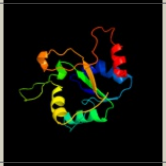
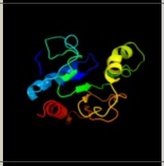
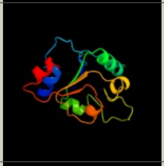
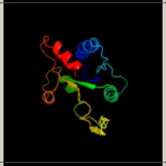
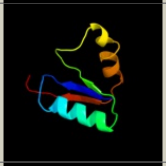
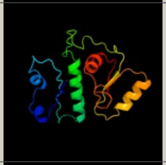
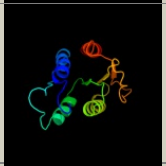
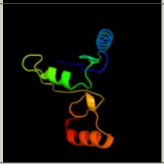
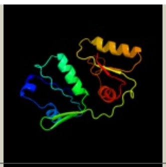
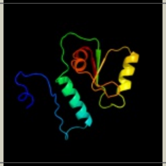
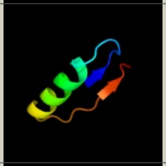
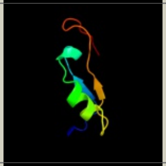
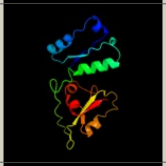
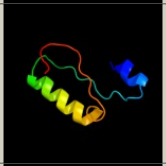
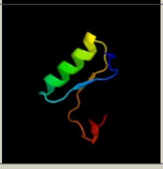
Email	l.a.kelley@imperial.ac.uk
Description	Q9JMR6
Date	Thu Jan 5 12:37:50 GMT 2012
Unique Job ID	6e7a4450c3df15c1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h16A_	Alignment		97.4	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tir protein; **PDBTitle:** crystal structure of a bacteria tir domain, pdtir from2 paracoccus denitrificans
2	d1fyva_	Alignment		97.2	16	**Fold:**Flavodoxin-like **Superfamily:**Toll/Interleukin receptor TIR domain **Family:**Toll/Interleukin receptor TIR domain
3	c2y92A_	Alignment		97.0	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll/interleukin-1 receptor domain-containing adapter **PDBTitle:** crystal structure of mal adaptor protein
4	c2z5vA_	Alignment		97.0	12	**PDB header:**immune system **Chain:** A: **PDB Molecule:**myeloid differentiation primary response protein **PDBTitle:** solution structure of the tir domain of human myd88
5	c1t3gB_	Alignment		95.9	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**x-linked interleukin-1 receptor accessory **PDBTitle:** crystal structure of the toll/interleukin-1 receptor (tir)2 domain of human il-1rapl
6	d1fyxa_	Alignment		95.0	10	**Fold:**Flavodoxin-like **Superfamily:**Toll/Interleukin receptor TIR domain **Family:**Toll/Interleukin receptor TIR domain
7	c3oziB_	Alignment		94.2	5	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**l6tr; **PDBTitle:** crystal structure of the tir domain from the flax disease resistance2 protein l6
8	d2f62a1	Alignment		84.9	16	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
9	d1m1nb_	Alignment		84.3	19	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
10	c2khzB_	Alignment		82.7	24	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**c-myc-responsive protein rcl; **PDBTitle:** solution structure of rcl
11	c2i34B_	Alignment		77.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** the crystal structure of class c acid phosphatase from bacillus2 anthracis with tungstate bound

12	d1qh8b_	Alignment		76.0	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
13	d1miob_	Alignment		60.4	18	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
14	d1wdka3	Alignment		50.4	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
15	c3pdiB_	Alignment		47.5	12	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nifn; **PDBTitle:** precursor bound nifen
16	d2i7xa1	Alignment		46.3	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
17	c2i7xA_	Alignment		46.3	17	**PDB header:**rna binding protein, protein binding **Chain:** A: **PDB Molecule:**protein cft2; **PDBTitle:** structure of yeast cpsf-100 (ydh1p)
18	c3pdiG_	Alignment		45.7	7	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nife; **PDBTitle:** precursor bound nifen
19	c3kbqA_	Alignment		43.4	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ta0487; **PDBTitle:** the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
20	c2xr1B_	Alignment		43.3	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cleavage and polyadenylation specificity factor 100 kd **PDBTitle:** dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
21	c3jrnA_	Alignment	not modelled	39.2	13	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**at1g72930 protein; **PDBTitle:** crystal structure of tir domain from arabidopsis thaliana
22	d2d81a1	Alignment	not modelled	39.2	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PHB depolymerase-like
23	c2ycbA_	Alignment	not modelled	38.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor; **PDBTitle:** structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermautotrophicus
24	d1jq5a_	Alignment	not modelled	36.8	14	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
25	c3sirD_	Alignment	not modelled	34.6	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**caspase; **PDBTitle:** crystal structure of drice
26	c3ox4D_	Alignment	not modelled	33.9	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 2; **PDBTitle:** structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
27	d2dkfa1	Alignment	not modelled	33.6	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
