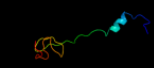
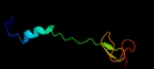
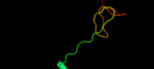
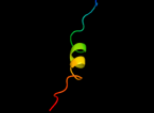
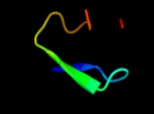
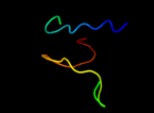
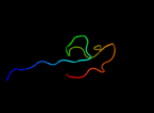
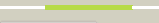
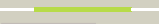
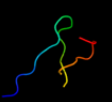
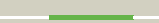
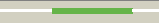
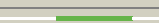
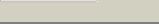
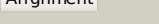
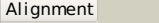
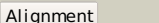
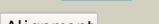


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qam01	 Alignment		100.0	100	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
2	d2zjr1	 Alignment		99.9	50	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
3	d2j0151	 Alignment		99.9	35	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
4	c3bbo2_	 Alignment		97.0	21	PDB header: ribosome Chain: 2: PDB Molecule: ribosomal protein l32; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
5	d2apob1	 Alignment		83.9	21	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
6	c2f9iD_	 Alignment		82.9	5	PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl PDBTitle: crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
7	d2ey4e1	 Alignment		81.1	16	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
8	d1hk8a_	 Alignment		78.9	17	Fold: PFL-like glycol radical enzymes Superfamily: PFL-like glycol radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit
9	c1hk8A_	 Alignment		78.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic ribonucleotide-triphosphate reductase; PDBTitle: structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
10	c1dvbA_	 Alignment		69.8	9	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
11	c2kdxA_	 Alignment		67.1	3	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein

12	d2f9yb1	 Alignment		64.9	9	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
13	c2f9yB_	 Alignment		64.9	9	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
14	c1i3ql_	 Alignment		64.5	17	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii 14.2kd PDBTitle: rna polymerase ii crystal form i at 3.1 a resolution
15	d2akla2	 Alignment		62.7	5	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
16	c2hr5B_	 Alignment		59.4	9	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
17	c2lcqA_	 Alignment		58.2	22	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
18	c1yuzB_	 Alignment		57.1	10	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
19	c2aklA_	 Alignment		56.7	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phna-like protein pa0128; PDBTitle: solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
20	d2gnra1	 Alignment		54.0	10	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: SSO2064-like
21	c3k7aM_	 Alignment	not modelled	53.5	12	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of an rna polymerase ii-tfiib complex
22	d1dl6a_	 Alignment	not modelled	52.9	10	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
23	d2k4xa1	 Alignment	not modelled	52.6	26	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
24	d2ct7a1	 Alignment	not modelled	52.6	7	Fold: RING/U-box Superfamily: RING/U-box Family: IBR domain
25	c3a44D_	 Alignment	not modelled	51.2	8	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
26	c2qkdA_	 Alignment	not modelled	44.4	20	PDB header: signaling protein, cell cycle Chain: A: PDB Molecule: zinc finger protein zpr1; PDBTitle: crystal structure of tandem zpr1 domains
27	d1pfta_	 Alignment	not modelled	38.4	21	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
28	c2gb5B_	 Alignment	not modelled	36.8	6	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
29	c3nn5B_	 Alignment	not modelled	32.8	10	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa

29	c3gnbB_	Alignment	not modelled	32.8	19	(ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
30	c3h0gl_	Alignment	not modelled	30.6	5	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
31	d1lkoa2	Alignment	not modelled	29.2	16	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
32	c3na7A_	Alignment	not modelled	26.2	10	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
33	c3mkrB_	Alignment	not modelled	25.5	13	PDB header: transport protein Chain: B: PDB Molecule: coatomer subunit alpha; PDBTitle: crystal structure of yeast alpha/epsilon-cop subcomplex of the cop12 vesicular coat
34	c3mv2A_	Alignment	not modelled	25.4	17	PDB header: protein transport Chain: A: PDB Molecule: coatomer subunit alpha; PDBTitle: crystal structure of a-cop in complex with e-cop
35	c3cngC_	Alignment	not modelled	24.8	29	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
36	c2zkr2_	Alignment	not modelled	24.4	23	PDB header: ribosomal protein/rna Chain: 2: PDB Molecule: 60s ribosomal protein l37e; 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
37	d1odha_	Alignment	not modelled	22.9	12	Fold: GCM domain Superfamily: GCM domain Family: GCM domain
38	d2g45a1	Alignment	not modelled	21.8	5	Fold: RING/U-box Superfamily: RING/U-box Family: Zf-UBP
39	c3jywY_	Alignment	not modelled	21.0	23	PDB header: ribosome Chain: Y: PDB Molecule: 60s ribosomal protein l37(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
40	cls1iY_	Alignment	not modelled	19.4	20	PDB header: ribosome Chain: Y: PDB Molecule: 60s ribosomal protein l37-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, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
41	d1nuia2	Alignment	not modelled	19.2	11	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger
42	d2vuti1	Alignment	not modelled	19.1	19	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
43	d2aqaa1	Alignment	not modelled	18.8	40	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
44	d1yuza2	Alignment	not modelled	18.8	11	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
45	c2k2dA_	Alignment	not modelled	18.7	8	PDB header: metal binding protein Chain: A: PDB Molecule: ring finger and chy zinc finger domain- PDBTitle: solution nmr structure of c-terminal domain of human pirh2.2 northeast structural genomics consortium (nesg) target ht2c
46	c3lpeF_	Alignment	not modelled	17.7	5	PDB header: transferase Chain: F: PDB Molecule: dna-directed rna polymerase subunit e''; PDBTitle: crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
47	d1d5ta2	Alignment	not modelled	17.2	40	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GDI-like
48	d2cona1	Alignment	not modelled	17.2	18	Fold: Rubredoxin-like Superfamily: NOB1 zinc finger-like Family: NOB1 zinc finger-like
49	c1x31D_	Alignment	not modelled	16.6	25	PDB header: oxidoreductase Chain: D: PDB Molecule: sarcosine oxidase delta subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
50	d2bcgg3	Alignment	not modelled	16.2	30	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GDI-like
51	c3bvoA_	Alignment	not modelled	15.9	12	PDB header: chaperone Chain: A: PDB Molecule: co-chaperone protein hscb, mitochondrial precursor; PDBTitle: crystal structure of human co-chaperone protein hscb
52	d1vqo11	Alignment	not modelled	15.2	14	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37e
53	c2y0fD_	Alignment	not modelled	15.1	5	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispq) from thermus thermophilus hb27
54	d2dloa1	Alignment	not modelled	14.5	18	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
						PDB header: hydrolase/dna

55	c2opfA_	Alignment	not modelled	14.2	6	Chain: A: PDB Molecule: endonuclease viii; PDBTitle: crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
56	c2nn6I_	Alignment	not modelled	13.7	11	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
57	c2ktvA_	Alignment	not modelled	13.3	32	PDB header: translation Chain: A: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: human erf1 c-domain, "open" conformer
58	c4a17Y_	Alignment	not modelled	13.2	11	PDB header: ribosome Chain: Y: PDB Molecule: rpl37a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
59	c2ba1B_	Alignment	not modelled	13.0	15	PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core
60	dlwgma_	Alignment	not modelled	13.0	3	Fold: RING/U-box Superfamily: RING/U-box Family: U-box
61	c2k5cA_	Alignment	not modelled	13.0	10	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein pf0385; PDBTitle: nmr structure for pf0385
62	c2ecvA_	Alignment	not modelled	12.9	13	PDB header: ligase Chain: A: PDB Molecule: tripartite motif-containing protein 5; PDBTitle: solution structure of the zinc finger, c3hc4 type (ring2 finger) domain of tripartite motif-containing protein 5
63	c3n40P_	Alignment	not modelled	12.7	19	PDB header: viral protein Chain: P: PDB Molecule: p62 envelope glycoprotein; PDBTitle: crystal structure of the immature envelope glycoprotein complex of2 chikungunya virus.
64	c2gviA_	Alignment	not modelled	12.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of a putative formylmethanofuran dehydrogenase2 subunit e (ta1109) from thermoplasma acidophilum at 1.87 a resolution
65	dlvqoz1	Alignment	not modelled	12.3	21	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
66	c2odxA_	Alignment	not modelled	12.2	8	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c oxidase polypeptide iv; PDBTitle: solution structure of zn(ii)cox4
67	dljj2y_	Alignment	not modelled	12.1	32	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
68	dlq1aa_	Alignment	not modelled	12.1	10	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
69	clyshD_	Alignment	not modelled	12.0	16	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
70	dlpfva3	Alignment	not modelled	12.0	6	Fold: Rubredoxin-like Superfamily: Methionyl-tRNA synthetase (MetRS), Zn-domain Family: Methionyl-tRNA synthetase (MetRS), Zn-domain
71	c2zkrz_	Alignment	not modelled	11.7	11	PDB header: ribosomal protein/rna Chain: Z: PDB Molecule: e site t-rna; 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
72	c1s1i9_	Alignment	not modelled	11.7	16	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; 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, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
73	c3jyw9_	Alignment	not modelled	11.3	16	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
74	c2qa4Z_	Alignment	not modelled	10.8	21	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
75	c3cc4Z_	Alignment	not modelled	10.7	21	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
76	c1u5kA_	Alignment	not modelled	10.7	8	PDB header: recombination,replication Chain: A: PDB Molecule: hypothetical protein; PDBTitle: recombinational repair protein reco
77	dl1v3a_	Alignment	not modelled	10.6	23	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Hypothetical zinc finger protein YacG
78	c3glsC_	Alignment	not modelled	10.5	0	PDB header: hydrolase Chain: C: PDB Molecule: nad-dependent deacetylase sirtuin-3, PDBTitle: crystal structure of human sirt3
79	c2joxA_	Alignment	not modelled	10.4	25	PDB header: transcription Chain: A: PDB Molecule: churchill protein; PDBTitle: embryonic neural inducing factor churchill is not a dna-2 binding zinc finger protein: solution structure reveals a3 solvent-

					exposed beta-sheet and zinc binuclear cluster Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA methyltransferase RlmA
80	d1p91a_	Alignment	not modelled	10.3	11
81	d1y0ja1	Alignment	not modelled	10.2	40
82	d1ffkw_	Alignment	not modelled	10.2	26
83	c2kreA_	Alignment	not modelled	10.0	9
84	c3noyA_	Alignment	not modelled	9.6	20
85	d1yc5a1	Alignment	not modelled	9.3	0
86	c1ee8A_	Alignment	not modelled	9.0	12
87	d1wiia_	Alignment	not modelled	8.9	7
88	c3d00A_	Alignment	not modelled	8.8	9
89	c2pziA_	Alignment	not modelled	8.8	11
90	c1vddC_	Alignment	not modelled	8.5	11
91	c2ecyA_	Alignment	not modelled	8.2	13
92	c1pqvS_	Alignment	not modelled	8.2	15
93	c1k82D_	Alignment	not modelled	8.1	6
94	d1k81a_	Alignment	not modelled	8.1	11
95	c1nnjA_	Alignment	not modelled	8.1	6
96	d1m2ka_	Alignment	not modelled	7.9	11
97	c1y1yS_	Alignment	not modelled	7.8	15
98	d6rxna_	Alignment	not modelled	7.7	11
99	d1hcna_	Alignment	not modelled	7.7	44