Phyre^2

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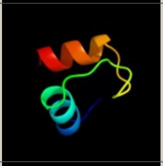
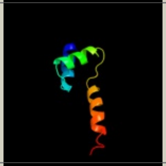
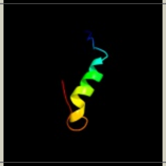
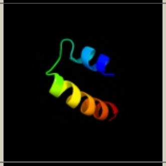
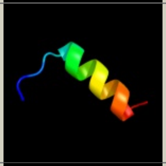
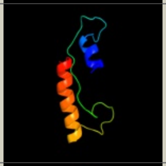
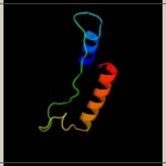
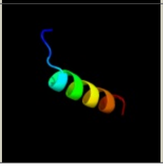
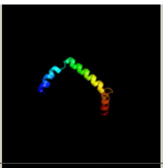
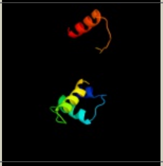
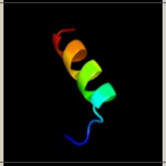
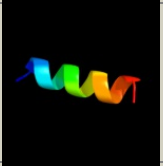
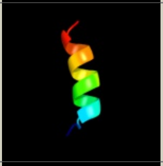
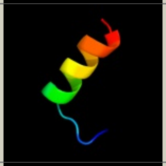
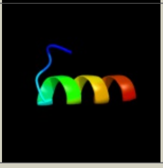
Description	P0C243
Date	Thu Jan 5 11:30:03 GMT 2012
Unique Job ID	9bb3bc59da89eff9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1f6va_	Alignment		73.4	22	**Fold:**C-terminal domain of B transposition protein **Superfamily:**C-terminal domain of B transposition protein **Family:**C-terminal domain of B transposition protein
2	c2elhA_	Alignment		54.9	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
3	d2f2ac1	Alignment		47.3	31	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Glu-tRNAGln amidotransferase C subunit **Family:**Glu-tRNAGln amidotransferase C subunit
4	d1hlva1	Alignment		45.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
5	c3thgA_	Alignment		43.6	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase activase 1, **PDBTitle:** crystal structure of the creosote rubisco activase c-domain
6	c2znrA_	Alignment		36.2	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amsh-like protease; **PDBTitle:** crystal structure of the dub domain of human amsh-lp
7	c3kfuJ_	Alignment		33.8	19	**PDB header:**ligase/rna **Chain:** J: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit c; **PDBTitle:** crystal structure of the transamidosome
8	c2l4dA_	Alignment		33.5	24	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**sco1/senc family protein/cytochrome c; **PDBTitle:** cytochrome c domain of pp3183 protein from pseudomonas putida
9	c3iwpK_	Alignment		32.7	33	**PDB header:**metal binding protein **Chain:** K: **PDB Molecule:**copper homeostasis protein cutc homolog; **PDBTitle:** crystal structure of human copper homeostasis protein cutc
10	d1twda_	Alignment		32.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
11	c3cp5A_	Alignment		31.8	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** cytochrome c from rhodothermus marinus

12	c1k87A_	Alignment		30.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**proline dehydrogenase; **PDBTitle:** crystal structure of e.coli puta (residues 1-669)
13	d1c75a_	Alignment		30.2	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
14	c2w7nA_	Alignment		27.5	19	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**trfb transcriptional repressor protein; **PDBTitle:** crystal structure of kora bound to operator dna: insight2 into repressor cooperation in rp4 gene regulation
15	d1dvva_	Alignment		26.4	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
16	c2k7wB_	Alignment		25.5	20	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** bax activation is initiated at a novel interaction site
17	d1fcdc1	Alignment		23.4	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
18	d1gksa_	Alignment		23.3	11	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
19	d1cora_	Alignment		22.8	6	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
20	d1ynra1	Alignment		22.4	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
21	d1a56a_	Alignment	not modelled	22.4	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
22	d1dvha_	Alignment	not modelled	22.2	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
23	c3h0mU_	Alignment	not modelled	22.1	28	**PDB header:**ligase **Chain:** U: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit c; **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
24	d1c53a_	Alignment	not modelled	21.5	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
25	d1fi3a_	Alignment	not modelled	21.3	6	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
26	c2zzsW_	Alignment	not modelled	21.1	25	**PDB header:**electron transport **Chain:** W: **PDB Molecule:** **PDBTitle:** crystal structure of cytochrome c554 from vibrio2 parahaemolyticus strain rimd2210633
27	d1ls9a_	Alignment	not modelled	20.4	26	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
28	c3o0rC_	Alignment	not modelled	20.2	19	**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
						PDB header:oxygen binding, transport protein

