
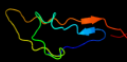



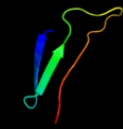



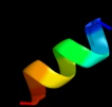



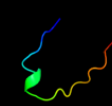










# Phyre2

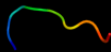
Email	I.a.kelley@imperial.ac.uk
Description	P0AAY4
Date	Thu Jan 5 11:14:07 GMT 2012
Unique Job ID	eb46913e1d318ffd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2kywA_</a>	 Alignment		43.0	31	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> adhesion exoprotein; <b>PDBTitle:</b> solution nmr structure of a domain of adhesion exoprotein from2 pediococcus pentosaceus, northeast structural genomics consortium3 target ptr41o
2	<a href="#">c1zy3B_</a>	 Alignment		28.4	64	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bh3-peptide from bh3 interacting domain death <b>PDBTitle:</b> structural model of complex of bcl-w protein with bid bh3-2 peptide
3	<a href="#">c2oy7A_</a>	 Alignment		16.8	38	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer surface protein a; <b>PDBTitle:</b> the crystal structure of ospa mutant
4	<a href="#">c2voiB_</a>	 Alignment		16.0	50	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bh3-interacting domain death agonist p13; <b>PDBTitle:</b> structure of mouse a1 bound to the bid bh3-domain
5	<a href="#">c1erfA_</a>	 Alignment		11.5	58	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane glycoprotein; <b>PDBTitle:</b> conformational mapping of the n-terminal fusion peptide of2 hiv-1 gp41 using 13c-enhanced fourier transform infrared3 spectroscopy (ftir)
6	<a href="#">c2pjvA_</a>	 Alignment		11.2	58	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> solution structure of hiv-1 gp41 fusion domain bound to dpc2 micelle
7	<a href="#">c3kd4A_</a>	 Alignment		10.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative protease; <b>PDBTitle:</b> crystal structure of a putative protease (bdi_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
8	<a href="#">d1kwga3</a>	 Alignment		8.2	50	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> A4 beta-galactosidase middle domain
9	<a href="#">c2jpwA_</a>	 Alignment		6.7	58	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> troponin i, cardiac muscle; <b>PDBTitle:</b> solution structure of the bisphosphorylated cardiac2 specific n-extension of cardiac troponin i
10	<a href="#">d1jzta_</a>	 Alignment		6.1	67	<b>Fold:</b> YjeF N-terminal domain-like <b>Superfamily:</b> YjeF N-terminal domain-like <b>Family:</b> YjeF N-terminal domain-like
11	<a href="#">c2wtoB_</a>	 Alignment		6.1	29	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> orf131 protein; <b>PDBTitle:</b> crystal structure of apo-form czce from c. metallidurans ch34

12 [c2zkr9\\_](#)

Alignment



6.0

44

**PDB header:**ribosomal protein/rna  
**Chain:** 9: **PDB Molecule:**60s ribosomal protein l32;  
**PDBTitle:** structure of a mammalian ribosomal 60s subunit within  
an2 80s complex obtained by docking homology models of the rna3  
and proteins into an 8.7 a cryo-em map

13	<a href="#">c2ariA_</a>	Alignment		5.6	58	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope polyprotein gp160; <b>PDBTitle:</b> solution structure of micelle-bound fusion domain of hiv-12 gp41
----	-------------------------	-----------	--	-----	----	--