28	c3et4A_	Alignment	not modelled	32.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**outer membrane protein p4, nadp phosphatase; **PDBTitle:** structure of recombinant haemophilus influenzae e(p4)

						acid phosphatase
29	c2xr1A_	Alignment	not modelled	31.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor 100 kd **PDBTitle:** dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
30	d1ycga1	Alignment	not modelled	30.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
31	d2i52a1	Alignment	not modelled	30.6	27	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like
32	d2ieca1	Alignment	not modelled	30.0	27	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like
33	c2ogfD_	Alignment	not modelled	29.5	33	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0408; **PDBTitle:** crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
34	d2obba1	Alignment	not modelled	27.3	11	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
35	d1u0sy_	Alignment	not modelled	26.1	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
36	c3pctA_	Alignment	not modelled	25.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class c acid phosphatase; **PDBTitle:** structure of the class c acid phosphatase from pasteurella multocida
37	c2ia5C_	Alignment	not modelled	23.6	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**polynucleotide kinase; **PDBTitle:** t4 polynucleotide kinase/phosphatase with bound sulfate and2 magnesium.
38	d1ltqa1	Alignment	not modelled	23.3	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
39	d2b82a1	Alignment	not modelled	22.4	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Class B acid phosphatase, AphA
40	c1tjnA_	Alignment	not modelled	22.3	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**sirohydrochlorin cobaltochelatase; **PDBTitle:** crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
41	d1tjna_	Alignment	not modelled	22.3	18	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**CbiX-like
42	c3ehdA_	Alignment	not modelled	21.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of conserved protein from enterococcus faecalis v583
43	d1uxoa_	Alignment	not modelled	21.1	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**YdeN-like
44	c3af5A_	Alignment	not modelled	20.9	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1404; **PDBTitle:** the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
45	c2ofhX_	Alignment	not modelled	20.0	17	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
46	c2xdqB_	Alignment	not modelled	19.6	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**light-independent protochlorophyllide reductase subunit b; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
47	c2kbzA_	Alignment	not modelled	18.9	25	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**15 protein (bacteriophage spp1 complete **PDBTitle:** nmr structure of protein gp15 of bacteriophage spp1
48	d1f8ya_	Alignment	not modelled	17.1	21	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
49	d1vh3a_	Alignment	not modelled	17.0	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
50	c3bfjK_	Alignment	not modelled	17.0	19	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase; **PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase
51	c3lyhB_	Alignment	not modelled	16.8	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cobalamin (vitamin b12) biosynthesis cbix protein; **PDBTitle:** crystal structure of putative cobalamin (vitamin b12) biosynthesis2 cbix protein (yp_958415.1) from marinobacter aquaeolei vt8 at 1.60 a3 resolution
52	d2d9ia1	Alignment	not modelled	16.3	5	**Fold:**IF3-like **Superfamily:**SMR domain-like **Family:**Smr domain
53	d1vlja_	Alignment	not modelled	15.9	17	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
						Fold: Ribosomal protein S5 domain 2-like

54	d1kija1	Alignment	not modelled	15.7	8	**Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
55	d2i76a2	Alignment	not modelled	15.6	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
56	d1xi8a3	Alignment	not modelled	15.4	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
57	d1ssqa_	Alignment	not modelled	15.4	11	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
58	c1htjF_	Alignment	not modelled	15.3	22	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**kiaa0380; **PDBTitle:** structure of the rgs-like domain from pdz-rhogef
59	d1htjf_	Alignment	not modelled	15.3	22	**Fold:**Regulator of G-protein signaling, RGS **Superfamily:**Regulator of G-protein signaling, RGS **Family:**Regulator of G-protein signaling, RGS
60	d2fcja1	Alignment	not modelled	15.3	20	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
61	c2v0xB_	Alignment	not modelled	15.2	19	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**lamina-associated polypeptide 2 isoforms **PDBTitle:** the dimerization domain of lap2alpha
62	c2l3mA_	Alignment	not modelled	14.8	10	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
63	c3nohA_	Alignment	not modelled	14.4	29	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative peptide binding protein; **PDBTitle:** crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution
64	d2cpqa1	Alignment	not modelled	14.3	35	**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)
65	d2hk6a1	Alignment	not modelled	14.1	14	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
66	c1wqaB_	Alignment	not modelled	13.7	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phospho-sugar mutase; **PDBTitle:** crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
67	c3u0vA_	Alignment	not modelled	13.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysophospholipase-like protein 1; **PDBTitle:** crystal structure analysis of human lyplal1
68	d1q8la_	Alignment	not modelled	13.3	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
69	d2hiya1	Alignment	not modelled	13.2	6	**Fold:**SP0830-like **Superfamily:**SP0830-like **Family:**SP0830-like
70	c2k29A_	Alignment	not modelled	13.1	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
71	c2rafC_	Alignment	not modelled	13.1	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dinucleotide-binding oxidoreductase; **PDBTitle:** crystal structure of putative dinucleotide-binding2 oxidoreductase (np_786167.1) from lactobacillus plantarum3 at 1.60 a resolution
72	d1e5da1	Alignment	not modelled	13.0	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
73	c3gx1A_	Alignment	not modelled	12.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1832 protein; **PDBTitle:** crystal structure of a domain of lin1832 from listeria innocua
74	c3nhzA_	Alignment	not modelled	12.8	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
75	d1s6ua_	Alignment	not modelled	12.6	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
76	d1cvra1	Alignment	not modelled	12.6	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Gingipain R (RgpB), C-terminal domain
77	c2j48A_	Alignment	not modelled	12.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
78	c3cf4A_	Alignment	not modelled	12.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetyl-coa decarboxylase/synthase alpha subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
79	d1afia_	Alignment	not modelled	12.3	6	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
						PDB header:lyase

80	c3clhA_	Alignment	not modelled	12.2	7	**Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of 3-dehydroquinate synthase (dhqs)from2 helicobacter pylori
81	c2vq3B_	Alignment	not modelled	12.1	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**metalloreductase steap3; **PDBTitle:** crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle
82	d1mioa_	Alignment	not modelled	12.0	11	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
83	d1kvja_	Alignment	not modelled	11.9	9	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
84	d1l8qa2	Alignment	not modelled	11.5	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
85	c3okfA_	Alignment	not modelled	11.4	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** 2.5 angstrom resolution crystal structure of 3-dehydroquinate synthase2 (arob) from vibrio cholerae
86	c2r98A_	Alignment	not modelled	11.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetylglutamate synthase; **PDBTitle:** crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
87	c3trdA_	Alignment	not modelled	11.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha/beta hydrolase; **PDBTitle:** structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
88	d1p6ta1	Alignment	not modelled	11.2	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
89	d1bxca_	Alignment	not modelled	11.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
90	c2yvqA_	Alignment	not modelled	11.1	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
91	d1p9oa_	Alignment	not modelled	11.0	19	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
92	d1zesa1	Alignment	not modelled	10.9	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
93	d1wu2a3	Alignment	not modelled	10.7	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
94	d1w25a1	Alignment	not modelled	10.4	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
95	c3qd7X_	Alignment	not modelled	10.3	25	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein ydal; **PDBTitle:** crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
96	d2auna2	Alignment	not modelled	10.2	10	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
97	c2ldiA_	Alignment	not modelled	10.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
98	d1qh8a_	Alignment	not modelled	10.1	9	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
99	d1mb3a_	Alignment	not modelled	10.0	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related