

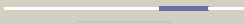




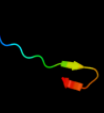



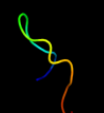


# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P75980
Date	Thu Jan 5 12:16:53 GMT 2012
Unique Job ID	cbe2896b14ba5d08

Detailed template information

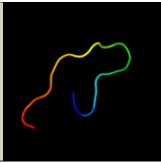
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3kdrC_</a>	 Alignment		92.1	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hk97 family phage portal protein; <b>PDBTitle:</b> the crystal structure of a hk97 family phage portal protein from2 corynebacterium diphtheriae to 2.9a
2	<a href="#">c3fo8D_</a>	 Alignment		16.1	26	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> tail sheath protein gp18; <b>PDBTitle:</b> crystal structure of the bacteriophage t4 tail sheath2 protein, protease resistant fragment gp18pr
3	<a href="#">dlc0ma1</a>	 Alignment		8.1	15	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> DNA-binding domain of retroviral integrase <b>Family:</b> DNA-binding domain of retroviral integrase
4	<a href="#">dlhq0a_</a>	 Alignment		6.4	27	<b>Fold:</b> CNF1/YfiH-like putative cysteine hydrolases <b>Superfamily:</b> CNF1/YfiH-like putative cysteine hydrolases <b>Family:</b> Type 1 cytotoxic necrotizing factor, catalytic domain
5	<a href="#">c3zrhA_</a>	 Alignment		6.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin thioesterase zranb1; <b>PDBTitle:</b> crystal structure of the lys29, lys33-linkage-specific traid otu2 deubiquitinase domain reveals an ankyrin-repeat ubiquitin binding3 domain (ankubd)
6	<a href="#">c3hjdA_</a>	 Alignment		5.1	41	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> human neutrophil peptide 1; <b>PDBTitle:</b> x-ray structure of monomeric variant of hnp1

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[c3hjdB\\_](#)



Alignment



5.1

41

**PDB header:**antimicrobial protein  
**Chain:** B: **PDB Molecule:**human neutrophil peptide 1;  
**PDBTitle:** x-ray structure of monomeric variant of hnp1