Phyre2

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Description	P0ABK9
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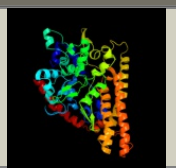
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qdba_	Alignment		100.0	47	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
2	d2rdza1	Alignment		100.0	100	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
3	c2j7aE_	Alignment		100.0	32	**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
4	c1fs9A_	Alignment		100.0	48	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c nitrite reductase; **PDBTitle:** cytochrome c nitrite reductase from wolinella succinogenes-azide2 complex
5	c2vr0A_	Alignment		100.0	32	**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
6	d1fs7a_	Alignment		100.0	48	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
7	d1oaha_	Alignment		100.0	32	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
8	c1oahA_	Alignment		100.0	32	**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).
9	c3f29A_	Alignment		100.0	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
10	d1fgja_	Alignment		99.6	16	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
11	c1fgjA_	Alignment		99.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxylamine oxidoreductase; **PDBTitle:** x-ray structure of hydroxylamine oxidoreductase

12	d1ft5a_	Alignment		98.1	18	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
13	c2p0bA_	Alignment		98.0	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c-type protein nrfb; **PDBTitle:** crystal structure of chemically-reduced e.coli nrfb
14	d1sp3a_	Alignment		98.0	22	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
15	d1y0pa1	Alignment		97.8	34	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
16	c3oueA_	Alignment		97.7	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** structure of c-terminal hexaheme fragment of gsu1996
17	c3ouqA_	Alignment		97.6	15	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** structure of n-terminal hexaheme fragment of gsu1996
18	c3ov0A_	Alignment		97.4	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** structure of dodecaheme cytochrome c gsu1996
19	d1qo8a1	Alignment		97.1	28	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
20	d1d4ca1	Alignment		96.9	29	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
21	c2j7aC_	Alignment	not modelled	96.8	18	**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
22	d1m1qa_	Alignment	not modelled	96.8	26	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
23	d1aqea_	Alignment	not modelled	96.8	26	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
24	c3pmqA_	Alignment	not modelled	96.5	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**decaheme cytochrome c mtrf; **PDBTitle:** crystal structure of the outer membrane decaheme cytochrome mtrf
25	d1duwa_	Alignment	not modelled	96.4	15	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
26	c2e84A_	Alignment	not modelled	96.3	20	**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
27	c2k3vA_	Alignment	not modelled	96.3	38	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**tetraheme cytochrome c-type; **PDBTitle:** solution structure of a tetrahaem cytochrome from2 shewanella frigidimarina
28	c1eysC_	Alignment	not modelled	95.9	16	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum

29	d1eysc_	Alignment	not modelled	95.9	16	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Photosynthetic reaction centre (cytochrome subunit)
30	d1ogyb_	Alignment	not modelled	95.9	17	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
31	d1ofwa_	Alignment	not modelled	95.8	15	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
32	c2bq4A_	Alignment	not modelled	95.6	25	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**basic cytochrome c3; **PDBTitle:** crystal structure of type i cytochrome c3 from2 desulfovibrio africanus
33	c2jblC_	Alignment	not modelled	95.2	17	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**photosynthetic reaction center cytochrome c **PDBTitle:** photosynthetic reaction center from blastochloris viridis
34	d2i5nc1	Alignment	not modelled	95.2	17	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Photosynthetic reaction centre (cytochrome subunit)
35	c1z1nX_	Alignment	not modelled	95.2	18	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**sixteen heme cytochrome; **PDBTitle:** crystal structure of the sixteen heme cytochrome from desulfovibrio2 gigas
36	d19hca_	Alignment	not modelled	95.2	13	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
37	d2cvca1	Alignment	not modelled	95.1	20	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
38	c2cvcA_	Alignment	not modelled	94.5	19	**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)
39	c3o5aB_	Alignment	not modelled	93.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diheme cytochrome c napb; **PDBTitle:** crystal structure of partially reduced periplasmic nitrate reductase2 from cupriavidus necator using ionic liquids
40	d1j0pa_	Alignment	not modelled	92.3	27	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
41	d1i77a_	Alignment	not modelled	92.0	22	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
42	d1jnia_	Alignment	not modelled	91.8	29	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
43	c1jniA_	Alignment	not modelled	91.8	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**diheme cytochrome c napb; **PDBTitle:** structure of the napb subunit of the periplasmic nitrate2 reductase from haemophilus influenzae.
44	c2a3mA_	Alignment	not modelled	91.5	16	**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)
45	d1gyoa_	Alignment	not modelled	89.5	20	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
46	d1wada_	Alignment	not modelled	89.2	16	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
47	c2c1dC_	Alignment	not modelled	88.6	25	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**soxa; **PDBTitle:** crystal structure of soxxa from p. pantotrophus
48	c1qo8A_	Alignment	not modelled	88.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c3 fumarate reductase; **PDBTitle:** the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
49	d2ctha_	Alignment	not modelled	88.2	17	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
50	c3h4nB_	Alignment	not modelled	88.0	26	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c7; **PDBTitle:** ppcd, a cytochrome c7 from geobacter sulfurreducens
51	c1h32A_	Alignment	not modelled	87.5	28	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**diheme cytochrome c; **PDBTitle:** reduced soxax complex from rhodovulum sulfidophilum
52	d1up9a_	Alignment	not modelled	84.9	22	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
53	d2cy3a_	Alignment	not modelled	84.4	15	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
54	c3h34A_	Alignment	not modelled	81.8	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c7; **PDBTitle:** ppce, a cytochrome c7 from geobacter sulfurreducens
55	c1nbvA_	Alignment	not modelled	81.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein amine dehydrogenase 60 kda

55	c1pbyA_	Alignment	not modelled	81.0	22	**PDBTitle:** structure of the phenylhydrazine adduct of the2 quinohemoprotein amine dehydrogenase from paracoccus3 denitrificans at 1.7 a resolution
56	c1jmxA_	Alignment	not modelled	80.3	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**amine dehydrogenase; **PDBTitle:** crystal structure of a quinohemoprotein amine dehydrogenase2 from pseudomonas putida
57	d3caoa_	Alignment	not modelled	80.0	18	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
58	c3h33A_	Alignment	not modelled	79.5	14	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c7; **PDBTitle:** ppcc, a cytochrome c7 from geobacter sulfurreducens
59	d1nmla1	Alignment	not modelled	74.7	10	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
60	c1jrxA_	Alignment	not modelled	74.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
61	d1rwja_	Alignment	not modelled	73.6	17	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
62	d1os6a_	Alignment	not modelled	70.6	21	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
63	d1eb7a1	Alignment	not modelled	68.8	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
64	c2c1uB_	Alignment	not modelled	63.2	25	**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
65	c1nmlA_	Alignment	not modelled	62.9	21	**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)
66	c3o5cA_	Alignment	not modelled	62.7	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** cytochrome c peroxidase bccp of shewanella oneidensis
67	c3l4oB_	Alignment	not modelled	62.6	13	**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
68	c1d4cB_	Alignment	not modelled	62.6	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
69	d1iqca1	Alignment	not modelled	62.3	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
70	c3oa8A_	Alignment	not modelled	62.0	21	**PDB header:**heme-binding protein/heme-binding protei **Chain:** A: **PDB Molecule:**soxa; **PDBTitle:** diheme soxax
71	c1iqcB_	Alignment	not modelled	58.2	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**di-heme peroxidase; **PDBTitle:** crystal structure of di-heme peroxidase from nitrosomonas europaea
72	d1h21a_	Alignment	not modelled	55.0	38	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
73	c1zzhA_	Alignment	not modelled	54.4	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c peroxidase; **PDBTitle:** structure of the fully oxidized di-heme cytochrome c2 peroxidase from r. capsulatus
74	d1hh5a_	Alignment	not modelled	52.7	20	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
75	d1h32a2	Alignment	not modelled	51.7	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c SoxA
76	d1h32a1	Alignment	not modelled	51.0	42	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c SoxA
77	d1wejf_	Alignment	not modelled	50.0	35	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
78	d1co6a_	Alignment	not modelled	48.2	32	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
79	d1lfma_	Alignment	not modelled	47.7	35	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
80	d1pbya1	Alignment	not modelled	47.2	16	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
81	c2vhdB_	Alignment	not modelled	46.7	17	**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

82	d1yeba_	Alignment	not modelled	46.0	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
83	d1j3sa_	Alignment	not modelled	46.0	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
84	d1ytca_	Alignment	not modelled	45.2	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
85	d3c2ca_	Alignment	not modelled	45.1	32	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
86	c3hq7A_	Alignment	not modelled	45.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** ccpa from g. sulfurreducens, g94k/k97q/r100i variant
87	d1jdla_	Alignment	not modelled	44.2	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
88	c1w2lA_	Alignment	not modelled	44.2	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome oxidase subunit ii; **PDBTitle:** cytochrome c domain of caa3 oxygen oxidoreductase
89	d1ycca_	Alignment	not modelled	43.6	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
90	d1ccra_	Alignment	not modelled	43.2	35	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
91	d1ynra1	Alignment	not modelled	41.6	40	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
92	d351ca_	Alignment	not modelled	40.0	40	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
93	c2zxyA_	Alignment	not modelled	39.6	40	**PDB header:**oxygen binding, transport protein **Chain:** A: **PDB Molecule:**cytochrome c552; **PDBTitle:** crystal structure of cytochrome c555 from aquifex aeolicus
94	c2d0sA_	Alignment	not modelled	39.6	40	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
95	d1lmsa_	Alignment	not modelled	39.3	32	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
96	c3b42B_	Alignment	not modelled	38.9	16	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**methyl-accepting chemotaxis protein, putative; **PDBTitle:** periplasmic sensor domain of chemotaxis protein gsu0935
97	d1m70a2	Alignment	not modelled	38.0	23	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
98	d1fcdc1	Alignment	not modelled	36.9	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
99	d1nmla2	Alignment	not modelled	36.8	26	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
100	c3oa8B_	Alignment	not modelled	36.5	25	**PDB header:**heme-binding protein/heme-binding protei **Chain:** B: **PDB Molecule:**soxx; **PDBTitle:** diheme soxax
101	d1jmxa1	Alignment	not modelled	35.9	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
102	d1h1oa2	Alignment	not modelled	35.5	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
103	c2yiuE_	Alignment	not modelled	34.9	29	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
104	d1fi3a_	Alignment	not modelled	34.8	40	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
105	d1a56a_	Alignment	not modelled	34.8	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
106	c2fynH_	Alignment	not modelled	34.6	29	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c1; **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
107	d1c53a_	Alignment	not modelled	34.2	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
108	d1cora_	Alignment	not modelled	33.6	40	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c

109	c2bpbB_	Alignment	not modelled	33.2	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit b; **PDBTitle:** sulfite dehydrogenase from starkeya novella
110	c3mk7B_	Alignment	not modelled	32.3	36	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit o; **PDBTitle:** the structure of cbb3 cytochrome oxidase
111	c1m70D_	Alignment	not modelled	31.9	32	**PDB header:**electron transport **Chain:** D: **PDB Molecule:**cytochrome c4; **PDBTitle:** crystal structure of oxidized recombinant cytochrome c4 from2 pseudomonas stutzeri
112	c3o0rC_	Alignment	not modelled	31.6	17	**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
113	d1dvva_	Alignment	not modelled	31.5	40	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
114	d1pbya2	Alignment	not modelled	29.6	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
115	d1gu2a_	Alignment	not modelled	29.4	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
116	d1m70a1	Alignment	not modelled	28.9	32	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
117	d1iqca2	Alignment	not modelled	28.8	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
118	d1kb0a1	Alignment	not modelled	28.0	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinoprotein alcohol dehydrogenase, C-terminal domain
119	c2w9kA_	Alignment	not modelled	27.6	26	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crithidia fasciculata cytochrome c
120	d1dw0a_	Alignment	not modelled	27.6	23	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c