Email	l.a.kelley@imperial.ac.uk
Description	P0A6T5
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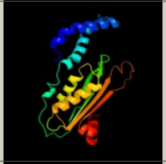
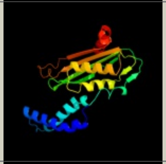
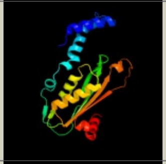
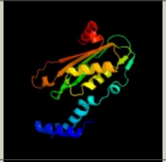
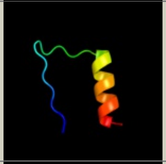
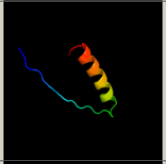
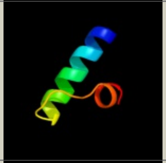
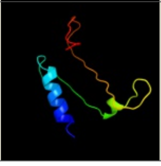
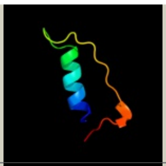
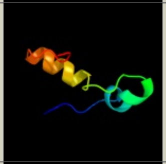
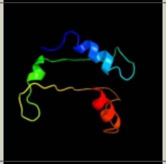
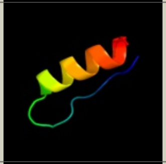
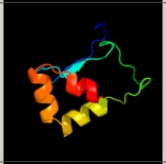
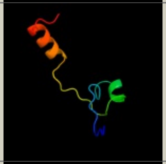
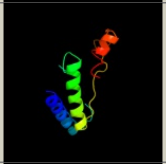
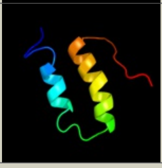
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1a8ra_	Alignment		100.0	100	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
2	d1wpla_	Alignment		100.0	36	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
3	c1is7F_	Alignment		100.0	36	**PDB header:**hydrolase/protein binding **Chain:** F: **PDB Molecule:**gtp cyclohydrolase i; **PDBTitle:** crystal structure of rat gtpchi/gfrp stimulatory complex
4	d1wura1	Alignment		100.0	35	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
5	c1wm9D_	Alignment		100.0	35	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase i; **PDBTitle:** structure of gtp cyclohydrolase i from thermus thermophilus hb8
6	c3bp1A_	Alignment		93.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-dependent 7-cyano-7-deazaguanine reductase; **PDBTitle:** crystal structure of putative 7-cyano-7-deazaguanine2 reductase quef from vibrio cholerae o1 biovar eltor
7	c3ugsB_	Alignment		40.1	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
8	c3pg6D_	Alignment		39.7	22	**PDB header:**ligase **Chain:** D: **PDB Molecule:**e3 ubiquitin-protein ligase dtx3l; **PDBTitle:** the carboxyl terminal domain of human deltex 3-like
9	d1ku2a1	Alignment		33.6	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
10	c3lk6A_	Alignment		33.4	3	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipoprotein ybbd; **PDBTitle:** beta-n-hexosaminidase n318d mutant (ybbd_n318d) from bacillus subtilis
11	c2xczA_	Alignment		29.6	22	**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

12	d1vqoj1	Alignment		28.8	10	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
13	c2d2rA_	Alignment		27.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
14	d1cmca_	Alignment		25.6	20	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Met repressor, MetJ (MetR)
15	d1dpta_	Alignment		25.6	15	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
16	c1jp3A_	Alignment		22.1	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** structure of e.coli undecaprenyl pyrophosphate synthase
17	c3iraA_	Alignment		19.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
18	d1vhxa_	Alignment		19.2	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
19	c3tevA_	Alignment		19.1	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hyrolase, family 3; **PDBTitle:** the crystal structure of glycosyl hydrolase from deinococcus2 radiodurans r1
20	d2veaa1	Alignment		19.1	9	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
21	d2nn6f2	Alignment	not modelled	18.5	44	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
22	d1ueha_	Alignment	not modelled	18.2	32	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
23	c3d5bN_	Alignment	not modelled	17.8	20	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
24	c3cf5G_	Alignment	not modelled	17.8	17	**PDB header:**ribosome/antibiotic **Chain:** G: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** thiopeptide antibiotic thiostrepton bound to the large ribosomal2 subunit of deinococcus radiodurans
25	d2zjrg1	Alignment	not modelled	17.8	17	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
26	d1uiza_	Alignment	not modelled	17.2	15	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
27	d1j3aa_	Alignment	not modelled	17.0	16	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
28	d1f75a_	Alignment	not modelled	16.2	32	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase

29	c3bmxB_	Alignment	not modelled	14.9	5	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized lipoprotein ybbd; **PDBTitle:** beta-n-hexosaminidase (ybbd) from bacillus subtilis
30	d1fima_	Alignment	not modelled	14.7	12	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
31	d1l0oc_	Alignment	not modelled	14.5	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
32	c1l0oC_	Alignment	not modelled	14.5	8	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**sigma factor; **PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
33	d1sjya_	Alignment	not modelled	13.2	13	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
34	c3gacD_	Alignment	not modelled	12.7	14	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** structure of mif with hpp
35	c3b64A_	Alignment	not modelled	12.3	17	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
36	d1aopa2	Alignment	not modelled	12.1	11	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
37	c2o90A_	Alignment	not modelled	11.6	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroneopterin aldolase; **PDBTitle:** atomic resolution crystal structure of e.coli2 dihydroneopterin aldolase in complex with neopterin
38	d2j01n1	Alignment	not modelled	11.4	20	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
39	c2vfwB_	Alignment	not modelled	11.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**short-chain z-isoprenyl diphosphate synthetase; **PDBTitle:** rv1086 native
40	d1gd0a_	Alignment	not modelled	10.6	9	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
41	d1tr9a_	Alignment	not modelled	10.5	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**NagZ-like
42	d2ba0g2	Alignment	not modelled	10.5	22	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
43	d1vhma_	Alignment	not modelled	10.3	20	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
44	c3fwtA_	Alignment	not modelled	10.2	11	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** crystal structure of leishmania major mif2
45	d1lfpa_	Alignment	not modelled	10.0	29	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
46	d2o3bb1	Alignment	not modelled	9.9	23	**Fold:**Nuclease A inhibitor (NuiA) **Superfamily:**Nuclease A inhibitor (NuiA) **Family:**Nuclease A inhibitor (NuiA)
47	d1b9la_	Alignment	not modelled	9.8	28	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**DHN aldolase/epimerase
48	d1u8va1	Alignment	not modelled	9.6	16	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**Medium chain acyl-CoA dehydrogenase-like, C-terminal domain
49	c2kduB_	Alignment	not modelled	9.3	67	**PDB header:**metal binding protein/exocytosis **Chain:** B: **PDB Molecule:**protein unc-13 homolog a; **PDBTitle:** structural basis of the munc13-1/ca2+-calmodulin2 interaction: a novel 1-26 calmodulin binding motif with a3 bipartite binding mode
50	c3us8A_	Alignment	not modelled	9.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase [nadp]; **PDBTitle:** crystal structure of an isocitrate dehydrogenase from sinorhizobium2 meliloti 1021
51	d1vixa1	Alignment	not modelled	9.1	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
52	d1vmea1	Alignment	not modelled	9.1	5	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
53	c3izcK_	Alignment	not modelled	9.1	16	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein rpl16 (l13p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
54	c3nyyA_	Alignment	not modelled	8.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycyl-glycine endopeptidase lytm; **PDBTitle:** crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus

						atcc 29149 at 1.60 a3 resolution
55	d1u9da_	Alignment	not modelled	8.6	31	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**VC0714-like
56	d2veaa2	Alignment	not modelled	8.4	16	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**Phytochrome-specific domain
57	d2je6a2	Alignment	not modelled	8.4	28	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
58	d1nbua_	Alignment	not modelled	8.4	13	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**DHN aldolase/epimerase
59	c2vg2C_	Alignment	not modelled	8.3	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
60	c1vixA_	Alignment	not modelled	8.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** crystal structure of a putative peptidase t
61	d1mw7a_	Alignment	not modelled	8.2	7	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
62	c1s1iM_	Alignment	not modelled	8.2	16	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l16-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
63	d1n62b2	Alignment	not modelled	8.2	12	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
64	c2uxqB_	Alignment	not modelled	7.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase native; **PDBTitle:** isocitrate dehydrogenase from the psychrophilic bacterium2 desulfotalea psychrophila: biochemical properties and3 crystal structure analysis
65	c3hlyA_	Alignment	not modelled	7.6	24	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
66	c2f7tA_	Alignment	not modelled	7.5	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mos1 transposase; **PDBTitle:** crystal structure of the catalytic domain of mos1 mariner2 transposase
67	d1rp3a1	Alignment	not modelled	7.2	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
68	d5nula_	Alignment	not modelled	7.0	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
69	d1d8ja_	Alignment	not modelled	6.9	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**The central core domain of TFIIE beta
70	d2fz5a1	Alignment	not modelled	6.9	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
71	d1t0la_	Alignment	not modelled	6.8	13	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
72	c2x3mA_	Alignment	not modelled	6.7	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein orf239; **PDBTitle:** crystal structure of hypothetical protein orf239 from pyrobaculum2 spherical virus
73	c3fniA_	Alignment	not modelled	6.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
74	c3l8jA_	Alignment	not modelled	6.5	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**programmed cell death protein 10; **PDBTitle:** crystal structure of ccm3, a cerebral cavernous malformation protein2 critical for vascular integrity
75	d1lwda_	Alignment	not modelled	6.4	18	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
76	d1nbwa2	Alignment	not modelled	6.4	32	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
77	d1vj7a2	Alignment	not modelled	6.4	9	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**RelA/SpoT domain
78	c3f6sI_	Alignment	not modelled	6.3	24	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
79	c3sqlB_	Alignment	not modelled	6.3	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycosyl hydrolase family 3; **PDBTitle:** crystal structure of glycoside hydrolase from synechococcus
						PDB header:dna binding protein

80	c3nr7A_	Alignment	not modelled	6.1	18	**Chain:** A: **PDB Molecule:**dna-binding protein h-ns; **PDBTitle:** crystal structure of s. typhimurium h-ns 1-83
81	c3czxA_	Alignment	not modelled	6.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** the crystal structure of the putative n-acetylmuramoyl-l-2 alanine amidase from neisseria meningitidis
82	c3jywM_	Alignment	not modelled	5.8	16	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l16(a); **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
83	d2a0sa1	Alignment	not modelled	5.7	29	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**6-pyruvoyl tetrahydropterin synthase
84	c3c5tB_	Alignment	not modelled	5.6	9	**PDB header:**signaling protein/signaling protein **Chain:** B: **PDB Molecule:**exendin-4; **PDBTitle:** crystal structure of the ligand-bound glucagon-like peptide-1 receptor2 extracellular domain
85	d1qwda_	Alignment	not modelled	5.6	8	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
86	d2nn6e2	Alignment	not modelled	5.6	22	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
87	d1pdaa1	Alignment	not modelled	5.6	31	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
88	d1dhna_	Alignment	not modelled	5.4	16	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**DHN aldolase/epimerase
89	c2fnzA_	Alignment	not modelled	5.4	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** crystal structure of the lactate dehydrogenase from cryptosporidium2 parvum complexed with cofactor (b-nicotinamide adenine dinucleotide)3 and inhibitor (oxamic acid)
90	d2nn6a2	Alignment	not modelled	5.2	11	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
91	d1otfa_	Alignment	not modelled	5.2	32	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
92	c1bvyF_	Alignment	not modelled	5.2	10	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
93	d1bvyf_	Alignment	not modelled	5.2	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
94	c2ftcH_	Alignment	not modelled	5.1	23	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**39s ribosomal protein l13, mitochondrial; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
95	c2h8bB_	Alignment	not modelled	5.1	71	**PDB header:**hormone/growth factor **Chain:** B: **PDB Molecule:**insulin-like 3; **PDBTitle:** solution structure of insl3
96	d2fgca2	Alignment	not modelled	5.0	23	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like