





















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1tqA_</a>	 Alignment		99.9	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ypqj; <b>PDBTitle:</b> crystal structure of protein ypqj from bacillus subtilis, pfam duf64
2	<a href="#">d1tqa_</a>	 Alignment		99.9	28	<b>Fold:</b> YutG-like <b>Superfamily:</b> YutG-like <b>Family:</b> YutG-like
3	<a href="#">d1rfza_</a>	 Alignment		99.9	23	<b>Fold:</b> YutG-like <b>Superfamily:</b> YutG-like <b>Family:</b> YutG-like
4	<a href="#">d1y9ia_</a>	 Alignment		99.9	20	<b>Fold:</b> YutG-like <b>Superfamily:</b> YutG-like <b>Family:</b> YutG-like
5	<a href="#">c1loiA_</a>	 Alignment		15.2	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic 3',5'-amp specific phosphodiesterase rd1; <b>PDBTitle:</b> n-terminal splice region of rat c-amp phosphodiesterase, 2 nmr, 7 structures
6	<a href="#">c2zxiC_</a>	 Alignment		12.9	28	<b>PDB header:</b> fad-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl <b>PDBTitle:</b> structure of aquifex aeolicus gida in the form ii crystal
7	<a href="#">c3cp8C_</a>	 Alignment		10.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl <b>PDBTitle:</b> crystal structure of gida from chlorobium tepidum
8	<a href="#">d1ctda_</a>	 Alignment		9.6	67	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
9	<a href="#">d2b6ca1</a>	 Alignment		7.9	0	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> BC3264-like
10	<a href="#">c3eeqB_</a>	 Alignment		7.4	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative cobalamin biosynthesis protein g <b>PDBTitle:</b> crystal structure of a putative cobalamin biosynthesis2 protein g homolog from sulfobolus solfataricus

11 [d3eeqa2](#)

Alignment



5.8

17

**Fold:**CbiG N-terminal domain-like  
**Superfamily:**CbiG N-terminal domain-like  
**Family:**CbiG N-terminal domain-like