
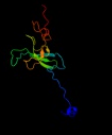
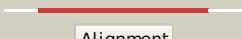


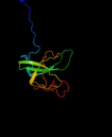







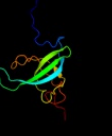



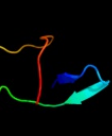



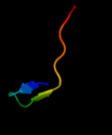
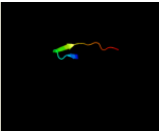
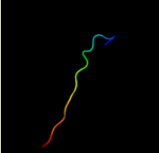
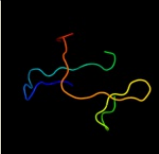


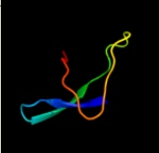

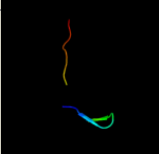
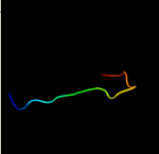


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0A0H0
Date	Tue Jul 17 17:05:06 BST 2012
Unique Job ID	c60cf05d72fae754

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1i94l_	 Alignment		100.0	70	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
2	d2qall1	 Alignment		100.0	71	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
3	d2uubl1	 Alignment		100.0	69	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
4	c1zn1l_	 Alignment		100.0	75	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	31	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	c1s1hl_	 Alignment		100.0	30	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.
7	c2zskl_	 Alignment		100.0	29	PDB header: ribosomal protein/rna Chain: L: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
8	d1ah9a_	 Alignment		85.5	30	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
9	c3i4oA_	 Alignment		85.4	27	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
10	d1hr0w_	 Alignment		71.0	37	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
11	d1jt8a_	 Alignment		46.7	38	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like

12	c2oqkA	Alignment		38.3	13	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	c2d1cB	Alignment		28.5	33	PDB header: oxidoreductase Chain: B: PDB Molecule: isocitrate dehydrogenase; PDBTitle: crystal structure of tt0538 protein from thermus thermophilus hb8
14	d2ix0a3	Alignment		24.3	43	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
15	c1y80A	Alignment		23.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iiiiim)-binding protein from2 moorella thermoacetica
16	d1v7wa1	Alignment		21.1	21	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyltransferase family 36 C-terminal domain
17	d1d7qa	Alignment		20.9	13	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
18	d1ju2a1	Alignment		18.0	30	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
19	d1pbl_a	Alignment		16.1	39	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
20	d3bula2	Alignment		15.0	24	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
21	d1dwna	Alignment	not modelled	13.9	36	Fold: RNA bacteriophage capsid protein Superfamily: RNA bacteriophage capsid protein Family: RNA bacteriophage capsid protein
22	d1leara1	Alignment	not modelled	12.0	13	Fold: Urease metallochaperone UreE, N-terminal domain Superfamily: Urease metallochaperone UreE, N-terminal domain Family: Urease metallochaperone UreE, N-terminal domain
23	d2dipa1	Alignment	not modelled	11.0	11	Fold: RING/U-box Superfamily: RING/U-box Family: ZZ domain
24	d1yrra1	Alignment	not modelled	10.5	21	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
25	d1e32a1	Alignment	not modelled	10.4	24	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
26	d1o7ia	Alignment	not modelled	10.0	7	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
27	d2fcta1	Alignment	not modelled	9.2	18	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: PhyH-like
28	d1rub4	Alignment	not modelled	8.5	29	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
29	d1hqsa	Alignment	not modelled	8.4	33	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases

30	c2jx5A_	Alignment	not modelled	8.0	32	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
31	c3swnA_	Alignment	not modelled	7.9	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
32	d1x7fa2	Alignment	not modelled	7.8	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Outer surface protein, N-terminal domain
33	d1rxta1	Alignment	not modelled	7.2	18	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-myristoyl transferase, NMT
34	d1w98b1	Alignment	not modelled	7.1	31	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
35	d1ccwa_	Alignment	not modelled	6.7	11	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
36	c3n0vD_	Alignment	not modelled	6.6	10	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
37	c1x7fa_	Alignment	not modelled	6.1	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: outer surface protein; PDBTitle: crystal structure of an uncharacterized b. cereus protein
38	d1d3ba_	Alignment	not modelled	6.0	5	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
39	d2vo1a1	Alignment	not modelled	6.0	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
40	c2e0cA_	Alignment	not modelled	5.9	28	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	c2r8cB_	Alignment	not modelled	5.6	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative amidohydrolase; PDBTitle: crystal structure of uncharacterized protein eaj56179
42	c3louB_	Alignment	not modelled	5.5	11	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
43	c1xyr6_	Alignment	not modelled	5.5	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	c3bw1A_	Alignment	not modelled	5.3	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