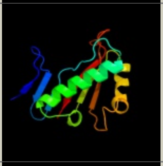
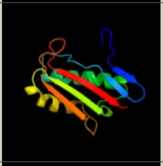
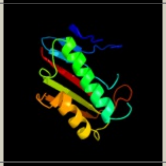
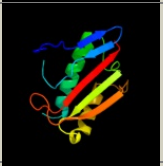
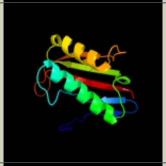
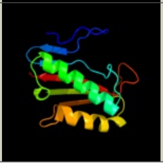
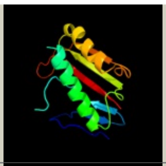
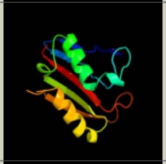
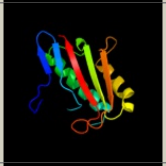
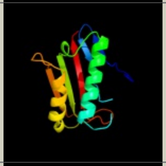
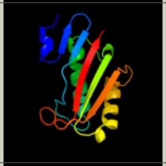
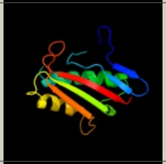
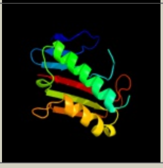
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AEB7
Date	Thu Jan 5 11:22:58 GMT 2012
Unique Job ID	061465d94ebd30fd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gtzA_	Alignment		100.0	92	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative translation initiation inhibitor; **PDBTitle:** crystal structure of a putative translation initiation inhibitor from2 salmonella typhimurium
2	c3k12F_	Alignment		100.0	35	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein a6v7t0; **PDBTitle:** crystal structure of an uncharacterized protein a6v7t0 from2 pseudomonas aeruginosa
3	c3kjjL_	Alignment		100.0	43	**PDB header:**unknown function **Chain:** L: **PDB Molecule:**nmb1025 protein; **PDBTitle:** crystal structure of nmb1025, a member of yjgf protein family, from2 neisseria meningitidis (hexagonal crystal form)
4	d2ewca1	Alignment		100.0	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
5	c3k0tA_	Alignment		100.0	21	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**endoribonuclease l-psp, putative; **PDBTitle:** crystal structure of pspto -psp protein in complex with d-beta-glucose2 from pseudomonas syringae pv. tomato str. dc3000
6	d1jd1a_	Alignment		100.0	26	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
7	c3m4sC_	Alignment		100.0	26	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**putative endoribonuclease l-psp; **PDBTitle:** crystal structure of a putative endoribonuclease l-psp from entamoeba2 histolytica, orthorhombic form
8	c3l7qD_	Alignment		100.0	25	**PDB header:**translation **Chain:** D: **PDB Molecule:**putative translation initiation inhibitor, aldr regulator- **PDBTitle:** crystal structure of aldr from streptococcus mutans
9	c3r0pB_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-psp putative endoribonuclease; **PDBTitle:** crystal structure of l-psp putative endoribonuclease from uncultured2 organism
10	c3lmeE_	Alignment		100.0	17	**PDB header:**translation **Chain:** E: **PDB Molecule:**possible translation initiation inhibitor; **PDBTitle:** structure of probable translation initiation inhibitor from2 (rpa2473) from rhodopseudomonas palustris
11	c3v4dC_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aminoacrylate peracid reductase rutc; **PDBTitle:** crystal structure of rutc protein a member of the yjgf family from2 e.coli

12	c3quwA_	Alignment		100.0	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein mmf1; **PDBTitle:** crystal structure of yeast mmf1
13	d2cvla1	Alignment		100.0	28	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
14	d1onia_	Alignment		100.0	24	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
15	d1nq3a_	Alignment		100.0	26	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
16	c1xrgB_	Alignment		100.0	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative translation initiation inhibitor, yjgf **PDBTitle:** conserved hypothetical protein from clostridium2 thermocellum cth-2968
17	d2b33a1	Alignment		100.0	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
18	d1xrga_	Alignment		100.0	23	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
19	d1qd9a_	Alignment		100.0	31	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
20	d1x25a1	Alignment		100.0	24	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
21	d1qaha_	Alignment	not modelled	100.0	24	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
22	c3i7tA_	Alignment	not modelled	100.0	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of rv2704, a member of highly conserved2 yjgf/yer057c/uk114 family, from mycobacterium tuberculosis
23	c2ig8C_	Alignment	not modelled	100.0	27	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein pa3499; **PDBTitle:** crystal structure of a protein of unknown function pa3499 from2 pseudomonas aeruginosa
24	d1pf5a_	Alignment	not modelled	100.0	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
25	d1j7ha_	Alignment	not modelled	100.0	26	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
26	c2dyyG_	Alignment	not modelled	100.0	26	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**upf0076 protein ph0854; **PDBTitle:** crystal structure of putative translation initiation2 inhibitor ph0854 from pyrococcus horikoshii
27	d2cwja1	Alignment	not modelled	99.9	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
28	d2otma1	Alignment	not modelled	99.9	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP

29	d1qu9a_	Alignment	not modelled	99.9	25	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
30	c3i3fB_	Alignment	not modelled	99.9	25	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** hypothetical protein from giardia lamblia gl50803_14299
31	c3d01G_	Alignment	not modelled	99.9	21	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the protein atu1372 with unknown function from2 agrobacterium tumefaciens
32	c3lybC_	Alignment	not modelled	99.9	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative endoribonuclease; **PDBTitle:** structure of putative endoribonuclease(kp1_3112) from2 klebsiella pneumoniae
33	d1qnaa1	Alignment	not modelled	56.8	7	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
34	d1mp9a1	Alignment	not modelled	48.5	14	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
35	d1cdwa1	Alignment	not modelled	45.6	11	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
36	d1nh2a1	Alignment	not modelled	43.4	7	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
37	d1aisa1	Alignment	not modelled	43.1	14	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
38	c1mp9B_	Alignment	not modelled	29.1	16	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**tata-binding protein; **PDBTitle:** tbp from a mesothermophilic archaeon, sulfolobus2 acidocaldarius
39	c2z8uQ_	Alignment	not modelled	29.1	15	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** methanococcus jannaschii tbp
40	c1d3uA_	Alignment	not modelled	24.3	11	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**tata-binding protein; **PDBTitle:** tata-binding protein/transcription factor (ii)b/bre+tata-2 box complex from pyrococcus woesei
41	d1cdwa2	Alignment	not modelled	20.5	12	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
42	d1mp9a2	Alignment	not modelled	19.1	10	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
43	d1qnaa2	Alignment	not modelled	18.2	18	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
44	c1rm1A_	Alignment	not modelled	17.3	11	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**tata-box binding protein; **PDBTitle:** structure of a yeast tfiia/tbp/tata-box dna complex
45	c1ngmM_	Alignment	not modelled	17.2	11	**PDB header:**transcription/dna **Chain:** M: **PDB Molecule:**transcription initiation factor tfiid; **PDBTitle:** crystal structure of a yeast brf1-tbp-dna ternary complex
46	d1nh2a2	Alignment	not modelled	17.1	14	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
47	c3fqmA_	Alignment	not modelled	15.5	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**non-structural protein 5a; **PDBTitle:** crystal structure of a novel dimeric form of hcv ns5a domain i protein
48	d1aisa2	Alignment	not modelled	15.0	15	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
49	c3eikB_	Alignment	not modelled	14.0	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** double stranded dna binding protein
50	d1xhja_	Alignment	not modelled	13.6	16	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
51	d1qh4a1	Alignment	not modelled	13.5	13	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
52	d1g0wa1	Alignment	not modelled	13.2	17	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
53	d1r5pa_	Alignment	not modelled	12.6	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**KaiB-like
54	d1u6ra1	Alignment	not modelled	10.6	13	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
55	c3d87A_	Alignment	not modelled	9.4	24	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**interleukin-23 subunit p19; **PDBTitle:** crystal structure of interleukin-23
						PDB header:transcription/membrane protein **Chain:** A: **PDB Molecule:**rna polymerase sigma factor;

56	c3hugA_	Alignment	not modelled	9.2	6	**PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
57	d1vrpa1	Alignment	not modelled	9.1	15	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
58	c3i4tA_	Alignment	not modelled	9.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**diphthine synthase; **PDBTitle:** crystal structure of putative diphthine synthase from2 entamoeba histolytica
59	d1crka1	Alignment	not modelled	8.7	17	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
60	d2qeda1	Alignment	not modelled	8.2	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
61	d1i0ea1	Alignment	not modelled	8.0	12	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
62	d2a6aa1	Alignment	not modelled	8.0	3	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
63	d1nbwa2	Alignment	not modelled	7.6	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
64	c3mlcC_	Alignment	not modelled	7.5	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**fg41 malonate semialdehyde decarboxylase; **PDBTitle:** crystal structure of fg41msad inactivated by 3-chloropropiolate
65	d1sxjc1	Alignment	not modelled	7.1	8	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
66	d1xb2b1	Alignment	not modelled	6.5	16	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
67	c1j4aA_	Alignment	not modelled	6.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus
68	d1qk1a1	Alignment	not modelled	6.5	15	**Fold:**Guanido kinase N-terminal domain **Superfamily:**Guanido kinase N-terminal domain **Family:**Guanido kinase N-terminal domain
69	d2ix4a2	Alignment	not modelled	6.2	11	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
70	c3a1yF_	Alignment	not modelled	6.1	24	**PDB header:**ribosomal protein **Chain:** F: **PDB Molecule:**50s ribosomal protein p1 (l12p); **PDBTitle:** the structure of protein complex
71	c1okjB_	Alignment	not modelled	6.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protease yeaz; **PDBTitle:** crystal structure of the essential e. coli yeaz2 protein by mad method using the gadolinium complex3 "dotma"
72	d1qh5a_	Alignment	not modelled	5.7	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
73	c2dvzA_	Alignment	not modelled	5.7	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of a periplasmic transporter
74	d1y9ia_	Alignment	not modelled	5.5	19	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
75	c2xd4A_	Alignment	not modelled	5.5	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
76	c2qbbF_	Alignment	not modelled	5.3	14	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** crystal structure of the bacterial ribosome from2 escherichia coli in complex with gentamicin. this file3 contains the 30s subunit of the second 70s ribosome, with4 gentamicin bound. the entire crystal structure contains5 two 70s ribosomes and is described in remark 400.
77	d2qalf1	Alignment	not modelled	5.3	14	**Fold:**Ferredoxin-like **Superfamily:**Ribosomal protein S6 **Family:**Ribosomal protein S6
78	d1iqpa1	Alignment	not modelled	5.3	21	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain