





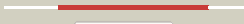

















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1kskA_	 Alignment		100.0	98	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: structure of rsua
2	c1vioA_	 Alignment		100.0	58	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: crystal structure of pseudouridylate synthase
3	c3dh3C_	 Alignment		100.0	28	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
4	d1kska4	 Alignment		100.0	98	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RluD
5	d1vioa1	 Alignment		100.0	66	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RluD
6	c2gmlA_	 Alignment		100.0	29	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase f; PDBTitle: crystal structure of catalytic domain of e.coli rluf
7	c2olwB_	 Alignment		100.0	35	PDB header: isomerase Chain: B: PDB Molecule: ribosomal large subunit pseudouridine synthase e; PDBTitle: crystal structure of e. coli pseudouridine synthase rlue
8	c2omlA_	 Alignment		100.0	35	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase e; PDBTitle: crystal structure of e. coli pseudouridine synthase rlue
9	d1v9ka_	 Alignment		100.0	22	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RluD
10	c1v9fA_	 Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: crystal structure of catalytic domain of pseudouridine2 synthase rlud from escherichia coli
11	d1v9fa_	 Alignment		100.0	22	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RluD

12	c2i82D_	Alignment		100.0	17	PDB header: lyase/rna Chain: D: PDB Molecule: ribosomal large subunit pseudouridine synthase a; PDBTitle: crystal structure of pseudouridine synthase rlua: indirect2 sequence readout through protein-induced rna structure
13	c1qyuA_	Alignment		100.0	23	PDB header: lyase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: structure of the catalytic domain of 23s rrna pseudouridine2 synthase rlud
14	d1vioa2	Alignment		99.2	34	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
15	c2k6pA_	Alignment		99.1	21	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein hp_1423; PDBTitle: solution structure of hypothetical protein, hp1423
16	c3bbnD_	Alignment		99.1	21	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s4; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
17	d1p9ka_	Alignment		99.0	21	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: YbcJ-like
18	d1dm9a_	Alignment		99.0	20	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kD
19	c1dm9A_	Alignment		99.0	20	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka PDBTitle: heat shock protein 15 kd
20	d1c06a_	Alignment		98.9	19	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
21	d2ey4a2	Alignment	not modelled	98.8	20	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
22	d2uubd1	Alignment	not modelled	98.7	27	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
23	c2cqjA_	Alignment	not modelled	98.6	19	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
24	d2apoa2	Alignment	not modelled	98.6	17	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
25	d1r3ea2	Alignment	not modelled	98.6	22	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
26	d2gy9d1	Alignment	not modelled	98.6	23	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
27	c2ey4A_	Alignment	not modelled	98.5	21	PDB header: isomerase/biosynthetic protein Chain: A: PDB Molecule: probable trna pseudouridine synthase b; PDBTitle: crystal structure of a cbf5-nop10-gar1 complex
28	d1k8wa5	Alignment	not modelled	98.3	20	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
29	c2apoA_	Alignment	not modelled	98.3	15	PDB header: isomerase/rna binding protein Chain: A: PDB Molecule: probable trna pseudouridine synthase b; PDBTitle: crystal structure of the methanococcus jannaschii cbf52

						nop10 complex
30	c1sgvA	Alignment	not modelled	98.3	21	PDB header: lyase Chain: A: PDB Molecule: trna pseudouridine synthase b; PDBTitle: structure of trna psi55 pseudouridine synthase (trub)
31	d1sgva2	Alignment	not modelled	98.2	21	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
32	d1kska3	Alignment	not modelled	98.2	98	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsaA N-terminal domain
33	c3uiaiA	Alignment	not modelled	98.1	16	PDB header: isomerase/chaperone Chain: A: PDB Molecule: h/aca ribonucleoprotein complex subunit 4; PDBTitle: structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
34	c1k8wA	Alignment	not modelled	98.1	18	PDB header: lyase/rna Chain: A: PDB Molecule: trna pseudouridine synthase b; PDBTitle: crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna
35	c3hp7A	Alignment	not modelled	97.9	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hemolysin, putative; PDBTitle: putative hemolysin from streptococcus thermophilus.
36	c1s1hD	Alignment	not modelled	97.8	19	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.
37	c2xzmD	Alignment	not modelled	97.6	15	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
38	d1jh3a	Alignment	not modelled	97.3	17	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
39	d1h3fa2	Alignment	not modelled	97.1	16	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
40	c1ze2B	Alignment	not modelled	96.9	27	PDB header: lyase/rna Chain: B: PDB Molecule: trna pseudouridine synthase b; PDBTitle: conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
41	c2janD	Alignment	not modelled	96.5	16	PDB header: ligase Chain: D: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
42	c1h3eA	Alignment	not modelled	96.3	16	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
43	c3iz6C	Alignment	not modelled	94.5	22	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
44	c3kbG	Alignment	not modelled	94.4	29	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.
45	c3iz6D	Alignment	not modelled	93.7	18	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
46	c2xzmW	Alignment	not modelled	93.1	15	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
47	c3izbD	Alignment	not modelled	92.1	14	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
48	d2g1la1	Alignment	not modelled	50.7	20	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
49	c2eh0A	Alignment	not modelled	48.8	17	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
50	c3fm8A	Alignment	not modelled	44.6	19	PDB header: transport protein/hydrolase activator Chain: A: PDB Molecule: kinesin-like protein kif13b; PDBTitle: crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
51	d1rwsa	Alignment	not modelled	44.4	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
52	c2jq1A	Alignment	not modelled	42.0	12	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
53	c3dwmA	Alignment	not modelled	34.5	22	PDB header: transferase Chain: A: PDB Molecule: 9.5 kda culture filtrate antigen cfp10a; PDBTitle: crystal structure of mycobacterium tuberculosis cyso, an

						antigen
54	c3rpfC_	Alignment	not modelled	32.6	7	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
55	c3hvyB_	Alignment	not modelled	30.6	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the tgs domain of the cleop_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
56	c2qjIA_	Alignment	not modelled	28.7	7	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin-related modifier 1; PDBTitle: crystal structure of urm1
57	d1xo3a_	Alignment	not modelled	28.7	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: C9orf74 homolog
58	d1fm0d_	Alignment	not modelled	28.3	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: Moad
59	d1wlna1	Alignment	not modelled	27.9	14	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
60	c2kmmA_	Alignment	not modelled	26.4	19	PDB header: hydrolase Chain: A: PDB Molecule: guanosine-3',5'-bis(diphosphate) 3'- PDBTitle: solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis, northeast structural genomics3 consortium target pgr122a (418-481)
61	c3po0A_	Alignment	not modelled	26.0	15	PDB header: protein binding Chain: A: PDB Molecule: small archaeal modifier protein 1; PDBTitle: crystal structure of samp1 from haloferax volcanii
62	d1vjka_	Alignment	not modelled	25.8	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: Moad
63	d1tkea1	Alignment	not modelled	20.4	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
64	c2g1eA_	Alignment	not modelled	19.2	7	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ta0895; PDBTitle: solution structure of ta0895
65	d1v8ca1	Alignment	not modelled	18.3	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: Moad
66	c2r9qD_	Alignment	not modelled	18.1	14	PDB header: hydrolase Chain: D: PDB Molecule: 2'-deoxycytidine 5'-triphosphate deaminase; PDBTitle: crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens
67	c2qieB_	Alignment	not modelled	17.4	28	PDB header: transferase Chain: B: PDB Molecule: molybdopterin synthase small subunit; PDBTitle: staphylococcus aureus molybdopterin synthase in complex2 with precursor z
68	c1v8cA_	Alignment	not modelled	17.2	23	PDB header: protein binding Chain: A: PDB Molecule: moad related protein; PDBTitle: crystal structure of moad related protein from thermus2 thermophilus hb8
69	d1zl0a1	Alignment	not modelled	17.1	15	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LD-carboxypeptidase A C-terminal domain-like Family: LD-carboxypeptidase A C-terminal domain-like
70	c2I52A_	Alignment	not modelled	17.0	11	PDB header: protein binding Chain: A: PDB Molecule: methanosarcina acetivorans samp1 homolog; PDBTitle: solution structure of the small archaeal modifier protein 1 (samp1)2 from methanosarcina acetivorans
71	d2ff4a3	Alignment	not modelled	17.0	28	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
72	d2affa1	Alignment	not modelled	16.6	16	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
73	c3poaA_	Alignment	not modelled	16.5	17	PDB header: peptide binding protein Chain: A: PDB Molecule: putative uncharacterized protein tb39.8; PDBTitle: structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
74	d1nyra2	Alignment	not modelled	16.4	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
75	d1wgka_	Alignment	not modelled	15.5	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: C9orf74 homolog
76	c3h7hA_	Alignment	not modelled	15.0	11	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt4; PDBTitle: crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
77	c3hx1B_	Alignment	not modelled	13.9	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: slr1951 protein; PDBTitle: crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a
78	c1mzwB_	Alignment	not modelled	13.9	31	PDB header: isomerase Chain: B: PDB Molecule: u4/u6 snrnp 60kda protein; PDBTitle: crystal structure of a u4/u6 snrnp complex between human2 spliceosomal cyclophilin h and a u4/u6-60k peptide

79	d1o48a_	Alignment	not modelled	13.6	10	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
80	d1j9ia_	Alignment	not modelled	13.6	19	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
81	d1xnea_	Alignment	not modelled	13.1	0	Fold: PUA domain-like Superfamily: PUA domain-like Family: ProFAR isomerase associated domain
82	d1wxqa2	Alignment	not modelled	12.8	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
83	c2qxxA_	Alignment	not modelled	11.7	15	PDB header: hydrolase Chain: A: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: bifunctional dctp deaminase: dtpase from mycobacterium tuberculosis2 in complex with dttp
84	d1f2fa_	Alignment	not modelled	11.5	9	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
85	c2kklA_	Alignment	not modelled	11.4	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mb1858; PDBTitle: solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
86	c2k9xA_	Alignment	not modelled	11.4	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of urm1 from trypanosoma brucei
87	d2hzab1	Alignment	not modelled	11.1	28	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
88	c2kd2A_	Alignment	not modelled	10.6	13	PDB header: apoptosis Chain: A: PDB Molecule: fas apoptotic inhibitory molecule 1; PDBTitle: nmr structure of faim-ctd
89	c1r21A_	Alignment	not modelled	9.8	16	PDB header: cell cycle Chain: A: PDB Molecule: antigen ki-67; PDBTitle: solution structure of human ki67 fha domain
90	d1zud21	Alignment	not modelled	9.7	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
91	c1z4hA_	Alignment	not modelled	8.9	24	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of2 atypical excisionase
92	d1dmza_	Alignment	not modelled	8.6	9	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
93	d1s04a_	Alignment	not modelled	8.6	14	Fold: PUA domain-like Superfamily: PUA domain-like Family: ProFAR isomerase associated domain
94	c2wwaj_	Alignment	not modelled	8.4	13	PDB header: ribosome Chain: J: PDB Molecule: 60s ribosomal protein l19; PDBTitle: cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
95	d1lgpa_	Alignment	not modelled	8.2	10	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
96	c2yujA_	Alignment	not modelled	7.9	11	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin fusion degradation 1-like; PDBTitle: solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
97	c1tygG_	Alignment	not modelled	7.9	17	PDB header: biosynthetic protein Chain: G: PDB Molecule: yjbs; PDBTitle: structure of the thiazole synthase/this complex
98	c2hj1A_	Alignment	not modelled	7.8	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
99	d2hj1a1	Alignment	not modelled	7.8	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: HI0395-like