Phyre²

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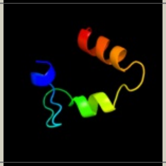
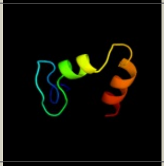
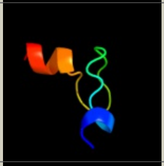
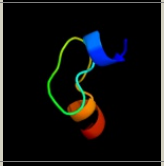
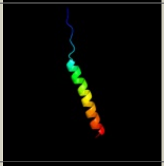
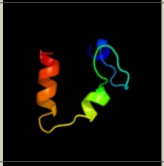
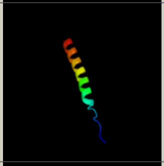
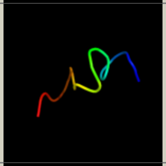
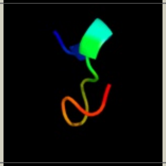
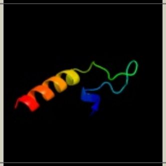
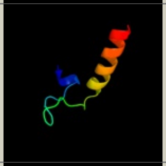
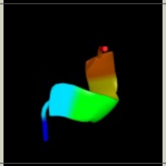
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3g27A_	Alignment		100.0	99	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**82 prophage-derived uncharacterized protein ybco; **PDBTitle:** structure of a putative bacteriophage protein from escherichia coli2 str. k-12 substr. mg1655
2	d351ca_	Alignment		40.5	23	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
3	d1fi3a_	Alignment		39.5	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
4	c2d0sA_	Alignment		34.6	26	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
5	c2zxyA_	Alignment		34.1	17	**PDB header:**oxygen binding, transport protein **Chain:** A: **PDB Molecule:**cytochrome c552; **PDBTitle:** crystal structure of cytochrome c555 from aquifex aeolicus
6	d1cora_	Alignment		30.8	26	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
7	d1dvva_	Alignment		25.7	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
8	d2izpa1	Alignment		23.1	25	**Fold:**IpaD-like **Superfamily:**IpaD-like **Family:**IpaD-like
9	d1ynra1	Alignment		23.0	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
10	c2izpB_	Alignment		22.8	25	**PDB header:**toxin **Chain:** B: **PDB Molecule:**putative membrane antigen; **PDBTitle:** bipd - an invasion prtein associated with the type-iii2 secretion system of burkholderia pseudomallei.
11	d1mz4a_	Alignment		22.3	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c

12	d1f1ca_	Alignment		17.2	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
13	c3dr0B_	Alignment		17.0	27	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c6; **PDBTitle:** structure of reduced cytochrome c6 from synechococcus sp.2 pcc 7002
14	d1a56a_	Alignment		16.8	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
15	d1qn2a_	Alignment		16.2	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
16	d2gc4d1	Alignment		13.7	36	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
17	d2i5nc1	Alignment		12.8	31	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Photosynthetic reaction centre (cytochrome subunit)
18	c2jblC_	Alignment		12.8	31	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**photosynthetic reaction center cytochrome c **PDBTitle:** photosynthetic reaction center from blastochloris viridis
19	d1h1oa2	Alignment		12.6	67	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
20	c2d0wA_	Alignment		12.5	33	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome cl; **PDBTitle:** crystal structure of cytochrome cl from hyphomicrobium2 denitrificans
21	d1fcdc1	Alignment	not modelled	12.4	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
22	d1lmsa_	Alignment	not modelled	12.3	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
23	d1ql3a_	Alignment	not modelled	12.1	42	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
24	c1fcdD_	Alignment	not modelled	11.9	20	**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
25	c1w5cT_	Alignment	not modelled	11.7	21	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**cytochrome c-550; **PDBTitle:** photosystem ii from thermosynechococcus elongatus
26	d1gnta_	Alignment	not modelled	11.3	35	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Hybrid cluster protein (prismane protein)
27	d2ccya_	Alignment	not modelled	11.2	67	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
28	d1cpqa_	Alignment	not modelled	11.1	83	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like

29	d1mqva_	Alignment	not modelled	11.0	67	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
30	d1iqca1	Alignment	not modelled	11.0	57	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
31	c3dmiA_	Alignment	not modelled	10.9	29	**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
32	d1gnla_	Alignment	not modelled	10.9	35	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Hybrid cluster protein (prismane protein)
33	d1f1fa_	Alignment	not modelled	10.8	57	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
34	c2zzsW_	Alignment	not modelled	10.7	57	**PDB header:**electron transport **Chain:** W: **PDB Molecule:** **PDBTitle:** crystal structure of cytochrome c554 from vibrio2 parahaemolyticus strain rimd2210633
35	d1gqaa_	Alignment	not modelled	10.6	67	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
36	d2j8wa1	Alignment	not modelled	10.6	67	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
37	c3oa8A_	Alignment	not modelled	10.5	57	**PDB header:**heme-binding protein/heme-binding protei **Chain:** A: **PDB Molecule:**soxa; **PDBTitle:** diheme soxax
38	c1m70D_	Alignment	not modelled	10.5	33	**PDB header:**electron transport **Chain:** D: **PDB Molecule:**cytochrome c4; **PDBTitle:** crystal structure of oxidized recombinant cytochrome c4 from2 pseudomonas stutzeri
39	d1gksa_	Alignment	not modelled	10.4	83	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
40	d1e85a_	Alignment	not modelled	10.2	83	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
41	d1cyja_	Alignment	not modelled	10.2	57	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
42	d1e29a_	Alignment	not modelled	10.2	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
43	d1hzua1	Alignment	not modelled	10.1	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
44	d2rdza1	Alignment	not modelled	10.1	20	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
45	d1cc5a_	Alignment	not modelled	10.1	80	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
46	d1ctja_	Alignment	not modelled	10.0	57	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
47	d1c6ra_	Alignment	not modelled	9.9	57	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
48	d1i8oa_	Alignment	not modelled	9.8	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
49	d1s05a_	Alignment	not modelled	9.8	50	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
50	c2hgoA_	Alignment	not modelled	9.7	33	**PDB header:**toxin **Chain:** A: **PDB Molecule:**cassiicolin; **PDBTitle:** nmr structure of cassiicolin
51	d1bbha_	Alignment	not modelled	9.7	50	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
52	d1c75a_	Alignment	not modelled	9.7	43	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
53	d1nmla1	Alignment	not modelled	9.6	50	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
54	d1h32a2	Alignment	not modelled	9.4	23	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c SoxA
55	d1dvha_	Alignment	not modelled	9.3	60	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
56	d1m70a2	Alignment	not modelled	9.3	67	**Fold:**Cytochrome c **Superfamily:**Cytochrome c

						Family: Two-domain cytochrome c
57	d1tbxa_	Alignment	not modelled	9.1	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**F93-like
58	d1gu2a_	Alignment	not modelled	9.1	57	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
59	d1kb0a1	Alignment	not modelled	9.0	60	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinoprotein alcohol dehydrogenase, C-terminal domain
60	d1c52a_	Alignment	not modelled	9.0	60	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
61	d1h1oa1	Alignment	not modelled	8.9	60	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
62	c1h32A_	Alignment	not modelled	8.8	43	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**diheme cytochrome c; **PDBTitle:** reduced soxax complex from rhodovulum sulfidophilum
63	d1nira1	Alignment	not modelled	8.6	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
64	d1h9xa1	Alignment	not modelled	8.6	60	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
65	d1gdva_	Alignment	not modelled	8.5	57	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
66	d1nmla2	Alignment	not modelled	8.5	67	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
67	c2zonG_	Alignment	not modelled	8.5	50	**PDB header:**oxidoreductase/electron transport **Chain:** G: **PDB Molecule:**cytochrome c551; **PDBTitle:** crystal structure of electron transfer complex of nitrite2 reductase with cytochrome c
68	c1w2lA_	Alignment	not modelled	8.4	67	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome oxidase subunit ii; **PDBTitle:** cytochrome c domain of caa3 oxygen oxidoreductase
69	d1hj3a1	Alignment	not modelled	8.4	60	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
70	c1fs9A_	Alignment	not modelled	8.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c nitrite reductase; **PDBTitle:** cytochrome c nitrite reductase from wolinella succinogenes-azide2 complex
71	c2c1dC_	Alignment	not modelled	8.0	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**soxa; **PDBTitle:** crystal structure of soxxa from p. pantotrophus
72	d1wvec1	Alignment	not modelled	8.0	60	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
73	d1kv9a1	Alignment	not modelled	8.0	80	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinoprotein alcohol dehydrogenase, C-terminal domain
74	d1eb7a1	Alignment	not modelled	7.9	50	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
75	d1dw0a_	Alignment	not modelled	7.8	43	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
76	d1qksa1	Alignment	not modelled	7.8	60	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
77	d1e2rb1	Alignment	not modelled	7.8	60	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
78	d3cx5d1	Alignment	not modelled	7.7	80	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
79	d1kx7a_	Alignment	not modelled	7.6	43	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
80	d1wada_	Alignment	not modelled	7.6	22	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
81	c2fwtA_	Alignment	not modelled	7.5	63	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**dhc, diheme cytochrome c; **PDBTitle:** crystal structure of dhc purified from rhodobacter2 sphaeroides
82	c3a1gD_	Alignment	not modelled	7.5	29	**PDB header:**transferase **Chain:** D: **PDB Molecule:**polymerase basic protein 2; **PDBTitle:** high-resolution crystal structure of rna polymerase pb1-pb22 subunits from influenza a virus
83	c1pbyA	Alignment	not modelled	7.5	44	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein amine dehydrogenase 60 kda

83	c1pbyA_	Alignment	not modelled	7.5	44	**PDBTitle:** structure of the phenylhydrazine adduct of the2 quinohemoprotein amine dehydrogenase from paracoccus3 denitrificans at 1.7 a resolution
84	d1u5sb1	Alignment	not modelled	7.5	45	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
85	d1dy7b1	Alignment	not modelled	7.4	60	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
86	c1p84D_	Alignment	not modelled	7.4	80	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
87	c2yiuE_	Alignment	not modelled	7.2	100	**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
88	d1fuia1	Alignment	not modelled	7.2	28	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**FucI/AraA C-terminal domain-like **Family:**L-fucose isomerase, C-terminal domain
89	c3mk7B_	Alignment	not modelled	7.2	50	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit o; **PDBTitle:** the structure of cbb3 cytochrome oxidase
90	c1zzhA_	Alignment	not modelled	7.2	43	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c peroxidase; **PDBTitle:** structure of the fully oxidized di-heme cytochrome c2 peroxidase from r. capsulatus
91	d1ppjd1	Alignment	not modelled	7.0	80	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
92	d1fs7a_	Alignment	not modelled	7.0	16	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
93	c3hq7A_	Alignment	not modelled	6.9	57	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** ccpa from g. sulfurreducens, g94k/k97q/r100i variant
94	d1c53a_	Alignment	not modelled	6.9	50	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
95	d1m70a1	Alignment	not modelled	6.9	80	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
96	c2echA_	Alignment	not modelled	6.9	30	**PDB header:**blood coagulation inhibitor **Chain:** A: **PDB Molecule:**echistatin; **PDBTitle:** echistatin-the refined structure of a disintegrin in2 solution by 1h nmr
97	d1pbya1	Alignment	not modelled	6.8	80	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
98	c2v07A_	Alignment	not modelled	6.7	71	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**cytochrome c6; **PDBTitle:** structure of the arabidopsis thaliana cytochrome c6a v52q2 variant
99	c3cwbQ_	Alignment	not modelled	6.6	100	**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