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Description	P0A7W1
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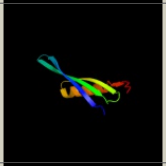
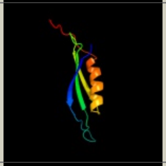
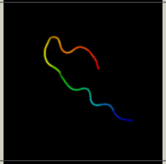
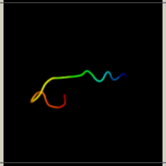
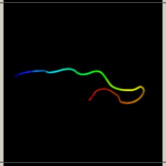
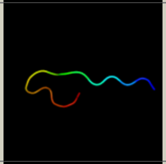
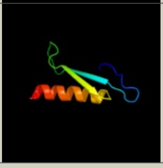
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bbnE_	Alignment		100.0	47	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**ribosomal protein s5; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
2	c1p6gE_	Alignment		100.0	100	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**30s ribosomal protein s5; **PDBTitle:** real space refined coordinates of the 30s subunit fitted2 into the low resolution cryo-em map of the ef-g.gtp state3 of e. coli 70s ribosome
3	c2ow8f_	Alignment		100.0	47	**PDB header:**ribosome **Chain:** F: **PDB Molecule:** **PDBTitle:** crystal structure of a 70s ribosome-trna complex reveals functional2 interactions and rearrangements. this file, 2ow8, contains the 30s3 ribosome subunit, two trna, and mrna molecules. 50s ribosome subunit4 is in the file 1vsa.
4	c2xzmE_	Alignment		100.0	29	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**ribosomal protein s5 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
5	c1eg0B_	Alignment		100.0	54	**PDB header:**ribosome **PDB COMPND:**
6	c2zkqe_	Alignment		100.0	29	**PDB header:**ribosomal protein/rna **Chain:** E: **PDB Molecule:**rna expansion segment es6 part ii; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
7	c1s1hE_	Alignment		100.0	31	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**40s ribosomal protein s2; **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.
8	c3izbE_	Alignment		100.0	30	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**40s ribosomal protein rps2 (s5p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
9	c3iz6E_	Alignment		100.0	33	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**40s ribosomal protein s2 (s5p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
10	d2qale1	Alignment		100.0	100	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
11	d2uube1	Alignment		100.0	41	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components

12	d1pkpa1	Alignment		99.9	51	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
13	d2uube2	Alignment		99.9	55	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Ribosomal S5 protein, N-terminal domain
14	d1pkpa2	Alignment		99.9	59	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Ribosomal S5 protein, N-terminal domain
15	d2qale2	Alignment		99.9	100	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Ribosomal S5 protein, N-terminal domain
16	d1p42a1	Alignment		58.3	47	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
17	c2go4A_	Alignment		54.3	47	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine **PDBTitle:** crystal structure of aquifex aeolicus lpxc complexed with tu-514
18	c3nzkB_	Alignment		51.9	40	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine **PDBTitle:** structure of lpxc from yersinia enterocolitica complexed with chir0902 inhibitor
19	c2vesA_	Alignment		50.3	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine **PDBTitle:** crystal structure of lpxc from pseudomonas aeruginosa2 complexed with the potent bb-78485 inhibitor
20	d2b7ta1	Alignment		49.0	22	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
21	d2nuga2	Alignment	not modelled	46.6	15	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
22	d2pifa1	Alignment	not modelled	46.5	22	**Fold:**PSTPO5379-like **Superfamily:**PSTPO5379-like **Family:**PSTPO5379-like
23	c3adjA_	Alignment	not modelled	43.1	21	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**f21m12.9 protein; **PDBTitle:** structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
24	d1x47a1	Alignment	not modelled	42.1	24	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
25	d2vapa2	Alignment	not modelled	41.7	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
26	d1stua_	Alignment	not modelled	40.5	18	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
27	d1qu6a2	Alignment	not modelled	40.1	19	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
28	d1w5fa2	Alignment	not modelled	39.2	36	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
29	d2b7va1	Alignment	not modelled	38.1	28	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like

						Family: Double-stranded RNA-binding domain (dsRBD)
30	c2ljhA_	Alignment	not modelled	37.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**double-stranded rna-specific editase adar; **PDBTitle:** nmr structure of double-stranded rna-specific editase adar
31	d1rq2a2	Alignment	not modelled	37.4	24	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
32	d1ofua2	Alignment	not modelled	34.2	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
33	d1o0wa2	Alignment	not modelled	33.9	25	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
34	c3adiC_	Alignment	not modelled	30.5	25	**PDB header:**gene regulation/rna **Chain:** C: **PDB Molecule:**f21m12.9 protein; **PDBTitle:** structure of arabidopsis hyl1 and its molecular implications for mirna2 processing
35	c2zqeA_	Alignment	not modelled	25.8	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2
36	d1bf4a_	Alignment	not modelled	24.2	26	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**"Histone-like" proteins from archaea
37	d1x48a1	Alignment	not modelled	23.4	24	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
38	d2dixa1	Alignment	not modelled	22.4	20	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
39	d1tzza2	Alignment	not modelled	21.5	26	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
40	c1t4oA_	Alignment	not modelled	21.4	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease iii; **PDBTitle:** crystal structure of rnt1p dsrbd
41	d1t4oa_	Alignment	not modelled	21.4	30	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
42	c3c4tA_	Alignment	not modelled	20.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoribonuclease dicer; **PDBTitle:** structure of rnaseiiib and dsrna binding domains of mouse dicer
43	d1sr9a3	Alignment	not modelled	20.3	15	**Fold:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain **Superfamily:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain **Family:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain
44	c2l3jA_	Alignment	not modelled	17.9	27	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**double-stranded rna-specific editase 1; **PDBTitle:** the solution structure of the adar2 dsrbm-rna complex reveals a2 sequence-specific read out of the minor groove
45	d1r4ca_	Alignment	not modelled	17.3	11	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cystatins
46	c2ch9A_	Alignment	not modelled	16.7	8	**PDB header:**inhibitor **Chain:** A: **PDB Molecule:**cystatin f; **PDBTitle:** crystal structure of dimeric human cystatin f
47	d2dmya1	Alignment	not modelled	15.8	17	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
48	d1bqga2	Alignment	not modelled	14.9	20	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
49	c2fkpC_	Alignment	not modelled	14.6	13	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**n-acylamino acid racemase; **PDBTitle:** the mutant g127c-t313c of deinococcus radiodurans n-2 acylamino acid racemase
50	d1uila_	Alignment	not modelled	14.5	16	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
51	d1wi9a_	Alignment	not modelled	14.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
52	c1yywB_	Alignment	not modelled	14.2	19	**PDB header:**hydrolase/rna **Chain:** B: **PDB Molecule:**ribonuclease iii; **PDBTitle:** crystal structure of rnase iii from aquifex aeolicus2 complexed with double stranded rna at 2.8-angstrom3 resolution
53	c3kk4B_	Alignment	not modelled	14.1	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bp1543; **PDBTitle:** uncharacterized protein bp1543 from bordetella pertussis tohama i
54	c3adlA_	Alignment	not modelled	14.0	19	**PDB header:**gene regulation/rna **Chain:** A: **PDB Molecule:**risc-loading complex subunit tarbp2; **PDBTitle:** structure of trbp2 and its molecule implications for mirna processing
55	d1r0ma2	Alignment	not modelled	13.7	12	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like

56	d1jpdx2	Alignment	not modelled	13.6	9	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
57	d1jdfa2	Alignment	not modelled	13.2	15	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
58	d1cewi_	Alignment	not modelled	13.2	5	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cystatins
59	d1nu5a2	Alignment	not modelled	12.9	15	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
60	c3llhB_	Alignment	not modelled	12.8	31	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**risc-loading complex subunit tarbp2; **PDBTitle:** crystal structure of the first dsrbd of tar rna-binding protein 2
61	d1kn0a_	Alignment	not modelled	12.7	20	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**The homologous-pairing domain of Rad52 recombinase
62	c1znnF_	Alignment	not modelled	12.2	19	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**plp synthase; **PDBTitle:** structure of the synthase subunit of plp synthase
63	d1znna1	Alignment	not modelled	12.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**PdxS-like
64	d1t4lb_	Alignment	not modelled	12.2	33	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
65	d1di2a_	Alignment	not modelled	11.8	23	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
66	c1w5fA_	Alignment	not modelled	11.8	36	**PDB header:**cell division **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz, t7 mutated, domain swapped (t. maritima)
67	d1uhza_	Alignment	not modelled	10.7	17	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
