Email	l.a.kelley@imperial.ac.uk
Description	P52127
Date	Thu Jan 5 12:05:31 GMT 2012
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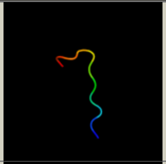
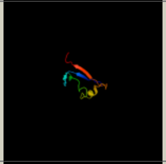
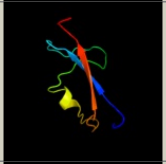
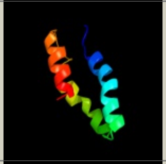
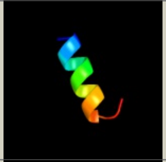
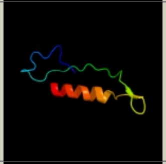
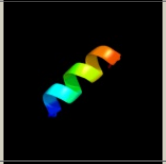
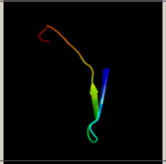
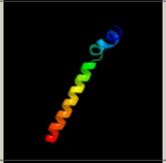
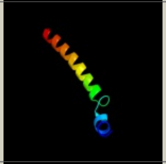
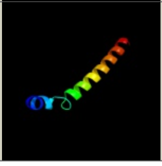
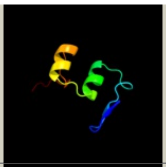
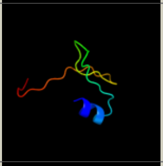
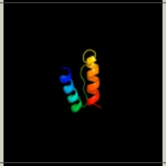
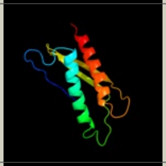
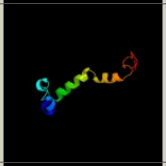
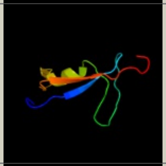
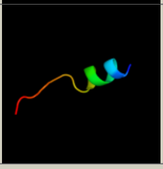
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2j7ja2	Alignment		40.3	36	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
2	d2c1ha1	Alignment		39.9	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
3	d1l6sa_	Alignment		35.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
4	d1wgwa_	Alignment		23.7	18	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
5	d1x6va2	Alignment		22.7	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
6	c1e1hC_	Alignment		21.1	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**botulinum neurotoxin type a light chain; **PDBTitle:** crystal structure of recombinant botulinum neurotoxin type2 a light chain, self-inhibiting zn endopeptidase.
7	d1jhda2	Alignment		19.0	36	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
8	d1gefa_	Alignment		18.7	23	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
9	c2py8B_	Alignment		18.7	21	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**hypothetical protein rbcx; **PDBTitle:** rbcx
10	c2peoA_	Alignment		16.9	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**rbcx protein; **PDBTitle:** crystal structure of rbcx from anabaena ca
11	d2peoa1	Alignment		16.9	16	**Fold:**RbcX-like **Superfamily:**RbcX-like **Family:**RbcX-like

12	c3gk7A_	Alignment		16.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum
13	d1ob8a_	Alignment		15.8	22	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
14	c2pt7G_	Alignment		14.4	10	**PDB header:**hydrolase/protein binding **Chain:** G: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of cag virb11 (hp0525) and an inhibitory protein2 (hp1451)
15	d1jiha1	Alignment		14.1	17	**Fold:**Lesion bypass DNA polymerase (Y-family), little finger domain **Superfamily:**Lesion bypass DNA polymerase (Y-family), little finger domain **Family:**Lesion bypass DNA polymerase (Y-family), little finger domain
16	c2qjfB_	Alignment		13.8	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'- **PDBTitle:** crystal structure of atp-sulfurylase domain of human paps2 synthetase 1
17	d1v47a2	Alignment		13.5	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
18	d1c4ka3	Alignment		13.1	18	**Fold:**Ornithine decarboxylase C-terminal domain **Superfamily:**Ornithine decarboxylase C-terminal domain **Family:**Ornithine decarboxylase C-terminal domain
19	d1gzga_	Alignment		13.1	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
20	d1vzva_	Alignment		12.9	24	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
21	c1xnjB_	Alignment	not modelled	12.5	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'-phosphosulfate **PDBTitle:** aps complex of human paps synthetase 1
22	c2kmgA_	Alignment	not modelled	12.2	23	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**klca; **PDBTitle:** the structure of the klca and ardb proteins show a novel2 fold and antirestriction activity against type i dna3 restriction systems in vivo but not in vitro
23	c1jhdA_	Alignment	not modelled	12.0	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** crystal structure of bacterial atp sulfurylase from the2 riftia pachyptila symbiont
24	d1k8ke_	Alignment	not modelled	11.8	17	**Fold:**Arp2/3 complex 21 kDa subunit ARPC3 **Superfamily:**Arp2/3 complex 21 kDa subunit ARPC3 **Family:**Arp2/3 complex 21 kDa subunit ARPC3
25	c3ulxA_	Alignment	not modelled	11.7	40	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**stress-induced transcription factor nac1; **PDBTitle:** crystal structural of the conserved domain of rice stress-responsive2 nac1
26	d1wiia_	Alignment	not modelled	11.7	67	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
27	d1j8yf1	Alignment	not modelled	11.5	15	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
28	d2olra2	Alignment	not modelled	11.0	23	**Fold:**PEP carboxykinase N-terminal domain **Superfamily:**PEP carboxykinase N-terminal domain **Family:**PEP carboxykinase N-terminal domain

29	d1ls1a1	Alignment	not modelled	10.3	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
30	d1qzxa1	Alignment	not modelled	10.3	15	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
31	d1m8pa2	Alignment	not modelled	10.1	36	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
32	c2gjvF_	Alignment	not modelled	10.0	10	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** crystal structure of a protein of unknown function from salmonella2 typhimurium
33	c3ka1A_	Alignment	not modelled	10.0	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**rbcx protein; **PDBTitle:** crystal structure of rbcx from thermosynechococcus elongatus
34	c1v47B_	Alignment	not modelled	9.9	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp sulfurylase; **PDBTitle:** crystal structure of atp sulfurylase from thermus2 thermophillus hb8 in complex with aps
35	d2gjva1	Alignment	not modelled	9.8	10	**Fold:**Phage tail protein-like **Superfamily:**Phage tail protein-like **Family:**STM4215-like
36	d1j3ba2	Alignment	not modelled	9.8	26	**Fold:**PEP carboxykinase N-terminal domain **Superfamily:**PEP carboxykinase N-terminal domain **Family:**PEP carboxykinase N-terminal domain
37	c2wj0B_	Alignment	not modelled	9.7	15	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**archaeal hjc; **PDBTitle:** crystal structures of holliday junction resolvases from2 archaeoglobus fulgidus bound to dna substrate
38	d1g8fa2	Alignment	not modelled	9.3	29	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
39	d1na6a2	Alignment	not modelled	9.0	22	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Type II restriction endonuclease catalytic domain
40	d1at3a_	Alignment	not modelled	8.7	21	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
41	c2o9xA_	Alignment	not modelled	8.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**reductase, assembly protein; **PDBTitle:** crystal structure of a putative redox enzyme maturation protein from2 archaeoglobus fulgidus
42	c1r6xA_	Alignment	not modelled	8.5	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp:sulfate adenylyltransferase; **PDBTitle:** the crystal structure of a truncated form of yeast atp2 sulfurylase, lacking the c-terminal aps kinase-like domain,3 in complex with sulfate
43	d1jq6a_	Alignment	not modelled	8.3	6	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
44	d2gtad1	Alignment	not modelled	8.1	20	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
45	d1jixa_	Alignment	not modelled	7.7	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**beta-Glucosyltransferase (DNA-modifying)
46	c1g8gB_	Alignment	not modelled	7.6	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** atp sulfurylase from s. cerevisiae: the binary product complex with2 aps
47	d1snna_	Alignment	not modelled	7.5	19	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
48	d2ipqx1	Alignment	not modelled	7.0	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**STY4665 C-terminal domain-like
49	d1kn6a_	Alignment	not modelled	6.9	22	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Prohormone convertase 1 pro-domain
50	d2pbka1	Alignment	not modelled	6.8	18	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
51	d1afpa_	Alignment	not modelled	6.5	28	**Fold:**Antifungal protein (AGAFP) **Superfamily:**Antifungal protein (AGAFP) **Family:**Antifungal protein (AGAFP)
52	d1xg8a_	Alignment	not modelled	6.5	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**YuzD-like
53	d1ztpa1	Alignment	not modelled	6.4	12	**Fold:**eIF4e-like **Superfamily:**eIF4e-like **Family:**BLES03-like
54	d1iega_	Alignment	not modelled	6.3	6	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
55	d2p41a1	Alignment	not modelled	6.2	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap methylase

56	d1ahsa_	Alignment	not modelled	6.2	20	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Top domain of virus capsid protein
57	d1o6ea_	Alignment	not modelled	5.9	18	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
58	c1p4qA_	Alignment	not modelled	5.8	44	**PDB header:**transcription/transferase **Chain:** A: **PDB Molecule:**cbp/p300-interacting transactivator 2; **PDBTitle:** solution structure of the cited2 transactivation domain in2 complex with the p300 ch1 domain
59	c2pf4E_	Alignment	not modelled	5.8	12	**PDB header:**hydrolase regulator/viral protein **Chain:** E: **PDB Molecule:**small t antigen; **PDBTitle:** crystal structure of the full-length simian virus 40 small t antigen2 complexed with the protein phosphatase 2a aalpha subunit
60	d1k0ia2	Alignment	not modelled	5.8	13	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**PHBH-like
61	c3njqB_	Alignment	not modelled	5.7	18	**PDB header:**viral protein/inhibitor **Chain:** B: **PDB Molecule:**orf 17; **PDBTitle:** crystal structure of kaposi's sarcoma-associated herpesvirus protease2 in complex with dimer disruptor
62	d1knwa2	Alignment	not modelled	5.5	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
63	c2gutA_	Alignment	not modelled	5.5	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arc/mediator, positive cofactor 2 glutamine/q- **PDBTitle:** solution structure of the trans-activation domain of the2 human co-activator arc105
64	c3cr8C_	Alignment	not modelled	5.5	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sulfate adenylyltranferase, adenylylsulfate **PDBTitle:** hexameric aps kinase from thiobacillus denitrificans
65	c2nw0B_	Alignment	not modelled	5.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**plyb; **PDBTitle:** crystal structure of a lysin
66	d1pv8a_	Alignment	not modelled	5.4	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
67	c3p0sA_	Alignment	not modelled	5.4	53	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein vp; **PDBTitle:** crystal structure of bombyx mori densovirus 1 capsid
68	d1olta_	Alignment	not modelled	5.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
69	c2gksB_	Alignment	not modelled	5.3	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional sat/aps kinase; **PDBTitle:** crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
70	d1k4ia_	Alignment	not modelled	5.2	32	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
71	c3lhiA_	Alignment	not modelled	5.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative 6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-2 phosphogluconolactonase(yp_207848.1) from neisseria3 gonorrhoeae fa 1090 at 1.33 a resolution
72	d2vgna3	Alignment	not modelled	5.2	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
73	c3letB_	Alignment	not modelled	5.1	6	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosine monophosphate-protein transferase vops; **PDBTitle:** crystal structure of fic domain containing ampylator, vops