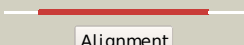
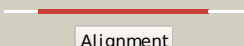
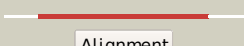
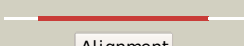
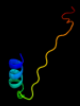
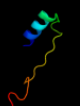
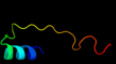
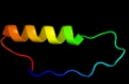
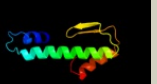


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P62617
Date	Thu Jan 5 12:07:42 GMT 2012
Unique Job ID	d615c0b3465af989

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f0ga_	 Alignment		100.0	63	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
2	d1t0aa_	 Alignment		100.0	67	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
3	d1gx1a_	 Alignment		100.0	97	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
4	c2pmpA_	 Alignment		100.0	48	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
5	d1w55a2	 Alignment		100.0	50	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
6	c1w57A_	 Alignment		100.0	50	PDB header: transferase Chain: A: PDB Molecule: ispd/ispf bifunctional enzyme; PDBTitle: structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
7	d1iv3a_	 Alignment		100.0	41	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
8	d1vh8a_	 Alignment		100.0	77	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
9	c2uzhB_	 Alignment		100.0	40	PDB header: lyase Chain: B: PDB Molecule: 2c-methyl-d-erythritol 2,4-cyclodiphosphate PDBTitle: mycobacterium smegmatis 2c-methyl-d-erythritol-2,4-2 cyclodiphosphate synthase (ispf)
10	c3re3B_	 Alignment		100.0	56	PDB header: lyase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from francisella tularensis
11	c3b6nA_	 Alignment		100.0	41	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate PDBTitle: crystal structure of 2c-methyl-d-erythritol 2,4-2 cyclodiphosphate synthase pv003920 from plasmodium vivax

12	c3fwta_	 Alignment		64.2	18	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: crystal structure of leishmania major mif2
13	c3b64A_	 Alignment		55.2	17	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: macrophage migration inhibitory factor (mif) from2 /leishmania major
14	d1hfoa_	 Alignment		54.9	14	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
15	d2gdga1	 Alignment		54.5	14	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
16	c1w25B_	 Alignment		53.8	20	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
17	c2os5C_	 Alignment		52.1	23	PDB header: cytokine Chain: C: PDB Molecule: acemif; PDBTitle: macrophage migration inhibitory factor from ancylostoma ceylanicum
18	c2xcza_	 Alignment		50.6	17	PDB header: immune system Chain: A: PDB Molecule: possible atls1-like light-inducible protein; PDBTitle: crystal structure of macrophage migration inhibitory factor2 homologue from prochlorococcus marinus
19	c3bb1A_	 Alignment		37.9	22	PDB header: regulatory protein Chain: A: PDB Molecule: regulatory protein of laci family; PDBTitle: crystal structure of a regulatory protein of laci family from2 chloroflexus aggregans
20	d1s5ja2	 Alignment		35.9	10	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
21	d1olta_	 Alignment	not modelled	34.0	17	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
22	d1wh9a_	 Alignment	not modelled	29.6	15	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
23	d2cc0a1	 Alignment	not modelled	27.1	13	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
24	d1ru8a_	 Alignment	not modelled	25.5	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
25	c3caiA_	 Alignment	not modelled	23.5	16	PDB header: transferase Chain: A: PDB Molecule: possible aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis rv3778c2 protein
26	c3hrdE_	 Alignment	not modelled	20.7	26	PDB header: oxidoreductase Chain: E: PDB Molecule: nicotinate dehydrogenase large molybdopterin PDBTitle: crystal structure of nicotinate dehydrogenase
27	c1xaxA_	 Alignment	not modelled	19.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0054 protein hi0004; PDBTitle: nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
28	d1yh5a1	 Alignment	not modelled	19.8	13	Fold: YggU-like Superfamily: YggU-like Family: YggU-like
						Fold: Thiolase-like

29	d1u6ea2	Alignment	not modelled	19.0	20	Superfamily: Thiolase-like Family: Chalcone synthase-like
30	c2ehtA	Alignment	not modelled	18.2	29	PDB header: lipid transport Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: crystal structure of acyl carrier protein from aquifex aeolicus (form2 2)
31	c3gacD	Alignment	not modelled	17.3	16	PDB header: cytokine Chain: D: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: structure of mif with hpp
32	d1q8ia2	Alignment	not modelled	17.2	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
33	d1h4ra2	Alignment	not modelled	16.6	23	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Third domain of FERM
34	c3ejbC	Alignment	not modelled	15.5	27	PDB header: oxidoreductase/lipid transport Chain: C: PDB Molecule: acyl carrier protein; PDBTitle: crystal structure of p450biol in complex with tetradecanoic2 acid ligated acyl carrier protein
35	c3izbU	Alignment	not modelled	15.4	20	PDB header: ribosome Chain: U: PDB Molecule: 40s ribosomal protein s24; PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
36	c3iz6U	Alignment	not modelled	15.4	15	PDB header: ribosome Chain: U: PDB Molecule: 40s ribosomal protein s24 (s24e); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
37	d1hnja2	Alignment	not modelled	15.1	25	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
38	d1tgoa2	Alignment	not modelled	14.8	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
39	c2hmaA	Alignment	not modelled	14.8	18	PDB header: transferase Chain: A: PDB Molecule: probable trna (5-methylaminomethyl-2-thiouridylate)- PDBTitle: the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
40	c3t5sA	Alignment	not modelled	14.4	8	PDB header: immune system Chain: A: PDB Molecule: macrophage migration inhibitory factor; PDBTitle: structure of macrophage migration inhibitory factor from giardia2 lamblia
41	d2j13a1	Alignment	not modelled	14.1	29	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
42	d1gyxa	Alignment	not modelled	13.2	10	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
43	d1qhta2	Alignment	not modelled	13.1	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
44	d1d5aa2	Alignment	not modelled	13.0	20	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
45	d2iboal	Alignment	not modelled	13.0	13	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
46	d1n62b2	Alignment	not modelled	12.8	18	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
47	c3lvmB	Alignment	not modelled	12.6	19	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
48	c1wygA	Alignment	not modelled	12.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
49	c2zkqc	Alignment	not modelled	12.2	15	PDB header: ribosomal protein/rna Chain: C: PDB Molecule: rna expansion segment es4; PDBTitle: structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
50	d2g1da1	Alignment	not modelled	12.2	17	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: Ribosomal protein S24e
51	c2epiA	Alignment	not modelled	12.2	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0045 protein mj1052; PDBTitle: crystal structure pf hypothetical protein mj1052 from2 methanocaldococcus jannaschii (form 2)
52	d1v97a5	Alignment	not modelled	12.0	24	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
53	d1wn7a2	Alignment	not modelled	11.9	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
54	c1cmIA	Alignment	not modelled	11.5	13	PDB header: transferase Chain: A: PDB Molecule: protein (chalcone synthase); PDBTitle: chalcone synthase from alfalfa complexed with malonyl-coa
						PDB header: transferase

55	c2l9fA_	Alignment	not modelled	11.5	13	Chain: A: PDB Molecule: cale8; PDBTitle: nmr solution structure of meacp
56	c2vfjA_	Alignment	not modelled	11.2	31	PDB header: hydrolase Chain: A: PDB Molecule: tumor necrosis factor; PDBTitle: structure of the a20 ovarian tumour (otu) domain
57	d2c1ia1	Alignment	not modelled	10.8	19	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
58	c3nctC_	Alignment	not modelled	10.7	35	PDB header: dna binding protein, chaperone Chain: C: PDB Molecule: protein psib; PDBTitle: x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
59	d2fi0a1	Alignment	not modelled	10.4	26	Fold: SP0561-like Superfamily: SP0561-like Family: SP0561-like
60	c3g8rA_	Alignment	not modelled	10.4	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable spore coat polysaccharide biosynthesis protein e; PDBTitle: crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
61	c2fq2A_	Alignment	not modelled	10.3	17	PDB header: lipid transport Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
62	c3hdoB_	Alignment	not modelled	10.3	16	PDB header: transferase Chain: B: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: crystal structure of a histidinol-phosphate aminotransferase from2 geobacter metallireducens
63	c3ffhA_	Alignment	not modelled	10.2	11	PDB header: transferase Chain: A: PDB Molecule: histidinol-phosphate aminotransferase; PDBTitle: the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
64	d1qz9a_	Alignment	not modelled	10.2	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
65	d1ywxal	Alignment	not modelled	10.2	11	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: Ribosomal protein S24e
66	d1eg5a_	Alignment	not modelled	10.1	23	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
67	c1x3oA_	Alignment	not modelled	10.0	26	PDB header: lipid transport Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: crystal structure of the acyl carrier protein from thermus2 thermophilus hb8
68	c1ffvB_	Alignment	not modelled	9.8	15	PDB header: hydrolase Chain: B: PDB Molecule: cutl, molybdoprotein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava
69	c1s5jA_	Alignment	not modelled	9.7	12	PDB header: transferase Chain: A: PDB Molecule: dna polymerase i; PDBTitle: insight in dna replication: the crystal structure of dna2 polymerase b1 from the archaeon sulfolobus solfataricus
70	d1rm6a2	Alignment	not modelled	9.6	21	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
71	c1vlbA_	Alignment	not modelled	9.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
72	d1vk8a_	Alignment	not modelled	9.4	14	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
73	d1nyla_	Alignment	not modelled	9.3	28	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
74	c1n62E_	Alignment	not modelled	9.2	19	PDB header: oxidoreductase Chain: E: PDB Molecule: carbon monoxide dehydrogenase large chain; PDBTitle: crystal structure of the mo,co-co dehydrogenase (codh), n-2 butylisocyanide-bound state
75	c3dkbA_	Alignment	not modelled	9.2	31	PDB header: hydrolase Chain: A: PDB Molecule: tumor necrosis factor, alpha-induced protein 3; PDBTitle: crystal structure of a20, 2.5 angstrom
76	c3a2kB_	Alignment	not modelled	9.2	11	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
77	d1t8ka_	Alignment	not modelled	9.1	26	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
78	d1otfa_	Alignment	not modelled	9.0	29	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
79	c3lkzB_	Alignment	not modelled	9.0	15	PDB header: viral protein Chain: B: PDB Molecule: non-structural protein 5; PDBTitle: structural and functional analyses of a conserved hydrophobic pocket2 of flavivirus methyltransferase
80	d2p81a1	Alignment	not modelled	8.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
						PDB header: isomerase

81	c2op8A	Alignment	not modelled	8.8	12	Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
82	c1w17A	Alignment	not modelled	8.8	28	PDB header: hydrolase Chain: A: PDB Molecule: probable polysaccharide deacetylase pdaa; PDBTitle: structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
83	c2hdyA	Alignment	not modelled	8.7	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: selenocysteine lyase; PDBTitle: structure of human selenocysteine lyase
84	c3ry0A	Alignment	not modelled	8.6	26	PDB header: isomerase Chain: A: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
85	d1elua	Alignment	not modelled	8.6	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
86	d1s6ya2	Alignment	not modelled	8.5	24	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
87	d1yqha1	Alignment	not modelled	8.4	19	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
88	d1xn9a	Alignment	not modelled	8.4	17	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: Ribosomal protein S24e
89	c3m20A	Alignment	not modelled	8.3	20	PDB header: isomerase Chain: A: PDB Molecule: 4-oxalocrotonate tautomerase, putative; PDBTitle: crystal structure of dmpl from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
90	d1ub7a2	Alignment	not modelled	8.3	21	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
91	c2oq2B	Alignment	not modelled	8.2	11	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
92	d3clsc1	Alignment	not modelled	8.0	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
93	c3lmoA	Alignment	not modelled	8.0	17	PDB header: transferase Chain: A: PDB Molecule: specialized acyl carrier protein; PDBTitle: crystal structure of specialized acyl carrier protein2 (rpa2022) from rhodopseudomonas palustris, northeast3 structural genomics consortium target rpr324
94	c3pfyA	Alignment	not modelled	7.9	31	PDB header: hydrolase Chain: A: PDB Molecule: otu domain-containing protein 5; PDBTitle: the catalytic domain of human otud5
95	d1mzja2	Alignment	not modelled	7.5	18	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
96	d1r57a	Alignment	not modelled	7.5	10	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
97	c1sb3D	Alignment	not modelled	7.5	21	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxybenzoyl-coa reductase alpha subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
98	c2bg5C	Alignment	not modelled	7.4	19	PDB header: transferase Chain: C: PDB Molecule: phosphoenolpyruvate-protein kinase; PDBTitle: crystal structure of the phosphoenolpyruvate-binding enzyme2 i-domain from the thermoanaerobacter tengcongensis pep:3 sugar phosphotransferase system (pts)
99	d1lc5a	Alignment	not modelled	7.3	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like