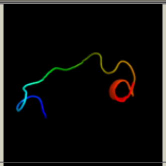
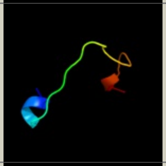
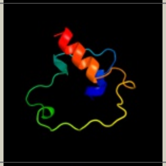
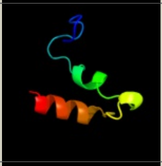
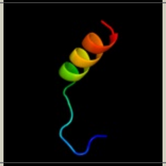
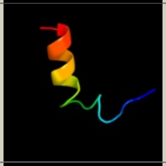
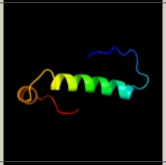
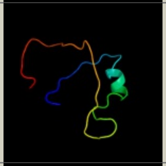
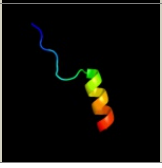
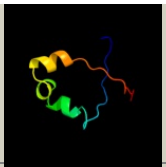
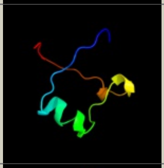
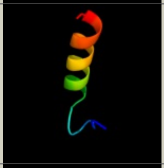
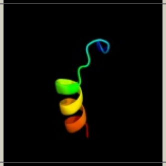
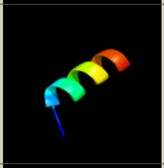
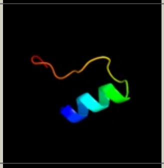
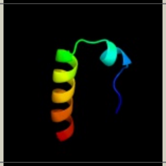
Email	l.a.kelley@imperial.ac.uk
Description	Q9S4W9
Date	Thu Jan 5 12:38:22 GMT 2012
Unique Job ID	6c67161201d43444

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1p42a2	Alignment		53.5	46	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
2	c3nzkB_	Alignment		39.8	50	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine **PDBTitle:** structure of lpxc from yersinia enterocolitica complexed with chir0902 inhibitor
3	d1lm6a_	Alignment		39.4	16	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
4	c1nmlA_	Alignment		37.4	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**di-haem cytochrome c peroxidase; **PDBTitle:** di-haemic cytochrome c peroxidase from pseudomonas nautica 617, form2 in (ph 4.0)
5	c2v07A_	Alignment		37.4	24	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**cytochrome c6; **PDBTitle:** structure of the arabidopsis thaliana cytochrome c6a v52q2 variant
6	c2c1uB_	Alignment		36.4	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**di-haem cytochrome c peroxidase; **PDBTitle:** crystal structure of the di-haem cytochrome c peroxidase2 from paracoccus pantotrophus - oxidised form
7	c2l4dA_	Alignment		31.0	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**sco1/senc family protein/cytochrome c; **PDBTitle:** cytochrome c domain of pp3183 protein from pseudomonas putida
8	c3o5cA_	Alignment		27.0	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** cytochrome c peroxidase bccp of shewanella oneidensis
9	d2a1va1	Alignment		26.9	23	**Fold:**Secretion chaperone-like **Superfamily:**YjbR-like **Family:**YjbR-like
10	d1miua3	Alignment		26.8	38	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
11	d1h32b_	Alignment		25.6	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c

12	c1iyjB_	Alignment		25.4	42	**PDB header:**gene regulation/antitumor protein **Chain:** B: **PDB Molecule:**breast cancer susceptibility; **PDBTitle:** structure of a brca2-dss1 complex
13	c1mjeA_	Alignment		24.0	42	**PDB header:**gene regulation/antitumor protein/dna **Chain:** A: **PDB Molecule:**breast cancer 2; **PDBTitle:** structure of a brca2-dss1-ssdna complex
14	c3cu4A_	Alignment		23.0	5	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** omcf, outer membrance cytochrome f from geobacter2 sulfurreducens
15	d1ccra_	Alignment		22.5	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
16	d1i8oa_	Alignment		21.6	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
17	c1iqcB_	Alignment		21.6	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**di-heme peroxidase; **PDBTitle:** crystal structure of di-heme peroxidase from nitrosomonas europaea
18	d1unld_	Alignment		20.6	30	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
19	d1b9ha_	Alignment		20.3	25	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
20	d3c2ca_	Alignment		20.0	36	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
21	d1nmla2	Alignment	not modelled	19.8	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
22	d1jdla_	Alignment	not modelled	19.3	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
23	c1unhD_	Alignment	not modelled	19.0	30	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**cyclin-dependent kinase 5 activator 1; **PDBTitle:** structural mechanism for the inhibition of cdk5-p25 by2 roscovitine, aloisine and indirubin.
24	d1eb7a2	Alignment	not modelled	18.7	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
25	d1gksa_	Alignment	not modelled	18.6	9	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
26	c1zxjB_	Alignment	not modelled	18.2	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein mg377 homolog; **PDBTitle:** crystal structure of the hypthetical mycoplasma protein,2 mpn555
27	c2w9kA_	Alignment	not modelled	17.7	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crithidia fasciculata cytochrome c
28	d1iqca2	Alignment	not modelled	17.6	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
29	d1iyjb3	Alignment	not modelled	17.6	38	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins

						Family: Single strand DNA-binding domain, SSB
30	c2vesA_	Alignment	not modelled	17.2	54	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine **PDBTitle:** crystal structure of lpxc from pseudomonas aeruginosa2 complexed with the potent bb-78485 inhibitor
31	c3l4oB_	Alignment	not modelled	17.0	21	**PDB header:**oxidoreductase/electron transport **Chain:** B: **PDB Molecule:**methylamine utilization protein maug; **PDBTitle:** crystal structure of the maug/pre-methylamine dehydrogenase complex2 after treatment with hydrogen peroxide
32	d2evra1	Alignment	not modelled	16.9	42	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**Spr N-terminal domain-like
33	c3hq7A_	Alignment	not modelled	16.7	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** ccpa from g. sulfurreducens, g94k/k97q/r100i variant
34	d1ls9a_	Alignment	not modelled	16.7	41	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
35	c3dmiA_	Alignment	not modelled	16.3	38	**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
36	d1hzua1	Alignment	not modelled	15.4	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
37	d2c8sa1	Alignment	not modelled	15.2	35	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
38	d1ufya_	Alignment	not modelled	15.0	25	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
39	d1c52a_	Alignment	not modelled	14.8	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
40	c2vhdB_	Alignment	not modelled	14.8	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** crystal structure of the di-haem cytochrome c peroxidase2 from pseudomonas aeruginosa - mixed valence form
41	c3oa8B_	Alignment	not modelled	13.7	47	**PDB header:**heme-binding protein/heme-binding protei **Chain:** B: **PDB Molecule:**soxx; **PDBTitle:** diheme soxax
42	d1gdva_	Alignment	not modelled	13.6	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
43	d1j3sa_	Alignment	not modelled	13.2	16	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
44	d1hroa_	Alignment	not modelled	13.2	7	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
45	c2krxA_	Alignment	not modelled	13.1	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**asl3597 protein; **PDBTitle:** solution nmr structure of asl3597 from nostoc sp. pcc7120.2 northeast structural genomics consortium target id nsr244.
46	c3f4mA_	Alignment	not modelled	13.0	19	**PDB header:**immune system **Chain:** A: **PDB Molecule:**tumor necrosis factor, alpha-induced protein 8- **PDBTitle:** crystal structure of tipe2
47	c1npyA_	Alignment	not modelled	12.7	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical shikimate 5-dehydrogenase-like **PDBTitle:** structure of shikimate 5-dehydrogenase-like protein hi0607
48	c1w2lA_	Alignment	not modelled	12.6	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome oxidase subunit ii; **PDBTitle:** cytochrome c domain of caa3 oxygen oxidoreductase
49	d1cyja_	Alignment	not modelled	12.4	38	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
50	d1npya1	Alignment	not modelled	12.2	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
51	d1co6a_	Alignment	not modelled	12.2	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
52	d1dy7b1	Alignment	not modelled	12.1	6	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
53	d1cxca_	Alignment	not modelled	11.4	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
54	d1fj2a_	Alignment	not modelled	11.2	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
55	d1ql3a_	Alignment	not modelled	10.9	15	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c

56	c1miuA_	Alignment	not modelled	10.7	38	**PDB header:**gene regulation/antitumor protein **Chain:** A: **PDB Molecule:**breast cancer type 2 susceptibility protein; **PDBTitle:** structure of a brca2-dss1 complex
57	d1c6sa_	Alignment	not modelled	10.7	38	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
58	c2c1dB_	Alignment	not modelled	10.4	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**soxx; **PDBTitle:** crystal structure of soxxa from p. pantotrophus
59	c2go4A_	Alignment	not modelled	10.3	45	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine **PDBTitle:** crystal structure of aquifex aeolicus lpxc complexed with tu-514
60	d1h9xa1	Alignment	not modelled	10.3	7	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
61	c2zzsW_	Alignment	not modelled	10.2	27	**PDB header:**electron transport **Chain:** W: **PDB Molecule:** **PDBTitle:** crystal structure of cytochrome c554 from vibrio2 parahaemolyticus strain rimd2210633
62	d1c6ra_	Alignment	not modelled	10.0	48	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
63	d1pmma_	Alignment	not modelled	9.1	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Pyridoxal-dependent decarboxylase
64	d1cota_	Alignment	not modelled	9.0	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
65	d1dvha_	Alignment	not modelled	9.0	11	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
66	c3mgjA_	Alignment	not modelled	8.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1480; **PDBTitle:** crystal structure of the saccharop_dh_n domain of mj14802 protein from methanococcus jannaschii. northeast structural3 genomics consortium target mjr83a.
67	d1e2rb1	Alignment	not modelled	8.8	7	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
68	d1lfma_	Alignment	not modelled	8.5	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
69	c3dr0B_	Alignment	not modelled	8.5	31	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c6; **PDBTitle:** structure of reduced cytochrome c6 from synechococcus sp.2 pcc 7002
70	c2js3B_	Alignment	not modelled	8.5	50	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of protein q6n9a4_rhopa. northeast structural genomics2 consortium target rpt8
71	c3l87A_	Alignment	not modelled	8.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** the crystal structure of smu.143c from streptococcus mutans ua159
72	d1lmsa_	Alignment	not modelled	8.4	7	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
73	c3o0rC_	Alignment	not modelled	8.2	17	**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
74	d1ctja_	Alignment	not modelled	8.0	48	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
75	c2zonG_	Alignment	not modelled	8.0	36	**PDB header:**oxidoreductase/electron transport **Chain:** G: **PDB Molecule:**cytochrome c551; **PDBTitle:** crystal structure of electron transfer complex of nitrite2 reductase with cytochrome c
76	d1m70a1	Alignment	not modelled	7.9	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
77	d1e6ya1	Alignment	not modelled	7.9	42	**Fold:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Superfamily:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Family:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
78	c2vofD_	Alignment	not modelled	7.7	47	**PDB header:**apoptosis **Chain:** D: **PDB Molecule:**bcl-2-binding component 3; **PDBTitle:** structure of mouse a1 bound to the puma bh3-domain
79	d1q3ja_	Alignment	not modelled	7.5	45	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Gurmarin-like **Family:**Antifungal peptide
80	c2vofB_	Alignment	not modelled	7.4	47	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2-binding component 3; **PDBTitle:** structure of mouse a1 bound to the puma bh3-domain
81	d1m70a2	Alignment	not modelled	7.1	15	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c

82	c3cp5A_	Alignment	not modelled	6.9	35	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** cytochrome c from rhodothermus marinus
83	d2gc4d1	Alignment	not modelled	6.5	35	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
84	d1yeba_	Alignment	not modelled	6.5	7	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
85	c3nswA_	Alignment	not modelled	6.4	32	**PDB header:**immune system **Chain:** A: **PDB Molecule:**excretory-secretory protein 2; **PDBTitle:** crystal structure of ancylostoma ceylanicum excretory-secretory2 protein 2
86	d1wvec1	Alignment	not modelled	6.3	5	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
87	c1m70D_	Alignment	not modelled	6.3	21	**PDB header:**electron transport **Chain:** D: **PDB Molecule:**cytochrome c4; **PDBTitle:** crystal structure of oxidized recombinant cytochrome c4 from2 pseudomonas stutzeri
88	c2jv2A_	Alignment	not modelled	6.3	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1500; **PDBTitle:** solution structure of the n-terminal domain of ph1500
89	d1h1oa2	Alignment	not modelled	6.0	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
90	c2fhyL_	Alignment	not modelled	6.0	15	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**fructose-1,6-bisphosphatase 1; **PDBTitle:** structure of human liver fpbase complexed with a novel2 benzoxazole as allosteric inhibitor
91	c2v5jB_	Alignment	not modelled	6.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
92	d2dbsa1	Alignment	not modelled	6.0	30	**Fold:**TTHC002-like **Superfamily:**TTHC002-like **Family:**TTHC002-like
93	d1qz9a_	Alignment	not modelled	5.9	9	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
94	c1txlA_	Alignment	not modelled	5.9	34	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**metal-binding protein yoda; **PDBTitle:** crystal structure of metal-binding protein yoda from e.2 coli, pfam duf149
95	d1txla_	Alignment	not modelled	5.9	34	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Hypothetical protein YodA
96	c2jmbA_	Alignment	not modelled	5.9	60	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu4866; **PDBTitle:** solution structure of the protein atu4866 from agrobacterium2 tumefaciens
97	d2inca1	Alignment	not modelled	5.8	100	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
98	d1c53a_	Alignment	not modelled	5.8	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
99	c2huuA_	Alignment	not modelled	5.8	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine glyoxylate aminotransferase; **PDBTitle:** crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine