

























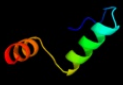


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P39354
Date	Thu Jan 5 11:59:43 GMT 2012
Unique Job ID	f79aa359a220a73a

Detailed template information

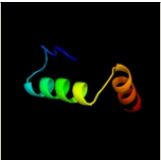
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2yugA</a>	 Alignment		14.3	22	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> protein frg1; <b>PDBTitle:</b> solution structure of mouse frg1 protein
2	<a href="#">d1dfca3</a>	 Alignment		12.9	20	<b>Fold:</b> beta-Trefoil <b>Superfamily:</b> Actin-crosslinking proteins <b>Family:</b> Fascin
3	<a href="#">d1ecfa1</a>	 Alignment		11.9	40	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
4	<a href="#">c1ecjB</a>	 Alignment		11.1	40	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamine phosphoribosylpyrophosphate <b>PDBTitle:</b> escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
5	<a href="#">c3sooB</a>	 Alignment		10.9	33	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> line-1 type transposase domain-containing protein 1; <b>PDBTitle:</b> crystal structure of a line-1 type transposase domain-containing2 protein 1 (l1td1) from homo sapiens at 2.73 a resolution
6	<a href="#">d1cgme</a>	 Alignment		10.7	11	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> TMV-like viral coat proteins <b>Family:</b> TMV-like viral coat proteins
7	<a href="#">d1gph11</a>	 Alignment		9.8	50	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
8	<a href="#">d1c0ma1</a>	 Alignment		9.6	33	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> DNA-binding domain of retroviral integrase <b>Family:</b> DNA-binding domain of retroviral integrase
9	<a href="#">c1gph1</a>	 Alignment		9.5	50	<b>PDB header:</b> transferase(glutamine amidotransferase) <b>Chain:</b> 1: <b>PDB Molecule:</b> glutamine phosphoribosyl-pyrophosphate amidotransferase; <b>PDBTitle:</b> structure of the allosteric regulatory enzyme of purine biosynthesis
10	<a href="#">d2vv5a1</a>	 Alignment		9.4	10	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Mechanosensitive channel protein MscS (YggB), middle domain
11	<a href="#">d1dfca1</a>	 Alignment		8.5	19	<b>Fold:</b> beta-Trefoil <b>Superfamily:</b> Actin-crosslinking proteins <b>Family:</b> Fascin

12	<a href="#">d1dfca2</a>	Alignment		7.5	22	<b>Fold:</b> beta-Trefoil <b>Superfamily:</b> Actin-crosslinking proteins <b>Family:</b> Fascin
13	<a href="#">c3aqbC_</a>	Alignment		6.2	45	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> component a of hexaprenyl diphosphate synthase; <b>PDBTitle:</b> m. luteus b-p 26 heterodimeric hexaprenyl diphosphate synthase in2 complex with magnesium
14	<a href="#">c2w0cC_</a>	Alignment		5.8	18	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> major capsid protein p2; <b>PDBTitle:</b> x-ray structure of the entire lipid-containing2 bacteriophage pm2
15	<a href="#">d1qopa_</a>	Alignment		5.6	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
16	<a href="#">c3navB_</a>	Alignment		5.6	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961

17

[c2ekcA](#)

Alignment



5.5

23

**PDB header:**lyase  
**Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain;  
**PDBTitle:** structural study of project id aq\_1548 from aquifex  
aeolicus vf5