
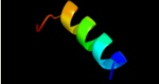



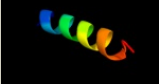




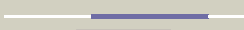







# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0C7Z3
Date	Tue Jul 17 17:05:08 BST 2012
Unique Job ID	e38ff2908a915b00

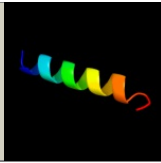
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1dtcA_</a>	 Alignment		13.4	39	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-delta-toxin; <b>PDBTitle:</b> delta-toxin and analogues as peptide models for protein ion2 channels
2	<a href="#">c2dtbA_</a>	 Alignment		13.4	39	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> delta-toxin; <b>PDBTitle:</b> delta-toxin and analogues as peptide models for protein ion2 channels
3	<a href="#">c2kamA_</a>	 Alignment		13.1	39	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> delta-hemolysin; <b>PDBTitle:</b> nmr structure of delta-toxin from staphylococcus aureus in2 cd3oh
4	<a href="#">c1fmeA_</a>	 Alignment		12.0	46	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> fsd-ey peptide; <b>PDBTitle:</b> solution structure of fsd-ey, a novel peptide assuming a2 beta-beta-alpha fold
5	<a href="#">c1fsvA_</a>	 Alignment		10.8	46	<b>PDB header:</b> beta beta alpha motif <b>Chain:</b> A: <b>PDB Molecule:</b> full sequence design 1 of beta beta alpha motif; <b>PDBTitle:</b> full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, minimized average structure
6	<a href="#">c1fsdA_</a>	 Alignment		10.8	46	<b>PDB header:</b> novel sequence <b>Chain:</b> A: <b>PDB Molecule:</b> full sequence design 1 of beta beta alpha motif; <b>PDBTitle:</b> full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, 41 structures
7	<a href="#">c2dalA_</a>	 Alignment		10.0	67	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein kiaa0794; <b>PDBTitle:</b> solution structure of the novel identified uba-like domain2 in the n-terminal of human fas associated factor 1 protein
8	<a href="#">d1rp3b_</a>	 Alignment		5.2	73	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Anti-sigma factor FlgM <b>Family:</b> Anti-sigma factor FlgM

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[c2zxeG](#)

Alignment



5.1

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**PDB header:**hydrolase/transport protein  
**Chain:** G: **PDB Molecule:**phospholemman-like protein;  
**PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state