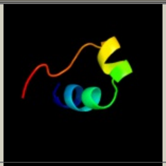
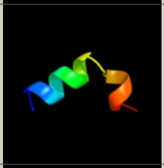
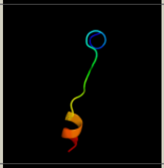
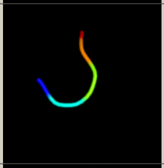
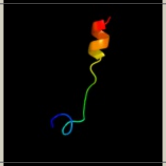
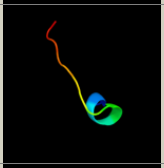
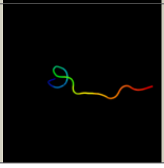
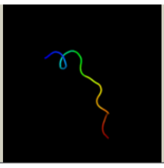
Email	l.a.kelley@imperial.ac.uk
Description	Q46795
Date	Thu Jan 5 12:34:15 GMT 2012
Unique Job ID	6d1c04130a31ddbe

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pp7u_	Alignment		54.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**39 kda initiator binding protein, IBP39, N-terminal domain
2	d2ga1a1	Alignment		20.8	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Alr1493-like
3	c3s81A_	Alignment		12.8	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aspartate racemase; **PDBTitle:** crystal structure of putative aspartate racemase from salmonella2 typhimurium
4	c2i4cA_	Alignment		10.5	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**bicarbonate transporter; **PDBTitle:** crystal structure of bicarbonate transport protein cmpa from2 synechocystis sp. pcc 6803 in complex with bicarbonate and calcium
5	c2fhwA_	Alignment		6.9	80	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**relaxin 3 (prorelaxin h3) (insulin-like peptide **PDBTitle:** solution structure of human relaxin-3
6	c2g29A_	Alignment		6.7	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrate transport protein nrta; **PDBTitle:** crystal structure of the periplasmic nitrate-binding2 protein nrta from synechocystis pcc 6803
7	d1sxja1	Alignment		6.2	55	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
8	d2h7aa1	Alignment		5.9	20	**Fold:**YcgL-like **Superfamily:**YcgL-like **Family:**YcgL-like
9	d1xkpc1	Alignment		5.8	24	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
10	d1itwa_	Alignment		5.8	29	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Monomeric isocitrate dehydrogenase

11	c2b0tA_	Alignment		5.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp isocitrate dehydrogenase; **PDBTitle:** structure of monomeric nadp isocitrate dehydrogenase