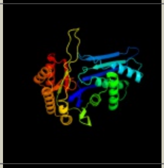
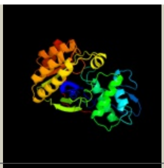
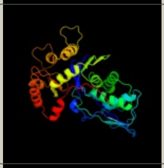
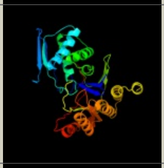
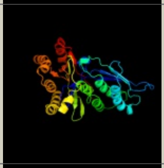
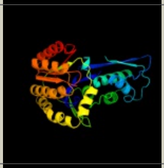
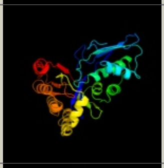
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P00547
Date	Thu Jan 5 10:56:41 GMT 2012
Unique Job ID	2a793123967a329d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1fwlD_	Alignment		100.0	29	**PDB header:**transferase **Chain:** D: **PDB Molecule:**homoserine kinase; **PDBTitle:** crystal structure of homoserine kinase
2	c3hulA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine kinase; **PDBTitle:** structure of putative homoserine kinase thrb from listeria2 monocytogenes
3	c2cz9A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable galactokinase; **PDBTitle:** crystal structure of galactokinase from pyrococcus horikoshi
4	c2v34B_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-diphosphocytidyl-2c-methyl-d-erythritol kinase; **PDBTitle:** ispe in complex with cytidine and ligand
5	c1pieA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**galactokinase; **PDBTitle:** crystal structure of lactococcus lactis galactokinase2 complexed with galactose
6	c3k17A_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lin0012 protein; **PDBTitle:** crystal structure of a lin0012 protein from listeria innocua
7	c2hfuB_	Alignment		100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mevalonate kinase, putative; **PDBTitle:** crystal structure of l. major mevalonate kinase in complex2 with r-mevalonate
8	c1uekA_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-(cytidine 5'-diphospho)-2c-methyl-d-erythritol **PDBTitle:** crystal structure of 4-(cytidine 5'-diphospho)-2c-methyl-d-2 erythritol kinase
9	c2hk3A_	Alignment		100.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diphosphomevalonate decarboxylase; **PDBTitle:** crystal structure of mevalonate diphosphate decarboxylase2 from staphylococcus aureus (orthorhombic form)
10	c2x7iA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mevalonate kinase; **PDBTitle:** crystal structure of mevalonate kinase from methicillin-2 resistant staphylococcus aureus mrsa252
11	c1oj4B_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-diphosphocytidyl-2-c-methyl-d-erythritol **PDBTitle:** ternary complex of2 4-diphosphocytidyl-2-c-methyl-d-erythritol kinase

12	c1wuuA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**galactokinase; **PDBTitle:** crystal structure of human galactokinase complexed with2 mgamppnp and galactose
13	c3k85B_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**d-glycero-d-manno-heptose 1-phosphate kinase; **PDBTitle:** crystal structure of a d-glycero-d-manno-heptose 1-phosphate2 kinase from bacteriodes thetaiotaomicron
14	c1k47F_	Alignment		100.0	12	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphomevalonate kinase; **PDBTitle:** crystal structure of the streptococcus pneumoniae2 phosphomevalonate kinase (pmk)
15	c2a2cA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetylgalactosamine kinase; **PDBTitle:** x-ray structure of human n-acetyl galactosamine kinase2 complexed with mg-adp and n-acetyl galactosamine 1-3 phosphate
16	c2gs8A_	Alignment		100.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mevalonate pyrophosphate decarboxylase; **PDBTitle:** structure of mevalonate pyrophosphate decarboxylase from streptococcus2 pyogenes
17	c2oi2A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mevalonate kinase; **PDBTitle:** streptococcus pneumoniae mevalonate kinase in complex with2 diphosphomevalonate
18	c1kkhA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mevalonate kinase; **PDBTitle:** crystal structure of the methanococcus jannaschii2 mevalonate kinase
19	c2aj4B_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**galactokinase; **PDBTitle:** crystal structure of saccharomyces cerevisiae galactokinase2 in complex with galactose and mg:amppnp
20	c2r42A_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mevalonate kinase; **PDBTitle:** the biochemical and structural basis for feedback2 inhibition of mevalonate kinase and isoprenoid metabolism
21	d1h72c1	Alignment	not modelled	100.0	31	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
22	c3ltoB_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**mevalonate diphosphate decarboxylase; **PDBTitle:** crystal structure of a mevalonate diphosphate decarboxylase2 from legionella pneumophila
23	c2hkeB_	Alignment	not modelled	99.9	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**diphosphomevalonate decarboxylase, putative; **PDBTitle:** mevalonate diphosphate decarboxylase from trypanosoma brucei
24	d1k47a1	Alignment	not modelled	99.9	12	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
25	d1kkha1	Alignment	not modelled	99.9	14	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
26	d1oj4a1	Alignment	not modelled	99.9	18	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
27	d1ueka1	Alignment	not modelled	99.9	25	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
28	d1piea1	Alignment	not modelled	99.9	15	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
						Fold: Ribosomal protein S5 domain 2-like

29	d1s4ea1	Alignment	not modelled	99.9	16	**Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
30	c1fi4A_	Alignment	not modelled	99.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mevalonate 5-diphosphate decarboxylase; **PDBTitle:** the x-ray crystal structure of mevalonate 5-diphosphate decarboxylase2 at 2.3 angstrom resolution.
31	d1wuua1	Alignment	not modelled	99.9	19	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
32	d1kvka1	Alignment	not modelled	99.9	18	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
33	d1h72c2	Alignment	not modelled	99.9	27	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Homoserine kinase
34	d1fi4a1	Alignment	not modelled	99.9	20	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
35	c3f0nB_	Alignment	not modelled	99.7	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**mevalonate pyrophosphate decarboxylase; **PDBTitle:** mus musculus mevalonate pyrophosphate decarboxylase
36	d1k47a2	Alignment	not modelled	99.6	11	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Phosphomevalonate kinase (PMK)
37	d1kvka2	Alignment	not modelled	99.6	13	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Mevalonate kinase
38	d1ueka2	Alignment	not modelled	99.6	22	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
39	d1piea2	Alignment	not modelled	99.5	13	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Galactokinase
40	d1wuua2	Alignment	not modelled	99.5	15	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Galactokinase
41	d1s4ea2	Alignment	not modelled	99.5	16	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Galactokinase
42	d1kkha2	Alignment	not modelled	99.5	14	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Mevalonate kinase
43	d1oj4a2	Alignment	not modelled	99.4	16	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
44	d1fi4a2	Alignment	not modelled	96.8	15	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Mevalonate 5-diphosphate decarboxylase
45	c3m05A_	Alignment	not modelled	65.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pepe_1480; **PDBTitle:** the crystal structure of a functionally unknown protein2 pepe_1480 from pediococcus pentosaceus atcc 25745
46	c3dfeA_	Alignment	not modelled	38.8	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative pii-like signaling protein; **PDBTitle:** crystal structure of a putative pii-like signaling protein2 (yp_323533.1) from anabaena variabilis atcc 29413 at 2.35 a3 resolution
47	d1o51a_	Alignment	not modelled	35.7	20	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**DUF190/COG1993
48	d2cz4a1	Alignment	not modelled	31.2	20	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
49	d1wg1a_	Alignment	not modelled	29.4	16	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
50	c2j9dG_	Alignment	not modelled	25.1	15	**PDB header:**membrane transport **Chain:** G: **PDB Molecule:**hypothetical nitrogen regulatory pii-like **PDBTitle:** structure of glnk1 with bound effectors indicates2 regulatory mechanism for ammonia uptake
51	c3gaaB_	Alignment	not modelled	24.8	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ta1441; **PDBTitle:** the crystal structure of the protein with unknown function from2 thermoplasma acidophilum
52	c3bzqA_	Alignment	not modelled	24.4	15	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**nitrogen regulatory protein p-ii; **PDBTitle:** high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
53	d1xxaa_	Alignment	not modelled	22.2	12	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
54	d2p90a1	Alignment	not modelled	21.8	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Cgl1923-like **Family:**Cgl1923-like
55	d2p5ma1	Alignment	not modelled	20.5	18	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor

56	d1b4ba_	Alignment	not modelled	20.0	20	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
57	c3mnfA_	Alignment	not modelled	19.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pac2 family protein; **PDBTitle:** crystal structure of pac2 family protein from streptomyces avermitilis2 ma
58	c3cagF_	Alignment	not modelled	19.7	20	**PDB header:**dna binding protein **Chain:** F: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
59	c1vkrA_	Alignment	not modelled	19.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific pts system enzyme iiabc components; **PDBTitle:** structure of iib domain of the mannitol-specific permease enzyme ii
60	d1vkra_	Alignment	not modelled	19.0	24	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
61	c2p90B_	Alignment	not modelled	18.7	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein cgl1923; **PDBTitle:** the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
62	d2ns1b1	Alignment	not modelled	17.7	18	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
63	d1or5a_	Alignment	not modelled	17.2	16	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
64	c3ncpD_	Alignment	not modelled	15.6	18	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**nitrogen regulatory protein p-ii (glnb-2); **PDBTitle:** glnk2 from archaeoglobus fulgidus
65	d1hwua_	Alignment	not modelled	15.0	15	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
66	c2wamB_	Alignment	not modelled	14.5	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical alanine and leucine rich **PDBTitle:** crystal structure of mycobacterium tuberculosis unknown2 function protein rv2714
67	c2cq8A_	Alignment	not modelled	14.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**10-formyltetrahydrofolate dehydrogenase; **PDBTitle:** solution structure of rsgi ruh-033, a pp-binding domain of2 10-fthfdh from human cdna
68	d2gdwa1	Alignment	not modelled	14.0	17	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Peptidyl carrier domain
69	d1ul3a_	Alignment	not modelled	13.9	16	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
70	c2qnwA_	Alignment	not modelled	13.9	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** toxoplasma gondii apicoplast-targeted acyl carrier protein
71	d1vkua_	Alignment	not modelled	12.6	14	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
72	c2l4bA_	Alignment	not modelled	12.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
73	c3ieiD_	Alignment	not modelled	12.2	27	**PDB header:**transferase **Chain:** D: **PDB Molecule:**leucine carboxyl methyltransferase 1; **PDBTitle:** crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine
74	c1x3oA_	Alignment	not modelled	11.6	13	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of the acyl carrier protein from thermus2 thermophilus hb8
75	c2dclB_	Alignment	not modelled	11.3	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical upf0166 protein ph1503; **PDBTitle:** structure of ph1503 protein from pyrococcus horikoshii ot3
76	c3czcA_	Alignment	not modelled	11.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
77	c3mntA_	Alignment	not modelled	10.9	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucine carboxyl methyltransferase 1; **PDBTitle:** crystal structure of human leucine carboxyl methyltransferase 1
78	c2zwaA_	Alignment	not modelled	10.9	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucine carboxyl methyltransferase 2; **PDBTitle:** crystal structure of trna wybutosine synthesizing enzyme2 tyw4
79	d1aopa1	Alignment	not modelled	10.7	13	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
80	d1mg7a1	Alignment	not modelled	10.4	14	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Early switch protein XOL-1, N-terminal domain

81	d1rjda_	Alignment	not modelled	10.1	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Leucine carboxy methyltransferase Ppm1
82	d2piia_	Alignment	not modelled	9.9	16	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
83	c2kwlA_	Alignment	not modelled	9.6	10	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of acyl carrier protein from borrelia burgdorferi
84	d1uhva1	Alignment	not modelled	9.0	57	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
85	d1wi6a1	Alignment	not modelled	8.6	9	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
86	c2jvfA_	Alignment	not modelled	8.2	16	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
87	d3begb1	Alignment	not modelled	8.0	16	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
88	c2btqB_	Alignment	not modelled	7.9	24	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**tubulin btubb; **PDBTitle:** structure of btubab heterodimer from prosthecobacter2 dejongeii
89	d2axtj1	Alignment	not modelled	7.6	83	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein J, PsbJ **Family:**PsbJ-like
90	c2btoA_	Alignment	not modelled	7.4	15	**PDB header:**cytoskeletal protein **Chain:** A: **PDB Molecule:**tubulin btuba; **PDBTitle:** structure of btuba from prosthecobacter dejongeii
91	c3mhyC_	Alignment	not modelled	7.3	15	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**pii-like protein pz; **PDBTitle:** a new pii protein structure
92	c2liuA_	Alignment	not modelled	7.1	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cura; **PDBTitle:** nmr structure of holo-acpi domain from cura module from lyngbya2 majuscula
93	d2dfaa1	Alignment	not modelled	7.0	55	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
94	d1wg4a_	Alignment	not modelled	7.0	14	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
95	d1a6qa1	Alignment	not modelled	6.9	26	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
96	d1tubb1	Alignment	not modelled	6.9	17	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
97	d1v6ta_	Alignment	not modelled	6.7	36	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
98	c1b4aA_	Alignment	not modelled	6.7	20	**PDB header:**repressor **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** structure of the arginine repressor from bacillus stearothermophilus
99	c2x5eA_	Alignment	not modelled	6.6	36	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**upf0271 protein pa4511; **PDBTitle:** crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa