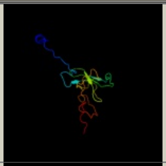
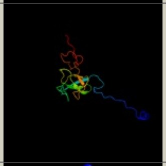
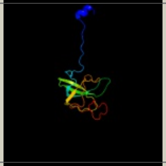
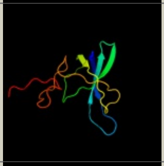
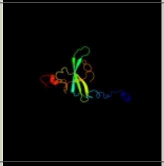
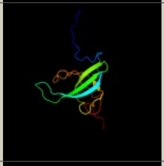
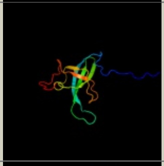
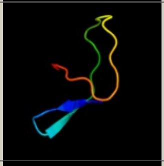
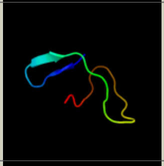
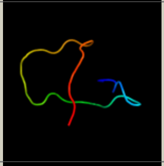
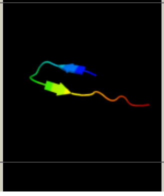
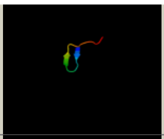
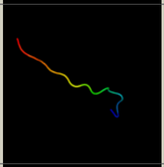
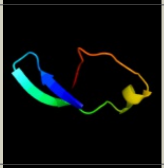
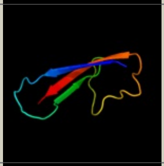
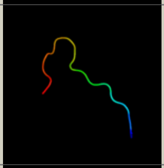
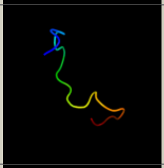
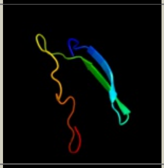
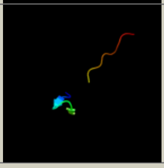
Email	l.a.kelley@imperial.ac.uk
Description	P0A7S3
Date	Thu Jan 5 11:06:07 GMT 2012
Unique Job ID	399ae7550a169953

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qall1	Alignment		100.0	100	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
2	d1i94l_	Alignment		100.0	72	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
3	d2uubl1	Alignment		100.0	73	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
4	c1zn1L_	Alignment		100.0	100	**PDB header:**biosynthetic/structural protein/rna **Chain:** L: **PDB Molecule:**30s ribosomal protein s12; **PDBTitle:** coordinates of rrf fitted into cryo-em map of the 70s post-2 termination complex
5	c2xzmL_	Alignment		100.0	28	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**40s ribosomal protein s12; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
6	c2zkql_	Alignment		100.0	27	**PDB header:**ribosomal protein/rna **Chain:** L: **PDB Molecule:** **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
7	c1s1hL_	Alignment		100.0	29	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**40s ribosomal protein s23; **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, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
8	c3i4oA_	Alignment		85.1	23	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
9	d1ah9a_	Alignment		85.0	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
10	d1hr0w_	Alignment		69.8	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
11	d1jt8a_	Alignment		45.4	38	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

12	c2oqkA_	Alignment		37.8	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
13	d2ix0a3	Alignment		29.8	41	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
14	c2d1cB_	Alignment		27.8	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** crystal structure of tt0538 protein from thermus thermophilus hb8
15	d1d7qa_	Alignment		26.9	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
16	d1v7wa1	Alignment		24.0	19	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
17	c1y80A_	Alignment		22.9	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted cobalamin binding protein; **PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica
18	d1ju2a1	Alignment		19.0	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
19	d1eara1	Alignment		15.9	13	**Fold:**Urease metallochaperone UreE, N-terminal domain **Superfamily:**Urease metallochaperone UreE, N-terminal domain **Family:**Urease metallochaperone UreE, N-terminal domain
20	d1pb1a_	Alignment		15.7	44	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
21	d3bula2	Alignment	not modelled	13.6	35	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
22	d1o7ia_	Alignment	not modelled	12.6	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
23	d1e32a1	Alignment	not modelled	12.0	18	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
24	d1yrra1	Alignment	not modelled	12.0	29	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
25	d1dwna_	Alignment	not modelled	11.9	32	**Fold:**RNA bacteriophage capsid protein **Superfamily:**RNA bacteriophage capsid protein **Family:**RNA bacteriophage capsid protein
26	d1rutx4	Alignment	not modelled	10.7	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
27	c2jx5A_	Alignment	not modelled	10.0	16	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**glub(s27a); **PDBTitle:** solution structure of the ubiquitin domain n-terminal to2 the s27a ribosomal subunit of giardia lamblia
28	c3swnA_	Alignment	not modelled	9.7	9	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u6 snrna-associated sm-like protein lsm5; **PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
29	d1hqsa_	Alignment	not modelled	8.9	33	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like

						Family: Dimeric isocitrate & isopropylmalate dehydrogenases
30	d1rxta1	Alignment	not modelled	8.2	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
31	d2dipa1	Alignment	not modelled	8.2	17	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**ZZ domain
32	d2vo1a1	Alignment	not modelled	8.0	32	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
33	c3n0vD_	Alignment	not modelled	7.5	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
34	d1x7fa2	Alignment	not modelled	7.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Outer surface protein, N-terminal domain
35	d1ccwa_	Alignment	not modelled	6.8	22	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
36	d1w98b1	Alignment	not modelled	6.6	38	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
37	d2fcta1	Alignment	not modelled	6.5	24	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
38	c2r8cB_	Alignment	not modelled	6.4	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative amidohydrolase; **PDBTitle:** crystal structure of uncharacterized protein eaj56179
39	c3bw1A_	Alignment	not modelled	6.3	9	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u6 snrna-associated sm-like protein lsm3; **PDBTitle:** crystal structure of homomeric yeast lsm3 exhibiting novel octameric2 ring organisation
40	c2e0cA_	Alignment	not modelled	6.2	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**409aa long hypothetical nadp-dependent isocitrate **PDBTitle:** crystal structure of isocitrate dehydrogenase from sulfolobus tokodaii2 strain7 at 2.0 a resolution
41	c3louB_	Alignment	not modelled	6.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
42	c3cw1D_	Alignment	not modelled	6.1	9	**PDB header:**splicing **Chain:** D: **PDB Molecule:**small nuclear ribonucleoprotein sm d3; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
43	c1xyr6_	Alignment	not modelled	6.0	45	**PDB header:**virus **Chain:** 6: **PDB Molecule:**genome polyprotein, coat protein vp3; **PDB Fragment:**residues 620-630 **PDBTitle:** poliovirus 135s cell entry intermediate
44	d1d3ba_	Alignment	not modelled	5.9	10	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
45	c3hx6A_	Alignment	not modelled	5.6	25	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**type 4 fimbrial biogenesis protein pily1; **PDBTitle:** crystal structure of pseudomonas aeruginosa pily1 c-terminal2 domain
46	c1x7fA_	Alignment	not modelled	5.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**outer surface protein; **PDBTitle:** crystal structure of an uncharacterized b. cereus protein