Phyre^2

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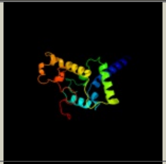
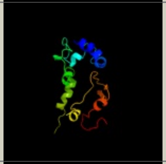
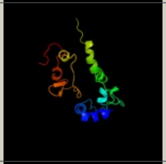
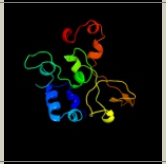
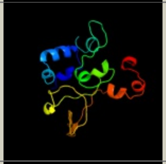
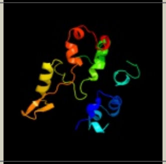
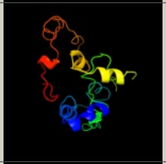
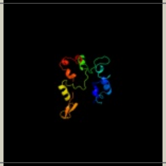
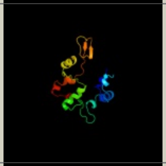
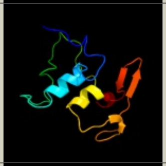
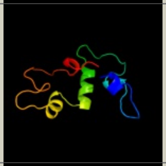
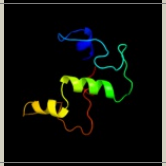
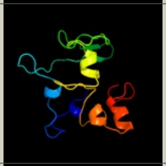
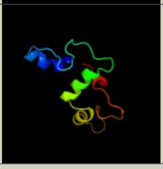
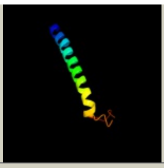
Description	P0ABL5
Date	Thu Jan 5 11:15:47 GMT 2012
Unique Job ID	5025faf37de61ec3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j7aC_	Alignment		99.9	30	**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		98.7	25	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
3	c1fgjA_	Alignment		98.7	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxylamine oxidoreductase; **PDBTitle:** x-ray structure of hydroxylamine oxidoreductase
4	c2p0bA_	Alignment		98.5	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c-type protein nrfb; **PDBTitle:** crystal structure of chemically-reduced e.coli nrfb
5	d2rdza1	Alignment		98.3	24	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
6	d1oaha_	Alignment		98.1	15	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
7	c1oahA_	Alignment		98.1	15	**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).
8	d1qdba_	Alignment		98.0	15	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
9	d1fs7a_	Alignment		98.0	11	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
10	d1sp3a_	Alignment		98.0	19	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
11	c1fs9A_	Alignment		98.0	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c nitrite reductase; **PDBTitle:** cytochrome c nitrite reductase from wolinella succinogenes-azide2 complex

12	d1ft5a_	Alignment		97.9	18	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
13	c2vr0A_	Alignment		97.9	15	**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
14	c2j7aE_	Alignment		97.8	15	**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
15	c3f29A_	Alignment		97.7	18	**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	c3pmqA_	Alignment		97.3	23	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**decaheme cytochrome c mtrf; **PDBTitle:** crystal structure of the outer membrane decaheme cytochrome mtrf
17	d1y0pa1	Alignment		97.1	23	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
18	d1d4ca1	Alignment		97.0	22	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
19	c2a3mA_	Alignment		96.6	18	**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)
20	c1jrxA_	Alignment		96.5	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
21	c3ougA_	Alignment	not modelled	96.4	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** structure of n-terminal hexaheme fragment of gsu1996
22	d1i77a_	Alignment	not modelled	96.1	15	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
23	d1j0pa_	Alignment	not modelled	96.1	35	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
24	d2ctha_	Alignment	not modelled	95.8	38	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
25	c2k3vA_	Alignment	not modelled	95.7	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**tetraheme cytochrome c-type; **PDBTitle:** solution structure of a tetrahaem cytochrome from2 shewanella frigidimarina
26	d1wada_	Alignment	not modelled	95.6	31	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
27	d1m1qa_	Alignment	not modelled	95.5	31	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
28	d1qo8a1	Alignment	not modelled	95.4	19	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
29	d1gyoa_	Alignment	not modelled	95.1	30	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes

