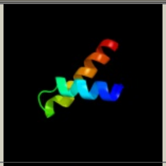
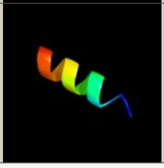
Email	l.a.kelley@imperial.ac.uk
Description	P0AF73
Date	Thu Jan 5 11:25:27 GMT 2012
Unique Job ID	4f83408e4079dc99

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fd5a2	Alignment		8.4	8	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
2	d1z21a1	Alignment		6.4	38	**Fold:**Type III secretion system domain **Superfamily:**Type III secretion system domain **Family:**YopR Core
3	c1yfnG_	Alignment		5.7	50	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**sigma-e factor negative regulatory protein; **PDBTitle:** versatile modes of peptide recognition by the aaa+ adaptor2 protein sspb- the crystal structure of a sspb-rsea complex
4	c1emzA_	Alignment		5.3	29	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein e1; **PDBTitle:** solution structure of fragment (350-370) of the2 transmembrane domain of hepatitis c envelope glycoprotein3 e1