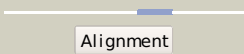
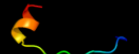
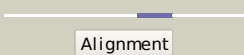
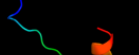
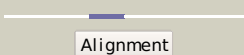




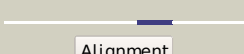



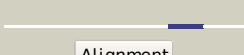


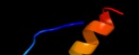









# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P28697
Date	Thu Jan 5 11:45:10 GMT 2012
Unique Job ID	44f06355961278d6

Detailed template information

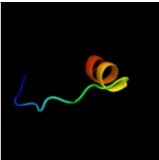
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1bdta_</a>	 Alignment		20.3	44	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
2	<a href="#">d1b28a_</a>	 Alignment		19.4	44	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
3	<a href="#">c2wfuA_</a>	 Alignment		14.5	81	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable insulin-like peptide 5 a chain; <b>PDBTitle:</b> crystal structure of dilp5 variant db
4	<a href="#">c2wfvA_</a>	 Alignment		14.0	81	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable insulin-like peptide 5 a chain; <b>PDBTitle:</b> crystal structure of dilp5 variant c4
5	<a href="#">d1myla_</a>	 Alignment		10.0	41	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
6	<a href="#">d1baza_</a>	 Alignment		8.8	44	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
7	<a href="#">d1myka_</a>	 Alignment		8.3	41	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
8	<a href="#">d1xhja_</a>	 Alignment		7.8	35	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> NifU C-terminal domain-like
9	<a href="#">d1veha_</a>	 Alignment		7.4	22	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> NifU C-terminal domain-like
10	<a href="#">c3i3aC_</a>	 Alignment		6.7	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> acyl-[acyl-carrier-protein]-udp-n- <b>PDBTitle:</b> structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
11	<a href="#">d1th5a1</a>	 Alignment		6.6	7	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> NifU C-terminal domain-like

12	<a href="#">c1z2tA_</a>	Alignment		6.4	50	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> anchor peptide ser65-leu87 of almgs; <b>PDBTitle:</b> nmr structure study of anchor peptide ser65-leu87 of enzyme2 acholeplasma laidlawii monoglycosyldiacyl glycerol3 synthase (almgs) in dhpc micelles
13	<a href="#">c2jnvA_</a>	Alignment		6.3	29	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> nifu-like protein 1, chloroplast; <b>PDBTitle:</b> solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
14	<a href="#">d1n12a_</a>	Alignment		6.2	22	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Bacterial adhesins <b>Family:</b> Pilus subunits

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[c2h8bB\\_](#)

Alignment



6.1

40

**PDB header:**hormone/growth factor  
**Chain:** B: **PDB Molecule:**insulin-like 3;  
**PDBTitle:** solution structure of insl3