						Family: Cytochrome c3-like
30	d1up9a_	Alignment	not modelled	94.9	16	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
31	c2e84A_	Alignment	not modelled	94.7	37	**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
32	d1ofwa_	Alignment	not modelled	94.6	31	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
33	c1qo8A_	Alignment	not modelled	94.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c3 fumarate reductase; **PDBTitle:** the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
34	d1duwa_	Alignment	not modelled	94.4	25	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
35	c3oueA_	Alignment	not modelled	94.2	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** structure of c-terminal hexaheme fragment of gsu1996
36	d2i5nc1	Alignment	not modelled	94.1	23	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Photosynthetic reaction centre (cytochrome subunit)
37	d1aqea_	Alignment	not modelled	93.9	19	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
38	c2jblC_	Alignment	not modelled	93.8	23	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**photosynthetic reaction center cytochrome c **PDBTitle:** photosynthetic reaction center from blastochloris viridis
39	c1z1nX_	Alignment	not modelled	93.0	20	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**sixteen heme cytochrome; **PDBTitle:** crystal structure of the sixteen heme cytochrome from desulfovibrio2 gigas
40	d1ogyb_	Alignment	not modelled	93.0	29	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
41	c2cvcA_	Alignment	not modelled	92.9	31	**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)
42	c3o5aB_	Alignment	not modelled	92.8	27	**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
43	d2cvca1	Alignment	not modelled	92.3	29	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
44	d3caoa_	Alignment	not modelled	91.6	28	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
45	c3h4nB_	Alignment	not modelled	91.2	30	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c7; **PDBTitle:** ppcd, a cytochrome c7 from geobacter sulfurreducens
46	c3h34A_	Alignment	not modelled	90.9	32	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c7; **PDBTitle:** ppce, a cytochrome c7 from geobacter sulfurreducens
47	d19hca_	Alignment	not modelled	90.8	27	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
48	c3ov0A_	Alignment	not modelled	90.4	15	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** structure of dodecaheme cytochrome c gsu1996
49	c1eysC_	Alignment	not modelled	89.0	13	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
50	d1eysc_	Alignment	not modelled	89.0	13	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Photosynthetic reaction centre (cytochrome subunit)
51	c2bq4A_	Alignment	not modelled	88.3	24	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**basic cytochrome c3; **PDBTitle:** crystal structure of type i cytochrome c3 from2 desulfovibrio africanus
52	d2cy3a_	Alignment	not modelled	87.5	22	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
53	c1jniA_	Alignment	not modelled	87.3	27	**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.
54	d1jnia_	Alignment	not modelled	87.3	27	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
55	c2fwtA_	Alignment	not modelled	86.8	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**dhc, diheme cytochrome c; **PDBTitle:** crystal structure of dhc purified from rhodobacter2 sphaeroides

56	c3o0rC_	Alignment		84.3	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
57	d1h21a_	Alignment	not modelled	84.2	29	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
58	d1rwja_	Alignment	not modelled	79.6	31	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
59	c3h33A_	Alignment	not modelled	79.5	35	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c7; **PDBTitle:** ppcc, a cytochrome c7 from geobacter sulfurreducens
60	d1hh5a_	Alignment	not modelled	77.1	33	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
61	c1d4cB_	Alignment	not modelled	76.7	28	**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
62	c2fynH_	Alignment	not modelled	67.7	50	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c1; **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
63	c1p84D_	Alignment	not modelled	63.2	40	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
64	c1zrtD_	Alignment	not modelled	62.7	50	**PDB header:**oxidoreductase/metal transport **Chain:** D: **PDB Molecule:**cytochrome c1; **PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
65	d3cx5d1	Alignment	not modelled	60.0	40	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
66	c1m70D_	Alignment	not modelled	59.9	11	**PDB header:**electron transport **Chain:** D: **PDB Molecule:**cytochrome c4; **PDBTitle:** crystal structure of oxidized recombinant cytochrome c4 from2 pseudomonas stutzeri
67	c2yiuE_	Alignment	not modelled	58.5	50	**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
68	d1ppjd1	Alignment	not modelled	55.3	40	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
69	c3mk7B_	Alignment	not modelled	54.8	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit o; **PDBTitle:** the structure of cbb3 cytochrome oxidase
70	c3cwbQ_	Alignment	not modelled	53.9	27	**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
71	d1otsa_	Alignment	not modelled	51.0	22	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
72	d1os6a_	Alignment	not modelled	50.7	24	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
73	c2hydB_	Alignment	not modelled	49.0	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
74	d1h32a2	Alignment	not modelled	39.7	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c SoxA
75	d2axtj1	Alignment	not modelled	38.4	16	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein J, PsbJ **Family:**PsbJ-like
76	d1h32a1	Alignment	not modelled	36.1	42	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c SoxA
77	c2c1dC_	Alignment	not modelled	36.0	32	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**soxa; **PDBTitle:** crystal structure of soxxa from p. pantotrophus
78	d1jdla_	Alignment	not modelled	33.1	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
79	c3hd7A_	Alignment	not modelled	32.4	15	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
80	d1i8oa_	Alignment	not modelled	31.7	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
						Fold: Cytochrome c

81	d1cxca_	Alignment	not modelled	31.6	33	**Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
82	d1wejf_	Alignment	not modelled	29.8	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
83	c3a0bl_	Alignment	not modelled	28.2	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
84	c3a0bL_	Alignment	not modelled	27.9	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
85	c2l4dA_	Alignment	not modelled	27.8	56	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**sco1/senc family protein/cytochrome c; **PDBTitle:** cytochrome c domain of pp3183 protein from pseudomonas putida
86	d1ql3a_	Alignment	not modelled	27.5	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
87	d3c2ca_	Alignment	not modelled	27.5	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
88	c1h32A_	Alignment	not modelled	27.4	42	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**diheme cytochrome c; **PDBTitle:** reduced soxax complex from rhodovulum sulfidophilum
89	d1lfma_	Alignment	not modelled	27.2	44	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
90	d1cota_	Alignment	not modelled	26.6	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
91	c3bz1L_	Alignment	not modelled	26.1	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
92	c3prrL_	Alignment	not modelled	26.1	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
93	c3prqL_	Alignment	not modelled	26.1	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
94	c3kziL_	Alignment	not modelled	26.1	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
95	c3bz2L_	Alignment	not modelled	26.1	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer
96	c3arcL_	Alignment	not modelled	26.1	30	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
97	c1s5ll_	Alignment	not modelled	26.0	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
98	c1s5lL_	Alignment	not modelled	26.0	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
99	d2axtl1	Alignment	not modelled	26.0	30	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein L, PsbL **Family:**PsbL-like
100	c2axtL_	Alignment	not modelled	26.0	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
101	c2axtl_	Alignment	not modelled	26.0	30	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
102	d1j3sa_	Alignment	not modelled	26.0	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
103	d1nmla2	Alignment	not modelled	25.8	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
104	c3cp5A_	Alignment	not modelled	25.7	27	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** cytochrome c from rhodothermus marinus
105	d1qn2a_	Alignment	not modelled	25.1	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
106	d2hyda2	Alignment	not modelled	23.9	11	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
107	c3m97X_	Alignment	not modelled	23.1	33	**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
108	c2czsB_	Alignment	not modelled	22.3	32	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c, putative; **PDBTitle:** crystal structure analysis of the diheme c-type cytochrome dhc2
109	c3b47A_	Alignment	not modelled	22.1	44	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** periplasmic sensor domain of chemotaxis protein gsu0582
110	c2fqcA_	Alignment	not modelled	22.0	50	**PDB header:**toxin **Chain:** A: **PDB Molecule:**conotoxin pl14a; **PDBTitle:** solution structure of conotoxin pl14a
111	d1lmsa_	Alignment	not modelled	21.8	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
112	c2c1dB_	Alignment	not modelled	21.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**soxx; **PDBTitle:** crystal structure of soxxa from p. pantotrophus
113	d1vyda_	Alignment	not modelled	21.3	50	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
114	d1h32b_	Alignment	not modelled	20.9	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
115	d1eb7a1	Alignment	not modelled	20.7	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
116	d1hzua1	Alignment	not modelled	20.7	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
117	c3oa8B_	Alignment	not modelled	20.5	33	**PDB header:**heme-binding protein/heme-binding protei **Chain:** B: **PDB Molecule:**soxx; **PDBTitle:** diheme soxax
118	d1ytca_	Alignment	not modelled	20.5	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
119	c1ciiA_	Alignment	not modelled	20.5	22	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
120	d1nmla1	Alignment	not modelled	20.4	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase