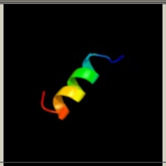
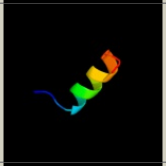
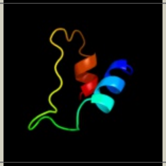
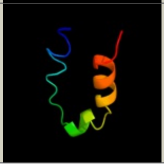
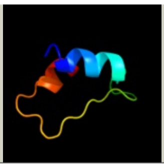
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AEH8
Date	Thu Jan 5 11:23:22 GMT 2012
Unique Job ID	885b769baa53da92

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3buxb3	Alignment		65.0	44	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
2	c1fbvA_	Alignment		19.9	44	**PDB header:**ligase **Chain:** A: **PDB Molecule:**signal transduction protein cbl; **PDBTitle:** structure of a cbl-ubch7 complex: ring domain function in2 ubiquitin-protein ligases
3	c2zifB_	Alignment		7.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative modification methylase; **PDBTitle:** crystal structure of ttha0409, putative dna modification2 methylase from thermus thermophilus hb8- complexed with s-3 adenosyl-l-methionine
4	c2xpnA_	Alignment		6.8	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iws1; **PDBTitle:** crystal structure of a spt6-iws1(spn1) complex from2 encephalitozoon cuniculi, form i

5	c1nw6A_	Alignment		5.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**modification methylase rsri; **PDBTitle:** structure of the beta class n6-adenine dna methyltransferase rsri2 bound to sinefungin