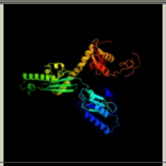
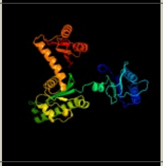
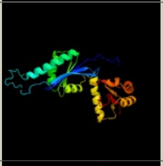
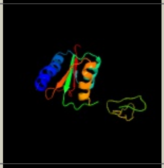
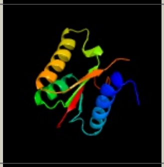
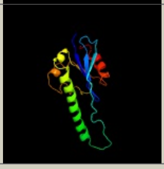
Email	mdejesus@rockefeller.edu
Description	RVBD2629_(-)_2955777_2956901
Date	Wed Aug 7 12:50:27 BST 2019
Unique Job ID	ed41dbb70651394d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4af1A_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** archeal release factor arf1
2	c1dt9A_	Alignment		100.0	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**protein (eukaryotic peptide chain release factor **PDBTitle:** the crystal structure of human eukaryotic release factor2 erf1-mechanism of stop codon recognition and peptidyl-trna3 hydrolysis
3	c4crnX_	Alignment		100.0	18	**PDB header:**translation **Chain:** X: **PDB Molecule:**erf1 in ribosome-bound erf1-erf3-gdpnp complex; **PDBTitle:** cryo-em of a pretermination complex with erf1 and erf3
4	c3agkA_	Alignment		100.0	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** crystal structure of archaeal translation termination factor, arf1
5	c3e1yD_	Alignment		100.0	19	**PDB header:**translation **Chain:** D: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** crystal structure of human erf1/erf3 complex
6	c3mcaB_	Alignment		100.0	12	**PDB header:**translation regulation/hydrolase **Chain:** B: **PDB Molecule:**protein dom34; **PDBTitle:** structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
7	c3agjD_	Alignment		100.0	18	**PDB header:**translation/hydrolase **Chain:** D: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
8	c3agjB_	Alignment		100.0	18	**PDB header:**translation/hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
9	c3j15A_	Alignment		100.0	20	**PDB header:**translation/transport protein **Chain:** A: **PDB Molecule:**protein pelota; **PDBTitle:** model of ribosome-bound archaeal pelota and abce1
10	c3e20C_	Alignment		99.9	21	**PDB header:**translation **Chain:** C: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** crystal structure of s.pombe erf1/erf3 complex
11	c3obwA_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of two archaeal pelotas reveal inter-domain2 structural plasticity

12	c2vgmA_	Alignment		99.9	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dom34; **PDBTitle:** structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
13	c3ir9A_	Alignment		99.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** c-terminal domain of peptide chain release factor from methanosarcina2 mazei.
14	c3obyB_	Alignment		99.9	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
15	d1dt9a2	Alignment		99.8	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
16	c2qi2A_	Alignment		99.8	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein pelota related protein; **PDBTitle:** crystal structure of the thermoplasma acidophilum pelota2 protein
17	c2ktvA_	Alignment		99.8	21	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** human erf1 c-domain, "open" conformer
18	c3e20H_	Alignment		99.7	26	**PDB header:**translation **Chain:** H: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** crystal structure of s.pombe erf1/erf3 complex
19	d1x52a1	Alignment		99.5	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
20	d1dt9a1	Alignment		99.5	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**ERF1/Dom34 middle domain-like
21	d2vgna3	Alignment	not modelled	99.5	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
22	d2qi2a3	Alignment	not modelled	99.3	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
23	d1dt9a3	Alignment	not modelled	99.0	11	**Fold:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 **Superfamily:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 **Family:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1
24	d2qi2a2	Alignment	not modelled	97.9	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**ERF1/Dom34 middle domain-like
25	d2vgna2	Alignment	not modelled	96.7	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**ERF1/Dom34 middle domain-like
26	c3on1A_	Alignment	not modelled	76.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2414 protein; **PDBTitle:** the structure of a protein with unknown function from bacillus2 halodurans c
27	c3v7qB_	Alignment	not modelled	73.0	12	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**probable ribosomal protein ylxq; **PDBTitle:** crystal structure of b. subtilis ylxq at 1.55 a resolution
28	d1t0kb_	Alignment	not modelled	71.0	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins

29	c3o85A_	Alignment	not modelled	67.4	11	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**ribosomal protein l7ae; **PDBTitle:** giardia lamblia 15.5kd rna binding protein
30	c2zkr6_	Alignment	not modelled	64.9	13	**PDB header:**ribosomal protein/rna **Chain:** 6: **PDB Molecule:**60s ribosomal protein l30e; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
31	c3zf7g_	Alignment	not modelled	64.5	17	**PDB header:**ribosome **Chain:** G: **PDB Molecule:** **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
32	c1dvbA_	Alignment	not modelled	63.5	8	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
33	c1yuzB_	Alignment	not modelled	62.7	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
34	c5ewrA_	Alignment	not modelled	59.5	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**box c/d snornp and u4 snrnp component snu13p; **PDBTitle:** c merolae u4 snrnp protein snu13
35	c4a1dG_	Alignment	not modelled	59.4	21	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**rpl30; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
36	c3cpqB_	Alignment	not modelled	58.6	11	**PDB header:**ribosomal protein **Chain:** B: **PDB Molecule:**50s ribosomal protein l30e; **PDBTitle:** crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044)
37	d1w41a1	Alignment	not modelled	58.3	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
38	d2bo1a1	Alignment	not modelled	56.1	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
39	c3v7eB_	Alignment	not modelled	56.0	20	**PDB header:**ribosomal protein/rna **Chain:** B: **PDB Molecule:**ribosome-associated protein l7ae-like; **PDBTitle:** crystal structure of ybxf bound to the sam-i riboswitch aptamer
40	c2hr5B_	Alignment	not modelled	55.1	21	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
41	c3j21Z_	Alignment	not modelled	53.3	13	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l30e; **PDBTitle:** promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
42	d1rlga_	Alignment	not modelled	52.2	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
43	d1vqof1	Alignment	not modelled	49.7	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
44	c3j3aM_	Alignment	not modelled	49.0	14	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**40s ribosomal protein s12; **PDBTitle:** structure of the human 40s ribosomal proteins
45	c3zeyF_	Alignment	not modelled	48.2	20	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**40s ribosomal protein s12; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
46	c5xyiM_	Alignment	not modelled	48.2	20	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**ribosomal protein l7ae, putative; **PDBTitle:** small subunit of trichomonas vaginalis ribosome
47	d1xbia1	Alignment	not modelled	45.3	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
48	d1gz0a2	Alignment	not modelled	45.2	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
49	d2alea1	Alignment	not modelled	43.5	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
50	d1jj2f_	Alignment	not modelled	40.5	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
51	c5xxuM_	Alignment	not modelled	40.1	24	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**ribosomal protein es12; **PDBTitle:** small subunit of toxoplasma gondii ribosome
52	d2ozba1	Alignment	not modelled	37.9	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
53	d1gz0f2	Alignment	not modelled	36.8	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
54	c2xznU_	Alignment	not modelled	35.4	17	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**ribosomal protein l7ae 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 2

55	d2czwa1	Alignment	not modelled	35.0	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
56	d2fc3a1	Alignment	not modelled	33.4	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
57	d2hyma2	Alignment	not modelled	30.6	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
58	c3j38M_	Alignment	not modelled	26.7	17	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**40s ribosomal protein s12; **PDBTitle:** structure of the d. melanogaster 40s ribosomal proteins
59	c2lbwA_	Alignment	not modelled	26.7	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 2; **PDBTitle:** solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant
60	c6hmsB_	Alignment	not modelled	25.8	17	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna polymerase ii large subunit,dna polymerase ii large **PDBTitle:** cryo-em map of dna polymerase d from pyrococcus abyssi in complex with2 dna
61	c4e0uB_	Alignment	not modelled	25.4	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cyclic dipeptide n-prenyltransferase; **PDBTitle:** crystal structure of cdpnpt in complex with thiolodiphosphate and (s)-2 benzodiazependione
62	d2gnra1	Alignment	not modelled	24.6	6	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
63	c1vddC_	Alignment	not modelled	23.3	16	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
64	c5wb4H_	Alignment	not modelled	22.6	5	**PDB header:**transferase **Chain:** H: **PDB Molecule:**n-acetylglucosaminyldiphosphoundecaprenol n-acetyl-beta-d- **PDBTitle:** crystal structure of the tara wall teichoic acid glycosyltransferase
65	c3mayE_	Alignment	not modelled	22.6	15	**PDB header:**heme-binding protein **Chain:** E: **PDB Molecule:**possible exported protein; **PDBTitle:** crystal structure of a secreted mycobacterium tuberculosis heme-2 binding protein
66	c4ld7N_	Alignment	not modelled	22.4	10	**PDB header:**transferase **Chain:** N: **PDB Molecule:**dimethylallyl tryptophan synthase; **PDBTitle:** crystal structure of anapt from neosartorya fischeri
67	d2aifa1	Alignment	not modelled	22.2	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
68	c5ijlA_	Alignment	not modelled	21.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase ii large subunit; **PDBTitle:** d-family dna polymerase - dp2 subunit (catalytic subunit)
69	c5zvqA_	Alignment	not modelled	19.4	12	**PDB header:**recombination **Chain:** A: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombination mediator protein recr
70	d2aa4a2	Alignment	not modelled	16.9	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
71	c4u3eA_	Alignment	not modelled	16.6	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside triphosphate reductase; **PDBTitle:** anaerobic ribonucleotide reductase
72	c3ve5D_	Alignment	not modelled	15.2	16	**PDB header:**recombination **Chain:** D: **PDB Molecule:**recombination protein recr; **PDBTitle:** structure of recombination mediator protein recr16-196 deletion mutant
73	c6ok1B_	Alignment	not modelled	15.1	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chsh2(duf35); **PDBTitle:** ltp2-chsh2(duf35) aldolase
74	c2aa4B_	Alignment	not modelled	13.9	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative n-acetylmannosamine kinase; **PDBTitle:** crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
75	c3u5cM_	Alignment	not modelled	13.7	18	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**40s ribosomal protein s12; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
76	d2ap1a1	Alignment	not modelled	13.4	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
77	c4htlA_	Alignment	not modelled	13.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-glucoside kinase; **PDBTitle:** lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
78	c5mg5W_	Alignment	not modelled	13.2	0	**PDB header:**transferase **Chain:** W: **PDB Molecule:**2,4-diacetylphloroglucinol biosynthesis protein; **PDBTitle:** a multi-component acyltransferase phlabc from pseudomonas protegens2 soaked with the monoacetylphloroglucinol (mapg)
79	d1vdda_	Alignment	not modelled	13.0	16	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
						PDB header:transferase

80	c6et9H_	Alignment	not modelled	12.9	10	**Chain:** H: **PDB Molecule:**pfam duf35; **PDBTitle:** structure of the acetoacetyl-coa-thiolase/hmg-coa-synthase complex2 from methanothermococcus thermolithotrophicus at 2.75 a
81	c6mrrA_	Alignment	not modelled	12.1	20	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**foldit1; **PDBTitle:** de novo designed protein foldit1
82	c2mxtA_	Alignment	not modelled	12.1	20	**PDB header:**splicing **Chain:** A: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein q; **PDBTitle:** nmr structure of the acidic domain of syncrip (hnrnpq)
83	c4ijaA_	Alignment	not modelled	11.7	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**xylr protein; **PDBTitle:** structure of s. aureus methicillin resistance factor mecr2
84	d1z05a2	Alignment	not modelled	11.5	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
85	c5z2vB_	Alignment	not modelled	10.9	18	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recr from pseudomonas aeruginosa pao1
86	d1woqa2	Alignment	not modelled	10.8	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
87	c2nykA_	Alignment	not modelled	10.6	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**m157; **PDBTitle:** crystal structure of m157 from mouse cytomegalovirus
88	c5heaA_	Alignment	not modelled	9.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase (galt1); **PDBTitle:** cgt structure in hexamer
89	c3o3nB_	Alignment	not modelled	8.9	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**beta-subunit 2-hydroxyacyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
90	c3qocD_	Alignment	not modelled	8.9	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative metallopeptidase; **PDBTitle:** crystal structure of n-terminal domain (creatinase/prolidase like2 domain) of putative metallopeptidase from corynebacterium diphtheriae
91	c5f9yB_	Alignment	not modelled	8.5	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**aminoacyl-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from cryptosporidium2 parvum complexed with l-proline and amp
92	c4db3A_	Alignment	not modelled	8.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyl-d-glucosamine kinase; **PDBTitle:** 1.95 angstrom resolution crystal structure of n-acetyl-d-glucosamine2 kinase from vibrio vulnificus.
93	c3d6xA_	Alignment	not modelled	8.3	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(3r)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase; **PDBTitle:** crystal structure of campylobacter jejuni fabz
94	c3ns5B_	Alignment	not modelled	8.3	21	**PDB header:**translation **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit b; **PDBTitle:** crystal structure of the rna recognition motif of yeast eif3b residues2 76-161
95	c2atmA_	Alignment	not modelled	7.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure of the recombinant allergen ves v 2
96	c2ap1A_	Alignment	not modelled	7.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
97	d2apob1	Alignment	not modelled	7.8	9	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
98	c4ltyD_	Alignment	not modelled	7.8	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**exonuclease subunit sbcd; **PDBTitle:** crystal structure of e.coli sbcd at 1.8 a resolution
99	c1s1iG_	Alignment	not modelled	7.5	12	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**60s ribosomal protein l8-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.