
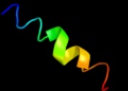

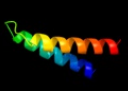











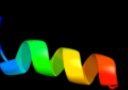



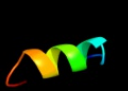
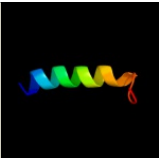


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2wssT_</a>	 Alignment		28.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> T: <b>PDB Molecule:</b> atp synthase subunit b, mitochondrial; <b>PDBTitle:</b> the structure of the membrane extrinsic region of bovine2 atp synthase
2	<a href="#">c3d19E_</a>	 Alignment		25.4	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> conserved metalloprotein; <b>PDBTitle:</b> crystal structure of a conserved metalloprotein from bacillus cereus
3	<a href="#">d1d8ba_</a>	 Alignment		15.3	10	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> HRDC domain from helicases
4	<a href="#">c3dbyN_</a>	 Alignment		15.2	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> N: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein from bacillus cereus2 g9241 (csap target)
5	<a href="#">c2lf0A_</a>	 Alignment		8.7	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yibl; <b>PDBTitle:</b> solution structure of sf3636, a two-domain unknown function protein2 from shigella flexneri 2a, determined by joint refinement of nmr,3 residual dipolar couplings and small-angle x-ray scattering, nesg4 target sfr339/ocsp target sf3636
6	<a href="#">c2k47A_</a>	 Alignment		7.0	18	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> solution structure of the c-terminal n-rna binding domain2 of the vesicular stomatitis virus phosphoprotein
7	<a href="#">d1q2za_</a>	 Alignment		6.8	18	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> C-terminal domain of Ku80 <b>Family:</b> C-terminal domain of Ku80
8	<a href="#">c2kelB_</a>	 Alignment		6.4	27	<b>PDB header:</b> transcription repressor <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein 56b; <b>PDBTitle:</b> structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
9	<a href="#">d3d19a1</a>	 Alignment		5.8	11	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Bacillus cereus metalloprotein-like <b>Family:</b> Bacillus cereus metalloprotein-like
10	<a href="#">d1s58a_</a>	 Alignment		5.5	12	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> ssDNA viruses <b>Family:</b> Parvoviridae-like VP

11	<a href="#">c2k59B_</a>	Alignment		5.4	18	<p><b>PDB header:</b>transport protein</p> <p><b>Chain:</b> B: <b>PDB Molecule:</b>neuronal acetylcholine receptor subunit beta-2;</p> <p><b>PDBTitle:</b> nmr structures of the second transmembrane domain of the2 neuronal acetylcholine receptor beta 2 subunit</p>
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