


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">dlycca_</a>	 Alignment		100.0	100	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
2	<a href="#">dlyeba_</a>	 Alignment		100.0	91	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
3	<a href="#">dlwejf_</a>	 Alignment		99.9	62	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
4	<a href="#">dlytca_</a>	 Alignment		99.9	82	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
5	<a href="#">dlj3sa_</a>	 Alignment		99.9	63	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
6	<a href="#">dlifma_</a>	 Alignment		99.9	62	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
7	<a href="#">dlccra_</a>	 Alignment		99.9	57	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
8	<a href="#">c3m97X_</a>	 Alignment		99.9	36	<b>PDB header:</b> electron transport <b>Chain:</b> X: <b>PDB Molecule:</b> cytochrome c-552; <b>PDBTitle:</b> structure of the soluble domain of cytochrome c552 with its flexible2 linker segment from paracoccus denitrificans
9	<a href="#">dlql3a_</a>	 Alignment		99.9	37	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
10	<a href="#">dlhroa_</a>	 Alignment		99.9	43	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
11	<a href="#">dlco6a_</a>	 Alignment		99.9	47	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c

12	<a href="#">c2w9kA_</a>	Alignment		99.9	49	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c; <b>PDBTitle:</b> crithidia fasciculata cytochrome c
13	<a href="#">d1lmsa_</a>	Alignment		99.9	97	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
14	<a href="#">d1qn2a_</a>	Alignment		99.9	42	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
15	<a href="#">d1jdla_</a>	Alignment		99.8	32	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
16	<a href="#">d3c2ca_</a>	Alignment		99.8	37	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
17	<a href="#">dli8oa_</a>	Alignment		99.8	39	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
18	<a href="#">dlvyda_</a>	Alignment		99.8	28	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
19	<a href="#">dlcxca_</a>	Alignment		99.8	36	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
20	<a href="#">d155ca_</a>	Alignment		99.8	32	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
21	<a href="#">c2yevB_</a>	Alignment	not modelled	99.8	27	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase subunit 2; <b>PDBTitle:</b> structure of caa3-type cytochrome oxidase
22	<a href="#">d1cota_</a>	Alignment	not modelled	99.8	31	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
23	<a href="#">d1h32b_</a>	Alignment	not modelled	99.6	33	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
24	<a href="#">d1kb0a1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinoprotein alcohol dehydrogenase, C-terminal domain
25	<a href="#">c1w21A_</a>	Alignment	not modelled	99.6	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome oxidase subunit ii; <b>PDBTitle:</b> cytochrome c domain of caa3 oxygen oxidoreductase
26	<a href="#">c3oa8B_</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> heme-binding protein/heme-binding protei <b>Chain:</b> B: <b>PDB Molecule:</b> soxx; <b>PDBTitle:</b> diheme soxx
27	<a href="#">c3cp5A_</a>	Alignment	not modelled	99.6	29	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c; <b>PDBTitle:</b> cytochrome c from rhodothermus marinus
28	<a href="#">c2c1dB_</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> soxx; <b>PDBTitle:</b> crystal structure of soxxa from p. pantotrophus
29	<a href="#">c2d0wA_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome cl; <b>PDBTitle:</b> crystal structure of cytochrome cl from hyphomicrobium2

					denitrificans
30	<a href="#">c3dr0B_</a>	Alignment	not modelled	99.6	18 <b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c6; <b>PDBTitle:</b> structure of reduced cytochrome c6 from synechococcus sp. pcc 7002
31	<a href="#">c3o0rC_</a>	Alignment	not modelled	99.6	18 <b>PDB header:</b> immune system/oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nitric oxide reductase subunit c; <b>PDBTitle:</b> crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
32	<a href="#">c1w5cT_</a>	Alignment	not modelled	99.5	15 <b>PDB header:</b> photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> cytochrome c-550; <b>PDBTitle:</b> photosystem ii from thermosynechococcus elongatus
33	<a href="#">d2gc4d1</a>	Alignment	not modelled	99.5	14 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
34	<a href="#">c3mk7B_</a>	Alignment	not modelled	99.5	31 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit o; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
