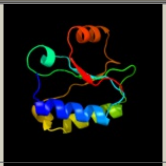
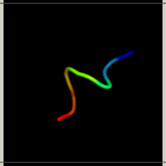
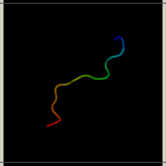
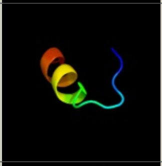
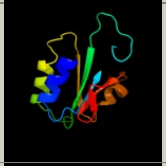
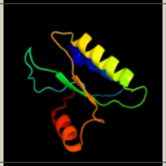
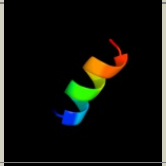
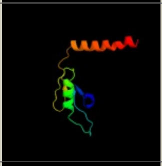
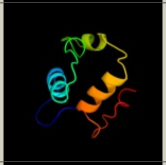
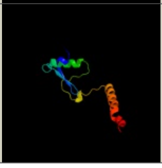
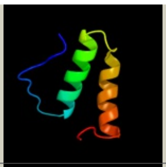
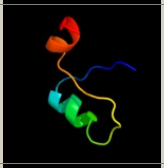
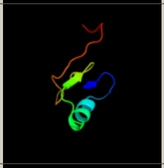
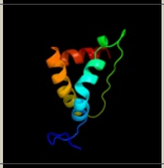
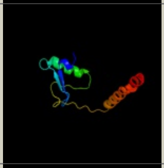
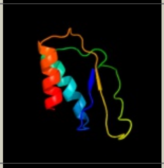
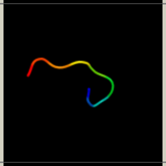
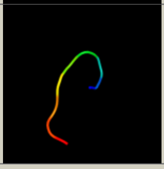
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AFZ1
Date	Thu Jan 5 11:27:37 GMT 2012
Unique Job ID	d67136d18eff568b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1no5a_	Alignment		40.2	13	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
2	c1r7gA_	Alignment		29.2	57	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** nmr structure of the membrane anchor domain (1-31) of the2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 100mm dpc)
3	c2l8tA_	Alignment		20.9	47	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**transposon tn557 toxic shock syndrome toxin-1; **PDBTitle:** staphylococcus aureus pathogenicity island 1 protein gp6, an internal2 scaffold in size determination
4	c2abyA_	Alignment		12.4	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0743; **PDBTitle:** solution structure of ta0743 from thermoplasma acidophilum
5	c2rffA_	Alignment		12.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotidyltransferase; **PDBTitle:** crystal structure of a putative nucleotidyltransferase2 (np_343093.1) from sulfolobus solfataricus at 1.40 a3 resolution
6	d1wota_	Alignment		11.8	14	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
7	d2foka2	Alignment		9.0	42	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Restriction endonuclease FokI, N-terminal (recognition) domain
8	d1dd5a_	Alignment		8.6	14	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
9	c3r1fO_	Alignment		8.0	18	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
10	d1ge9a_	Alignment		7.4	12	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
11	d1ek8a_	Alignment		7.3	15	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF

12	d1a3aa_	Alignment		6.9	17	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
13	d1s6la2	Alignment		6.2	19	**Fold:**NosL/MerB-like **Superfamily:**NosL/MerB-like **Family:**MerB-like
14	c3cu2A_	Alignment		6.1	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribulose-5-phosphate 3-epimerase; **PDBTitle:** crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
15	d1eh1a_	Alignment		5.9	9	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
16	d1sm4a2	Alignment		5.8	10	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
17	d1is1a_	Alignment		5.8	10	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
18	d2qmwa2	Alignment		5.5	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
19	c3gnyA_	Alignment		5.4	33	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1; **PDBTitle:** crystal structure of human alpha-defensin 1 (hnp1)
20	c3hj2B_	Alignment		5.2	33	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**human neutrophil peptide 1; **PDBTitle:** crystal structure of covalent dimer of hnp1
21	c3ns5B_	Alignment	not modelled	5.1	17	**PDB header:**translation **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit b; **PDBTitle:** crystal structure of the rna recognition motif of yeast eif3b residues2 76-161