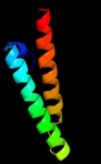
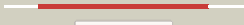
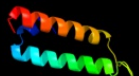
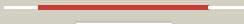
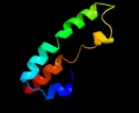
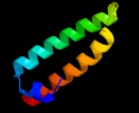
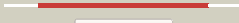
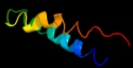
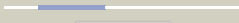
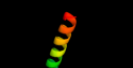
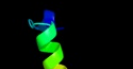
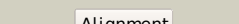
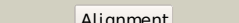
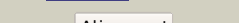
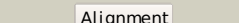


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1r73a_	 Alignment		99.9	44	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
2	d2zjrv1	 Alignment		99.9	38	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
3	c2j375_	 Alignment		99.9	32	PDB header: ribosome Chain: 5: PDB Molecule: ribosomal protein l35; PDBTitle: model of mammalian srp bound to 80s rncs
4	d2gycw1	 Alignment		99.9	100	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
5	d1vqov1	 Alignment		99.9	33	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
6	c2zkrv_	 Alignment		99.9	36	PDB header: ribosomal protein/rna Chain: V: PDB Molecule: rna expansion segment es9 part2; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
7	c3bboZ_	 Alignment		99.9	32	PDB header: ribosome Chain: Z: PDB Molecule: ribosomal protein l29; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
8	d2hgq11	 Alignment		99.9	39	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
9	c3jywX_	 Alignment		99.9	38	PDB header: ribosome Chain: X: PDB Molecule: 60s ribosomal protein l35; PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
10	c1sliX_	 Alignment		99.8	40	PDB header: ribosome Chain: X: PDB Molecule: 60s ribosomal protein l35; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1sli,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
11	c4a1eU_	 Alignment		99.7	29	PDB header: ribosome Chain: U: PDB Molecule: rpl35; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1

12	d2j0121	 Alignment		99.3	39	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
13	c2a8vA_	 Alignment		26.0	38	PDB header: protein/rna Chain: A: PDB Molecule: rna binding domain of rho transcription PDBTitle: rho transcription termination factor/rna complex
14	c2hv8D_	 Alignment		21.0	26	PDB header: protein transport Chain: D: PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of gtp-bound rab11 in complex with fip3
15	c2o1sC_	 Alignment		18.0	26	PDB header: transferase Chain: C: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from2 escherichia coli
16	d1gjjA2	 Alignment		14.9	25	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
17	d1xwya1	 Alignment		13.9	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
18	c2o1xA_	 Alignment		12.9	27	PDB header: transferase Chain: A: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from2 deinococcus radiodurans
19	c2xusA_	 Alignment		11.7	19	PDB header: protein binding Chain: A: PDB Molecule: breast cancer metastasis-suppressor 1; PDBTitle: crystal structure of the brms1 n-terminal region
20	c1sy9B_	 Alignment		11.2	42	PDB header: calcium-binding protein Chain: B: PDB Molecule: cyclic-nucleotide-gated olfactory channel; PDBTitle: structure of calmodulin complexed with a fragment of the2 olfactory cng channel
21	c1envA_	 Alignment	not modelled	11.0	26	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 envelope protein chimera consisting of a fragment of PDBTitle: atomic structure of the ectodomain from hiv-1 gp41
22	c1gcmC_	 Alignment	not modelled	10.9	25	PDB header: transcription regulation Chain: C: PDB Molecule: gcn4p-ii; PDBTitle: gcn4 leucine zipper core mutant p-li
23	d2odgc1	 Alignment	not modelled	10.8	31	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
24	c2rg8A_	 Alignment	not modelled	9.4	16	PDB header: apoptosis, translation Chain: A: PDB Molecule: programmed cell death protein 4; PDBTitle: crystal structure of programmed for cell death 4 middle ma32 domain
25	d1jeia_	 Alignment	not modelled	8.5	36	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
26	c1kd8E_	 Alignment	not modelled	8.3	22	PDB header: de novo protein Chain: E: PDB Molecule: gcn4 acid base heterodimer base- d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16v base-d12la16l
27	c1j1eB_	 Alignment	not modelled	6.9	17	PDB header: contractile protein Chain: B: PDB Molecule: troponin t; PDBTitle: crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
28	d1r8ja1	 Alignment	not modelled	6.8	15	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain

29	c1ce9C_	Alignment	not modelled	6.6	35	PDB header: helix capping Chain: C: PDB Molecule: protein (gcn4-pmse); PDBTitle: helix capping in the gcn4 leucine zipper
30	c1ce9A_	Alignment	not modelled	6.6	35	PDB header: helix capping Chain: A: PDB Molecule: protein (gcn4-pmse); PDBTitle: helix capping in the gcn4 leucine zipper
31	c1ce9B_	Alignment	not modelled	6.6	35	PDB header: helix capping Chain: B: PDB Molecule: protein (gcn4-pmse); PDBTitle: helix capping in the gcn4 leucine zipper
32	c1ce9D_	Alignment	not modelled	6.6	35	PDB header: helix capping Chain: D: PDB Molecule: protein (gcn4-pmse); PDBTitle: helix capping in the gcn4 leucine zipper
33	d1dd3a1	Alignment	not modelled	6.2	17	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
34	c2wq2A_	Alignment	not modelled	6.2	13	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4 leucine zipper mutant with three ixnntx motifs2 coordinating iodide
35	c3czqA_	Alignment	not modelled	6.1	19	PDB header: transferase Chain: A: PDB Molecule: putative polyphosphate kinase 2; PDBTitle: crystal structure of putative polyphosphate kinase 2 from2 sinorhizobium meliloti
36	d1ov9a_	Alignment	not modelled	6.1	35	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
37	d1sv1a_	Alignment	not modelled	6.0	15	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
38	d2a1ja1	Alignment	not modelled	6.0	23	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
39	c2wq0A_	Alignment	not modelled	5.9	13	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4 leucine zipper mutant with three ixnntx motifs2 coordinating chloride
40	d1hf8a1	Alignment	not modelled	5.8	17	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: Phosphoinositide-binding clathrin adaptor, domain 2
41	d1hljs_	Alignment	not modelled	5.8	19	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
42	d2oa5a1	Alignment	not modelled	5.7	32	Fold: BLRF2-like Superfamily: BLRF2-like Family: BLRF2-like
43	c2kztA_	Alignment	not modelled	5.7	16	PDB header: apoptosis Chain: A: PDB Molecule: programmed cell death protein 4; PDBTitle: structure of the tandem ma-3 region of pdcd4
44	d1zrja1	Alignment	not modelled	5.6	38	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
45	d1hx8a1	Alignment	not modelled	5.3	30	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: Phosphoinositide-binding clathrin adaptor, domain 2
46	c2outA_	Alignment	not modelled	5.1	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mu-like prophage flumu protein gp35, protein PDBTitle: solution structure of hi1506, a novel two domain protein2 from haemophilus influenzae
47	c1gcmB_	Alignment	not modelled	5.1	26	PDB header: transcription regulation Chain: B: PDB Molecule: gcn4p-ii; PDBTitle: gcn4 leucine zipper core mutant p-li
48	c3layF_	Alignment	not modelled	5.1	14	PDB header: metal binding protein Chain: F: PDB Molecule: zinc resistance-associated protein; PDBTitle: alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
49	c2jo8B_	Alignment	not modelled	5.1	35	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase 4; PDBTitle: solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)