Email	l.a.kelley@imperial.ac.uk
Description	P32157
Date	Thu Jan 5 11:49:39 GMT 2012
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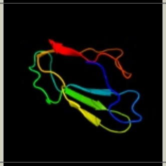
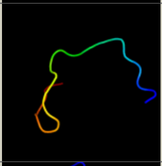
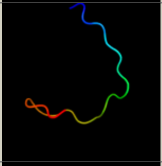
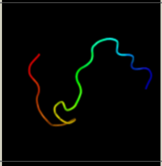
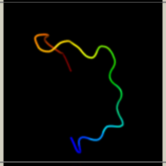
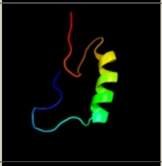
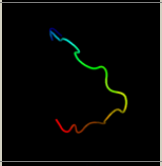
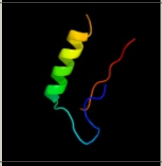
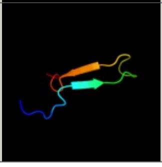
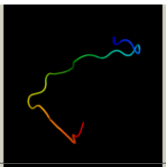
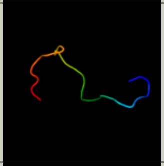
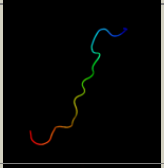
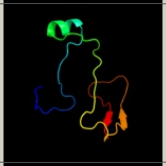
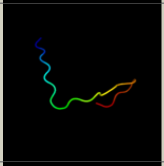
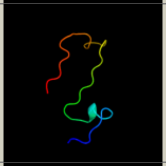
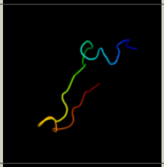
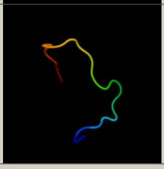
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1o65a_	Alignment		100.0	95	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**MOSC (MOCO sulphurase C-terminal) domain
2	d1orua_	Alignment		100.0	20	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**MOSC (MOCO sulphurase C-terminal) domain
3	c2q8iB_	Alignment		44.3	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of **PDBTitle:** pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
4	d1jvwa_	Alignment		42.1	33	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
5	d1q6ha_	Alignment		33.7	24	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
6	c2vcdA_	Alignment		32.0	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**outer membrane protein mip; **PDBTitle:** solution structure of the fkbp-domain of legionella2 pneumophila mip in complex with rapamycin
7	d1fd9a_	Alignment		28.7	33	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
8	d1vjea_	Alignment		26.9	15	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
9	c1q6uA_	Alignment		25.7	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase fkpa; **PDBTitle:** crystal structure of fkpa from escherichia coli
10	d1j98a_	Alignment		25.1	18	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
11	d2qamn1	Alignment		24.7	29	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17

12	c2ke0A_	Alignment		24.6	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of peptidyl-prolyl cis-trans isomerase from2 burkholderia pseudomallei
13	c2vn1A_	Alignment		20.6	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**70 kda peptidylprolyl isomerase; **PDBTitle:** crystal structure of the fk506-binding domain of plasmodium2 falciparum fkbp35 in complex with fk506
14	d1gd8a_	Alignment		17.6	10	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17
15	d2gpra_	Alignment		17.4	15	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
16	c2lgoA_	Alignment		17.0	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp; **PDBTitle:** solution nmr structure of a fkbp-type peptidyl-prolyl cis-trans2 isomerase from giardia lamblia, seattle structural genomics center3 for infectious disease target gilaa.00840.a
17	c2p39A_	Alignment		16.0	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fibroblast growth factor 23; **PDBTitle:** crystal structure of human fgf23
18	d1auya_	Alignment		15.4	24	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tymoviridae-like VP
19	d1ddla_	Alignment		15.4	18	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tymoviridae-like VP
20	c2f4eB_	Alignment		14.6	29	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**atfkbp42; **PDBTitle:** n-terminal domain of fkbp42 from arabidopsis thaliana
21	c3b7xA_	Alignment	not modelled	14.3	42	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 6; **PDBTitle:** crystal structure of human fk506-binding protein 6
22	c2dneA_	Alignment	not modelled	14.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
23	d1zunb1	Alignment	not modelled	13.3	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
24	c1q1cA_	Alignment	not modelled	13.1	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 4; **PDBTitle:** crystal structure of n(1-260) of human fkbp52
25	d1q1ca1	Alignment	not modelled	13.0	14	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
26	d2f9ha1	Alignment	not modelled	13.0	15	**Fold:**PTSIIA/GutA-like **Superfamily:**PTSIIA/GutA-like **Family:**PTSIIA/GutA-like
27	c2qj8B_	Alignment	not modelled	12.8	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mlr6093 protein; **PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
28	d1auyb_	Alignment	not modelled	12.7	24	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tymoviridae-like VP

29	c2dncA_	Alignment	not modelled	12.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase protein x component; **PDBTitle:** solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
30	c3oe2A_	Alignment	not modelled	12.4	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** 1.6 a crystal structure of peptidyl-prolyl cis-trans isomerase ppiase2 from pseudomonas syringae pv. tomato str. dc3000 (pspto dc3000)
31	d2ppna1	Alignment	not modelled	12.2	20	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
32	c3poaA_	Alignment	not modelled	11.7	33	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
33	d2cqma1	Alignment	not modelled	11.0	8	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17
34	d1y8ob1	Alignment	not modelled	11.0	16	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
35	c3o4aC_	Alignment	not modelled	10.2	20	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed beta-trefoil architecture with symmetric **PDBTitle:** crystal structure of symfoil-2: de novo designed beta-trefoil2 architecture with symmetric primary structure
36	d1kt0a3	Alignment	not modelled	10.0	21	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
37	d2pnrc1	Alignment	not modelled	9.8	16	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
38	c2kklA_	Alignment	not modelled	9.6	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mb1858; **PDBTitle:** solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
39	c2p23A_	Alignment	not modelled	9.4	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fibroblast growth factor 19; **PDBTitle:** crystal structure of human fgf19
40	d2qn6a1	Alignment	not modelled	9.3	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
41	d1r9ha_	Alignment	not modelled	9.2	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
42	d1e57a_	Alignment	not modelled	9.1	24	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tymoviridae-like VP
43	c3sf4F_	Alignment	not modelled	9.0	47	**PDB header:**signaling protein/protein binding **Chain:** F: **PDB Molecule:**protein inscuteable homolog; **PDBTitle:** crystal structure of the complex between the conserved cell polarity2 proteins inscuteable and lgn
44	d1s0ua1	Alignment	not modelled	9.0	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
45	c3jxvA_	Alignment	not modelled	8.7	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**70 kda peptidyl-prolyl isomerase; **PDBTitle:** crystal structure of the 3 fkbp domains of wheat fkbp73
46	c2lezA_	Alignment	not modelled	8.6	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**secreted effector protein pipb2; **PDBTitle:** solution nmr structure of n-terminal domain of salmonella effector2 protein pipb2. northeast structural genomics consortium (nesg) target3 stt318a
47	d1u79a_	Alignment	not modelled	8.5	14	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
48	d1ne3a_	Alignment	not modelled	7.8	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
49	c2vriA_	Alignment	not modelled	7.8	11	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** structure of the nsp3 x-domain of human coronavirus nl63
50	c3bboP_	Alignment	not modelled	7.6	11	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**ribosomal protein l17; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
51	c3ogfA_	Alignment	not modelled	7.2	21	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed dimeric trefoil-fold sub-domain which **PDBTitle:** crystal structure of difoil-4p homo-trimer: de novo designed dimeric2 trefoil-fold sub-domain which forms homo-trimer assembly
52	c3rrrM_	Alignment	not modelled	7.1	50	**PDB header:**viral protein **Chain:** M: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structure of the rsv f protein in the post-fusion conformation
53	d2zjrk1	Alignment	not modelled	7.0	11	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17

54	d2r48a1	Alignment	not modelled	7.0	18	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
55	d1r5ba1	Alignment	not modelled	6.8	13	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
56	c3o5dB_	Alignment	not modelled	6.8	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase fkbp5; **PDBTitle:** crystal structure of a fragment of fkbp51 comprising the fk1 and fk22 domains
57	d1q1ua_	Alignment	not modelled	6.6	13	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)
58	d2r4qa1	Alignment	not modelled	6.5	9	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
59	d1efca1	Alignment	not modelled	6.4	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
60	d1c9ha_	Alignment	not modelled	6.4	25	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
61	d1qqka_	Alignment	not modelled	6.4	27	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)
62	c2xzm1_	Alignment	not modelled	6.3	31	**PDB header:**ribosome **Chain:** 1: **PDB Molecule:**ribosomal protein s28e containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
63	c2gezE_	Alignment	not modelled	6.2	22	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**l-asparaginase alpha subunit; **PDBTitle:** crystal structure of potassium-independent plant asparaginase
64	d1g7sa1	Alignment	not modelled	6.2	27	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
65	c3ol0C_	Alignment	not modelled	6.2	21	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
66	d1a1qa_	Alignment	not modelled	6.1	26	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
67	c2ejyA_	Alignment	not modelled	6.0	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**55 kda erythrocyte membrane protein; **PDBTitle:** solution structure of the p55 pdz t85c domain complexed2 with the glycophorin c f127c peptide
68	d1ghja_	Alignment	not modelled	5.8	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
69	d1blaa_	Alignment	not modelled	5.7	27	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)
70	c3hbwA_	Alignment	not modelled	5.7	20	**PDB header:**hormone **Chain:** A: **PDB Molecule:**fibroblast growth factor 13; **PDBTitle:** crystal structure of human fibroblast growth factor2 homologous factor 2a (fhf2a), also referred to as3 fibroblast growth factor 13a (fgf13a)
71	d1bara_	Alignment	not modelled	5.7	20	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Fibroblast growth factors (FGF)
72	d1yata_	Alignment	not modelled	5.5	14	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
73	c1rouA_	Alignment	not modelled	5.5	19	**PDB header:**rotamase (isomerase) **Chain:** A: **PDB Molecule:**fkbp59-i; **PDBTitle:** structure of fkbp59-i, the n-terminal domain of a 59 kda2 fk506-binding protein, nmr, 22 structures
74	c2o7pA_	Alignment	not modelled	5.4	19	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**riboflavin biosynthesis protein ribd; **PDBTitle:** the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
75	d1liua1	Alignment	not modelled	5.4	25	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
76	d1kk1a1	Alignment	not modelled	5.3	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
77	c3gqsB_	Alignment	not modelled	5.3	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**adenylate cyclase-like protein; **PDBTitle:** crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
78	c1b34B_	Alignment	not modelled	5.3	23	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**protein (small nuclear ribonucleoprotein sm d2); **PDBTitle:** crystal structure of the d1d2 sub-complex from the human snrnp core2 domain

79	d1b34b_	Alignment	not modelled	5.3	23	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
80	d1igna2	Alignment	not modelled	5.1	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**DNA-binding domain of rap1
81	d1jnya1	Alignment	not modelled	5.0	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors