

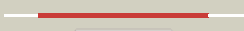
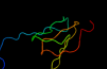

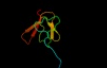



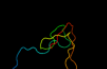

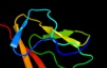













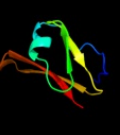
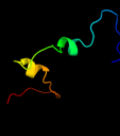






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fin0_	 Alignment		100.0	60	PDB header: ribosome Chain: 0: PDB Molecule: 50s ribosomal protein l27; PDBTitle: t. thermophilus 70s ribosome in complex with mrna, trnas2 and ef-tu.gdp.kirromycin ternary complex, fitted to a 6.43 a cryo-em map. this file contains the 50s subunit.
2	d2gycu1	 Alignment		100.0	100	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: Ribosomal L27 protein
3	d2zjrt1	 Alignment		100.0	71	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: Ribosomal L27 protein
4	c3bboX_	 Alignment		100.0	61	PDB header: ribosome Chain: X: PDB Molecule: ribosomal protein l27; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
5	c2ftcO_	 Alignment		100.0	44	PDB header: ribosome Chain: O: PDB Molecule: mitochondrial 39s ribosomal protein l27; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
6	d1v8qa_	 Alignment		100.0	52	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: Ribosomal L27 protein
7	d2ba0a2	 Alignment		94.0	17	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
8	d2je6i2	 Alignment		93.0	9	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
9	d2nn6h2	 Alignment		91.5	32	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
10	c2ba1B_	 Alignment		86.2	26	PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core
11	c2nn6H_	 Alignment		86.0	32	PDB header: hydrolase/transferase Chain: H: PDB Molecule: exosome complex exonuclease rrp4; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40

12	d2nn6i2	Alignment		83.6	13	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
13	c2nn6G_	Alignment		82.5	16	PDB header: hydrolase/transferase Chain: G: PDB Molecule: exosome complex exonuclease rrp40; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
14	c2nn6l_	Alignment		80.0	13	PDB header: hydrolase/transferase Chain: I: PDB Molecule: 3'-5' exoribonuclease csl4 homolog; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
15	c2ba0A_	Alignment		67.1	17	PDB header: rna binding protein Chain: A: PDB Molecule: archeal exosome rna binding protein rrp4; PDBTitle: archaeal exosome core
16	c2aukA_	Alignment		36.3	22	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
17	c2yyoA_	Alignment		35.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: spry domain-containing protein 3; PDBTitle: crystal sturcture of human spry domain
18	c2b44A_	Alignment		34.4	19	PDB header: hydrolase Chain: A: PDB Molecule: glycyl-glycine endopeptidase lytm; PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form
19	d1qwya_	Alignment		34.0	21	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Peptidoglycan hydrolase LytM
20	d1eyba_	Alignment		26.1	26	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Homogentisate dioxygenase
21	c1ey2A_	Alignment	not modelled	26.1	26	PDB header: oxidoreductase Chain: A: PDB Molecule: homogentisate 1,2-dioxygenase; PDBTitle: human homogentisate dioxygenase with fe(ii)
22	c3c8vA_	Alignment	not modelled	19.2	26	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure of putative acetyltransferase (yp_390128.1) from2 desulfovibrio desulfuricans g20 at 2.28 a resolution
23	c2jz2A_	Alignment	not modelled	15.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ssl0352 protein; PDBTitle: solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
24	c2cupA_	Alignment	not modelled	11.3	30	PDB header: metal binding protein Chain: A: PDB Molecule: skeletal muscle lim-protein 1; PDBTitle: solution structure of the skeletal muscle lim-protein 1
25	d1qpoa2	Alignment	not modelled	9.8	15	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
26	c2dn8A_	Alignment	not modelled	9.8	30	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
27	d2incc1	Alignment	not modelled	9.1	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: TmoB-like Family: TmoB-like
28	d2fsqa1	Alignment	not modelled	9.0	23	Fold: LigT-like Superfamily: LigT-like Family: Atu0111-like

29	c2je6l_	Alignment	not modelled	8.4	6	PDB header: hydrolase Chain: I: PDB Molecule: exosome complex rna-binding protein 1; PDBTitle: structure of a 9-subunit archaeal exosome
30	c2kytA_	Alignment	not modelled	8.2	29	PDB header: hydrolase Chain: A: PDB Molecule: group xvi phospholipase a2; PDBTitle: solution struture of the h-rev107 n-terminal domain
31	d1a6ca3	Alignment	not modelled	8.1	26	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
32	d1o4ua2	Alignment	not modelled	8.0	20	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
33	d1x3ha1	Alignment	not modelled	7.2	14	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
34	c3lazB_	Alignment	not modelled	6.1	42	PDB header: lyase Chain: B: PDB Molecule: d-galactarate dehydratase; PDBTitle: the crystal structure of the n-terminal domain of d-2 galactarate dehydratase from escherichia coli cft073
35	c3tbiB_	Alignment	not modelled	6.0	45	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain
36	c3nyyA_	Alignment	not modelled	5.9	22	PDB header: hydrolase Chain: A: PDB Molecule: putative glycyl-glycine endopeptidase lytm; PDBTitle: crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
37	c2l1sA_	Alignment	not modelled	5.7	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yohn; PDBTitle: yp_001336205.1
38	c3h41A_	Alignment	not modelled	5.7	20	PDB header: hydrolase Chain: A: PDB Molecule: nlp/p60 family protein; PDBTitle: crystal structure of a nlpc/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
39	d1qapa2	Alignment	not modelled	5.6	19	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
40	c3es1A_	Alignment	not modelled	5.5	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cupin 2, conserved barrel domain protein; PDBTitle: crystal structure of protein with a cupin-like fold and unknown2 function (yp_001165807.1) from novosphingobium aromaticivorans dsm3 12444 at 1.91 a resolution
41	d1ne9a1	Alignment	not modelled	5.3	13	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: FemXAB nonribosomal peptidyltransferases