
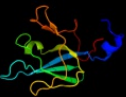



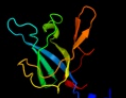




















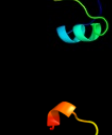


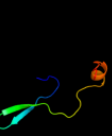
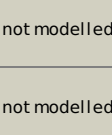


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1pxfa_</a>	 Alignment		100.0	100	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
2	<a href="#">c2cwpA_</a>	 Alignment		100.0	32	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> metrs related protein; <b>PDBTitle:</b> crystal structure of metrs related protein from pyrococcus horikoshii
3	<a href="#">d1pyba_</a>	 Alignment		100.0	28	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
4	<a href="#">d1gd7a_</a>	 Alignment		100.0	33	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
5	<a href="#">c2q2iA_</a>	 Alignment		100.0	30	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> secretion chaperone; <b>PDBTitle:</b> crystal structure of the protein secretion chaperone csaa from2 agrobacterium tumefaciens.
6	<a href="#">d1fl0a_</a>	 Alignment		100.0	37	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
7	<a href="#">d1mkha_</a>	 Alignment		100.0	49	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
8	<a href="#">d1ntga_</a>	 Alignment		100.0	43	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
9	<a href="#">c2nzoD_</a>	 Alignment		100.0	27	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> protein csaa; <b>PDBTitle:</b> crystal structure of a secretion chaperone csaa from bacillus subtilis2 in the space group p 32 2 1
10	<a href="#">c3bu2B_</a>	 Alignment		99.9	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative trna-binding protein; <b>PDBTitle:</b> crystal structure of a trna-binding protein from2 staphylococcus saprophyticus subsp. saprophyticus.3 northeast structural genomics consortium target syr77
11	<a href="#">c3pc0D_</a>	 Alignment		99.9	29	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> phenylalanyl-trna synthetase, beta chain; <b>PDBTitle:</b> crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp

12	<a href="#">c2e8gB_</a>	Alignment		99.9	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ph0536; <b>PDBTitle:</b> the structure of protein from p. horikoshii at 1.7 angstrom2 resolution
13	<a href="#">d1jjcb3</a>	Alignment		99.9	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
14	<a href="#">c2akwB_</a>	Alignment		99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> crystal structure of t.thermophilus phenylalanyl-trna synthetase2 complexed with p-cl-phenylalanine
15	<a href="#">c2rhsB_</a>	Alignment		99.7	28	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
16	<a href="#">c3l4gL_</a>	Alignment		89.2	7	<b>PDB header:</b> ligase <b>Chain:</b> L: <b>PDB Molecule:</b> phenylalanyl-trna synthetase beta chain; <b>PDBTitle:</b> crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
17	<a href="#">d1jjcb1</a>	Alignment		15.2	21	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Domains B1 and B5 of PheRS-beta, PheT
18	<a href="#">d1vjna_</a>	Alignment		10.6	21	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Hypothetical protein TM0207
19	<a href="#">c2fhdA_</a>	Alignment		8.3	19	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rhp9/crb2; <b>PDBTitle:</b> crystal structure of crb2 tandem tudor domains
20	<a href="#">d1qmga2</a>	Alignment		6.8	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
21	<a href="#">d2gyci1</a>	Alignment	not modelled	6.6	16	<b>Fold:</b> Ribosomal protein L14 <b>Superfamily:</b> Ribosomal protein L14 <b>Family:</b> Ribosomal protein L14
22	<a href="#">c3iz6D_</a>	Alignment	not modelled	6.3	26	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 40s ribosomal protein s4 (s4e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
23	<a href="#">c2xzmW_</a>	Alignment	not modelled	6.1	23	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> 40s ribosomal protein s4; <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
24	<a href="#">d1rbla2</a>	Alignment	not modelled	5.8	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RuBisCO, large subunit, small (N-terminal) domain <b>Family:</b> Ribulose 1,5-bisphosphate carboxylase-oxygenase
25	<a href="#">c3si5X_</a>	Alignment	not modelled	5.6	20	<b>PDB header:</b> cell cycle <b>Chain:</b> X: <b>PDB Molecule:</b> protein casc5; <b>PDBTitle:</b> kinetochore-bubr1 kinase complex