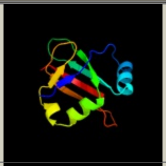
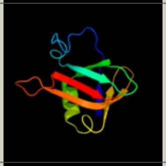
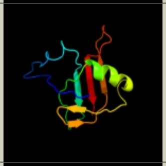
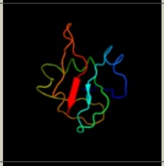
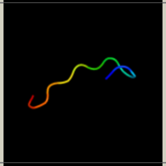
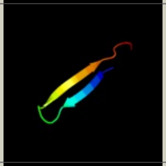
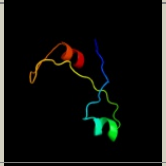
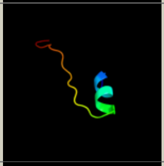
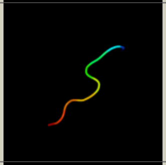
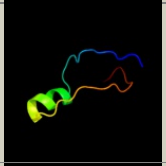
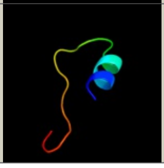
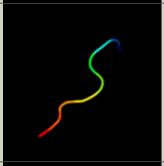
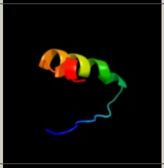
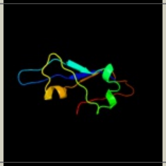
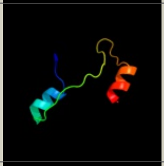
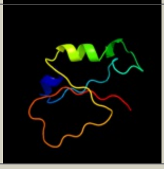
Email	l.a.kelley@imperial.ac.uk
Description	P68919
Date	Thu Jan 5 12:11:13 GMT 2012
Unique Job ID	1fd58fc39f756b8e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dfup_	Alignment		100.0	100	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Ribosomal protein L25-like
2	d1feua_	Alignment		100.0	18	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Ribosomal protein L25-like
3	d2zjrs1	Alignment		99.9	19	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Ribosomal protein L25-like
4	c2b9nZ_	Alignment		99.9	20	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein ctc; **PDBTitle:** 50s ribosomal subunit from a crystal structure of release factor rf2,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400.
5	d1zaka2	Alignment		52.9	25	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
6	d1htwa_	Alignment		47.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**YjeE-like
7	c1vhoA_	Alignment		24.0	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of a putative peptidase/endoglucanase
8	c1q7lB_	Alignment		18.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i
9	c3no8A_	Alignment		14.8	20	**PDB header:**isomerase regulator **Chain:** A: **PDB Molecule:**btb/poz domain-containing protein 2; **PDBTitle:** crystal structure of the phr domain from human btbd2 protein
10	c1vixA_	Alignment		14.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** crystal structure of a putative peptidase t
11	d2phpa1	Alignment		12.8	29	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**Phosphomethylpyrimidine kinase C-terminal domain-like

12	d1a6ca3	Alignment		12.2	10	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
13	c3hwjA_	Alignment		11.2	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase mycbp2; **PDBTitle:** crystal structure of the second phr domain of mouse myc-2 binding protein 2 (mycbp-2)
14	c3l7pA_	Alignment		11.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative nitrogen regulatory protein pii; **PDBTitle:** crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans
15	d1etha1	Alignment		10.6	14	**Fold:**Lipase/lipooxygenase domain (PLAT/LH2 domain) **Superfamily:**Lipase/lipooxygenase domain (PLAT/LH2 domain) **Family:**Colipase-binding domain
16	c3rzaA_	Alignment		9.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidase; **PDBTitle:** crystal structure of a tripeptidase (sav1512) from staphylococcus2 aureus subsp. aureus mu50 at 2.10 a resolution
17	c3na2C_	Alignment		9.5	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function from mine drainage2 metagenome leptospirillum rubarum
18	c3ls8A_	Alignment		9.3	67	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol 3-kinase catalytic subunit **PDBTitle:** crystal structure of human pik3c3 in complex with 3-[4-(4-2 morpholinyl)thieno[3,2-d]pyrimidin-2-yl]-phenol
19	d1z2la1	Alignment		9.3	10	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
20	d1vjna_	Alignment		8.9	24	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Hypothetical protein TM0207
21	c3gbwA_	Alignment	not modelled	8.8	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase mycbp2; **PDBTitle:** crystal structure of the first phr domain of the mouse myc-2 binding protein 2 (mycbp-2)
22	c2j8aA_	Alignment	not modelled	8.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-4 **PDBTitle:** x-ray structure of the n-terminus rrm domain of set1
23	d1e7ua4	Alignment	not modelled	8.3	56	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Phoshoinositide 3-kinase (PI3K), catalytic domain
24	c2x6kB_	Alignment	not modelled	7.5	67	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotidylinositol 3 kinase 59f; **PDBTitle:** the crystal structure of the drosophila class iii pi3-kinase2 vps34 in complex with pi-103
25	c3ifeA_	Alignment	not modelled	7.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** 1.55 angstrom resolution crystal structure of peptidase t (pept-1)2 from bacillus anthracis str. 'ames ancestor'.
26	d1qo5b_	Alignment	not modelled	7.1	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
27	c3mmtC_	Alignment	not modelled	7.0	26	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of fructose bisphosphate aldolase from bartonella2 henselae, bound to fructose bisphosphate
28	d1fdja_	Alignment	not modelled	6.6	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
						Fold: Phosphorylase/hydrolase-like

29	d1vixa1	Alignment	not modelled	6.4	14	**Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
30	d1xfba1	Alignment	not modelled	6.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
31	d1vkia_	Alignment	not modelled	6.3	5	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
32	d1zaia1	Alignment	not modelled	6.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
33	c2x0oA_	Alignment	not modelled	6.2	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**alcaligin biosynthesis protein; **PDBTitle:** apo structure of the alcaligin biosynthesis protein c (alcc)2 from bordetella bronchiseptica
34	c2pc4B_	Alignment	not modelled	6.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of fructose-bisphosphate aldolase from plasmodium2 falciparum in complex with trap-tail determined at 2.4 angstrom3 resolution
35	d1a5ca_	Alignment	not modelled	5.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
36	c2rb7A_	Alignment	not modelled	5.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase, m20/m25/m40 family; **PDBTitle:** crystal structure of co-catalytic metallopeptidase (yp_387682.1) from2 desulfovibrio desulfuricans g20 at 1.60 a resolution
37	d1fbaa_	Alignment	not modelled	5.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
38	d1f2ja_	Alignment	not modelled	5.4	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
39	d1nn7a_	Alignment	not modelled	5.3	17	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
40	c2y3aA_	Alignment	not modelled	5.1	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
41	c3ic1A_	Alignment	not modelled	5.1	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of zinc-bound succinyl-diaminopimelate desuccinylase2 from haemophilus influenzae
42	d1s1ga_	Alignment	not modelled	5.1	19	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
43	c1e8zA_	Alignment	not modelled	5.0	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol 3-kinase catalytic subunit; **PDBTitle:** structure determinants of phosphoinositide 3-kinase2 inhibition by wortmannin, ly294002, quercetin, myricetin3 and staurosporine
44	d2hgca1	Alignment	not modelled	5.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**YjcQ-like