29	c2zxyA_	Alignment	not modelled	19.6	23	**Chain:** A: **PDB Molecule:**cytochrome c552; **PDBTitle:** crystal structure of cytochrome c555 from aquifex aeolicus
30	d1b3qa1	Alignment	not modelled	19.3	37	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
31	d1f1ca_	Alignment	not modelled	19.2	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
32	c3kz0C_	Alignment	not modelled	18.5	20	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**mcl-1 specific peptide mb7; **PDBTitle:** mcl-1 complex with mcl-1-specific selected peptide
33	c3kz0D_	Alignment	not modelled	18.5	20	**PDB header:**apoptosis **Chain:** D: **PDB Molecule:**mcl-1 specific peptide mb7; **PDBTitle:** mcl-1 complex with mcl-1-specific selected peptide
34	c3kj1B_	Alignment	not modelled	18.3	20	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** mcl-1 in complex with bim bh3 mutant i2da
35	d1cyja_	Alignment	not modelled	17.8	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
36	d1cc5a_	Alignment	not modelled	17.7	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
37	d1kx5b_	Alignment	not modelled	17.3	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
38	d1f1fa_	Alignment	not modelled	17.2	32	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
39	d1m70a2	Alignment	not modelled	16.9	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
40	d1h1oa1	Alignment	not modelled	16.4	6	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
41	d1h1oa2	Alignment	not modelled	16.4	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
42	d1alna1	Alignment	not modelled	16.4	24	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
43	c2d0sA_	Alignment	not modelled	16.3	6	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
44	d1m70a1	Alignment	not modelled	15.9	31	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
45	d1kx7a_	Alignment	not modelled	15.7	7	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
46	d1e29a_	Alignment	not modelled	15.2	16	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
47	c2k9lA_	Alignment	not modelled	15.2	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54
48	c1w5cT_	Alignment	not modelled	15.0	21	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**cytochrome c-550; **PDBTitle:** photosystem ii from thermosynechococcus elongatus
49	d1ccra_	Alignment	not modelled	14.8	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
50	c1w2lA_	Alignment	not modelled	14.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome oxidase subunit ii; **PDBTitle:** cytochrome c domain of caa3 oxygen oxidoreductase
51	d1h9xa1	Alignment	not modelled	14.4	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
52	c2l66B_	Alignment	not modelled	14.2	35	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
53	d1lvaa3	Alignment	not modelled	14.2	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
54	d1hzua1	Alignment	not modelled	14.2	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
55	c2nl9B_	Alignment	not modelled	14.0	20	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** crystal structure of the mcl-1:bim bh3 complex
						PDB header:dna binding protein **Chain:** A: **PDB Molecule:**excisionase from transposon tn916;

56	c1y6uA_	Alignment	not modelled	13.9	15	**PDBTitle:** the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
57	d351ca_	Alignment	not modelled	13.5	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
58	d1pi1a_	Alignment	not modelled	13.2	15	**Fold:**Bromodomain-like **Superfamily:**Mob1/phocein **Family:**Mob1/phocein
59	d1cnoa_	Alignment	not modelled	13.1	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
60	c3dljB_	Alignment	not modelled	12.9	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-ala-his dipeptidase; **PDBTitle:** crystal structure of human carnosine dipeptidase 1
61	c2zonG_	Alignment	not modelled	12.8	15	**PDB header:**oxidoreductase/electron transport **Chain:** G: **PDB Molecule:**cytochrome c551; **PDBTitle:** crystal structure of electron transfer complex of nitrite2 reductase with cytochrome c
62	d1dcea2	Alignment	not modelled	12.8	33	**Fold:**C2 domain-like **Superfamily:**Rab geranylgeranyltransferase alpha-subunit, insert domain **Family:**Rab geranylgeranyltransferase alpha-subunit, insert domain
63	d1fcdc2	Alignment	not modelled	12.3	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
64	d1r3ba_	Alignment	not modelled	12.3	15	**Fold:**Bromodomain-like **Superfamily:**Mob1/phocein **Family:**Mob1/phocein
65	c2zooA_	Alignment	not modelled	11.9	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nitrite reductase; **PDBTitle:** crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125
66	c3cu4A_	Alignment	not modelled	11.8	6	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** omcf, outer membrance cytochrome f from geobacter2 sulfurreducens
67	c1pq1B_	Alignment	not modelled	11.5	20	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl2-like protein 11; **PDBTitle:** crystal structure of bcl-xl/bim
68	d1tj1a1	Alignment	not modelled	11.5	21	**Fold:**N-terminal domain of bifunctional PutA protein **Superfamily:**N-terminal domain of bifunctional PutA protein **Family:**N-terminal domain of bifunctional PutA protein
69	c2hjnA_	Alignment	not modelled	11.5	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**maintenance of ploidy protein mob1; **PDBTitle:** structural and functional analysis of saccharomyces2 cerevisiae mob1
70	d1ctja_	Alignment	not modelled	11.4	31	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
71	c1m70D_	Alignment	not modelled	10.8	19	**PDB header:**electron transport **Chain:** D: **PDB Molecule:**cytochrome c4; **PDBTitle:** crystal structure of oxidized recombinant cytochrome c4 from2 pseudomonas stutzeri
72	d1e2rb1	Alignment	not modelled	10.1	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
73	c3dmiA_	Alignment	not modelled	9.9	28	**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
74	c3g2bA_	Alignment	not modelled	9.7	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
75	c3io9B_	Alignment	not modelled	9.6	20	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** biml12y in complex with mcl-1
76	c2bpbB_	Alignment	not modelled	9.5	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit b; **PDBTitle:** sulfite dehydrogenase from starkeya novella
77	c3hj8A_	Alignment	not modelled	9.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2-dioxygenase; **PDBTitle:** crystal structure determination of catechol 1,2-dioxygenase from2 rhodococcus opacus 1cp in complex with 4-chlorocatechol
78	c3d7vB_	Alignment	not modelled	8.9	20	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-like protein 11; **PDBTitle:** crystal structure of mcl-1 in complex with an mcl-12 selective bh3 ligand
79	d1c6sa_	Alignment	not modelled	8.9	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
80	d1mz4a_	Alignment	not modelled	8.9	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
81	d1kv9a1	Alignment	not modelled	8.7	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinoprotein alcohol dehydrogenase, C-terminal domain
82	d1pira1	Alignment	not modelled	8.7	15	**Fold:**Cytochrome c **Superfamily:**Cytochrome c

82	d1nnra1	Alignment	not modelled	8.7	15	**Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
83	c2qneA_	Alignment	not modelled	8.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase (zp_00558420.1) from2 desulfitobacterium hafniense y51 at 2.30 a resolution
84	d1kb0a1	Alignment	not modelled	8.5	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinoprotein alcohol dehydrogenase, C-terminal domain
85	c2rd5D_	Alignment	not modelled	8.2	28	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**pii protein; **PDBTitle:** structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
86	c3dr0B_	Alignment	not modelled	8.2	29	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c6; **PDBTitle:** structure of reduced cytochrome c6 from synechococcus sp.2 pcc 7002
87	c2kvcA_	Alignment	not modelled	8.2	40	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
88	c1fcdD_	Alignment	not modelled	8.1	13	**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
89	d1ffva1	Alignment	not modelled	8.0	24	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
90	d2gc4d1	Alignment	not modelled	7.9	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
91	d1wvec1	Alignment	not modelled	7.7	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
92	d1gdva_	Alignment	not modelled	7.7	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
93	d1whua_	Alignment	not modelled	7.7	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 **Family:**Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3
94	c1tmxA_	Alignment	not modelled	7.6	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyquinol 1,2-dioxygenase; **PDBTitle:** crystal structure of hydroxyquinol 1,2-dioxygenase from2 nocardioides simplex 3e
95	d1c6ra_	Alignment	not modelled	7.5	32	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
96	d1dgja1	Alignment	not modelled	7.4	19	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
97	c1d1dA_	Alignment	not modelled	7.3	11	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (capsid protein); **PDBTitle:** nmr solution structure of the capsid protein from rous2 sarcoma virus
98	c3bh1A_	Alignment	not modelled	7.3	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0371 protein dip2346; **PDBTitle:** crystal structure of protein dip2346 from corynebacterium diphtheriae
99	c2pjxD_	Alignment	not modelled	7.3	41	**PDB header:**endocytosis/exocytosis **Chain:** D: **PDB Molecule:**syntaxin-4; **PDBTitle:** crystal structure of the munc18c/syntaxin4 n-peptide complex