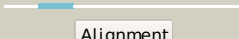
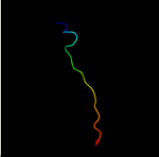
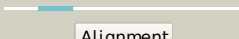
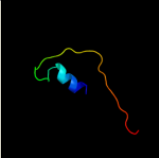
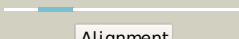
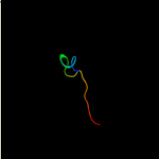

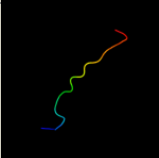

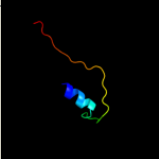

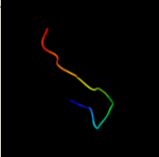

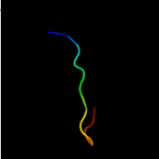

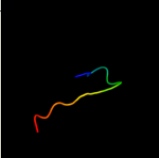

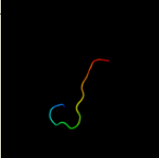

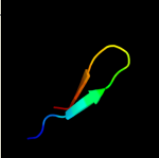


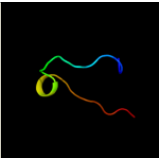
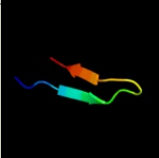
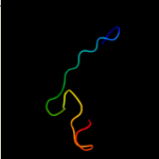
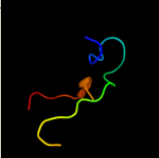
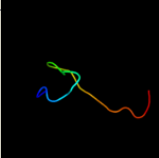
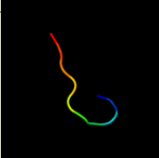
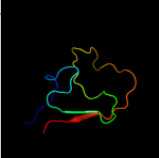
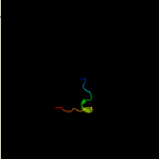
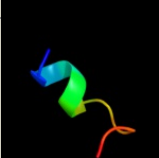


Phyre2

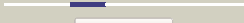
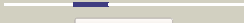


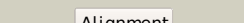
Email	I.a.kelley@imperial.ac.uk
Description	Q81XH6
Date	Thu Apr 26 09:34:36 BST 2012
Unique Job ID	544235acab21f8f4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3npeA	 Alignment		36.6	26	PDB header: oxidoreductase Chain: A; PDB Molecule: 9-cis-epoxycarotenoid dioxygenase 1, chloroplastic; PDBTitle: structure of vp14 in complex with oxygen
2	c3r8kB	 Alignment		34.5	15	PDB header: apoptosis Chain: B; PDB Molecule: heme-binding protein 2; PDBTitle: crystal structure of human soul protein (hexagonal form)
3	c3fsnA	 Alignment		30.4	18	PDB header: isomerase Chain: A; PDB Molecule: retinal pigment epithelium-specific 65 kda protein; PDBTitle: crystal structure of rpe65 at 2.14 angstrom resolution
4	c2biwC	 Alignment		29.0	29	PDB header: oxidoreductase Chain: C; PDB Molecule: apocarotenoid-cleaving oxygenase; PDBTitle: crystal structure of apocarotenoid cleavage oxygenase from2 synechocystis, native enzyme
5	d2gova1	 Alignment		28.4	3	Fold: Probable bacterial effector-binding domain Superfamily: Probable bacterial effector-binding domain Family: SOUL heme-binding protein
6	d2o5aa1	 Alignment		21.2	47	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Iojap/YbeB-like
7	d1sgva2	 Alignment		20.4	27	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
8	c3upsA	 Alignment		20.2	27	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: iojap-like protein; PDBTitle: crystal structure of iojap-like protein from zymomonas mobilis
9	d2id1a1	 Alignment		19.1	33	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Iojap/YbeB-like
10	d2cfua2	 Alignment		17.6	25	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Alkylsulfatase-like
11	d1ee8a2	 Alignment		17.3	23	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins

12	c1xk5A	Alignment		14.5	30	PDB header: transport protein Chain: A: PDB Molecule: snurportin-1; PDBTitle: crystal structure of the m3g-cap-binding domain of2 snurportin1 in complex with a m3gpppg-cap dinucleotide
13	c2cfuA	Alignment		13.3	25	PDB header: hydrolase Chain: A: PDB Molecule: sdsA1; PDBTitle: crystal structure of sdsA1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
14	c2i82D	Alignment		12.8	12	PDB header: lyase/rna Chain: D: PDB Molecule: ribosomal large subunit pseudouridine synthase a; PDBTitle: crystal structure of pseudouridine synthase rlua: indirect2 sequence readout through protein-induced rna structure
15	d1oa8a	Alignment		12.7	30	Fold: AXH domain Superfamily: AXH domain Family: AXH domain
16	c1k82D	Alignment		11.9	38	PDB header: hydrolase/dna Chain: D: PDB Molecule: formamido pyrimidine-dna glycosylase; PDBTitle: crystal structure of e.coli formamido pyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
17	d1q1oa	Alignment		11.5	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
18	c3km5B	Alignment		11.4	8	PDB header: cell invasion Chain: B: PDB Molecule: lysine specific cysteine protease; PDBTitle: crystal structure analysis of the k2 cleaved adhesin domain of lys-2 gingipain (kgp)
19	c3gjxE	Alignment		11.1	28	PDB header: protein transport Chain: E: PDB Molecule: snurportin-1; PDBTitle: crystal structure of the nuclear export complex crm1-2 snurportin1-rangtp
20	c3ce8A	Alignment		10.5	42	PDB header: unknown function Chain: A: PDB Molecule: putative pII-like nitrogen regulatory protein; PDBTitle: crystal structure of a duf3240 family protein (sbal_0098) from2 shewanella baltica os155 at 2.40 a resolution
21	c3hxrA	Alignment	not modelled	10.1	19	PDB header: structural protein Chain: A: PDB Molecule: nucleoporin nup120; PDBTitle: nucleoporin nup120 from s.cerevisiae (aa 1-757)
22	d2apoa2	Alignment	not modelled	9.9	21	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
23	d3proc2	Alignment	not modelled	9.6	67	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
24	d1sr4a	Alignment	not modelled	9.4	43	Fold: beta-Trefoil Superfamily: Ricin B-like lectins Family: Ricin B-like
25	c1sr4A	Alignment	not modelled	9.4	43	PDB header: toxin Chain: A: PDB Molecule: cytolethal distending toxin subunit a; PDBTitle: crystal structure of the haemophilus ducreyi cytolethal2 distending toxin
26	c2i7fB	Alignment	not modelled	9.3	50	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin component of dioxygenase; PDBTitle: sphingomonas yanoikuyae b1 ferredoxin
27	d1p5dx4	Alignment	not modelled	8.8	29	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
28	d1v9ka	Alignment	not modelled	8.7	24	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RluD
29	d1k3xa2	Alignment	not modelled	8.2	18	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins

							Family: N-terminal domain of MutM-like DNA repair proteins
30	c3i0uA_	Alignment	not modelled	8.2	59	PDB header: lyase Chain: A: PDB Molecule: phosphothreonine lyase ospf; PDBTitle: structure of the type iii effector/phosphothreonine lyase ospf from2 shigella flexneri	
31	c1k8wA_	Alignment	not modelled	8.0	29	PDB header: lyase/rna Chain: A: PDB Molecule: trna pseudouridine synthase b; PDBTitle: crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna	
32	c3zv0D_	Alignment	not modelled	7.7	44	PDB header: cell cycle Chain: D: PDB Molecule: h/aca ribonucleoprotein complex subunit 4; PDBTitle: structure of the shq1p-cbf5p complex	
33	d1aisb1	Alignment	not modelled	7.6	43	Fold: Cyclin-like Superfamily: Cyclin-like Family: Transcription factor IIB (TFIIB), core domain	
34	d1xzwa1	Alignment	not modelled	7.6	67	Fold: Immunoglobulin-like beta-sandwich Superfamily: Purple acid phosphatase, N-terminal domain Family: Purple acid phosphatase, N-terminal domain	
35	c3fkaD_	Alignment	not modelled	7.1	17	PDB header: unknown function Chain: D: PDB Molecule: uncharacterized ntf-2 like protein; PDBTitle: crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution	
36	d1usra_	Alignment	not modelled	7.0	29	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)	
37	d1pqsa_	Alignment	not modelled	6.9	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain	
38	c2fugC_	Alignment	not modelled	6.9	44	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-quinone oxidoreductase chain 3; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus	
39	c3dukD_	Alignment	not modelled	6.7	12	PDB header: unknown function Chain: D: PDB Molecule: ntf2-like protein of unknown function; PDBTitle: crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution	
40	c3s63B_	Alignment	not modelled	6.5	25	PDB header: lipid binding protein Chain: B: PDB Molecule: saposin-like protein; PDBTitle: saposin-like protein na-slp-1	
41	d1wjfa_	Alignment	not modelled	6.2	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase	
42	d2ey4a2	Alignment	not modelled	6.1	18	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB	
43	d1wfwA_	Alignment	not modelled	5.9	19	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain	
44	d1e0ea_	Alignment	not modelled	5.9	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase	
45	d1r3ea2	Alignment	not modelled	5.9	21	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB	
46	c2eouA_	Alignment	not modelled	5.8	100	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 473; PDBTitle: solution structure of the c2h2 type zinc finger (region 370-2 400) of human zinc finger protein 473	
47	d1d0qa_	Alignment	not modelled	5.8	50	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger	
48	c3hefB_	Alignment	not modelled	5.8	28	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small2 subunit	
49	c2v0xB_	Alignment	not modelled	5.7	22	PDB header: cell cycle Chain: B: PDB Molecule: lamina-associated polypeptide 2 isoforms PDBTitle: the dimerization domain of lap2alpha	
50	c2gu1A_	Alignment	not modelled	5.7	36	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae	
51	c3m1hB_	Alignment	not modelled	5.7	14	PDB header: cell invasion Chain: B: PDB Molecule: lysine specific cysteine protease; PDBTitle: crystal structure analysis of the k3 cleaved adhesin domain of lys-2 gingipain (kgp) from porphyromonas gingivalis w83	
52	c3cs5B_	Alignment	not modelled	5.7	86	PDB header: photosynthesis Chain: B: PDB Molecule: phycobilisome degradation protein nbla; PDBTitle: nbla protein from synechococcus elongatus pcc 7942	
53	d1xe0a_	Alignment	not modelled	5.6	32	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Nucleoplasmin-like core domain Family: Nucleoplasmin-like core domain	
54	d1v3ea_	Alignment	not modelled	5.5	29	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)	
55	d3d32a1	Alignment	not modelled	5.5	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: GABARAP-like	

56	c2jeuA_	 Alignment	not modelled	5.5	50	PDB header: transcription Chain: A: PDB Molecule: regulatory protein e2; PDBTitle: transcription activator structure reveals redox control of 2 a replication initiation reaction
57	d2f2fa1	 Alignment	not modelled	5.4	43	Fold: beta-Trefoil Superfamily: Ricin B-like lectins Family: Ricin B-like
58	c2c2xB_	 Alignment	not modelled	5.4	26	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase- PDBTitle: three dimensional structure of bifunctional 2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
59	d3e9fa1	 Alignment	not modelled	5.4	28	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Prp8 beta-finger domain-like
60	d1wj6a_	 Alignment	not modelled	5.3	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain