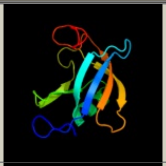
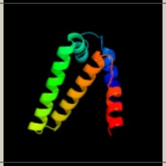
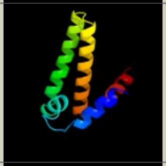
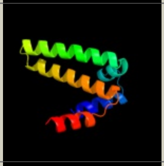
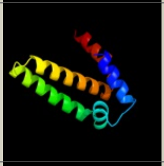
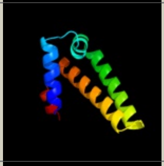
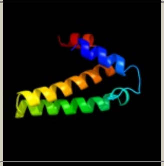
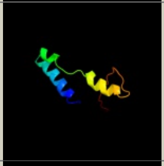
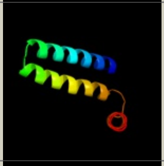
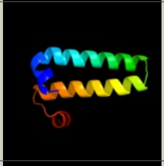
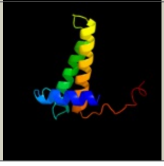
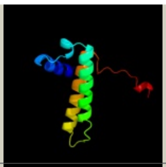
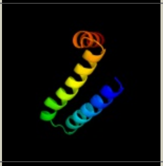
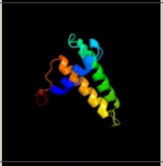
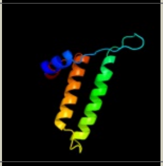
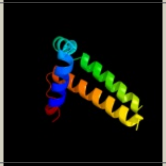
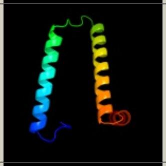
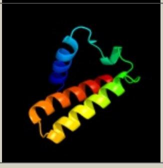
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P06989
Date	Thu Jan 5 10:59:47 GMT 2012
Unique Job ID	5e0299ff3582fa48

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1zpsa1	Alignment		100.0	37	**Fold:**HisI-like **Superfamily:**HisI-like **Family:**HisI-like
2	d2a7wa1	Alignment		100.0	36	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)
3	c2a7wF_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**phosphoribosyl-atp pyrophosphatase; **PDBTitle:** crystal structure of phosphoribosyl-atp pyrophosphatase2 from chromobacterium violaceum (atcc 12472). nesg target3 cvr7
4	d1yvwa1	Alignment		100.0	32	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)
5	c1yvwD_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**phosphoribosyl-atp pyrophosphatase; **PDBTitle:** crystal structure of phosphoribosyl-atp2 pyrophosphohydrolase from bacillus cereus. nesgc target3 bcr13.
6	d1y6xa1	Alignment		100.0	30	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)
7	d1yxba1	Alignment		99.9	33	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**HisE-like (PRA-PH)
8	c3crcB_	Alignment		98.8	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein mazg; **PDBTitle:** crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response
9	c2yxhB_	Alignment		98.8	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mazg-related protein; **PDBTitle:** crystal structure of mazg-related protein from thermotoga maritima
10	d1vmga_	Alignment		98.5	19	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
11	d2a3qa1	Alignment		98.3	23	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like

12	c3obcB_	Alignment		98.3	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pyrophosphatase; **PDBTitle:** crystal structure of a pyrophosphatase (af1178) from archaeoglobus2 fulgidus at 1.80 a resolution
13	d2gtad1	Alignment		98.3	15	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
14	c2q4pA_	Alignment		98.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein rs21-c6; **PDBTitle:** ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
15	d2gtaa1	Alignment		98.2	16	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
16	c2q9lA_	Alignment		98.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of imazg from vibrio dat 722: ctag-imazg (p43212)
17	d2oiea1	Alignment		98.0	22	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
18	c2yf3F_	Alignment		96.3	25	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**mazg-like nucleoside triphosphate pyrophosphohydrolase; **PDBTitle:** crystal structure of dr2231, the mazg-like protein from2 deinococcus radiodurans, complex with manganese
19	c2rfpA_	Alignment		84.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ntp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
20	c2p06A_	Alignment		71.2	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af_0060; **PDBTitle:** crystal structure of a predicted coding region af_0060 from2 archaeoglobus fulgidus dsm 4304
21	d2p06a1	Alignment	not modelled	71.2	23	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**AF0060-like
22	d1ulva4	Alignment	not modelled	41.9	11	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Bacterial glucoamylase N-terminal domain-like
23	d1lf6a2	Alignment	not modelled	38.2	21	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Bacterial glucoamylase N-terminal domain-like
24	d1m4ka2	Alignment	not modelled	33.8	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
25	d1nkra2	Alignment	not modelled	32.0	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
26	d1nvma1	Alignment	not modelled	31.1	15	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
27	d1qcqa_	Alignment	not modelled	25.1	17	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
28	d1j3ea_	Alignment	not modelled	23.0	21	**Fold:**Replication modulator SeqA, C-terminal DNA-binding domain **Superfamily:**Replication modulator SeqA, C-terminal DNA-binding domain **Family:**Replication modulator SeqA, C-terminal DNA-binding domain
						PDB header:transcription

29	c2a2oG_	Alignment	not modelled	21.7	11	**Chain:** G: **PDB Molecule:**hypothetical protein bt3146; **PDBTitle:** crystal structure of a putativetena family transcriptional regulator2 (bt_3146) from bacteroides thetaiotaomicron vpi-5482 at 2.16 a3 resolution
30	c2z1dA_	Alignment	not modelled	19.6	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hypd; **PDBTitle:** crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
31	d1axib1	Alignment	not modelled	18.1	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
32	c2i7uA_	Alignment	not modelled	17.1	28	**PDB header:**de novo protein/ligand binding protein **Chain:** A: **PDB Molecule:**four-alpha-helix bundle; **PDBTitle:** structural and dynamical analysis of a four-alpha-helix2 bundle with designed anesthetic binding pockets
33	d2od6a1	Alignment	not modelled	16.1	50	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Marine metagenome family DABB1
34	c1z6rC_	Alignment	not modelled	15.6	14	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
35	c3loeA_	Alignment	not modelled	13.8	31	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (f28a mutant)
36	d1z05a2	Alignment	not modelled	13.7	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
37	d1z2ua1	Alignment	not modelled	13.5	21	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
38	d2a2ma1	Alignment	not modelled	13.5	11	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**TENA/THI-4
39	c3gnyA_	Alignment	not modelled	13.3	31	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (hnp1)
40	c3lo7A_	Alignment	not modelled	13.2	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding protein a; **PDBTitle:** crystal structure of pbpa from mycobacterium tuberculosis
41	d1id3b_	Alignment	not modelled	13.1	10	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
42	d1pjua2	Alignment	not modelled	12.8	39	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
43	c3hj2B_	Alignment	not modelled	12.0	31	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**human neutrophil peptide 1; **PDBTitle:** crystal structure of covalent dimer of hnp1
44	c3ue3A_	Alignment	not modelled	11.9	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**septum formation, penicillin binding protein 3, **PDBTitle:** crystal structure of acinetobacter baumanni pbp3
45	c3equB_	Alignment	not modelled	11.6	44	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
46	d1nkra1	Alignment	not modelled	11.4	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
47	d1jeya1	Alignment	not modelled	11.2	13	**Fold:**SPOC domain-like **Superfamily:**SPOC domain-like **Family:**Ku70 subunit middle domain
48	c2ap1A_	Alignment	not modelled	11.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
49	d2zjrs1	Alignment	not modelled	11.0	6	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Ribosomal protein L25-like
50	c2kloA_	Alignment	not modelled	10.9	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna replication factor cdt1; **PDBTitle:** structure of the cdt1 c-terminal domain
51	d2afja1	Alignment	not modelled	10.9	9	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**SPRY domain
52	d1iqpa1	Alignment	not modelled	10.6	21	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
53	c1z05A_	Alignment	not modelled	10.5	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, rok family; **PDBTitle:** crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
54	d1m4ka1	Alignment	not modelled	10.1	36	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
55	c3r4rB_	Alignment	not modelled	9.9	25	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**hypothetical fimbrial assembly protein; **PDBTitle:** crystal structure of a hypothetical fimbrial assembly

