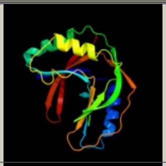
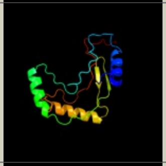
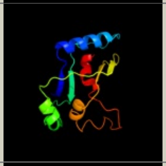
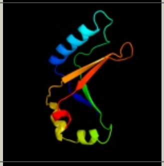
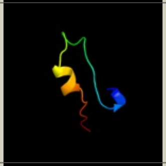
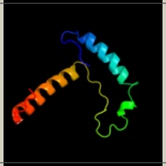
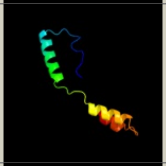
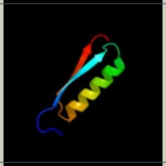
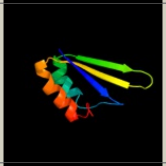
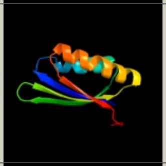
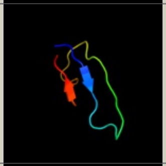
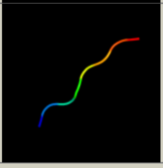
Email	l.a.kelley@imperial.ac.uk
Description	P37025
Date	Thu Jan 5 11:54:33 GMT 2012
Unique Job ID	ed86cb8f80ab72f6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1iuha_	Alignment		100.0	31	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**2'-5' RNA ligase LigT
2	c1vdxA_	Alignment		100.0	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**hypothetical protein ph0099; **PDBTitle:** crystal structure of a pyrococcus horikoshii protein with2 similarities to 2'5' rna-ligase
3	c2d4gA_	Alignment		100.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bsu11850; **PDBTitle:** structure of yjcg protein, a putative 2'-5' rna ligase from2 bacillus subtilis
4	c2vfyA_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**akap18 delta; **PDBTitle:** akap18 delta central domain
5	d1jh6a_	Alignment		100.0	14	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**tRNA splicing product Appr>p cyclic nucleotide phosphodiesterase
6	d2fsqa1	Alignment		98.2	12	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**Atu0111-like
7	d2ilxa1	Alignment		87.0	18	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**2',3'-cyclic nucleotide 3'-phosphodiesterase, catalytic domain
8	c2e5cA_	Alignment		38.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinamide phosphoribosyltransferase; **PDBTitle:** crystal structure of human nmprtase complexed with 5'-phosphoribosyl-2 1'-pyrophosphate
9	c2i3eA_	Alignment		28.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**g-rich; **PDBTitle:** solution structure of catalytic domain of goldfish rich2 protein
10	c3h0dB_	Alignment		18.8	11	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**ctsr; **PDBTitle:** crystal structure of ctsr in complex with a 26bp dna duplex
11	c3ce8A_	Alignment		18.6	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative pii-like nitrogen regulatory protein; **PDBTitle:** crystal structure of a duf3240 family protein (sbal_0098) from2 shewanella baltica os155 at 2.40 a resolution

12	d1gyxa_	Alignment		14.4	19	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
13	c2qpqC_	Alignment		11.0	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein bug27; **PDBTitle:** structure of bug27 from bordetella pertussis
14	c3itfA_	Alignment		9.2	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**periplasmic adaptor protein cpxp; **PDBTitle:** structural basis for the inhibitory function of the cpxp adaptor2 protein
15	c3nohA_	Alignment		9.2	11	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative peptide binding protein; **PDBTitle:** crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution
16	d1aopa2	Alignment		8.9	15	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
17	d1u8sa1	Alignment		8.5	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
18	c1zj8B_	Alignment		7.8	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable ferredoxin-dependent nitrite reductase nira; **PDBTitle:** structure of mycobacterium tuberculosis nira protein
19	d2ih2a2	Alignment		7.8	18	**Fold:**DNA methylase specificity domain **Superfamily:**DNA methylase specificity domain **Family:**TaqI C-terminal domain-like
20	c3dkuB_	Alignment		7.8	50	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of nudix hydrolase orf153, ymfb, from2 escherichia coli k-1
21	d1owfb_	Alignment	not modelled	6.0	10	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein