
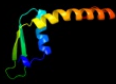


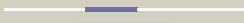
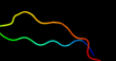

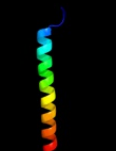




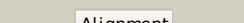
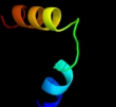










#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlavqa_	 Alignment		100.0	96	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: lambda exonuclease
2	c3k93A_	 Alignment		97.4	20	PDB header: hydrolase Chain: A: PDB Molecule: phage related exonuclease; PDBTitle: crystal structure of phage related exonuclease (yp_719632.1) from <i>Haemophilus somnus</i> 129pt at 2.15 Å resolution
3	dljbja2	 Alignment		15.8	24	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
4	d2gtsa1	 Alignment		14.0	15	Fold: Ferritin-like Superfamily: HP0062-like Family: HP0062-like
5	c1zawU_	 Alignment		10.5	15	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
6	c1zawW_	 Alignment		10.5	15	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
7	dlzavu1	 Alignment		10.5	15	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
8	c1zaxU_	 Alignment		10.5	15	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
9	c1zavU_	 Alignment		10.5	15	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
10	c1zaxW_	 Alignment		10.2	15	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
11	c1zavV_	 Alignment		10.0	15	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21

12	c1zaxV_	Alignment		10.0	15	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
13	c1zavW_	Alignment		9.7	15	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
14	c1zavV_	Alignment		8.7	15	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
15	c1dd3D_	Alignment		8.6	15	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of ribosomal protein l12 from thermotoga maritima
16	c1dd3C_	Alignment		8.6	15	PDB header: ribosome Chain: C: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of ribosomal protein l12 from thermotoga maritima
17	c2ktlA_	Alignment		8.2	19	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: structure of c-terminal domain from mtyrrs of a. nidulans
18	dlqzfa2	Alignment		7.7	50	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
19	dldd4c_	Alignment		6.4	15	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
20	dlj3kc_	Alignment		5.6	50	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
21	c1p9iA_	Alignment	not modelled	5.3	27	PDB header: unknown function Chain: A: PDB Molecule: cortexillin i/gcn4 hybrid peptide; PDBTitle: coiled-coil x-ray structure at 1.17 a resolution