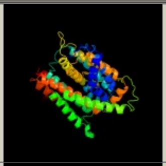
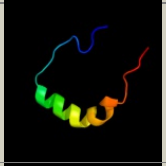
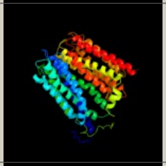
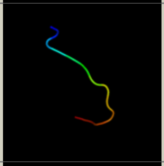
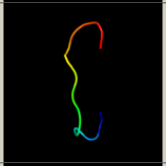
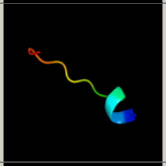
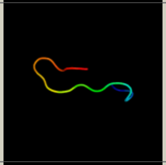
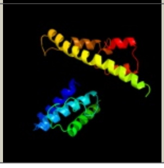
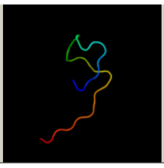
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AGM9
Date	Thu Jan 5 11:29:35 GMT 2012
Unique Job ID	ff3b70a26b477d42

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qe7A_	Alignment		100.0	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uracil permease; **PDBTitle:** crystal structure of uracil transporter--uraa
2	c1bzkA_	Alignment		43.6	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein (band 3 anion transport protein); **PDBTitle:** structural studies on the effects of the deletion in the2 red cell anion exchanger (band3, ae1) associated with3 south east asian ovalocytosis.
3	d1pw4a_	Alignment		37.6	11	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
4	d1prta_	Alignment		14.8	38	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
5	c1oyiA_	Alignment		14.3	43	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**double-stranded rna-binding protein; **PDBTitle:** solution structure of the z-dna binding domain of the2 vaccinia virus gene e3l
6	d1oyia_	Alignment		14.3	43	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
7	c3lpzA_	Alignment		12.6	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**get4 (yor164c homolog); **PDBTitle:** crystal structure of c. therm. get4
8	c3o7pA_	Alignment		6.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-fucose-proton symporter; **PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
9	d1xmka1	Alignment		5.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
10	c2ht2B_	Alignment		5.4	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**h(+)/cl(-) exchange transporter clca; **PDBTitle:** structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex

11	d1zt2a1	Alignment		5.2	15	**Fold:**Prim-pol domain **Superfamily:**Prim-pol domain **Family:**PriA-like