Phyre2

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Description	P0ABL3
Date	Thu Jan 5 11:15:46 GMT 2012
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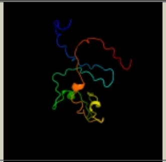
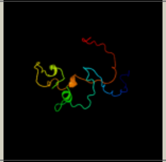
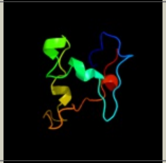
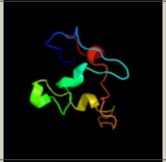
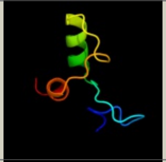
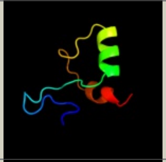
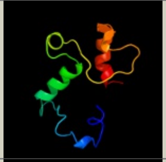
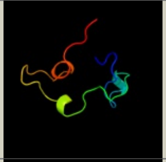
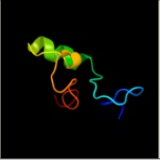
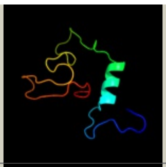
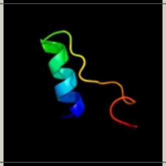
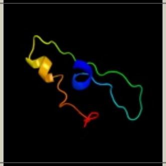
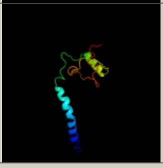
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ogyb_	Alignment		100.0	43	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
2	c3o5aB_	Alignment		100.0	47	**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
3	c1jniA_	Alignment		100.0	73	**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.
4	d1jnia_	Alignment		100.0	73	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
5	c2j7aE_	Alignment		95.5	29	**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
6	c2vr0A_	Alignment		95.0	29	**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
7	d2rdza1	Alignment		91.8	21	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
8	d1qdba_	Alignment		91.2	21	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
9	c2p0bA_	Alignment		87.8	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c-type protein nrfb; **PDBTitle:** crystal structure of chemically-reduced e.coli nrfb
10	d1fs7a_	Alignment		79.7	28	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
11	c1fs9A_	Alignment		79.7	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c nitrite reductase; **PDBTitle:** cytochrome c nitrite reductase from wolinella succinogenes-azide2 complex

12	c1qo8A_	Alignment		75.9	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c3 fumarate reductase; **PDBTitle:** the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
13	d1oaha_	Alignment		75.5	14	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
14	c1oahA_	Alignment		75.5	14	**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).
15	d1aqea_	Alignment		72.2	35	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
16	c3f29A_	Alignment		70.0	31	**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
17	d2cy3a_	Alignment		69.3	29	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
18	c1jrxA_	Alignment		65.1	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
19	d1i77a_	Alignment		63.5	15	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
20	c3mk7B_	Alignment		62.8	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit o; **PDBTitle:** the structure of cbb3 cytochrome oxidase
21	c2bq4A_	Alignment	not modelled	60.0	36	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**basic cytochrome c3; **PDBTitle:** crystal structure of type i cytochrome c3 from2 desulfovibrio africanus
22	c3ov0A_	Alignment	not modelled	59.9	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** structure of dodecaheme cytochrome c gsu1996
23	c2j7aC_	Alignment	not modelled	58.6	27	**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
24	d1d4ca1	Alignment	not modelled	58.2	26	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
25	d1ft5a_	Alignment	not modelled	55.2	22	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
26	c3oueA_	Alignment	not modelled	55.0	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** structure of c-terminal hexaheme fragment of gsu1996
27	d1m1qa_	Alignment	not modelled	51.5	25	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
28	d3caoa_	Alignment	not modelled	50.5	33	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
29	d1gyoa_	Alignment	not modelled	50.0	41	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes

						Family: Cytochrome c3-like
30	c2a3mA_	Alignment	not modelled	50.0	21	**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)
31	d1sp3a_	Alignment	not modelled	49.2	22	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
32	d1duwa_	Alignment	not modelled	49.2	23	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
33	d1y0pa1	Alignment	not modelled	49.0	22	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
34	d1h21a_	Alignment	not modelled	48.8	24	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
35	d1cota_	Alignment	not modelled	46.9	36	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
36	d1vyda_	Alignment	not modelled	45.3	36	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
37	d1up9a_	Alignment	not modelled	44.8	29	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
38	c3b47A_	Alignment	not modelled	43.8	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** periplasmic sensor domain of chemotaxis protein gsu0582
39	d3c2ca_	Alignment	not modelled	42.7	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
40	c3ouqA_	Alignment	not modelled	41.6	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** structure of n-terminal hexaheme fragment of gsu1996
41	c3pmqA_	Alignment	not modelled	37.3	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**decaheme cytochrome c mtrf; **PDBTitle:** crystal structure of the outer membrane decaheme cytochrome mtrf
42	c2czsB_	Alignment	not modelled	36.9	29	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c, putative; **PDBTitle:** crystal structure analysis of the diheme c-type cytochrome dhc2
43	d1yeba_	Alignment	not modelled	35.1	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
44	d1ql3a_	Alignment	not modelled	34.4	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
45	d1rwja_	Alignment	not modelled	34.0	21	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
46	c3m97X_	Alignment	not modelled	31.9	24	**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
47	c2elmA_	Alignment	not modelled	31.6	45	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 10th c2h2 zinc finger of human2 zinc finger protein 406
48	c3o0rC_	Alignment	not modelled	31.1	21	**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
49	d1i8oa_	Alignment	not modelled	30.8	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
50	d1qo8a1	Alignment	not modelled	30.6	21	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
51	c2je2A_	Alignment	not modelled	30.4	42	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cytochrome p460; **PDBTitle:** cytochrome p460 from nitrosomonas europaea - probable2 nonphysiological oxidized form
52	d155ca_	Alignment	not modelled	29.4	40	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
53	d1c6sa_	Alignment	not modelled	29.3	8	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
54	d1jdla_	Alignment	not modelled	28.5	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
55	d1ppjd1	Alignment	not modelled	28.3	38	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
56	d1qn2a_	Alignment	not modelled	27.0	36	**Fold:**Cytochrome c **Superfamily:**Cytochrome c

						Family:monodomain cytochrome c
57	d1j0pa_	Alignment	not modelled	25.8	19	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
58	d1pbya1	Alignment	not modelled	25.5	50	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
59	d1lmsa_	Alignment	not modelled	25.4	31	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
60	c3h34A_	Alignment	not modelled	25.3	47	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c7; **PDBTitle:** ppce, a cytochrome c7 from geobacter sulfurreducens
61	d1h32a2	Alignment	not modelled	24.9	16	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c SoxA
62	d1cxca_	Alignment	not modelled	24.8	44	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
63	d3cx5d1	Alignment	not modelled	24.4	38	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
64	c2zxyA_	Alignment	not modelled	24.4	30	**PDB header:**oxygen binding, transport protein **Chain:** A: **PDB Molecule:**cytochrome c552; **PDBTitle:** crystal structure of cytochrome c555 from aquifex aeolicus
65	c3oa8B_	Alignment	not modelled	24.4	18	**PDB header:**heme-binding protein/heme-binding protei **Chain:** B: **PDB Molecule:**soxx; **PDBTitle:** diheme soxax
66	c2yiuE_	Alignment	not modelled	24.3	30	**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
67	d1ofwa_	Alignment	not modelled	24.2	18	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
68	c1p84D_	Alignment	not modelled	24.1	38	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
69	c3cwbQ_	Alignment	not modelled	23.8	38	**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
70	c3b42B_	Alignment	not modelled	23.7	27	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**methyl-accepting chemotaxis protein, putative; **PDBTitle:** periplasmic sensor domain of chemotaxis protein gsu0935
71	c1zrtD_	Alignment	not modelled	23.7	50	**PDB header:**oxidoreductase/metal transport **Chain:** D: **PDB Molecule:**cytochrome c1; **PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
72	d1ycca_	Alignment	not modelled	23.3	31	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
73	d351ca_	Alignment	not modelled	23.2	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
74	d1wejf_	Alignment	not modelled	23.1	23	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
75	c2d0sA_	Alignment	not modelled	23.1	30	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
76	d1ytca_	Alignment	not modelled	22.9	26	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
77	d1jmxa1	Alignment	not modelled	22.9	50	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
78	c1z1nX_	Alignment	not modelled	22.9	40	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**sixteen heme cytochrome; **PDBTitle:** crystal structure of the sixteen heme cytochrome from desulfovibrio2 gigas
79	d1cora_	Alignment	not modelled	22.7	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
80	c2fynH_	Alignment	not modelled	22.0	22	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c1; **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
81	d1j3sa_	Alignment	not modelled	21.2	23	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
82	d1ccra_	Alignment	not modelled	20.8	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c

83	c2xtsD_	Alignment	not modelled	20.7	24	**PDB header:**oxidoreductase/electron transport **Chain:** D: **PDB Molecule:**cytochrome; **PDBTitle:** crystal structure of the sulfane dehydrogenase soxcd from paracoccus2 pantotrophus
84	d1h32b_	Alignment	not modelled	20.1	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
85	d1fi3a_	Alignment	not modelled	19.9	40	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
86	c3h4nB_	Alignment	not modelled	19.4	42	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c7; **PDBTitle:** ppcd, a cytochrome c7 from geobacter sulfurreducens
87	c2jneA_	Alignment	not modelled	19.3	57	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein yfgj; **PDBTitle:** nmr structure of e.coli yfgj modelled with two zn+2 bound.2 northeast structural genomics consortium target er317.
88	d2jnea1	Alignment	not modelled	19.3	57	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
89	c2bpbB_	Alignment	not modelled	18.8	50	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit b; **PDBTitle:** sulfite dehydrogenase from starkeya novella
90	d2cvca1	Alignment	not modelled	18.6	19	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
91	d1eb7a1	Alignment	not modelled	18.4	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
92	c2c1dB_	Alignment	not modelled	18.3	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**soxx; **PDBTitle:** crystal structure of soxxa from p. pantotrophus
93	c2l4dA_	Alignment	not modelled	18.2	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**sco1/senc family protein/cytochrome c; **PDBTitle:** cytochrome c domain of pp3183 protein from pseudomonas putida
94	d1os6a_	Alignment	not modelled	18.1	33	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
95	d1cc5a_	Alignment	not modelled	17.7	39	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
96	c2jrpA_	Alignment	not modelled	17.4	57	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
97	d1ynra1	Alignment	not modelled	17.3	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
98	c3facE_	Alignment	not modelled	17.0	27	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of rhodobacter sphaeroides protein2 rsp_2168. northeast structural genomics target rhr83.
99	d1nmla2	Alignment	not modelled	16.9	8	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase