




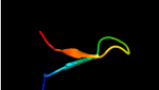

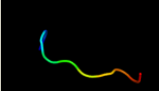


# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	C1P612
Date	Thu Jan 5 10:56:08 GMT 2012
Unique Job ID	135fdbc3aa4f2545

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dl8D_</a>	 Alignment		46.3	82	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> sece; <b>PDBTitle:</b> structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
2	<a href="#">c2wwaC_</a>	 Alignment		9.0	50	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> protein transport protein seb2; <b>PDBTitle:</b> cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
3	<a href="#">d2fnaa1</a>	 Alignment		7.0	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Helicase DNA-binding domain
4	<a href="#">c1dpuA_</a>	 Alignment		6.2	50	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a (rpa32) c-terminal domain; <b>PDBTitle:</b> solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)