


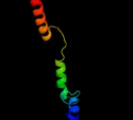







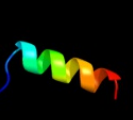



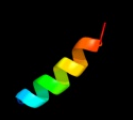











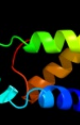
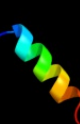


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	Q9S4X0
Date	Thu Jan 5 12:38:24 GMT 2012
Unique Job ID	9912a7446aa5aaa9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1f6va_	 Alignment		89.3	18	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	d2vcha1	 Alignment		45.7	18	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
3	c3cp5A_	 Alignment		38.8	32	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c; PDBTitle: cytochrome c from rhodothermus marinus
4	d1dvha_	 Alignment		31.7	18	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
5	c2l4dA_	 Alignment		30.6	27	PDB header: electron transport Chain: A: PDB Molecule: sco1/senc family protein/cytochrome c; PDBTitle: cytochrome c domain of pp3183 protein from pseudomonas putida
6	d1c53a_	 Alignment		30.5	18	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
7	c2zzsW_	 Alignment		30.1	29	PDB header: electron transport Chain: W: PDB Molecule: PDBTitle: crystal structure of cytochrome c554 from vibrio2 paraahaemolyticus strain rimd2210633
8	d1fcdc1	 Alignment		29.4	6	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
9	d1dvva_	 Alignment		29.1	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
10	d1ynra1	 Alignment		28.8	17	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
11	d2f2ac1	 Alignment		28.2	26	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Glu-tRNAGln amidotransferase C subunit Family: Glu-tRNAGln amidotransferase C subunit

12	dlcnoa_	Alignment		28.2	33	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
13	dlcc5a_	Alignment		28.1	19	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
14	dla56a_	Alignment		27.8	12	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
15	dlc75a_	Alignment		27.2	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
16	dlh1oa1	Alignment		26.7	11	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
17	c2zxyA_	Alignment		26.5	22	PDB header: oxygen binding, transport protein Chain: A: PDB Molecule: cytochrome c552; PDBTitle: crystal structure of cytochrome c555 from aquifex aeolicus
18	dlm70a1	Alignment		26.5	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
19	c2kvcA_	Alignment		25.9	25	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
20	dlwvec1	Alignment		25.4	24	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
21	dlh1oa2	Alignment	not modelled	25.2	18	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
22	dlcyja_	Alignment	not modelled	24.3	25	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
23	dlcora_	Alignment	not modelled	24.1	5	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
24	dlm70a2	Alignment	not modelled	23.6	18	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
25	d2ckxa1	Alignment	not modelled	23.6	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
26	dlfi3a_	Alignment	not modelled	22.9	6	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
27	dlf1ca_	Alignment	not modelled	22.8	14	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
28	clw2lA_	Alignment	not modelled	22.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome oxidase subunit ii; PDBTitle: cytochrome c domain of caa3 oxygen oxidoreductase
29	dlh9xa1	Alignment	not modelled	22.1	23	Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite

					reductase
30	d1ls9a_	Alignment	not modelled	21.8	20 Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
31	c3o0rC_	Alignment	not modelled	21.3	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
32	c2d0sA_	Alignment	not modelled	20.9	6 PDB header: electron transport Chain: A: PDB Molecule: cytochrome c; PDBTitle: crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
33	d1ctja_	Alignment	not modelled	20.8	27 Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
34	d1gksa_	Alignment	not modelled	19.7	5 Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
35	c3kfuj_	Alignment	not modelled	19.6	35 PDB header: ligase/rna Chain: J: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit c; PDBTitle: crystal structure of the transamidosome
36	c1m70D_	Alignment	not modelled	19.3	18 PDB header: electron transport Chain: D: PDB Molecule: cytochrome c4; PDBTitle: crystal structure of oxidized recombinant cytochrome c4 from2 pseudomonas stutzeri
37	d1hzua1	Alignment	not modelled	19.2	22 Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
38	d1e29a_	Alignment	not modelled	19.0	14 Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
39	d1dcea2	Alignment	not modelled	18.9	27 Fold: C2 domain-like Superfamily: Rab geranylgeranyltransferase alpha-subunit, insert domain Family: Rab geranylgeranyltransferase alpha-subunit, insert domain
40	d1kv9a1	Alignment	not modelled	18.8	14 Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinoprotein alcohol dehydrogenase, C-terminal domain
41	c2lkyA_	Alignment	not modelled	18.5	18 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msMeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
42	c3dmiA_	Alignment	not modelled	18.2	35 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
43	c2zonG_	Alignment	not modelled	18.1	17 PDB header: oxidoreductase/electron transport Chain: G: PDB Molecule: cytochrome c551; PDBTitle: crystal structure of electron transfer complex of nitrite2 reductase with cytochrome c
44	d3mdea2	Alignment	not modelled	17.5	7 Fold: Acyl-CoA dehydrogenase NM domain-like Superfamily: Acyl-CoA dehydrogenase NM domain-like Family: Medium chain acyl-CoA dehydrogenase, NM (N-terminal and middle) domains
45	d2o3aa1	Alignment	not modelled	17.3	28 Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF0751-like
46	d1c6ra_	Alignment	not modelled	17.2	30 Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
47	d1f1fa_	Alignment	not modelled	17.1	35 Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
48	d1z84a1	Alignment	not modelled	17.0	21 Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
49	c3cu4A_	Alignment	not modelled	16.9	0 PDB header: electron transport Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: omcf, outer membrane cytochrome f from geobacter2 sulfurreducens
50	c2yy8B_	Alignment	not modelled	16.8	29 PDB header: transferase Chain: B: PDB Molecule: upf0106 protein ph0461; PDBTitle: crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
51	d1iq8a1	Alignment	not modelled	16.7	14 Fold: TIM beta/alpha-barrel Superfamily: tRNA-guanine transglycosylase Family: tRNA-guanine transglycosylase
52	c2znrA_	Alignment	not modelled	16.6	37 PDB header: hydrolase Chain: A: PDB Molecule: amsh-like protease; PDBTitle: crystal structure of the dub domain of human amsh-lp
53	c3h0mU_	Alignment	not modelled	16.1	26 PDB header: ligase Chain: U: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit c; PDBTitle: structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
54	d1kx7a_	Alignment	not modelled	16.1	17 Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
					PDB header: structural genomics, unknown function

55	c3c4nB_	Alignment	not modelled	15.6	25	Chain: B: PDB Molecule: uncharacterized protein dr_0571; PDBTitle: crystal structure of dr_0571 protein from deinococcus2 radiodurans in complex with adp. northeast structural3 genomics consortium target drr125
56	d1dy7b1	Alignment	not modelled	15.6	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
57	d1ccra_	Alignment	not modelled	15.2	16	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
58	d1e2rb1	Alignment	not modelled	14.7	23	Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
59	d1muka_	Alignment	not modelled	14.4	32	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
60	c3hq2A_	Alignment	not modelled	14.3	14	PDB header: hydrolase Chain: A: PDB Molecule: bacillus subtilis m32 carboxypeptidase; PDBTitle: bsucp crystal structure
61	d351ca_	Alignment	not modelled	13.7	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
62	c1w5cT_	Alignment	not modelled	13.6	12	PDB header: photosynthesis Chain: T: PDB Molecule: cytochrome c-550; PDBTitle: photosystem ii from thermosynechococcus elongatus
63	d1syya_	Alignment	not modelled	13.5	40	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
64	c1syyaA_	Alignment	not modelled	13.5	40	PDB header: replication, oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase beta chain; PDBTitle: crystal structure of the r2 subunit of ribonucleotide reductase from2 chlamydia trachomatis
65	d5csma_	Alignment	not modelled	13.4	13	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Allosteric chorismate mutase
66	c3dr0B_	Alignment	not modelled	13.3	33	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c6; PDBTitle: structure of reduced cytochrome c6 from synechococcus sp.2 pcc 7002
67	c2v07A_	Alignment	not modelled	13.0	27	PDB header: photosynthesis Chain: A: PDB Molecule: cytochrome c6; PDBTitle: structure of the arabidopsis thaliana cytochrome c6a v52q2 variant
68	d1fcdc2	Alignment	not modelled	12.8	13	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
69	c2bpbB_	Alignment	not modelled	12.5	7	PDB header: oxidoreductase Chain: B: PDB Molecule: sulfite\cytochrome c oxidoreductase subunit b; PDBTitle: sulfite dehydrogenase from starkeya novella
70	c3thgA_	Alignment	not modelled	12.4	14	PDB header: protein binding Chain: A: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase activase 1, PDBTitle: crystal structure of the creosote rubisco activase c-domain
71	c1iq8B_	Alignment	not modelled	11.9	12	PDB header: transferase Chain: B: PDB Molecule: archaeosine trna-guanine transglycosylase; PDBTitle: crystal structure of archaeosine trna-guanine2 transglycosylase from pyrococcus horikoshii
72	c1smqD_	Alignment	not modelled	11.8	27	PDB header: oxidoreductase Chain: D: PDB Molecule: ribonucleoside-diphosphate reductase small chain PDBTitle: structure of the ribonucleotide reductase rnr2 homodimer2 from saccharomyces cerevisiae
73	d1kb0a1	Alignment	not modelled	11.7	15	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinoprotein alcohol dehydrogenase, C-terminal domain
74	d1b3qa1	Alignment	not modelled	11.5	26	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
75	d1wi9a_	Alignment	not modelled	11.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PCI domain (PINT motif)
76	d1c6sa_	Alignment	not modelled	11.4	32	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
77	c1fcdD_	Alignment	not modelled	11.2	12	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
78	d2h7aa1	Alignment	not modelled	10.9	24	Fold: YcgL-like Superfamily: YcgL-like Family: YcgL-like
79	c1h1oA_	Alignment	not modelled	10.9	18	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c-552; PDBTitle: acidithiobacillus ferrooxidans cytochrome c4 structure2 supports a complex-induced tuning of electron transfer

80	d1jk0a_	Alignment	not modelled	10.8	27	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
81	d1sqwa2	Alignment	not modelled	10.7	17	Fold: Cystatin-like Superfamily: Pre-PUA domain Family: Nip7p homolog, N-terminal domain
82	d1p7na_	Alignment	not modelled	10.6	21	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
83	d2bj7a1	Alignment	not modelled	10.2	28	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
84	c3r1fO_	Alignment	not modelled	9.8	11	PDB header: transcription Chain: O: PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
85	c2zw2B_	Alignment	not modelled	9.7	26	PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein sts178; PDBTitle: crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpus)
86	c3mk7F_	Alignment	not modelled	9.7	17	PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
87	d2hzaa1	Alignment	not modelled	9.7	22	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
88	d1hj3a1	Alignment	not modelled	9.6	29	Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
89	d1w68a_	Alignment	not modelled	9.6	23	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
90	d1pbya1	Alignment	not modelled	9.6	17	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
91	c2xtsD_	Alignment	not modelled	9.5	29	PDB header: oxidoreductase/electron transport Chain: D: PDB Molecule: cytochrome; PDBTitle: crystal structure of the sulfane dehydrogenase soxcd from paracoccus2 pantotrophus
92	d2hzab1	Alignment	not modelled	9.4	22	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
93	d1em9a_	Alignment	not modelled	8.8	21	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
94	c1k87A_	Alignment	not modelled	8.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: proline dehydrogenase; PDBTitle: crystal structure of e.coli puta (residues 1-669)
95	d1c52a_	Alignment	not modelled	8.8	43	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
96	c2yx5A_	Alignment	not modelled	8.8	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0062 protein mj1593; PDBTitle: crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
97	c3o0aB_	Alignment	not modelled	8.8	7	PDB header: ligase Chain: B: PDB Molecule: leucyl-trna synthetase subunit alpha; PDBTitle: crystal structure of the wild type cp1 hydrolytic domain from aquifex2 aeolicus leucyl-trna
98	d1s7ia_	Alignment	not modelled	8.5	14	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: DGPF domain (Pfam 04946)
99	c2dt5A_	Alignment	not modelled	8.4	26	PDB header: dna binding protein Chain: A: PDB Molecule: at-rich dna-binding protein; PDBTitle: crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8