						protein2 (bdi_3522) from parabacteroides distasonis atcc 8503 at 2.38 a3 resolution
56	d1z6ra3	Alignment	not modelled	9.9	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
57	c3a4cA_	Alignment	not modelled	9.7	16	**PDB header:**cell cycle, replication **Chain:** A: **PDB Molecule:**dna replication factor cdt1; **PDBTitle:** crystal structure of cdt1 c terminal domain
58	d1ex4a1	Alignment	not modelled	9.6	17	**Fold:**SH3-like barrel **Superfamily:**DNA-binding domain of retroviral integrase **Family:**DNA-binding domain of retroviral integrase
59	d1rp5a4	Alignment	not modelled	9.2	29	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
60	d1vqqa3	Alignment	not modelled	9.2	31	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
61	d2ayva1	Alignment	not modelled	8.8	23	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
62	d3b5ha2	Alignment	not modelled	8.8	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
63	d1z3da1	Alignment	not modelled	8.8	19	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
64	c2rkkA_	Alignment	not modelled	8.7	19	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein vta1; **PDBTitle:** crystal structure of s.cerevisiae vta1 n-terminal domain
65	d2zjrk1	Alignment	not modelled	8.5	18	**Fold:**Prokaryotic ribosomal protein L17 **Superfamily:**Prokaryotic ribosomal protein L17 **Family:**Prokaryotic ribosomal protein L17
66	d2ahme1	Alignment	not modelled	8.4	18	**Fold:**Coronavirus NSP8-like **Superfamily:**Coronavirus NSP8-like **Family:**Coronavirus NSP8-like
67	d1feua_	Alignment	not modelled	8.4	20	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Ribosomal protein L25-like
68	c2pmzQ_	Alignment	not modelled	8.4	27	**PDB header:**translation, transferase **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase subunit a; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
69	d2dl2a1	Alignment	not modelled	8.1	36	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
70	d1kx5b_	Alignment	not modelled	8.1	10	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
71	d1y6la_	Alignment	not modelled	8.0	17	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
72	d1k38a_	Alignment	not modelled	8.0	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
73	c3eo3B_	Alignment	not modelled	7.9	16	**PDB header:**isomerase, transferase **Chain:** B: **PDB Molecule:**bifunctional udp-n-acetylglucosamine 2-epimerase/n- **PDBTitle:** crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
74	c3ugfB_	Alignment	not modelled	7.7	0	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sucrose:(sucrose/fructan) 6-fructosyltransferase; **PDBTitle:** crystal structure of a 6-sst/6-sft from pachysandra terminalis
75	c3hjlA_	Alignment	not modelled	7.6	15	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**flagellar motor switch protein flig; **PDBTitle:** the structure of full-length flig from aquifex aeolicus
76	c2ahmG_	Alignment	not modelled	7.5	18	**PDB header:**viral protein, replication **Chain:** G: **PDB Molecule:**replicase polyprotein 1ab, heavy chain; **PDBTitle:** crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer
77	d2huec1	Alignment	not modelled	7.4	10	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
78	c2x48B_	Alignment	not modelled	7.2	16	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
79	d1k47a2	Alignment	not modelled	7.2	10	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Phosphomevalonate kinase (PMK)
80	c3tixA_	Alignment	not modelled	7.1	19	**PDB header:**gene regulation/protein binding **Chain:** A: **PDB Molecule:**ubiquitin-like protein smt3, rna-induced transcriptional **PDBTitle:** crystal structure of the chp1-tas3 complex core
81	c1mwuA_	Alignment	not modelled	7.1	31	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**penicillin-binding protein 2a; **PDBTitle:** structure of methicillin acyl-penicillin binding protein 2a2 from methicillin resistant staphylococcus aureus strain3 27r at 2.60 a resolution.

82	d1w1we_	Alignment	not modelled	7.1	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rad21/Rec8-like
83	c1w1wF_	Alignment	not modelled	7.1	29	**PDB header:**cell adhesion **Chain:** F: **PDB Molecule:**sister chromatid cohesion protein 1; **PDBTitle:** sc smc1hd:scc1-c complex, atpgs
84	d2aaka_	Alignment	not modelled	7.0	15	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
85	d1cg2a2	Alignment	not modelled	7.0	13	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
86	c2jtdA_	Alignment	not modelled	7.0	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**myomesin-1; **PDBTitle:** skelemin immunoglobulin c2 like domain 4
87	d1ov9a_	Alignment	not modelled	7.0	35	**Fold:**H-NS histone-like proteins **Superfamily:**H-NS histone-like proteins **Family:**H-NS histone-like proteins
88	d1ryqa_	Alignment	not modelled	6.9	42	**Fold:**Rubredoxin-like **Superfamily:**RNA polymerase subunits **Family:**RpoE2-like
89	d2ok3a1	Alignment	not modelled	6.9	24	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**Cyclophilin (peptidylprolyl isomerase)
90	d1kg1a_	Alignment	not modelled	6.9	33	**Fold:**Necrosis inducing protein 1, NIP1 **Superfamily:**Necrosis inducing protein 1, NIP1 **Family:**Necrosis inducing protein 1, NIP1
91	c2z56B_	Alignment	not modelled	6.9	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tk-subtilisin; **PDBTitle:** crystal structure of g56s-propeptide:s324a-subtilisin complex
92	c3oc2A_	Alignment	not modelled	6.8	19	**PDB header:**penicillin-binding protein **Chain:** A: **PDB Molecule:**penicillin-binding protein 3; **PDBTitle:** crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
93	d2fnja1	Alignment	not modelled	6.8	18	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**SPRY domain
94	c2wadB_	Alignment	not modelled	6.7	18	**PDB header:**peptide binding protein **Chain:** B: **PDB Molecule:**penicillin-binding protein 2b; **PDBTitle:** penicillin-binding protein 2b (pbp-2b) from streptococcus2 pneumoniae (strain 5204)
95	d2f09a1	Alignment	not modelled	6.6	19	**Fold:**Streptavidin-like **Superfamily:**YdhA-like **Family:**YdhA-like
96	d1k25a4	Alignment	not modelled	6.5	29	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
97	d1dfup_	Alignment	not modelled	6.5	9	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Ribosomal protein L25-like
98	d2z3qa1	Alignment	not modelled	6.4	28	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
99	d1pyya4	Alignment	not modelled	6.4	29	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase