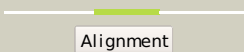
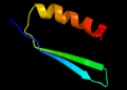
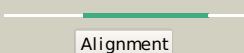

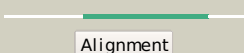
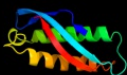
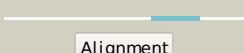

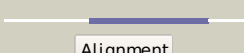

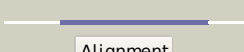

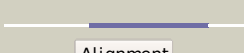
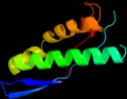








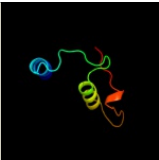


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2rrlA_</a>	 Alignment		60.7	21	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar hook-length control protein; <b>PDBTitle:</b> solution structure of the c-terminal domain of the flik
2	<a href="#">c2rpbA_</a>	 Alignment		42.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical membrane protein; <b>PDBTitle:</b> the solution structure of membrane protein
3	<a href="#">c3bk6C_</a>	 Alignment		42.7	10	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> ph stomatin; <b>PDBTitle:</b> crystal structure of a core domain of stomatin from2 pyrococcus horikoshii
4	<a href="#">c3gxqB_</a>	 Alignment		33.3	13	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> putative regulator of transfer genes arta; <b>PDBTitle:</b> structure of arta and dna complex
5	<a href="#">c3u5gB_</a>	 Alignment		19.7	19	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> 40s ribosomal protein s1-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution
6	<a href="#">d1wina_</a>	 Alignment		13.2	7	<b>Fold:</b> EF-Ts domain-like <b>Superfamily:</b> Band 7/SPFH domain <b>Family:</b> Band 7/SPFH domain
7	<a href="#">c2xzm4_</a>	 Alignment		11.0	9	<b>PDB header:</b> ribosome <b>Chain:</b> 4: <b>PDB Molecule:</b> 40s ribosomal protein s3a; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
8	<a href="#">d2od5a1</a>	 Alignment		7.5	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Marine metagenome family WH1
9	<a href="#">c2od5A_</a>	 Alignment		7.5	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative nucleic acid binding protein2 (jcvl_pep_1096688149193) from uncultured marine organism at 1.79 a3 resolution
10	<a href="#">c3dydB_</a>	 Alignment		7.1	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine aminotransferase; <b>PDBTitle:</b> human tyrosine aminotransferase
11	<a href="#">d2dyja1</a>	 Alignment		6.1	21	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Ribosome-binding factor A, RbfA <b>Family:</b> Ribosome-binding factor A, RbfA

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[c3pdxA](#)

Alignment



5.5

19

**PDB header:**transferase  
**Chain:** A: **PDB Molecule:**tyrosine aminotransferase;  
**PDBTitle:** crystal structural of mouse tyrosine aminotransferase