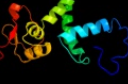
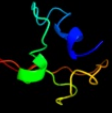
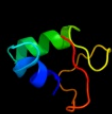
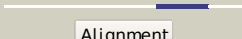
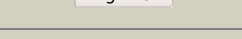
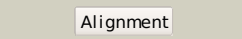
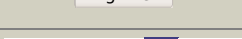


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xzmD_	 Alignment		100.0	63	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s4 containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
2	c3iz6C_	 Alignment		100.0	66	PDB header: ribosome Chain: C: PDB Molecule: 40s ribosomal protein s9 (s4p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
3	c1s1hD_	 Alignment		100.0	100	PDB header: ribosome Chain: D: PDB Molecule: 40s ribosomal protein s9-a; 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, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
4	d2uubd1	 Alignment		99.9	36	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
5	d2gy9d1	 Alignment		99.9	29	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
6	c3bbnD_	 Alignment		99.9	37	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s4; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
7	d1c06a_	 Alignment		99.8	33	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
8	c2cqiA_	 Alignment		99.8	28	PDB header: rna binding protein Chain: A: PDB Molecule: u3 small nucleolar ribonucleoprotein protein PDBTitle: solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
9	d1p9ka_	 Alignment		98.9	16	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: YbcJ-like
10	d1dm9a_	 Alignment		98.7	23	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kD
11	c1dm9A_	 Alignment		98.7	23	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka PDBTitle: heat shock protein 15 kd

12	c3hp7A_	Alignment		98.6	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hemolysin, putative; PDBTitle: putative hemolysin from streptococcus thermophilus.
13	d1vioa2	Alignment		98.6	22	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
14	c2k6pA_	Alignment		98.1	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein hp_1423; PDBTitle: solution structure of hypothetical protein, hp1423
15	c1kskA_	Alignment		97.8	21	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: structure of rsua
16	c1vioA_	Alignment		97.7	19	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: crystal structure of pseudouridylylase synthase
17	d1h3fa2	Alignment		97.7	23	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
18	d1jh3a_	Alignment		97.7	18	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
19	c3dh3C_	Alignment		97.7	16	PDB header: isomerase/rna Chain: C: PDB Molecule: ribosomal large subunit pseudouridine synthase f; PDBTitle: crystal structure of rluf in complex with a 22 nucleotide2 rna substrate
20	c1h3eA_	Alignment		97.6	22	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-tRNA synthetase; PDBTitle: tyrosyl-tRNA synthetase from thermus thermophilus complexed2 with wild-type trnatyr(gua) and with atp and tyrosinol
21	c2janD_	Alignment	not modelled	97.4	18	PDB header: ligase Chain: D: PDB Molecule: tyrosyl-tRNA synthetase; PDBTitle: tyrosyl-tRNA synthetase from mycobacterium tuberculosis in2 unliganded state
22	c3kbgA_	Alignment	not modelled	94.4	19	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s4e; PDBTitle: crystal structure of the 30s ribosomal protein s4e from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar28.
23	c3iz6D_	Alignment	not modelled	93.6	16	PDB header: ribosome Chain: D: PDB Molecule: 40s ribosomal protein s4 (s4e); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
24	c2xzmW_	Alignment	not modelled	92.7	12	PDB header: ribosome Chain: W: PDB Molecule: 40s ribosomal protein s4; PDBTitle: 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
25	c3izbD_	Alignment	not modelled	92.6	18	PDB header: ribosome Chain: D: PDB Molecule: 40s ribosomal protein rps4 (s4e); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
26	c2ktlA_	Alignment	not modelled	75.6	16	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-tRNA synthetase; PDBTitle: structure of c-terminal domain from mtttyrs of a. nidulans
27	c2eh0A_	Alignment	not modelled	63.5	18	PDB header: transport protein Chain: A: PDB Molecule: kinesin-like protein kif1b; PDBTitle: solution structure of the fha domain from human kinesin-2 like protein kif1b
						Fold: Alpha-L RNA-binding motif

28	d1kska3	Alignment	not modelled	35.0	22	Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
29	c2rohA	Alignment	not modelled	29.5	7	PDB header: dna binding protein Chain: A: PDB Molecule: telomere binding protein-1; PDBTitle: the dna binding domain of rtbp1
30	c2pjwV	Alignment	not modelled	28.4	20	PDB header: endocytosis/exocytosis Chain: V: PDB Molecule: vacuolar protein sorting-associated protein 27; PDBTitle: the vps27/hse1 complex is a gat domain-based scaffold for2 ubiquitin-dependent sorting
31	d2nn4a1	Alignment	not modelled	16.0	24	Fold: YqqQ-like Superfamily: YqqQ-like Family: YqqQ-like
32	c3rpfC	Alignment	not modelled	13.6	13	PDB header: transferase Chain: C: PDB Molecule: molybdopterin converting factor, subunit 1 (moad); PDBTitle: protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
33	d1dgsa1	Alignment	not modelled	13.1	37	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
34	d1nd9a	Alignment	not modelled	12.0	13	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: N-terminal subdomain of bacterial translation initiation factor IF2
35	d2v9va2	Alignment	not modelled	12.0	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
36	d2dkla1	Alignment	not modelled	10.9	24	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
37	d1gxla	Alignment	not modelled	10.5	7	Fold: Smc hinge domain Superfamily: Smc hinge domain Family: Smc hinge domain
38	d1gxja	Alignment	not modelled	9.8	5	Fold: Smc hinge domain Superfamily: Smc hinge domain Family: Smc hinge domain
39	c2kd2A	Alignment	not modelled	9.5	13	PDB header: apoptosis Chain: A: PDB Molecule: fas apoptotic inhibitory molecule 1; PDBTitle: nmr structure of faim-ctd
40	d1uila	Alignment	not modelled	9.3	20	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
41	c3e02A	Alignment	not modelled	8.8	15	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
42	c2jqlA	Alignment	not modelled	8.7	9	PDB header: cell cycle Chain: A: PDB Molecule: dna damage response protein kinase dun1; PDBTitle: nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1
43	c2juhA	Alignment	not modelled	8.2	11	PDB header: nuclear protein Chain: A: PDB Molecule: telomere binding protein tbp1; PDBTitle: solution structure of dna binding domain of ngtrf1
44	d2paja1	Alignment	not modelled	8.0	8	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: SAH/MTA deaminase-like
45	c3lotC	Alignment	not modelled	7.7	11	PDB header: structure genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
46	d2g1la1	Alignment	not modelled	7.5	17	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
47	d1vqop1	Alignment	not modelled	7.4	19	Fold: Ribosomal protein L19 (L19e) Superfamily: Ribosomal protein L19 (L19e) Family: Ribosomal protein L19 (L19e)
48	c3dwmA	Alignment	not modelled	7.3	17	PDB header: transferase Chain: A: PDB Molecule: 9.5 kda culture filtrate antigen cfp10a; PDBTitle: crystal structure of mycobacterium tuberculosis cyso, an antigen
49	d2pifa1	Alignment	not modelled	7.0	15	Fold: PSTPO5379-like Superfamily: PSTPO5379-like Family: PSTPO5379-like
50	c3iz5T	Alignment	not modelled	6.9	26	PDB header: ribosome Chain: T: PDB Molecule: 60s ribosomal protein l19 (l19e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of tritium aestivum translating 80s ribosome
51	d1v8ca1	Alignment	not modelled	6.9	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
52	c2xb0X	Alignment	not modelled	6.7	29	PDB header: hydrolase Chain: X: PDB Molecule: chromo domain-containing protein 1; PDBTitle: dna-binding domain from saccharomyces cerevisiae chromatin-2 remodelling protein chd1
53	c3e49A	Alignment	not modelled	6.7	17	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849 with a tim barrel fold; PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bx_e_c0966) from

						burkholderia xenovorans lb4003 at 1.75 a resolution
54	c3chvA_	 Alignment	not modelled	6.7	11	PDB header: metal binding protein Chain: A: PDB Molecule: prokaryotic domain of unknown function (dof849) with a tim PDBTitle: crystal structure of a prokaryotic domain of unknown function (dof849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
55	c3no5C_	 Alignment	not modelled	6.7	9	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam dof849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
56	c1dgsB_	 Alignment	not modelled	6.6	37	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
57	c1yseA_	 Alignment	not modelled	6.5	16	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein satb1; PDBTitle: solution structure of the mar-binding domain of satb1
58	d1f0la1	 Alignment	not modelled	6.4	21	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Diphtheria toxin, C-terminal domain Family: Diphtheria toxin, C-terminal domain
59	c3clqC_	 Alignment	not modelled	6.4	30	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a conserved protein of unknown function from2 enterococcus faecalis v583
60	c2g1eA_	 Alignment	not modelled	6.2	8	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ta0895; PDBTitle: solution structure of ta0895
61	d2q4qa1	 Alignment	not modelled	6.0	8	Fold: MTH938-like Superfamily: MTH938-like Family: MTH938-like
62	c1v9pB_	 Alignment	not modelled	5.9	37	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
63	c2y7eA_	 Alignment	not modelled	5.9	11	PDB header: lyase Chain: A: PDB Molecule: 3-keto-5-aminoheptanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-aminoheptanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
64	d1wf0a_	 Alignment	not modelled	5.7	21	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
65	c2wd5A_	 Alignment	not modelled	5.7	21	PDB header: cell cycle Chain: A: PDB Molecule: structural maintenance of chromosomes protein 1a; PDBTitle: smc hinge heterodimer (mouse)
66	d2cp8a1	 Alignment	not modelled	5.7	31	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
67	d2cqga1	 Alignment	not modelled	5.6	13	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
68	c2owoA_	 Alignment	not modelled	5.6	17	PDB header: ligase/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
69	d2gl5a1	 Alignment	not modelled	5.5	13	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
70	c2gm2A_	 Alignment	not modelled	5.2	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
71	c3m9hB_	 Alignment	not modelled	5.2	26	PDB header: chaperone Chain: B: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain of the2 mycobacterium tuberculosis proteasomal atpase mpa