



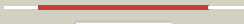

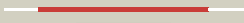




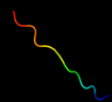

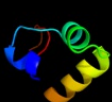







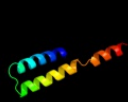


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qamn1	 Alignment		100.0	100	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17
2	c3bboP_	 Alignment		100.0	45	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein l17; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
3	d2zjrk1	 Alignment		100.0	52	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17
4	d1gd8a_	 Alignment		100.0	53	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17
5	d2cqma1	 Alignment		100.0	34	Fold: Prokaryotic ribosomal protein L17 Superfamily: Prokaryotic ribosomal protein L17 Family: Prokaryotic ribosomal protein L17
6	c3h0dB_	 Alignment		19.3	50	PDB header: transcription/dna Chain: B: PDB Molecule: ctsr; PDBTitle: crystal structure of ctrs in complex with a 26bp dna duplex
7	d1xd7a_	 Alignment		15.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator Rrf2
8	d1o65a_	 Alignment		15.0	25	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: MOSC (MOCO sulphurase C-terminal) domain
9	c2op8A_	 Alignment		14.1	5	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
10	c2z99A_	 Alignment		13.5	26	PDB header: cell cycle Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of scpb from mycobacterium tuberculosis
11	c2ic6B_	 Alignment		13.3	23	PDB header: viral protein Chain: B: PDB Molecule: nucleocapsid protein; PDBTitle: the coiled-coil domain (residues 1-75) structure of the sin2 nombre virus nucleocapsid protein

12	c1x4qA_	Alignment		10.9	26	PDB header: rna binding protein Chain: A: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: solution structure of pwi domain in u4/u6 small nuclear2 ribonucleoprotein prp3(hprp3)
13	d1v66a_	Alignment		10.8	26	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
14	d1otfa_	Alignment		9.9	10	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
15	d1bjpa_	Alignment		8.9	14	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
16	c3ry0A_	Alignment		8.7	10	PDB header: isomerase Chain: A: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
17	c2qsgX_	Alignment		7.5	22	PDB header: dna binding protein/dna Chain: X: PDB Molecule: uv excision repair protein rad23; PDBTitle: crystal structure of rad4-rad23 bound to a uv-damaged dna
18	d2a7wa1	Alignment		7.2	14	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)
19	c2x4kB_	Alignment		6.8	5	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
20	c2a7wF_	Alignment		6.7	14	PDB header: hydrolase Chain: F: PDB Molecule: phosphoribosyl-atp pyrophosphatase; PDBTitle: crystal structure of phosphoribosyl-atp pyrophosphatase2 from chromobacterium violaceum (atcc 12472). nesg target3 cvr7
21	d1x3zb1	Alignment	not modelled	6.5	25	Fold: XPC-binding domain Superfamily: XPC-binding domain Family: XPC-binding domain
22	c2wb1J_	Alignment	not modelled	6.2	19	PDB header: transcription Chain: J: PDB Molecule: dna-directed rna polymerase rpo13 subunit; PDBTitle: the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
23	c3mb2G_	Alignment	not modelled	6.1	10	PDB header: isomerase Chain: G: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - alpha subunit; PDBTitle: kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
24	d2fufa1	Alignment	not modelled	6.1	41	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: The origin DNA-binding domain of SV40 T-antigen
25	c2p9xB_	Alignment	not modelled	6.1	50	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ph0832; PDBTitle: crystal structure of ph0832 from pyrococcus horikoshii ot3
26	c2ormA_	Alignment	not modelled	5.9	10	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase hp0924; PDBTitle: crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
27	c3n4dF_	Alignment	not modelled	5.7	5	PDB header: hydrolase Chain: F: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of cg10062 inactivated by(r)-oxirane-2-carboxylate
28	d1y6xa1	Alignment	not modelled	5.7	45	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases

						Family: HisE-like (PRA-PH)
29	d1mwwa_	<div><div></div>Alignment</div>	not modelled	5.2	10	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: Hypothetical protein HI1388.1
30	c3abfB_	<div><div></div>Alignment</div>	not modelled	5.2	15	PDB header: isomerase Chain: B; PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)