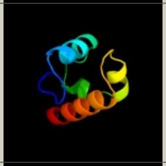
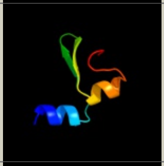
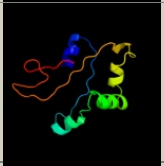
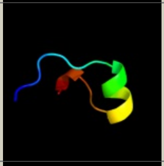
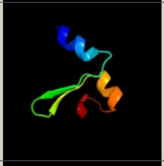
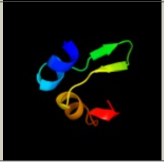
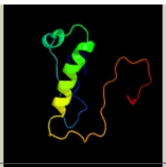
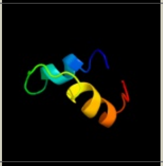
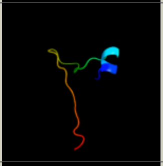
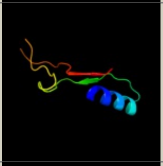
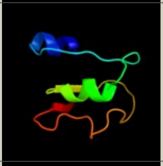
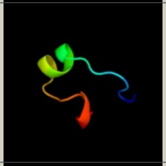
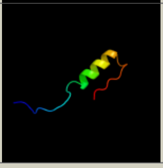
Email	l.a.kelley@imperial.ac.uk
Description	P31131
Date	Thu Jan 5 11:47:15 GMT 2012
Unique Job ID	4a0459e1ce9b6799

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2a9sa1	Alignment		100.0	33	**Fold:**Anticodon-binding domain-like **Superfamily:**CinA-like **Family:**CinA-like
2	d1pzna1	Alignment		55.5	14	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
3	d2i1qa1	Alignment		46.0	26	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
4	c3b33A_	Alignment		37.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the pas domain of nitrogen regulation protein2 nr(ii) from vibrio parahaemolyticus
5	c3a9lB_	Alignment		36.1	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly-gamma-glutamate hydrolase; **PDBTitle:** structure of bacteriophage poly-gamma-glutamate hydrolase
6	d1mzua_	Alignment		17.8	5	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
7	d1kfta_	Alignment		17.4	11	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
8	c1kftA_	Alignment		17.4	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excinuclease abc subunit c; **PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli
9	d1v9ya_	Alignment		17.0	18	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
10	c1v9yA_	Alignment		17.0	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**heme pas sensor protein; **PDBTitle:** crystal structure of the heme pas sensor domain of ec dos (ferric2 form)
11	c3mfxA_	Alignment		16.1	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sensory box/ggdef family protein; **PDBTitle:** crystal structure of the sensory box domain of the sensory-2 box/ggdef protein so_1695 from shewanella oneidensis,3 northeast structural genomics consortium target sor288b

12	d1saza1	Alignment		15.1	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
13	c2o8kA_	Alignment		13.8	9	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
14	c3h3yF_	Alignment		12.4	22	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**baseplate structural protein gp6; **PDBTitle:** fitting of the gp6 crystal structure into 3d cryo-em2 reconstruction of bacteriophage t4 star-shaped baseplate
15	d1j3ma_	Alignment		12.2	15	**Fold:**TBP-like **Superfamily:**TT1751-like **Family:**TT1751-like
16	d1nwza_	Alignment		11.6	14	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
17	d2phna1	Alignment		11.0	29	**Fold:**CofE-like **Superfamily:**CofE-like **Family:**CofE-like
18	d1a4ia1	Alignment		10.6	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
19	c3a0vA_	Alignment		10.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m)
20	c2w1tB_	Alignment		10.4	33	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt
21	d2bgwa1	Alignment	not modelled	9.8	10	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
22	c3mqoB_	Alignment	not modelled	9.7	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** the crystal structure of the pas domain in complex with isopropanol of2 a transcriptional regulator in the luxr family from burkholderia3 thailandensis to 1.7a
23	c3ju7B_	Alignment	not modelled	9.6	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative plp-dependent aminotransferase; **PDBTitle:** crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution
24	c3giuA_	Alignment	not modelled	8.9	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrrolidone-carboxylate peptidase; **PDBTitle:** 1.25 angstrom crystal structure of pyrrolidone-carboxylate peptidase2 (pcp) from staphylococcus aureus
25	d1xjca_	Alignment	not modelled	8.8	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
26	c2v1bA_	Alignment	not modelled	8.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nph1-1; **PDBTitle:** n- and c-terminal helices of oat lov2 (404-546) are2 involved in light-induced signal transduction (room3 temperature (293k) light structure of lov2 (404-546))
27	c1zpdA_	Alignment	not modelled	8.4	17	**PDB header:**alcohol fermentation **Chain:** A: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** pyruvate decarboxylase from zymomonas mobilis
						PDB header:structural genomics, unknown function

28	c1wu8B_	Alignment	not modelled	8.2	38	**Chain:** B: **PDB Molecule:**hypothetical protein ph0463; **PDBTitle:** crystal structure of project ph0463 from pyrococcus horikoshii ot3
29	c3p7nB_	Alignment	not modelled	8.1	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
30	c3fg8B_	Alignment	not modelled	7.9	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rha05790; **PDBTitle:** crystal structure of pas domain of rha05790
31	d1otda_	Alignment	not modelled	7.8	14	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
32	c2zbvC_	Alignment	not modelled	7.5	31	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from thermotoga2 maritima
33	d1rqpa2	Alignment	not modelled	7.5	31	**Fold:**Bacterial fluorinating enzyme, N-terminal domain **Superfamily:**Bacterial fluorinating enzyme, N-terminal domain **Family:**Bacterial fluorinating enzyme, N-terminal domain
34	d1iu8a_	Alignment	not modelled	7.2	50	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
35	c3lacA_	Alignment	not modelled	7.0	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrrolidone-carboxylate peptidase; **PDBTitle:** crystal structure of bacillus anthracis pyrrolidone-carboxylate2 peptidase, pcp
36	c3gdwA_	Alignment	not modelled	6.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma-54 interaction domain protein; **PDBTitle:** crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
37	c2ebjB_	Alignment	not modelled	6.7	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pyrrolidone carboxyl peptidase; **PDBTitle:** crystal structure of pyrrolidone carboxyl peptidase from thermus2 thermophilus
38	c2v3wC_	Alignment	not modelled	6.1	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**benzoylformate decarboxylase; **PDBTitle:** crystal structure of the benzoylformate decarboxylase2 variant l461a from pseudomonas putida
39	c3rtyA_	Alignment	not modelled	6.0	19	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** structure of an enclosed dimer formed by the drosophila period protein
40	d1s2da_	Alignment	not modelled	5.8	11	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
41	d1iofa_	Alignment	not modelled	5.7	44	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
42	c2cw5B_	Alignment	not modelled	5.6	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**bacterial fluorinating enzyme homolog; **PDBTitle:** crystal structure of a conserved hypothetical protein from2 thermus thermophilus hb8
43	c2q6oB_	Alignment	not modelled	5.5	38	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** sall-y70t with sam and cl
44	c2e62A_	Alignment	not modelled	5.3	12	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein at5g25060; **PDBTitle:** solution structure of the cwf21 domain in protein aak25922
45	d1auga_	Alignment	not modelled	5.3	44	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
46	c1rqrA_	Alignment	not modelled	5.2	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5'-fluoro-5'-deoxyadenosine synthase; **PDBTitle:** crystal structure and mechanism of a bacterial fluorinating enzyme,2 product complex
47	c2obxH_	Alignment	not modelled	5.2	11	**PDB header:**transferase **Chain:** H: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh2 from mesorhizobium loti (gene mll7281, swiss-2 prot entry q986n2) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
48	c1hvwA_	Alignment	not modelled	5.0	100	**PDB header:**toxin **Chain:** A: **PDB Molecule:**omega-atracotoxin-hv1a; **PDBTitle:** hairpinless mutant of omega-atracotoxin-hv1a