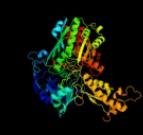
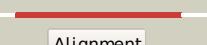
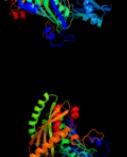
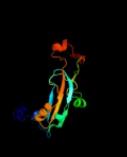
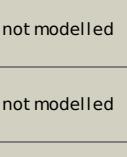


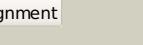
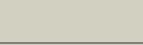
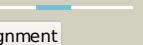
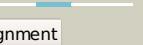
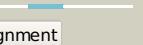
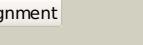
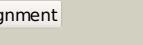
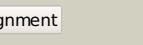
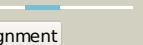
Phyre²

Email	i.a.kelley@imperial.ac.uk
Description	Q46799
Date	Thu Jan 5 12:34:21 GMT 2012
Unique Job ID	5f0c987a4aa10aac

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ffvB_			100.0	27	PDB header: hydrolase Chain: B; PDB Molecule: cutf, molybdoprotein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava
2	c1sb3D_			100.0	33	PDB header: oxidoreductase Chain: D; PDB Molecule: 4-hydroxybenzoyl-coa reductase alpha subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
3	c1n62E_			100.0	26	PDB header: oxidoreductase Chain: E; PDB Molecule: carbon monoxide dehydrogenase large chain; PDBTitle: crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
4	c1t3qB_			100.0	28	PDB header: oxidoreductase Chain: B; PDB Molecule: quinoline 2-oxidoreductase large subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
5	c2w54F_			100.0	25	PDB header: oxidoreductase Chain: F; PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of xanthine dehydrogenase from2 rhodobacter capsulatus in complex with bound inhibitor3 pterin-6-aldehyde
6	c1wygA_			100.0	25	PDB header: oxidoreductase Chain: A; PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
7	c3eubL_			100.0	25	PDB header: oxidoreductase Chain: L; PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of desulfo-xanthine oxidase with xanthine
8	c1vlba_			100.0	27	PDB header: oxidoreductase Chain: A; PDB Molecule: aldehyde oxidoreductase; PDBTitle: structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
9	c1dgjA_			100.0	25	PDB header: oxidoreductase Chain: A; PDB Molecule: aldehyde oxidoreductase; PDBTitle: crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
10	d1rm6a2			100.0	33	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
11	d1n62b2			100.0	24	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain

12	d1ffvb2	Alignment		100.0	26	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
13	d1jrob2	Alignment		100.0	25	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
14	d1t3qb2	Alignment		100.0	26	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
15	d1v97a5	Alignment		100.0	24	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
16	d1vlba4	Alignment		100.0	27	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
17	d1dgja4	Alignment		100.0	25	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
18	c3hrdE	Alignment		100.0	32	PDB header: oxidoreductase Chain: E: PDB Molecule: nicotinate dehydrogenase large molybdopterin PDBTitle: crystal structure of nicotinate dehydrogenase
19	c3hrdF	Alignment		100.0	28	PDB header: oxidoreductase Chain: F: PDB Molecule: nicotinate dehydrogenase medium molybdopterin PDBTitle: crystal structure of nicotinate dehydrogenase
20	d1t3qb1	Alignment		100.0	37	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
21	d1ffvb1	Alignment	not modelled	100.0	34	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
22	d1v97a3	Alignment	not modelled	100.0	26	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
23	d1n62b1	Alignment	not modelled	100.0	32	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
24	d3b9jc1	Alignment	not modelled	100.0	26	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
25	d1rm6a1	Alignment	not modelled	100.0	37	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
26	d1jrob1	Alignment	not modelled	100.0	30	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
27	d1vlba3	Alignment	not modelled	100.0	27	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
28	d1dgja3	Alignment	not modelled	100.0	24	Fold: alpha/beta-Hammerhead Superfamily: CO dehydrogenase molybdoprotein N-domain-like Family: CO dehydrogenase molybdoprotein N-domain-like
29	d1knwa2	Alignment	not modelled	52.5	16	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel

						Family: Alanine racemase-like, N-terminal domain
30	c2rghA_		not modelled	52.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
31	c2kwpA_		not modelled	49.4	23	PDB header: transcription Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: solution structure of the aminoterminal domain of e. coli nusa
32	d1hh2p4		not modelled	48.4	18	Fold: Transcription factor NusA, N-terminal domain Superfamily: Transcription factor NusA, N-terminal domain Family: Transcription factor NusA, N-terminal domain
33	c3n2oA_		not modelled	47.4	20	PDB header: lyase Chain: A: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
34	d1lotfa_		not modelled	46.0	22	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
35	c1vraA_		not modelled	43.8	31	PDB header: transferase Chain: A: PDB Molecule: arginine biosynthesis bifunctional protein argi; PDBTitle: crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
36	c2op8A_		not modelled	42.7	14	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
37	c3abfB_		not modelled	41.4	28	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
38	d2aal1a1		not modelled	40.7	13	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MSAD-like
39	d1mwwa_		not modelled	39.6	8	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: Hypothetical protein HI1388.1
40	d1uiza_		not modelled	39.4	14	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
41	c2xczA_		not modelled	39.0	18	PDB header: immune system Chain: A: PDB Molecule: possible atl51-like light-inducible protein; PDBTitle: crystal structure of macrophage migration inhibitory factor2 homologue from prochlorococcus marinus
42	c2ormA_		not modelled	38.1	16	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase hp0924; PDBTitle: crystal structure of the 4-oxalocrotonate tautomerase homologue dmp12 from helicobacter pylori.
43	d2cpqa1		not modelled	37.8	37	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
44	c3gacD_		not modelled	37.7	16	PDB header: cytokine Chain: D: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: structure of mif with hpp
45	c3mlcC_		not modelled	37.4	22	PDB header: isomerase Chain: C: PDB Molecule: fg41 malonate semialdehyde decarboxylase; PDBTitle: crystal structure of fg41msad inactivated by 3-chloropropionate
46	c3m20A_		not modelled	37.3	16	PDB header: isomerase Chain: A: PDB Molecule: 4-oxalocrotonate tautomerase, putative; PDBTitle: crystal structure of dmp1 from archaeoglobus fulgidus determined to 2.37 angstroms resolution
47	d1yh5a1		not modelled	37.2	13	Fold: YggU-like Superfamily: YggU-like Family: YggU-like
48	c3mb2G_		not modelled	37.1	37	PDB header: isomerase Chain: G: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - alpha subunit; PDBTitle: kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
49	c2lfcA_		not modelled	36.8	35	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase, flavoprotein subunit; PDBTitle: solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
50	d1t0aa_		not modelled	36.4	18	Fold: Bacillus chorismate mutase-like Superfamily: IpsF-like Family: IpsF-like
51	d1bjpa_		not modelled	36.1	24	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
52	c3fwta_		not modelled	36.1	15	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: crystal structure of leishmania major mif2
53	c3nzqB_		not modelled	35.8	20	PDB header: lyase Chain: B: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: crystal structure of biosynthetic arginine decarboxylase

						adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
54	c3ry0A_	Alignment	not modelled	35.8	36	PDB header: isomerase Chain: A: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
55	d1dpta_	Alignment	not modelled	34.3	10	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
56	d1hfoa_	Alignment	not modelled	34.2	17	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
57	c2x4kB_	Alignment	not modelled	33.8	16	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
58	d2fmra_	Alignment	not modelled	33.3	44	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
59	c3b64A_	Alignment	not modelled	32.6	11	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: macrophage migration inhibitory factor (mif) from2 /leishmania major
60	c2rgoA_	Alignment	not modelled	32.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
61	c3nzpA_	Alignment	not modelled	32.1	20	PDB header: lyase Chain: A: PDB Molecule: arginine decarboxylase; PDBTitle: crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
62	d1gd0a_	Alignment	not modelled	31.2	16	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
63	d2gdga1	Alignment	not modelled	31.1	19	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
64	c2dt5A_	Alignment	not modelled	30.1	12	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
65	d1fima_	Alignment	not modelled	30.1	14	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
66	c2v4iA_	Alignment	not modelled	29.2	26	PDB header: transferase Chain: A: PDB Molecule: glutamate n-acetyltransferase 2 alpha chain; PDBTitle: structure of a novel n-acyl-enzyme intermediate of an n-2 terminal nucleophile (tnn) hydrolase, oat2
67	c1d7kB_	Alignment	not modelled	29.0	17	PDB header: lyase Chain: B: PDB Molecule: human ornithine decarboxylase; PDBTitle: crystal structure of human ornithine decarboxylase at 2.12 angstroms resolution
68	d1nera_	Alignment	not modelled	28.4	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
69	d1w55a2	Alignment	not modelled	28.3	13	Fold: Bacillus chorismate mutase-like Superfamily: IpsF-like Family: IpsF-like
70	c3rr1B_	Alignment	not modelled	28.3	27	PDB header: lyase Chain: B: PDB Molecule: putative d-galactonate dehydratase; PDBTitle: crystal structure of enolase prk14017 (target efi-500653) from2 ralstonia pickettii 12j
71	d2dt5a1	Alignment	not modelled	27.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional repressor Rex, N-terminal domain
72	c2pmpA_	Alignment	not modelled	26.2	17	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
73	d1d4ca3	Alignment	not modelled	26.2	12	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
74	d1iv3a_	Alignment	not modelled	25.9	4	Fold: Bacillus chorismate mutase-like Superfamily: IpsF-like Family: IpsF-like
75	d1y0pa3	Alignment	not modelled	25.8	24	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
76	d1vh8a_	Alignment	not modelled	24.9	17	Fold: Bacillus chorismate mutase-like Superfamily: IpsF-like Family: IpsF-like
						PDB header: lyase

