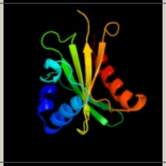
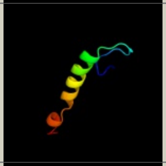
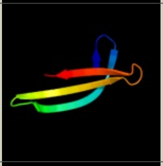
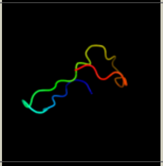
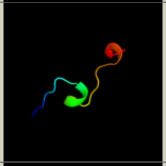
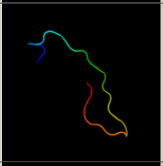
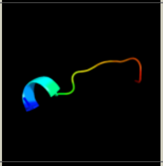
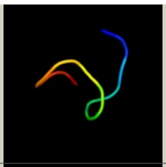
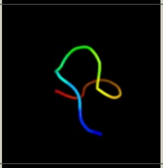
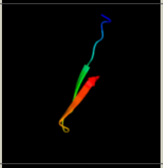
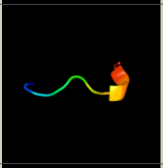
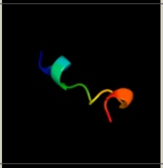
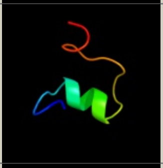
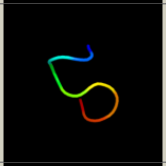
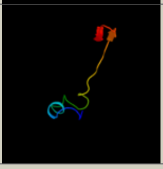
Email	l.a.kelley@imperial.ac.uk
Description	P0AD59
Date	Thu Jan 5 11:20:05 GMT 2012
Unique Job ID	15165b84afcaae80

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gpqa_	Alignment		100.0	100	**Fold:**Inhibitor of vertebrate lysozyme, Ivy **Superfamily:**Inhibitor of vertebrate lysozyme, Ivy **Family:**Inhibitor of vertebrate lysozyme, Ivy
2	d1uuza_	Alignment		100.0	26	**Fold:**Inhibitor of vertebrate lysozyme, Ivy **Superfamily:**Inhibitor of vertebrate lysozyme, Ivy **Family:**Inhibitor of vertebrate lysozyme, Ivy
3	d1fpoa1	Alignment		49.9	17	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
4	c2jkgA_	Alignment		37.9	23	**PDB header:**protein-binding **Chain:** A: **PDB Molecule:**profilin; **PDBTitle:** plasmodium falciparum profilin
5	d1k0ha_	Alignment		28.2	30	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**gpFII-like
6	d1h3ia2	Alignment		18.1	5	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
7	c3ebqA_	Alignment		14.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**molecule: pppde1 (permuted papain fold **PDBTitle:** crystal structure of human pppde1
8	c2xglB_	Alignment		13.5	25	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**colicin-m immunity protein; **PDBTitle:** the x-ray structure of the escherichia coli colicin m immunity2 protein demonstrates the presence of a disulphide bridge, which is3 functionally essential
9	d1xg8a_	Alignment		12.8	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**YuzD-like
10	c2ww9O_	Alignment		12.0	29	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**60s ribosomal protein l39; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
11	c3c5tB_	Alignment		11.3	30	**PDB header:**signaling protein/signaling protein **Chain:** B: **PDB Molecule:**exendin-4; **PDBTitle:** crystal structure of the ligand-bound glucagon-like peptide-1 receptor2 extracellular domain

12	d1ixta_	Alignment		10.3	46	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Conotoxin
13	c1ixtA_	Alignment		10.3	46	**PDB header:**toxin **Chain:** A: **PDB Molecule:**spasmodic protein tx9a-like protein; **PDBTitle:** structure of a novel p-superfamily spasmodic conotoxin2 reveals an inhibitory cystine knot motif
14	c2l23A_	Alignment		10.3	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 25; **PDBTitle:** nmr structure of the acid (activator interacting domain) of the human2 mediator med25 protein
15	c2zkr3_	Alignment		9.5	21	**PDB header:**ribosomal protein/rna **Chain:** 3: **PDB Molecule:**60s ribosomal protein l39e; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
16	d1vqo21	Alignment		9.4	60	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Ribosomal protein L39e **Family:**Ribosomal protein L39e
17	c4a1bB_	Alignment		9.4	29	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**rpl39; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 3.
18	c3if4C_	Alignment		9.1	44	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**integron cassette protein hfx_cass5; **PDBTitle:** structure from the mobile metagenome of north west arm2 sewage outfall: integron cassette protein hfx_cass5
19	c2jofA_	Alignment		8.9	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**trp-cage; **PDBTitle:** the trp-cage: optimizing the stability of a globular2 miniprotein
20	d1t27a_	Alignment		8.3	16	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Phoshatidylinositol transfer protein, PITP
21	d1bqka_	Alignment	not modelled	8.3	26	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
22	c1rijA_	Alignment	not modelled	8.1	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**e6apn1 peptide; **PDBTitle:** e6-bind trp-cage (e6apn1)
23	d1s7ea2	Alignment	not modelled	8.0	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
24	c2guzO_	Alignment	not modelled	7.3	30	**PDB header:**chaperone, protein transport **Chain:** O: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** structure of the tim14-tim16 complex of the mitochondrial2 protein import motor
25	c2d9tA_	Alignment	not modelled	7.2	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tudor domain-containing protein 3; **PDBTitle:** solution structure of the tudor domain of tudor domain2 containing protein 3 from mouse
26	c2yy8B_	Alignment	not modelled	7.0	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**upf0106 protein ph0461; **PDBTitle:** crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
27	c1l2yA_	Alignment	not modelled	6.6	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**tc5b; **PDBTitle:** nmr structure of trp-cage miniprotein construct tc5b
28	d8ruca1	Alignment	not modelled	6.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain

29	d1fm4a_	Alignment	not modelled	6.5	27	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
30	c3b4qA_	Alignment	not modelled	6.4	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a conserved protein domain (unknown2 function) from corynebacterium diphtheriae
31	d1ugja_	Alignment	not modelled	6.4	15	**Fold:**PRC-barrel domain **Superfamily:**PRC-barrel domain **Family:**RIKEN cDNA 2310057j16 protein (KIAA1543)
32	c2v36A_	Alignment	not modelled	6.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase large chain; **PDBTitle:** crystal structure of gamma-glutamyl transferase from2 bacillus subtilis
33	d2a8ea1	Alignment	not modelled	6.1	14	**Fold:**YktB/PF0168-like **Superfamily:**YktB/PF0168-like **Family:**YktB-like
34	d2ah2a2	Alignment	not modelled	6.1	18	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
35	c3a4cA_	Alignment	not modelled	5.9	26	**PDB header:**cell cycle, replication **Chain:** A: **PDB Molecule:**dna replication factor cdt1; **PDBTitle:** crystal structure of cdt1 c terminal domain
36	d1ykwa1	Alignment	not modelled	5.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
37	c2hw2A_	Alignment	not modelled	5.9	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in2 complex with rifampin
38	d1ooya2	Alignment	not modelled	5.9	8	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
39	d1qmra_	Alignment	not modelled	5.8	27	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
40	d1fafa_	Alignment	not modelled	5.7	32	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
41	d1e09a_	Alignment	not modelled	5.4	32	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
42	c3f9xA_	Alignment	not modelled	5.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setd8; **PDBTitle:** structural insights into lysine multiple methylation by set2 domain methyltransferases, set8-y334f / h4-lys20me2 /3 adohcy
43	c1zc1A_	Alignment	not modelled	5.3	19	**PDB header:**protein turnover **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation protein 1; **PDBTitle:** ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
44	d3d85d2	Alignment	not modelled	5.1	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
45	d1gh6a_	Alignment	not modelled	5.1	25	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain