























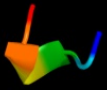



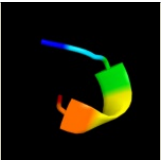
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2e74b1</a>	 Alignment		22.4	50	<b>Fold:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Superfamily:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
2	<a href="#">d1q90d</a>	 Alignment		21.8	40	<b>Fold:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Superfamily:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
3	<a href="#">d1bccc2</a>	 Alignment		18.6	50	<b>Fold:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Superfamily:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
4	<a href="#">d1ppjc1</a>	 Alignment		16.5	50	<b>Fold:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Superfamily:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
5	<a href="#">d3cx5c1</a>	 Alignment		16.4	70	<b>Fold:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Superfamily:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
6	<a href="#">c2ys9A</a>	 Alignment		16.2	67	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox and leucine zipper protein homez; <b>PDBTitle:</b> structure of the third homeodomain from the human homeobox2 and leucine zipper protein, homez
7	<a href="#">d1vf5b</a>	 Alignment		16.0	50	<b>Fold:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Superfamily:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
8	<a href="#">c1z65A</a>	 Alignment		14.7	50	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> prion-like protein doppel; <b>PDBTitle:</b> mouse doppel 1-30 peptide
9	<a href="#">d1tj1a1</a>	 Alignment		11.5	67	<b>Fold:</b> N-terminal domain of bifunctional PutA protein <b>Superfamily:</b> N-terminal domain of bifunctional PutA protein <b>Family:</b> N-terminal domain of bifunctional PutA protein
10	<a href="#">c3cx5N</a>	 Alignment		6.9	70	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N: <b>PDB Molecule:</b> cytochrome b; <b>PDBTitle:</b> structure of complex iii with bound cytochrome c in reduced2 state and definition of a minimal core interface for3 electron transfer.
11	<a href="#">c2qjkM</a>	 Alignment		6.8	60	<b>PDB header:</b> electron transport <b>Chain:</b> M: <b>PDB Molecule:</b> cytochrome b; <b>PDBTitle:</b> crystal structure analysis of mutant rhodobacter2 sphaeroides bc1 with stigmatellin and antimycin

12	<a href="#">c3cwbC_</a>	Alignment		6.4	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> cytochrome b; <b>PDBTitle:</b> chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
13	<a href="#">c2kneB_</a>	Alignment		6.0	57	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> atpase, ca++ transporting, plasma membrane 4; <b>PDBTitle:</b> calmodulin wraps around its binding domain in the plasma2 membrane ca2+ pump anchored by a novel 18-1 motif
14	<a href="#">c2wfvA_</a>	Alignment		5.8	83	<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
15	<a href="#">d2p7tc1</a>	Alignment		5.8	100	<b>Fold:</b> Voltage-gated potassium channels <b>Superfamily:</b> Voltage-gated potassium channels <b>Family:</b> Voltage-gated potassium channels

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[c2wfuA](#)

Alignment



5.8

83

**PDB header:**signaling protein  
**Chain:** A: **PDB Molecule:**probable insulin-like peptide 5 a chain;  
**PDBTitle:** crystal structure of dilp5 variant db