35	<a href="#">d1f1ca_</a>	Alignment	not modelled	99.5	17 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
36	<a href="#">d2c8sa1</a>	Alignment	not modelled	99.5	18 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
37	<a href="#">c3dmiA_</a>	Alignment	not modelled	99.5	19 <b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c6; <b>PDBTitle:</b> crystallization and structural analysis of cytochrome c62 from the diatom phaeodactylum tricornutum at 1.5 a3 resolution
38	<a href="#">d1e29a_</a>	Alignment	not modelled	99.5	22 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
39	<a href="#">c2xtsD_</a>	Alignment	not modelled	99.5	20 <b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome; <b>PDBTitle:</b> crystal structure of the sulfane dehydrogenase soxcd from paracoccus2 pantotrophus
40	<a href="#">d1m70a1</a>	Alignment	not modelled	99.5	25 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Two-domain cytochrome c
41	<a href="#">d1c52a_</a>	Alignment	not modelled	99.5	21 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
42	<a href="#">d1mz4a_</a>	Alignment	not modelled	99.5	16 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
43	<a href="#">d1fi3a_</a>	Alignment	not modelled	99.5	22 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
44	<a href="#">d1cnoa_</a>	Alignment	not modelled	99.5	17 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
45	<a href="#">d1c6ra_</a>	Alignment	not modelled	99.5	14 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
46	<a href="#">c3mk7F_</a>	Alignment	not modelled	99.5	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit p; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
47	<a href="#">c2zzsW_</a>	Alignment	not modelled	99.5	21 <b>PDB header:</b> electron transport <b>Chain:</b> W: <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure of cytochrome c554 from vibrio2 paraaemolyticus strain rimd2210633
48	<a href="#">d1c6sa_</a>	Alignment	not modelled	99.5	17 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
49	<a href="#">c2l4dA_</a>	Alignment	not modelled	99.5	33 <b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> sco1/senc family protein/cytochrome c; <b>PDBTitle:</b> cytochrome c domain of pp3183 protein from pseudomonas putida
50	<a href="#">d1ctja_</a>	Alignment	not modelled	99.5	15 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
51	<a href="#">d351ca_</a>	Alignment	not modelled	99.4	21 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
52	<a href="#">d1h9xa1</a>	Alignment	not modelled	99.4	17 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
53	<a href="#">c2v07A_</a>	Alignment	not modelled	99.4	25 <b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c6; <b>PDBTitle:</b> structure of the arabidopsis thaliana cytochrome c6a v52q2 variant
54	<a href="#">d1f1fa_</a>	Alignment	not modelled	99.4	15 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
55	<a href="#">d1gdva_</a>	Alignment	not modelled	99.4	21 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
56	<a href="#">d1hzua1</a>	Alignment	not modelled	99.4	14 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> N-terminal (heme c) domain of cytochrome cd1-nitrite

					reductase
57	<a href="#">d1dvva_</a>	Alignment	not modelled	99.4	20 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
58	<a href="#">d1nira1</a>	Alignment	not modelled	99.4	16 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
59	<a href="#">d1cyja_</a>	Alignment	not modelled	99.4	15 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
60	<a href="#">d1kv9a1</a>	Alignment	not modelled	99.4	14 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinoprotein alcohol dehydrogenase, C-terminal domain
61	<a href="#">d1cora_</a>	Alignment	not modelled	99.4	22 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
62	<a href="#">d1ls9a_</a>	Alignment	not modelled	99.4	15 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
63	<a href="#">d1h1oa2</a>	Alignment	not modelled	99.4	28 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Two-domain cytochrome c
64	<a href="#">c2zooA_</a>	Alignment	not modelled	99.4	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nitrite reductase; <b>PDBTitle:</b> crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125
65	<a href="#">c1m70D_</a>	Alignment	not modelled	99.4	21 <b>PDB header:</b> electron transport <b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome c4; <b>PDBTitle:</b> crystal structure of oxidized recombinant cytochrome c4 from2 pseudomonas stutzeri
66	<a href="#">d1ynra1</a>	Alignment	not modelled	99.4	17 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
67	<a href="#">d1c75a_</a>	Alignment	not modelled	99.3	19 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
68	<a href="#">d1e2rb1</a>	Alignment	not modelled	99.3	21 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
69	<a href="#">c2zxyA_</a>	Alignment	not modelled	99.3	25 <b>PDB header:</b> oxygen binding, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c552; <b>PDBTitle:</b> crystal structure of cytochrome c555 from aquifex aeolicus
70	<a href="#">d1a56a_</a>	Alignment	not modelled	99.3	22 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
71	<a href="#">d1cc5a_</a>	Alignment	not modelled	99.3	15 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
72	<a href="#">d1dy7b1</a>	Alignment	not modelled	99.3	16 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
73	<a href="#">d1kx7a_</a>	Alignment	not modelled	99.3	15 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
74	<a href="#">d1wvec1</a>	Alignment	not modelled	99.3	28 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
75	<a href="#">c2d0sA_</a>	Alignment	not modelled	99.3	22 <b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c; <b>PDBTitle:</b> crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
76	<a href="#">d1hj3a1</a>	Alignment	not modelled	99.3	18 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
77	<a href="#">d1qksa1</a>	Alignment	not modelled	99.3	19 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
78	<a href="#">d1fcdc2</a>	Alignment	not modelled	99.3	17 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Two-domain cytochrome c
79	<a href="#">d1m70a2</a>	Alignment	not modelled	99.3	19 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Two-domain cytochrome c
80	<a href="#">c2zonG_</a>	Alignment	not modelled	99.2	23 <b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> G: <b>PDB Molecule:</b> cytochrome c551; <b>PDBTitle:</b> crystal structure of electron transfer complex of nitrite2 reductase with cytochrome c
81	<a href="#">d1c53a_</a>	Alignment	not modelled	99.2	13 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
82	<a href="#">d1dvha_</a>	Alignment	not modelled	99.2	18 <b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
83	<a href="#">c3cu4A_</a>	Alignment	not modelled	99.2	22 <b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> omcf, outer membrane cytochrome f from geobacter2

						sulfurreducens
84	<a href="#">dlgksa_</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
85	<a href="#">c1fcdD_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> electron transport(flavocytochrome) <b>Chain:</b> D: <b>PDB Molecule:</b> flavocytochrome c sulfide dehydrogenase <b>PDBTitle:</b> the structure of flavocytochrome c sulfide dehydrogenase2 from a purple phototrophic bacterium chromatium vinosum at3 2.5 angstroms resolution
86	<a href="#">dlfcdc1</a>	Alignment	not modelled	99.1	18	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Two-domain cytochrome c
87	<a href="#">dlnmla2</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Di-heme cytochrome c peroxidase
88	<a href="#">c3o5cA_</a>	Alignment	not modelled	98.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c551 peroxidase; <b>PDBTitle:</b> cytochrome c peroxidase bccp of shewanella oneidensis
89	<a href="#">c1kb0A_</a>	Alignment	not modelled	98.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinohemoprotein alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of quinohemoprotein alcohol dehydrogenase from2 comamonas testosteroni
90	<a href="#">dlh1oa1</a>	Alignment	not modelled	98.8	22	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Two-domain cytochrome c
91	<a href="#">c1zzhA_</a>	Alignment	not modelled	98.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c peroxidase; <b>PDBTitle:</b> structure of the fully oxidized di-heme cytochrome c2 peroxidase from r. capsulatus
92	<a href="#">c1iqcB_</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> di-heme peroxidase; <b>PDBTitle:</b> crystal structure of di-heme peroxidase from nitrosomonas europaea
93	<a href="#">c1nnoA_</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite reductase; <b>PDBTitle:</b> conformational changes occurring upon no binding in nitrite2 reductase from pseudomonas aeruginosa
94	<a href="#">dlb7a2</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Di-heme cytochrome c peroxidase
95	<a href="#">c2vhdB_</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c551 peroxidase; <b>PDBTitle:</b> crystal structure of the di-haem cytochrome c peroxidase2 from pseudomonas aeruginosa - mixed valence form
96	<a href="#">dl1qca2</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Di-heme cytochrome c peroxidase
97	<a href="#">c1nmlA_</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> di-haem cytochrome c peroxidase; <b>PDBTitle:</b> di-haemic cytochrome c peroxidase from pseudomonas nautica 617, form2 in (ph 4.0)
98	<a href="#">c3hq7A_</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c551 peroxidase; <b>PDBTitle:</b> ccpa from g. sulfurreducens, g94k/k97q/r100i variant
99	<a href="#">c2c1uB_</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> di-haem cytochrome c peroxidase; <b>PDBTitle:</b> crystal structure of the di-haem cytochrome c peroxidase2 from paracoccus pantotrophus - oxidised form
100	<a href="#">c314oB_</a>	Alignment	not modelled	98.7	21	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> methylamine utilization protein mauG; <b>PDBTitle:</b> crystal structure of the mauG/pre-methylamine dehydrogenase complex2 after treatment with hydrogen peroxide
101	<a href="#">c1gq1B_</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome cd1 nitrite reductase; <b>PDBTitle:</b> cytochrome cd1 nitrite reductase, y25s mutant, oxidised2 form
102	<a href="#">c3oa8A_</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> heme-binding protein/heme-binding protei <b>Chain:</b> A: <b>PDB Molecule:</b> soxa; <b>PDBTitle:</b> di heme soxa
103	<a href="#">c1kv9A_</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> type ii quinohemoprotein alcohol dehydrogenase; <b>PDBTitle:</b> structure at 1.9 a resolution of a quinohemoprotein alcohol2 dehydrogenase from pseudomonas putida hk5
104	<a href="#">c1h1oA_</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-552; <b>PDBTitle:</b> acidithiobacillus ferrooxidans cytochrome c4 structure2 supports a complex-induced tuning of electron transfer
105	<a href="#">c2yiuE_</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome c1, heme protein; <b>PDBTitle:</b> x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
106	<a href="#">c1p84D_</a>	Alignment	not modelled	98.3	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome c1, heme protein; <b>PDBTitle:</b> hdbt inhibited yeast cytochrome bc1 complex
107	<a href="#">c3cwbQ_</a>	Alignment	not modelled	98.2	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> mitochondrial cytochrome c1, heme protein; <b>PDBTitle:</b> chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
108	<a href="#">c1h32A_</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> electron transfer <b>Chain:</b> A: <b>PDB Molecule:</b> di heme cytochrome c; <b>PDBTitle:</b> reduced soxa complex from rhodovulum sulfidophilum

109	<a href="#">c1zrtD_</a>	Alignment	not modelled	98.0	12	<b>PDB header:</b> oxidoreductase/metal transport <b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome c1; <b>PDBTitle:</b> rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
110	<a href="#">c2c1dC_</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> soxa; <b>PDBTitle:</b> crystal structure of soxxa from p. pantotrophus
111	<a href="#">d3cx5d1</a>	Alignment	not modelled	97.8	25	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Cytochrome bc1 domain
112	<a href="#">d1h32a2</a>	Alignment	not modelled	97.8	14	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Di-heme cytochrome c SoxA
113	<a href="#">c1yiqA_</a>	Alignment	not modelled	97.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinohemoprotein alcohol dehydrogenase; <b>PDBTitle:</b> molecular cloning and structural analysis of2 quinohemoprotein alcohol dehydrogenase adhiig from3 pseudomonas putida hk5. compariison to the other4 quinohemoprotein alcohol dehydrogenase adhiib found in the5 same microorganism.
114	<a href="#">d1ppjd1</a>	Alignment	not modelled	97.6	22	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Cytochrome bc1 domain
115	<a href="#">d1dw0a_</a>	Alignment	not modelled	97.5	21	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
116	<a href="#">d1gu2a_</a>	Alignment	not modelled	97.3	21	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
117	<a href="#">d1pbya1</a>	Alignment	not modelled	97.1	21	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
118	<a href="#">c2fynH_</a>	Alignment	not modelled	97.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome c1; <b>PDBTitle:</b> crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
119	<a href="#">c2bpbB_</a>	Alignment	not modelled	97.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfite\cytochrome c oxidoreductase subunit b; <b>PDBTitle:</b> sulfite dehydrogenase from starkeya novella
120	<a href="#">d1h32a1</a>	Alignment	not modelled	97.0	13	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Di-heme cytochrome c SoxA