







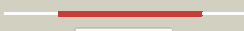








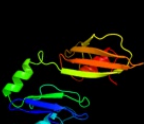

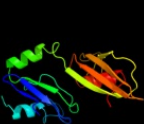









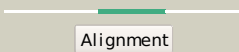
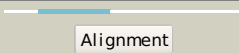
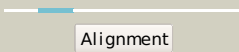
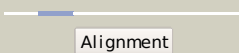
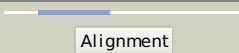
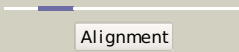
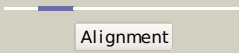
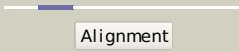


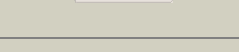
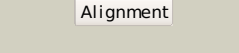
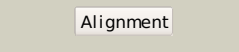
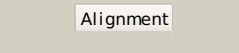

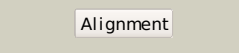
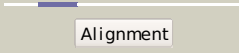



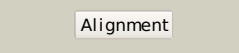
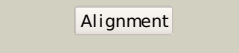

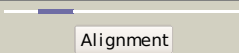
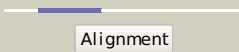
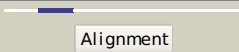


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dh3C_	 Alignment		100.0	31	PDB header: isomerase/rna Chain: C: PDB Molecule: ribosomal large subunit pseudouridine synthase f; PDBTitle: crystal structure of rluf in complex with a 22 nucleotide2 rna substrate
2	clvioA_	 Alignment		100.0	26	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: crystal structure of pseudouridylate synthase
3	clkskA_	 Alignment		100.0	30	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: structure of rsua
4	dlvioa1	 Alignment		100.0	28	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RluD
5	dlkska4	 Alignment		100.0	32	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RluD
6	c2gmlA_	 Alignment		100.0	30	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase f; PDBTitle: crystal structure of catalytic domain of e.coli rluf
7	c2omlA_	 Alignment		100.0	37	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase e; PDBTitle: crystal structure of e. coli pseudouridine synthase rlue
8	c2olwB_	 Alignment		100.0	36	PDB header: isomerase Chain: B: PDB Molecule: ribosomal large subunit pseudouridine synthase e; PDBTitle: crystal structure of e. coli pseudouridine synthase rlue
9	dlv9fa_	 Alignment		100.0	19	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/RluD
10	clv9fA_	 Alignment		100.0	19	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	c2i82D_	 Alignment		100.0	20	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

12	dlv9ka_	Alignment		100.0	17	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase RsuA/Rlud
13	clqyuA_	Alignment		100.0	18	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	dlvioa2	Alignment		99.1	25	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
15	d2ey4a2	Alignment		99.0	23	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
16	d2apoa2	Alignment		99.0	17	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
17	c2k6pA_	Alignment		99.0	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein hp_1423; PDBTitle: solution structure of hypothetical protein, hp1423
18	cldm9A_	Alignment		98.9	27	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka PDBTitle: heat shock protein 15 kd
19	dlldm9a_	Alignment		98.9	27	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kd
20	dlp9ka_	Alignment		98.9	26	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: YbcJ-like
21	c3bbnD_	Alignment	not modelled	98.9	16	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.
22	dlr3ea2	Alignment	not modelled	98.9	23	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
23	c2cqjA_	Alignment	not modelled	98.9	20	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	c2ey4A_	Alignment	not modelled	98.8	23	PDB header: isomerase/biosynthetic protein Chain: A: PDB Molecule: probable trna pseudouridine synthase b; PDBTitle: crystal structure of a cbf5-nop10-gar1 complex
25	dlk8wa5	Alignment	not modelled	98.8	23	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
26	c2apoA_	Alignment	not modelled	98.8	16	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
27	dlc06a_	Alignment	not modelled	98.7	20	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
28	clk8wA_	Alignment	not modelled	98.5	23	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

29	d2uubd1	Alignment	not modelled	98.5	28	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
30	c1sgvA	Alignment	not modelled	98.4	19	PDB header: lyase Chain: A: PDB Molecule: trna pseudouridine synthase b; PDBTitle: structure of trna psi55 pseudouridine synthase (trub)
31	d1sgva2	Alignment	not modelled	98.4	19	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase II TruB
32	c3uaiA	Alignment	not modelled	98.4	19	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
33	d2gy9d1	Alignment	not modelled	98.3	22	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
34	c3hp7A	Alignment	not modelled	97.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hemolysin, putative; PDBTitle: putative hemolysin from streptococcus thermophilus.
35	d1kska3	Alignment	not modelled	97.7	28	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
36	c1s1hD	Alignment	not modelled	97.6	16	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	c1ze2B	Alignment	not modelled	96.7	22	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
39	d1h3fa2	Alignment	not modelled	96.7	17	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
40	d1jh3a	Alignment	not modelled	96.3	28	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
41	c1h3eA	Alignment	not modelled	96.1	18	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
42	c2janD	Alignment	not modelled	95.3	22	PDB header: ligase Chain: D: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
43	c3kbgA	Alignment	not modelled	93.6	35	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.
44	c3iz6C	Alignment	not modelled	92.8	20	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
45	c3izbD	Alignment	not modelled	91.0	23	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
46	c3iz6D	Alignment	not modelled	91.0	26	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
47	c2xzmW	Alignment	not modelled	90.9	22	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
48	d2hzaa1	Alignment	not modelled	65.9	31	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
49	d2hzab1	Alignment	not modelled	64.6	31	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
50	c1q5vB	Alignment	not modelled	50.3	31	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
51	d2bj7a1	Alignment	not modelled	48.4	29	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
52	c3h7hA	Alignment	not modelled	47.7	20	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)
53	c2bj3D	Alignment	not modelled	47.3	29	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo

54	c2exuA	 Alignment	not modelled	40.3	20	PDB header: transcription Chain: A: PDB Molecule: transcription initiation protein spt4/spt5; PDBTitle: crystal structure of saccharomyces cerevisiae transcription elongation2 factors spt4-spt5nngn domain
55	d1d4ta	 Alignment	not modelled	32.1	18	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
56	c2ca9B	 Alignment	not modelled	30.9	23	PDB header: transcriptional regulation Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
57	c2ktiA	 Alignment	not modelled	24.6	32	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: structure of c-terminal domain from mtyrrs of a. nidulans
58	d1f2fa	 Alignment	not modelled	20.4	11	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
59	d2g1la1	 Alignment	not modelled	18.2	12	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
60	c3iz5w	 Alignment	not modelled	17.9	33	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l22 (l22e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
61	d1rwsa	 Alignment	not modelled	17.3	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
62	c2r9qD	 Alignment	not modelled	16.6	9	PDB header: hydrolase Chain: D: PDB Molecule: 2'-deoxycytidine 5'-triphosphate deaminase; PDBTitle: crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens
63	c2kmmA	 Alignment	not modelled	16.4	14	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)
64	c3hvvB	 Alignment	not modelled	15.6	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
65	d1o48a	 Alignment	not modelled	15.5	11	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
66	d1i3za	 Alignment	not modelled	15.0	22	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
67	d2cu3a1	 Alignment	not modelled	13.9	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
68	c1yj5C	 Alignment	not modelled	12.6	17	PDB header: transferase Chain: C: PDB Molecule: 5' polynucleotide kinase-3' phosphatase fha domain; PDBTitle: molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
69	d1tq5a1	 Alignment	not modelled	11.4	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Pirin-like
70	d1nyra2	 Alignment	not modelled	11.1	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
71	c1gxcA	 Alignment	not modelled	10.9	15	PDB header: phosphoprotein-binding domain Chain: A: PDB Molecule: serine/threonine-protein kinase chk2; PDBTitle: fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide
72	d1gxca	 Alignment	not modelled	10.9	15	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
73	d1tkea1	 Alignment	not modelled	10.8	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
74	c3po0A	 Alignment	not modelled	10.3	25	PDB header: protein binding Chain: A: PDB Molecule: small archaeal modifier protein 1; PDBTitle: crystal structure of samp1 from haloferax volcanii
75	c3izcw	 Alignment	not modelled	10.2	30	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein rpl22 (l22e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
76	d1fm0d	 Alignment	not modelled	10.2	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
77	c3mazA	 Alignment	not modelled	10.0	16	PDB header: signaling protein Chain: A: PDB Molecule: signal-transducing adaptor protein 1; PDBTitle: crystal structure of the human brdg1/stap-1 sh2 domain in complex with2 the ntal ptyr136 peptide
78	c3kt9A	 Alignment	not modelled	9.4	21	PDB header: hydrolase Chain: A: PDB Molecule: aprataxin; PDBTitle: aprataxin fha domain
79	d1fh5a	 Alignment	not modelled	9.3	13	Fold: SH2-like Superfamily: SH2 domain

					Family: SH2 domain
80	d1g6ga_	Alignment	not modelled	9.1	13 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
81	d1rpya_	Alignment	not modelled	9.1	27 Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
82	c1ka6A_	Alignment	not modelled	9.0	17 PDB header: immune system Chain: A: PDB Molecule: sh2 domain protein 1a; PDBTitle: sap/sh2d1a bound to peptide n-py
83	c1t6sB_	Alignment	not modelled	9.0	22 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of a conserved hypothetical protein from chlorobium2 tepidum
84	c2eh0A_	Alignment	not modelled	9.0	12 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
85	d1lgpa_	Alignment	not modelled	9.0	7 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
86	c1mzwB_	Alignment	not modelled	8.9	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
87	c2gsbA_	Alignment	not modelled	8.5	11 PDB header: signaling protein Chain: A: PDB Molecule: ras gtpase-activating protein 1; PDBTitle: solution structure of the second sh2 domain of human ras2 gtpase-activating protein 1
88	d1qcfa2	Alignment	not modelled	8.3	10 Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
89	d1vjka_	Alignment	not modelled	8.2	8 Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
90	d1t6sa2	Alignment	not modelled	8.1	22 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ScpB/YpuH-like
91	c2w1oA_	Alignment	not modelled	8.1	29 PDB header: translation Chain: A: PDB Molecule: 60s acidic ribosomal protein p2; PDBTitle: nmr structure of dimerization domain of human ribosomal2 protein p2
92	d1g3ga_	Alignment	not modelled	8.0	13 Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
93	c3b4sA_	Alignment	not modelled	7.5	29 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein luxt; PDBTitle: crystal structure of a luxt domain from vibrio2 parahaemolyticus rimd 2210633
94	c2qieB_	Alignment	not modelled	7.5	13 PDB header: transferase Chain: B: PDB Molecule: molybdopterin synthase small subunit; PDBTitle: staphylococcus aureus molybdopterin synthase in complex2 with precursor z
95	c2el8A_	Alignment	not modelled	7.4	9 PDB header: signaling protein Chain: A: PDB Molecule: signal-transducing adaptor protein 2; PDBTitle: solution structure of the human stap2 sh2 domain
96	c2ysxA_	Alignment	not modelled	7.1	9 PDB header: signaling protein Chain: A: PDB Molecule: signaling inositol polyphosphate phosphatase PDBTitle: solution structure of the human ship sh2 domain
97	d2exda1	Alignment	not modelled	7.0	25 Fold: OB-fold Superfamily: NfeD domain-like Family: NfeD domain-like
98	c2k5hA_	Alignment	not modelled	7.0	33 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
99	d1opka2	Alignment	not modelled	7.0	14 Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain