q2 variant
95	d2cvca1	Alignment	not modelled	94.7	38	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
96	d1ctja_	Alignment	not modelled	94.7	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
97	c3o0rC_	Alignment	not modelled	94.7	16	**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
98	d1c6sa_	Alignment	not modelled	94.6	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
99	c2zzsW_	Alignment	not modelled	94.6	22	**PDB header:**electron transport **Chain:** W: **PDB Molecule:** **PDBTitle:** crystal structure of cytochrome c554 from vibrio2 parahaemolyticus strain rimd2210633
100	c1eysC_	Alignment	not modelled	94.4	30	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
101	d1eysc_	Alignment	not modelled	94.4	30	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Photosynthetic reaction centre (cytochrome subunit)
102	d1gdva_	Alignment	not modelled	94.4	16	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
103	d1c6ra_	Alignment	not modelled	94.2	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
104	d1m70a2	Alignment	not modelled	94.2	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
105	d1dvha_	Alignment	not modelled	94.1	31	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
106	d1co6a_	Alignment	not modelled	94.0	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
107	c1w2lA_	Alignment	not modelled	93.8	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome oxidase subunit ii; **PDBTitle:** cytochrome c domain of caa3 oxygen oxidoreductase
						PDB header:electron transport

108	c2cvcA_	Alignment	not modelled	93.8	39	**Chain:** A: **PDB Molecule:**high-molecular-weight cytochrome c precursor; **PDBTitle:** crystal structure of high-molecular weight cytochrome c2 from desulfovibrio vulgaris (hildenborough)
109	c1gq1B_	Alignment	not modelled	93.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome cd1 nitrite reductase; **PDBTitle:** cytochrome cd1 nitrite reductase, y25s mutant, oxidised2 form
110	c2k3vA_	Alignment	not modelled	93.4	24	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**tetraheme cytochrome c-type; **PDBTitle:** solution structure of a tetrahaem cytochrome from2 shewanella frigidimarina
111	c2d0sA_	Alignment	not modelled	93.3	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
112	d1fi3a_	Alignment	not modelled	93.1	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
113	d2i5nc1	Alignment	not modelled	93.1	25	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Photosynthetic reaction centre (cytochrome subunit)
114	c2jblC_	Alignment	not modelled	93.1	25	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**photosynthetic reaction center cytochrome c **PDBTitle:** photosynthetic reaction center from blastochloris viridis
115	c1fcdD_	Alignment	not modelled	93.0	12	**PDB header:**electron transport(flavocytochrome) **Chain:** D: **PDB Molecule:**flavocytochrome c sulfide dehydrogenase **PDBTitle:** the structure of flavocytochrome c sulfide dehydrogenase2 from a purple phototrophic bacterium chromatium vinosum at3 2.5 angstroms resolution
116	d2cy3a_	Alignment	not modelled	93.0	26	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
117	c3m97X_	Alignment	not modelled	93.0	22	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**cytochrome c-552; **PDBTitle:** structure of the soluble domain of cytochrome c552 with its flexible2 linker segment from paracoccus denitrificans
118	d1qn2a_	Alignment	not modelled	92.9	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
119	c1z1nX_	Alignment	not modelled	92.9	29	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**sixteen heme cytochrome; **PDBTitle:** crystal structure of the sixteen heme cytochrome from desulfovibrio2 gigas
120	c3cwbQ_	Alignment	not modelled	92.8	19	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d