68	c1h2iG_	Alignment	not modelled	9.9	20	**PDB header:**dna-binding protein **Chain:** G: **PDB Molecule:**dna repair protein rad52 homolog; **PDBTitle:** human rad52 protein, n-terminal domain
69	d2cpna1	Alignment	not modelled	9.8	20	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
70	d2mnra2	Alignment	not modelled	9.6	21	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
71	d1iowa1	Alignment	not modelled	9.6	21	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
72	c1w59B_	Alignment	not modelled	9.4	20	**PDB header:**cell division **Chain:** B: **PDB Molecule:**cell division protein ftsz homolog 1; **PDBTitle:** ftsz dimer, empty (m. jannaschii)
73	d1x49a1	Alignment	not modelled	9.4	22	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
74	c2khxA_	Alignment	not modelled	9.4	26	**PDB header:**gene regulation,nuclear protein **Chain:** A: **PDB Molecule:**ribonuclease 3; **PDBTitle:** drosha double-stranded rna binding motif
75	d1t4na_	Alignment	not modelled	9.3	37	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
76	c3mwzA_	Alignment	not modelled	9.1	11	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**sialostatin l2; **PDBTitle:** crystal structure of the selenomethionine derivative of the l 22,47,2 100 m mutant of sialostatin l2
77	d2ux9a1	Alignment	not modelled	9.0	26	**Fold:**Dodecin subunit-like **Superfamily:**Dodecin-like **Family:**Dodecin-like
78	c3onrl_	Alignment	not modelled	9.0	15	**PDB header:**metal binding protein **Chain:** I: **PDB Molecule:**protein transport protein sece2; **PDBTitle:** crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
79	c2l2nA_	Alignment	not modelled	9.0	19	**PDB header:**rna binding protein, plant protein **Chain:** A: **PDB Molecule:**hyponastic leave 1; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for the first2 dsrbd of protein hyl1
80	c3oqtP_	Alignment	not modelled	8.9	26	**PDB header:**flavoprotein **Chain:** P: **PDB Molecule:**rv1498a protein; **PDBTitle:** crystal structure of rv1498a protein from mycobacterium tuberculosis
81	c3dfhC_	Alignment	not modelled	8.7	20	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**mandelate racemase; **PDBTitle:** crystal structure of putative mandelate racemase / muconate2 lactonizing enzyme from vibrionales bacterium swat-3
82	c2l33A_	Alignment	not modelled	8.7	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**interleukin enhancer-binding factor 3; **PDBTitle:** solution nmr structure of drbm 2 domain of interleukin enhancer-2 binding factor 3 from homo sapiens, northeast

						structural genomics3 consortium target hr4527e
83	c2rhoB_	Alignment	not modelled	8.5	22	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** synthetic gene encoded bacillus subtilis ftsz ncs dimer with2 bound gdp and gtp-gamma-s
84	c3l0rA_	Alignment	not modelled	8.5	17	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**cystatin-2; **PDBTitle:** crystal structure of salivary cystatin from the soft tick ornithodoros2 moubata
85	c1vz0B_	Alignment	not modelled	8.1	25	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**chromosome partitioning protein parb; chromosome segregation protein spo0j from thermus2 thermophilus
86	d2bv3a3	Alignment	not modelled	7.9	23	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
87	d1azpa_	Alignment	not modelled	7.8	28	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**"Histone-like" proteins from archaea
88	d1vz0a1	Alignment	not modelled	7.7	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
89	c2vxyA_	Alignment	not modelled	7.6	24	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** the structure of ftsz from bacillus subtilis at 1.7a2 resolution
90	c2vxaL_	Alignment	not modelled	7.5	12	**PDB header:**flavoprotein **Chain:** L: **PDB Molecule:**dodecin; **PDBTitle:** h.halophila dodecin in complex with riboflavin
91	c3n4fD_	Alignment	not modelled	7.3	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from geobacillus sp. y412mc10
92	c2vawA_	Alignment	not modelled	7.3	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz pseudomonas aeruginosa gdp
93	c1l0oC_	Alignment	not modelled	7.3	13	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**sigma factor; **PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
94	d1l0oc_	Alignment	not modelled	7.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
95	d1roaa_	Alignment	not modelled	7.1	15	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cystatins
96	d1ekza_	Alignment	not modelled	7.0	21	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
97	d1yeya2	Alignment	not modelled	6.8	12	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
98	c2ppgB_	Alignment	not modelled	6.7	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative isomerase; **PDBTitle:** crystal structure of putative isomerase from sinorhizobium meliloti
99	c2p88E_	Alignment	not modelled	6.7	15	**PDB header:**lyase **Chain:** E: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme **PDBTitle:** crystal structure of n-succinyl arg/lys racemase from2 bacillus cereus atcc 14579