77	c3f0gA	Alignment	not modelled	23.4	26	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
78	c2os5C	Alignment	not modelled	23.3	12	PDB header: cytokine Chain: C: PDB Molecule: acemif; PDBTitle: macrophage migration inhibitory factor from ancylostoma ceylanicum
79	d1d7ka2	Alignment	not modelled	23.3	17	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
80	c3re3B	Alignment	not modelled	23.1	17	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
81	d1gx1a	Alignment	not modelled	21.8	17	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
82	d1up7a2	Alignment	not modelled	20.6	13	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
83	c2on3A	Alignment	not modelled	20.2	19	PDB header: lyase Chain: A: PDB Molecule: ornithine decarboxylase; PDBTitle: a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminoxy-3 1-aminopropane
84	c3b6nA	Alignment	not modelled	19.4	26	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
85	d1s6ya2	Alignment	not modelled	19.4	22	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
86	c1m8pB	Alignment	not modelled	19.0	21	PDB header: transferase Chain: B: PDB Molecule: sulfate adenyllyltransferase; PDBTitle: crystal structure of p. chrysogenum atp sulfurylase in the t-state
87	d2g0ta1	Alignment	not modelled	18.8	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
88	c3ketA	Alignment	not modelled	18.3	24	PDB header: transcription/dna Chain: A: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
89	d7odca2	Alignment	not modelled	17.4	20	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
90	d1f3ta2	Alignment	not modelled	17.3	10	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
91	c3a1yF	Alignment	not modelled	16.1	28	PDB header: ribosomal protein Chain: F: PDB Molecule: 50s ribosomal protein p1 (l12p); PDBTitle: the structure of protein complex
92	c3e0mB	Alignment	not modelled	15.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra/msrb PDBTitle: crystal structure of fusion protein of msra and msrb
93	d1l0oc	Alignment	not modelled	15.8	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
94	c1l0oC	Alignment	not modelled	15.8	35	PDB header: protein binding Chain: C: PDB Molecule: sigma factor; PDBTitle: crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoIab with the sporulation sigma3 sigmaf
95	d1f80d	Alignment	not modelled	15.8	20	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
96	c2hlhA	Alignment	not modelled	15.6	21	PDB header: transferase Chain: A: PDB Molecule: nodulation fucosyltransferase; PDBTitle: crystal structure of fucosyltransferase nodz from bradyrhizobium
97	c2jxuA	Alignment	not modelled	15.4	39	PDB header: unknown function Chain: A: PDB Molecule: terb; PDBTitle: nmr solution structure of kp-terb, a tellurite resistance2 protein from klebsiella pneumoniae
98	c3mt1B	Alignment	not modelled	15.3	19	PDB header: lyase Chain: B: PDB Molecule: putative carboxynorspermidine decarboxylase protein; PDBTitle: crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
99	d2p3ra2	Alignment	not modelled	14.2	25	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase