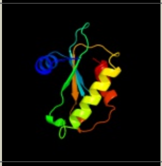
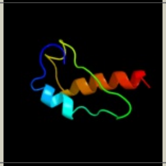
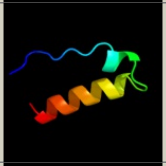
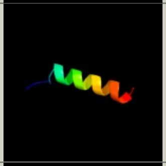
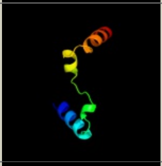
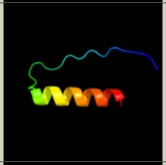
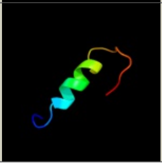
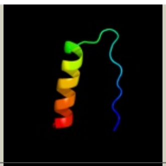
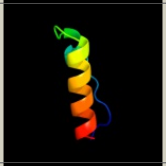
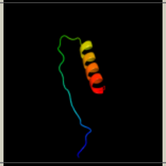
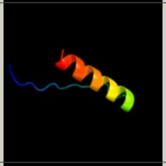
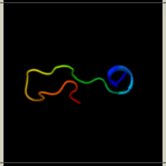
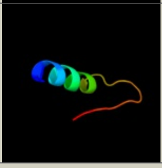
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A7Y8
Date	Thu Jan 5 11:06:29 GMT 2012
Unique Job ID	d85e045bb6dd5b5e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ljpA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease p protein component; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for e.coli2 ribonuclease p protein
2	d1d6ta_	Alignment		100.0	24	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**RNase P protein
3	d1a6fa_	Alignment		100.0	28	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**RNase P protein
4	d1nz0a_	Alignment		100.0	29	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**RNase P protein
5	c2c4rL_	Alignment		38.5	10	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
6	d1q6oa_	Alignment		15.9	0	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
7	c2y94C_	Alignment		11.7	14	**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
8	c3oqvA_	Alignment		11.0	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**albc; **PDBTitle:** albc, a cyclodipeptide synthase from streptomyces noursei
9	d1qjha_	Alignment		10.1	6	**Fold:**Ferredoxin-like **Superfamily:**Ribosomal protein S6 **Family:**Ribosomal protein S6
10	c3bvjA_	Alignment		9.7	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uridine 5'-monophosphate synthase; **PDBTitle:** crystal structure of human orotidine 5'-monophosphate decarboxylase2 complexed with xmp
11	c1tteA_	Alignment		9.4	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-conjugating enzyme e2-24 kda; **PDBTitle:** the structure of a class ii ubiquitin-conjugating enzyme,2 ubc1.

12	c2kjwA_	Alignment		8.6	7	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s6; **PDBTitle:** solution structure and backbone dynamics of the permutant2 p54-55
13	c2qcnA_	Alignment		8.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uridine 5'-monophosphate synthase; **PDBTitle:** covalent complex of the orotidine-5'-monophosphate decarboxylase2 domain of human ump synthase with 6-iodo-ump
14	d2j5aa1	Alignment		8.1	11	**Fold:**Ferredoxin-like **Superfamily:**Ribosomal protein S6 **Family:**Ribosomal protein S6
15	d1loua_	Alignment		7.7	6	**Fold:**Ferredoxin-like **Superfamily:**Ribosomal protein S6 **Family:**Ribosomal protein S6
16	c3bbnF_	Alignment		6.6	17	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**ribosomal protein s6; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
17	d1vsra_	Alignment		6.5	42	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
18	d2fsua1	Alignment		6.4	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PhnH-like **Family:**PhnH-like
19	c2fsuA_	Alignment		6.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein phnh; **PDBTitle:** crystal structure of the phnh protein from escherichia coli
20	d2ayva1	Alignment		5.4	17	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
21	d2jfga2	Alignment	not modelled	5.3	14	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
22	c3exsB_	Alignment	not modelled	5.1	6	**PDB header:**lyase **Chain:** B: **PDB Molecule:**rmpd (hexulose-6-phosphate synthase); **PDBTitle:** crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p