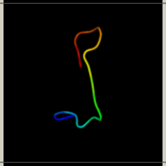
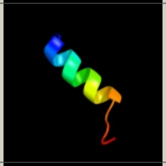
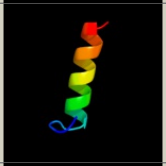
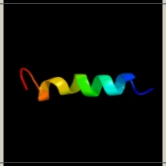
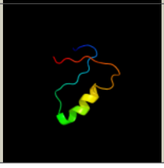
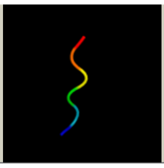
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q47042
Date	Thu Jan 5 12:36:10 GMT 2012
Unique Job ID	55142c23f438f47b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mxnA_	Alignment		17.1	11	**PDB header:**replication **Chain:** A: **PDB Molecule:**recq-mediated genome instability protein 1; **PDBTitle:** crystal structure of the rmi core complex
2	d1bcga_	Alignment		12.2	44	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
3	c2l1wB_	Alignment		9.8	41	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**vacuolar calcium atpase bca1 peptide; **PDBTitle:** the solution structure of soybean calmodulin isoform 4 complexed with2 the vacuolar calcium atpase bca1 peptide
4	c2rdcA_	Alignment		8.8	52	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative lipid binding protein (gsu0061) from2 geobacter sulfurreducens pca at 1.80 a resolution
5	c3rnvA_	Alignment		8.1	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**helper component proteinase; **PDBTitle:** structure of the autocatalytic cysteine protease domain of potyvirus2 helper-component proteinase
6	c1okgA_	Alignment		6.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major

7	c2cl2A_	Alignment		6.3	83	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative laminarinase; **PDBTitle:** endo-1,3(4)-beta-glucanase from phanerochaete chrysosporium,2 solved using native sulfur sad, exhibiting intact3 heptasaccharide glycosylation