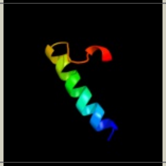
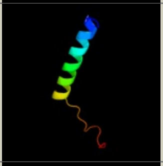
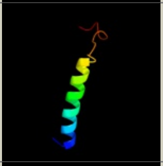
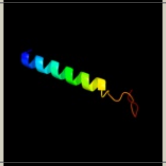
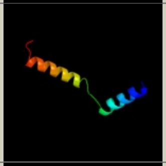
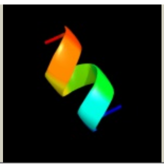
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	A5A614
Date	Thu Jan 5 10:55:19 GMT 2012
Unique Job ID	b979a54af45e5fa0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ldda_	Alignment		48.6	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**SCF ubiquitin ligase complex WHB domain
2	d1t5la1	Alignment		9.9	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
3	d1y76b1	Alignment		7.9	38	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
4	d1jqoa_	Alignment		7.9	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
5	c1jqoA_	Alignment		7.9	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
6	d1jqna_	Alignment		7.2	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
7	c1kyqC_	Alignment		6.4	12	**PDB header:**oxidoreductase, lyase **Chain:** C: **PDB Molecule:**siroheme biosynthesis protein met8; **PDBTitle:** met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
8	c3ogiC_	Alignment		6.2	56	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative esat-6-like protein 6; **PDBTitle:** crystal structure of the mycobacterium tuberculosis h37rv esxop2 complex (rv2346c-rv2347c)

9	d2dexx3	Alignment		5.3	67	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Peptidylarginine deiminase Pad4, catalytic C-terminal domain