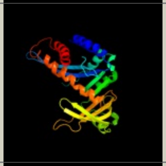
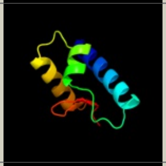
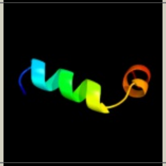
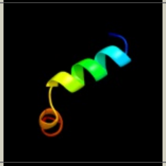
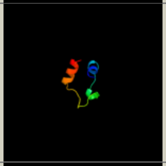
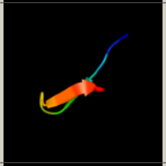
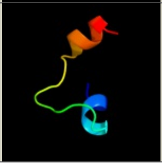
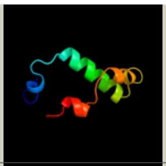
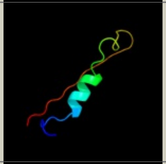
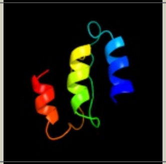
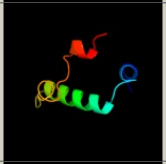
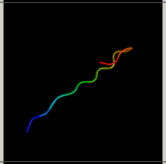
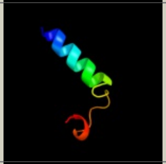
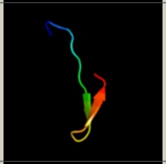
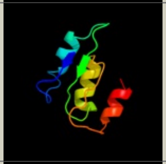
Email	l.a.kelley@imperial.ac.uk
Description	P28912
Date	Thu Jan 5 11:45:24 GMT 2012
Unique Job ID	7cd5438d21624744

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1musa_	Alignment		97.7	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
2	d1b7ea_	Alignment		97.7	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
3	d2v9va2	Alignment		79.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
4	c2v9vA_	Alignment		65.1	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** crystal structure of moorella thermoacetica selb(377-511)
5	d2ezha_	Alignment		50.9	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
6	d2ezia_	Alignment		49.1	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
7	c6paxA_	Alignment		43.9	22	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6; **PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
8	c3hefB_	Alignment		40.9	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
9	c2plyB_	Alignment		22.7	11	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
10	d1e8qa_	Alignment		20.2	36	**Fold:**Cellulose docking domain, dockering **Superfamily:**Cellulose docking domain, dockering **Family:**Cellulose docking domain, dockering
11	d1pdnc_	Alignment		19.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain

12	d1dlwa_	Alignment		19.4	11	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
13	c2rfpA_	Alignment		16.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ntp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
14	d1ajza_	Alignment		15.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
15	c3aq8A_	Alignment		15.3	4	**PDB header:**oxygen binding **Chain:** A: **PDB Molecule:**group 1 truncated hemoglobin; **PDBTitle:** crystal structure of truncated hemoglobin from tetrahymena pyriformis,2 q46e mutant, fe(iii) form
16	d2fgga1	Alignment		15.3	31	**Fold:**dsRBD-like **Superfamily:**Rv2632c-like **Family:**Rv2632c-like
17	c2kvcA_	Alignment		15.2	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
18	c3mx7A_	Alignment		14.8	29	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** crystal structure analysis of human faim-ntd
19	c2vp8A_	Alignment		14.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
20	d1s69a_	Alignment		14.5	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
21	d1iyxa1	Alignment	not modelled	13.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
22	c2k27A_	Alignment	not modelled	13.2	25	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
23	c3ol4B_	Alignment	not modelled	12.7	26	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
24	c3e2dB_	Alignment	not modelled	12.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** the 1.4 a crystal structure of the large and cold-active2 vibrio sp. alkaline phosphatase
25	c2j4mA_	Alignment	not modelled	11.9	36	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**endoglucanase 45a; **PDBTitle:** double dockerin from piromyces equi cel45a
26	d1idra_	Alignment	not modelled	11.7	7	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
27	c1qcrD_	Alignment	not modelled	11.3	8	**PDB header:** **PDB COMPND:**
28	d1mpga1	Alignment	not modelled	11.3	11	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
29	d1g9ga_	Alignment	not modelled	10.5	63	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases

						Family: Cellulases catalytic domain
30	d1md6a_	Alignment	not modelled	10.3	17	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Interleukin-1 (IL-1)
31	c2y5sA_	Alignment	not modelled	10.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
32	c2kzvA_	Alignment	not modelled	9.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of cv_0373(175-257) protein from2 chromobacterium violaceum, northeast structural genomics consortium3 target cvr118a
33	d3bpya1	Alignment	not modelled	9.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
34	d1osna_	Alignment	not modelled	9.7	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
35	c3rf7A_	Alignment	not modelled	9.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
36	c1e17A_	Alignment	not modelled	8.8	9	**PDB header:**dna binding domain **Chain:** A: **PDB Molecule:**afx; **PDBTitle:** solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
37	d2c6ya1	Alignment	not modelled	8.8	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
38	c3r1iB_	Alignment	not modelled	8.7	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
39	c1dlyA_	Alignment	not modelled	8.5	12	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**hemoglobin; **PDBTitle:** x-ray crystal structure of hemoglobin from the green2 unicellular alga chlamydomonas eugametos
40	d1dlya_	Alignment	not modelled	8.5	12	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
41	c3gk0H_	Alignment	not modelled	8.4	20	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
42	c1l2aD_	Alignment	not modelled	8.4	50	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
43	d1l1ya_	Alignment	not modelled	8.4	50	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
44	d1w6ta1	Alignment	not modelled	8.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
45	c3co7C_	Alignment	not modelled	8.4	14	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**forkhead box protein o1; **PDBTitle:** crystal structure of foxo1 dbd bound to dbe2 dna
46	d2ilaa_	Alignment	not modelled	8.1	22	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Interleukin-1 (IL-1)
47	c3cwbQ_	Alignment	not modelled	7.9	8	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
48	d2ptza1	Alignment	not modelled	7.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
49	c3nswA_	Alignment	not modelled	7.8	38	**PDB header:**immune system **Chain:** A: **PDB Molecule:**excretory-secretory protein 2; **PDBTitle:** crystal structure of ancylostoma ceylanicum excretory-secretory2 protein 2
50	d2ezla_	Alignment	not modelled	7.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
51	c2yf3F_	Alignment	not modelled	7.7	20	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**mazg-like nucleoside triphosphate pyrophosphohydrolase; **PDBTitle:** crystal structure of dr2231, the mazg-like protein from2 deinococcus radiodurans, complex with manganese
52	c2x4mD_	Alignment	not modelled	7.7	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
53	c1hj0A_	Alignment	not modelled	7.6	19	**PDB header:**actin binding peptide **Chain:** A: **PDB Molecule:**thymosin beta9; **PDBTitle:** thymosin beta9
54	d1g31a_	Alignment	not modelled	7.6	13	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES

55	d2abka_	Alignment	not modelled	7.3	13	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
56	c3hluA_	Alignment	not modelled	7.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf2179; **PDBTitle:** crystal structure of uncharacterized protein conserved in bacteria2 duf2179 from eubacterium ventriosum
57	c1p84D_	Alignment	not modelled	7.1	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
58	d1vi7a1	Alignment	not modelled	7.1	19	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like
59	c2jpiA_	Alignment	not modelled	7.1	17	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
60	d1rh6a_	Alignment	not modelled	7.0	15	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
61	d1eyea_	Alignment	not modelled	6.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
62	c3g73A_	Alignment	not modelled	6.8	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**forkhead box protein m1; **PDBTitle:** structure of the foxm1 dna binding
63	d2a22a1	Alignment	not modelled	6.7	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
64	d2giab1	Alignment	not modelled	6.7	63	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Guide RNA binding protein gBP
65	c2giaB_	Alignment	not modelled	6.7	63	**PDB header:**translation **Chain:** B: **PDB Molecule:**mitochondrial rna-binding protein 1; **PDBTitle:** crystal structures of trypanosoma bruciei mrp1/mrp2
66	d1m5wa_	Alignment	not modelled	6.6	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
67	d1pcna1	Alignment	not modelled	6.5	36	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Colipase-like **Family:**Colipase-like
68	c1gmuB_	Alignment	not modelled	6.5	9	**PDB header:**metallochaperone **Chain:** B: **PDB Molecule:**uree; **PDBTitle:** structure of uree
69	d1ogla_	Alignment	not modelled	6.5	18	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**Type II deoxyuridine triphosphatase
70	d1un2a_	Alignment	not modelled	6.4	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
71	c3douA_	Alignment	not modelled	6.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase j; **PDBTitle:** crystal structure of methyltransferase involved in cell2 division from thermoplasma volcanicum gss1
72	c3a44D_	Alignment	not modelled	6.4	0	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
73	c3k6qB_	Alignment	not modelled	6.4	14	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative ligand binding protein; **PDBTitle:** crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
74	d1d5va_	Alignment	not modelled	6.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
75	d1xb4a2	Alignment	not modelled	6.4	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
76	c1c94B_	Alignment	not modelled	6.3	63	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**retro-gcn4 leucine zipper; **PDBTitle:** reversing the sequence of the gcn4 leucine zipper does not2 affect its fold.
77	d1ha7a_	Alignment	not modelled	6.2	17	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
78	c2iucB_	Alignment	not modelled	6.1	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
79	c2b99A_	Alignment	not modelled	6.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin synthase; **PDBTitle:** crystal structure of an archaeal pentameric riboflavin2 synthase complex with a substrate analog inhibitor
80	d2hfha_	Alignment	not modelled	6.0	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
81	c3a52A_	Alignment	not modelled	6.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase;

81	c3a52A_	Alignment	not modelled	6.0	18	**PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
82	d1pm6a_	Alignment	not modelled	6.0	15	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
83	d1j3aa_	Alignment	not modelled	6.0	13	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
84	d2czda1	Alignment	not modelled	5.9	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
85	c2kl8A_	Alignment	not modelled	5.9	14	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or15; **PDBTitle:** solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15
86	d2o0ma1	Alignment	not modelled	5.9	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
87	c2o0mA_	Alignment	not modelled	5.9	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, sorc family; **PDBTitle:** the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis
88	c3emkA_	Alignment	not modelled	5.8	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose/ribitol dehydrogenase; **PDBTitle:** 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
89	d2a07f1	Alignment	not modelled	5.8	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
90	d1f6ya_	Alignment	not modelled	5.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
91	c2y6xA_	Alignment	not modelled	5.8	11	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii 11 kd protein; **PDBTitle:** structure of psb27 from thermosynechococcus elongatus
92	d1yqea1	Alignment	not modelled	5.8	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
93	d2i7pa1	Alignment	not modelled	5.6	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
94	d1dqwa_	Alignment	not modelled	5.6	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
95	c2dfjA_	Alignment	not modelled	5.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosinetetraphosphatase; **PDBTitle:** crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
96	c2wdzD_	Alignment	not modelled	5.5	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of the short chain dehydrogenase2 galactitol-dehydrogenase (gatdh) of rhodobacter3 sphaeroides in complex with nad+ and 1,2-pentandiol
97	d1xi8a3	Alignment	not modelled	5.5	21	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
98	c3n1uA_	Alignment	not modelled	5.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, had superfamily, subfamily iii a; **PDBTitle:** structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
99	c3pk0B_	Alignment	not modelled	5.5	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis