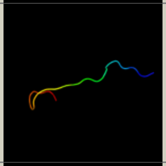
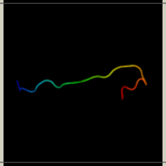
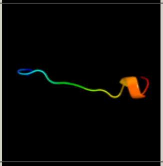
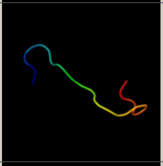
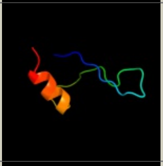
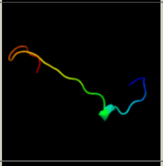
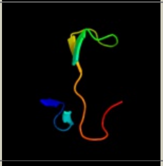
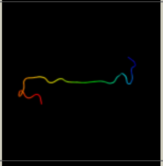
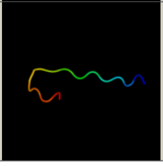
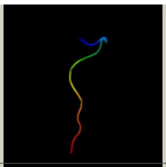
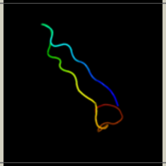
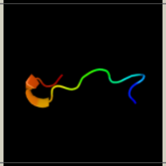
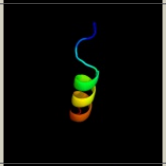
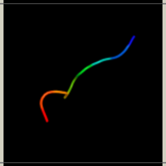
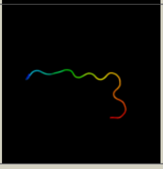
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P15033
Date	Thu Jan 5 11:34:19 GMT 2012
Unique Job ID	a805268fc2c42a3f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2o14a1	Alignment		31.3	23	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**YxiM N-terminal domain-like
2	c2gesA_	Alignment		25.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase; **PDBTitle:** pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt)
3	d1sq5a_	Alignment		25.5	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
4	c2qkdA_	Alignment		20.1	63	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains
5	d1rz3a_	Alignment		16.2	42	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
6	c3b7xA_	Alignment		15.5	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 6; **PDBTitle:** crystal structure of human fk506-binding protein 6
7	d1odfa_	Alignment		14.3	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
8	d2cp6a1	Alignment		12.7	25	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
9	d1nija2	Alignment		12.2	40	**Fold:**Hypothetical protein YjiA, C-terminal domain **Superfamily:**Hypothetical protein YjiA, C-terminal domain **Family:**Hypothetical protein YjiA, C-terminal domain
10	c3tqcB_	Alignment		11.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pantothenate kinase; **PDBTitle:** structure of the pantothenate kinase (coaa) from coxiella burnetii
11	c3asyB_	Alignment		11.2	47	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine kinase; **PDBTitle:** ligand-free structure of uridine kinase from thermus thermophilus hb8

12	d1umga_	Alignment		10.8	53	**Fold:**Sulfolobus fructose-1,6-bisphosphatase-like **Superfamily:**Sulfolobus fructose-1,6-bisphosphatase-like **Family:**Sulfolobus fructose-1,6-bisphosphatase-like
13	c3iz5j_	Alignment		9.0	45	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l12 (l11p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
14	d2f1la1	Alignment		8.6	20	**Fold:**PRC-barrel domain **Superfamily:**PRC-barrel domain **Family:**RimM C-terminal domain-like
15	d1vm6a2	Alignment		7.7	35	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
16	d1xmka1	Alignment		7.1	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
17	d1tj1a1	Alignment		6.9	56	**Fold:**N-terminal domain of bifunctional PutA protein **Superfamily:**N-terminal domain of bifunctional PutA protein **Family:**N-terminal domain of bifunctional PutA protein
18	c2bpsA_	Alignment		6.3	38	**PDB header:**ubiquitin **Chain:** A: **PDB Molecule:**yukd protein; **PDBTitle:** ubiquitin-like protein yukd of bacillus subtilis
19	c2ajmA_	Alignment		6.1	42	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**nonstructural protein 5a; **PDBTitle:** nmr structure of the in-plane membrane anchor domain [1-28]2 of the monotopic nonstructural protein 5a (ns5a) from the3 bovine viral diarrhea virus (bvdv)
20	d2oo3a1	Alignment		6.0	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**LPG1296-like
21	c1h8bB_	Alignment	not modelled	5.8	64	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**titin; **PDBTitle:** ef-hands 3,4 from alpha-actinin / z-repeat 7 from titin
22	d1yl7a2	Alignment	not modelled	5.6	24	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
23	d1iqca2	Alignment	not modelled	5.5	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
24	c3bguA_	Alignment	not modelled	5.5	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ferredoxin-like protein of unknown function; **PDBTitle:** crystal structure of a dimeric ferredoxin-like protein of unknown2 function (tfu_0763) from thermobifida fusca yx at 1.50 a resolution
25	d2b1ya1	Alignment	not modelled	5.4	36	**Fold:**Atu1913-like **Superfamily:**Atu1913-like **Family:**Atu1913-like
26	d1ou8a_	Alignment	not modelled	5.4	42	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**Stringent starvation protein B, SspB
27	c2wwiC_	Alignment	not modelled	5.2	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidilate kinase, putative; **PDBTitle:** plasmodium falciparum thymidylate kinase in complex with2 aztmp and adp
28	c3c8uA_	Alignment	not modelled	5.1	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of putative fructose transport system kinase2 (yp 612366.1) from silicibacter sp. tm1040 at 1.95 a

		resolution