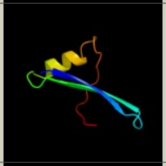
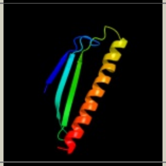
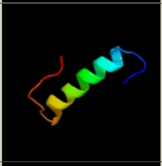
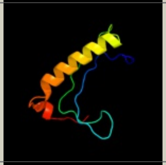
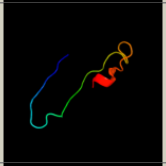
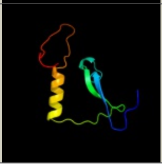
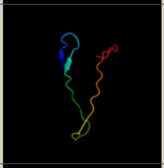
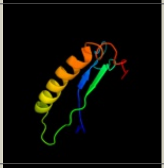
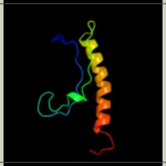
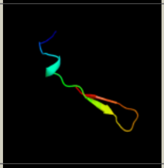
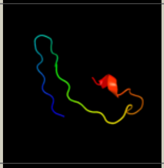
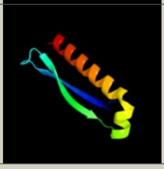
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P76160
Date	Thu Jan 5 12:19:53 GMT 2012
Unique Job ID	8772bc30d04a440e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jkxa_	Alignment		27.5	9	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
2	c2eenA_	Alignment		25.4	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1819; **PDBTitle:** structure of ph1819 protein from pyrococcus horikoshii ot3
3	d1fmta2	Alignment		21.8	10	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
4	c2zfdB_	Alignment		17.2	11	**PDB header:**signaling protein/transferase **Chain:** B: **PDB Molecule:**putative uncharacterized protein t20l15_90; **PDBTitle:** the crystal structure of plant specific calcium binding protein atcbl22 in complex with the regulatory domain of atcipk14
5	d2bw0a2	Alignment		17.2	8	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
6	c2v4oB_	Alignment		17.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**multifunctional protein sur e; **PDBTitle:** crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
7	c3oquB_	Alignment		17.0	19	**PDB header:**hormone receptor **Chain:** B: **PDB Molecule:**abscisic acid receptor pyl9; **PDBTitle:** crystal structure of native abscisic acid receptor pyl9 with aba
8	d1wjwa_	Alignment		16.4	10	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
9	d2blna2	Alignment		15.2	14	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
10	d2ae8a2	Alignment		12.7	18	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
11	d1civa2	Alignment		11.8	10	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain

12	c2fjtA_	Alignment		11.4	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylyl cyclase class iv; **PDBTitle:** adenylyl cyclase class iv from yersinia pestis
13	d1xo8a_	Alignment		11.3	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**LEA14-like **Family:**LEA14-like
14	c3rfoA_	Alignment		10.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** crystal structure of methyionyl-trna formyltransferase from bacillus2 anthracis
15	c3p9xB_	Alignment		9.9	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
16	d2ldxa2	Alignment		9.3	8	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
17	d1ev0a_	Alignment		8.8	27	**Fold:**Cell division protein MinE topological specificity domain **Superfamily:**Cell division protein MinE topological specificity domain **Family:**Cell division protein MinE topological specificity domain
18	d2f1da2	Alignment		8.6	21	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
19	d1s3ia2	Alignment		8.6	10	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
20	c1ybxA_	Alignment		8.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** conserved hypothetical protein cth-383 from clostridium thermocellum
21	c2y94C_	Alignment	not modelled	8.4	36	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5'-amp-activated protein kinase catalytic subunit alpha-1; **PDBTitle:** structure of an active form of mammalian ampk
22	d1gsoa1	Alignment	not modelled	8.1	6	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
23	c2f1dP_	Alignment	not modelled	7.6	21	**PDB header:**lyase **Chain:** P: **PDB Molecule:**imidazoleglycerol-phosphate dehydratase 1; **PDBTitle:** x-ray structure of imidazoleglycerol-phosphate dehydratase
24	c3n5fB_	Alignment	not modelled	7.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**n-carbamoyl-l-amino acid hydrolase; **PDBTitle:** crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43
25	d1rhya2	Alignment	not modelled	7.4	11	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
26	c1rhyB_	Alignment	not modelled	7.3	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**imidazole glycerol phosphate dehydratase; **PDBTitle:** crystal structure of imidazole glycerol phosphate dehydratase
27	c2ae8C_	Alignment	not modelled	7.2	19	**PDB header:**lyase **Chain:** C: **PDB Molecule:**imidazoleglycerol-phosphate dehydratase; **PDBTitle:** crystal structure of imidazoleglycerol-phosphate dehydratase from2 staphylococcus aureus subsp. aureus n315
						Fold:LDH C-terminal domain-like

28	d2cmda2	Alignment	not modelled	7.0	16	**Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
29	c1s1hJ_	Alignment	not modelled	7.0	11	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**40s ribosomal protein s20; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
30	c2i3fA_	Alignment	not modelled	6.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glycolipid transfer-like protein; **PDBTitle:** crystal structure of a glycolipid transfer-like protein2 from galdieria sulphuraria
31	c2dc4A_	Alignment	not modelled	6.7	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**165aa long hypothetical protein; **PDBTitle:** structure of ph1012 protein from pyrococcus horikoshii ot3
32	c3dcjA_	Alignment	not modelled	6.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable 5'-phosphoribosylglycinamide **PDBTitle:** crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
33	c2hjqA_	Alignment	not modelled	6.5	14	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein yqbf; **PDBTitle:** nmr structure of bacillus subtilis protein yqbf, northeast2 structural genomics target sr449
34	d1a6da3	Alignment	not modelled	6.4	10	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**Group II chaperonin (CCT, TRIC), intermediate domain
35	c1yrwA_	Alignment	not modelled	5.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of e.coli arna transformylase domain
36	d1q3qa3	Alignment	not modelled	5.4	14	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**Group II chaperonin (CCT, TRIC), intermediate domain