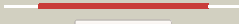



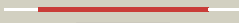
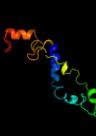

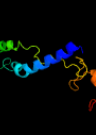

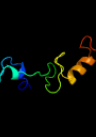

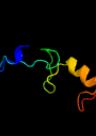





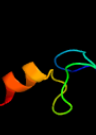

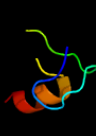



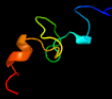









# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD2056c\_(rpsN)\_2314362\_2314667  
 Date Mon Aug 5 13:25:16 BST 2019  
 Unique Job ID 7a9b49165a679ca7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6dzkN_</a>	 Alignment		100.0	72	<b>PDB header:</b> ribosome <b>Chain:</b> N; <b>PDB Molecule:</b> 30s ribosomal protein s14; <b>PDBTitle:</b> cryo-em structure of mycobacterium smegmatis c(minus) 30s ribosomal2 subunit with mpy
2	<a href="#">c3j6vN_</a>	 Alignment		100.0	32	<b>PDB header:</b> ribosome <b>Chain:</b> N; <b>PDB Molecule:</b> 28s ribosomal protein s14, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
3	<a href="#">c3bbnN_</a>	 Alignment		100.0	34	<b>PDB header:</b> ribosome <b>Chain:</b> N; <b>PDB Molecule:</b> ribosomal protein s14; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
4	<a href="#">d2qaln1</a>	 Alignment		100.0	48	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Ribosomal protein S14
5	<a href="#">c2gy9N_</a>	 Alignment		99.9	56	<b>PDB header:</b> ribosome <b>Chain:</b> N; <b>PDB Molecule:</b> 30s ribosomal subunit protein s14; <b>PDBTitle:</b> structure of the 30s subunit of a pre-translocational e. coli ribosome2 obtained by fitting atomic models for rna and protein components into3 cryo-em map emd-1056
6	<a href="#">d2uubn1</a>	 Alignment		99.9	48	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Ribosomal protein S14
7	<a href="#">c3j20P_</a>	 Alignment		94.1	25	<b>PDB header:</b> ribosome <b>Chain:</b> P; <b>PDB Molecule:</b> 30s ribosomal protein s14p type z; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
8	<a href="#">c3jyvN_</a>	 Alignment		93.8	21	<b>PDB header:</b> ribosome <b>Chain:</b> N; <b>PDB Molecule:</b> 40s ribosomal protein s29(a); <b>PDBTitle:</b> structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
9	<a href="#">c3zey8_</a>	 Alignment		93.8	21	<b>PDB header:</b> ribosome <b>Chain:</b> 8; <b>PDB Molecule:</b> ribosomal protein s29, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
10	<a href="#">c2xzN_</a>	 Alignment		93.7	21	<b>PDB header:</b> ribosome <b>Chain:</b> N; <b>PDB Molecule:</b> rps29e; <b>PDBTitle:</b> 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
11	<a href="#">c5xxud_</a>	 Alignment		93.4	21	<b>PDB header:</b> ribosome <b>Chain:</b> D; <b>PDB Molecule:</b> ribosomal protein us3; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome

12	<a href="#">c6az1S_</a>	Alignment		93.1	21	<b>PDB header:</b> ribosome/antibiotic <b>Chain:</b> S: <b>PDB Molecule:</b> ribosomal protein s14; <b>PDBTitle:</b> cryo-em structure of the small subunit of leishmania ribosome bound to2 paromomycin
13	<a href="#">c5xyid_</a>	Alignment		92.9	28	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein s3, putative; <b>PDBTitle:</b> small subunit of trichomonas vaginalis ribosome
14	<a href="#">c2zkqn_</a>	Alignment		91.6	26	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> N: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into a 3.8.7 a cryo-em map
15	<a href="#">c1s1hN_</a>	Alignment		83.0	27	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 40s ribosomal protein s29-b; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
16	<a href="#">c3uz0A_</a>	Alignment		47.7	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> stage iii sporulation protein ah; <b>PDBTitle:</b> crystal structure of spoiii and spoiiiq complex
17	<a href="#">c3tufA_</a>	Alignment		40.4	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> stage iii sporulation protein ah; <b>PDBTitle:</b> structure of the spoiii-spoiiiq pore forming complex.
18	<a href="#">c6amaO_</a>	Alignment		36.7	23	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> O: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to 2.3.09 angstrom
19	<a href="#">c4j2nB_</a>	Alignment		35.7	36	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
20	<a href="#">c4j2nA_</a>	Alignment		29.7	36	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
21	<a href="#">d2bmfa1</a>	Alignment	not modelled	23.4	35	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
22	<a href="#">c2zhhA_</a>	Alignment	not modelled	22.5	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensitive transcriptional activator soxr; <b>PDBTitle:</b> crystal structure of soxr
23	<a href="#">c4lhfa_</a>	Alignment	not modelled	20.5	35	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein cox; <b>PDBTitle:</b> crystal structure of a dna binding protein from phage p2
24	<a href="#">d1r8da_</a>	Alignment	not modelled	16.4	12	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
25	<a href="#">c3gpvA_</a>	Alignment	not modelled	15.0	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
26	<a href="#">c1yuzB_</a>	Alignment	not modelled	13.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nigerythrin; <b>PDBTitle:</b> partially reduced state of nigerythrin
27	<a href="#">d2ieaa3</a>	Alignment	not modelled	12.9	14	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
28	<a href="#">c1y6uA_</a>	Alignment	not modelled	11.6	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> excisionase from transposon tn916; <b>PDBTitle:</b> the structure of the excisionase (xis) protein from 2 conjugative transposon tn916 provides insights into the 3 regulation of heterobivalent tyrosine recombinases <b>PDB header:</b> ribosome

29	<a href="#">c3zeyU_</a>	Alignment	not modelled	11.1	22	<b>Chain:</b> U: <b>PDB Molecule:</b> 40s ribosomal protein s25, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
30	<a href="#">c3izbV_</a>	Alignment	not modelled	10.6	30	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 40s ribosomal protein rps25 (s25e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
31	<a href="#">c5ntbB_</a>	Alignment	not modelled	10.5	28	<b>PDB header:</b> protease inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> papain inhibitor; <b>PDBTitle:</b> streptomyces papain inhibitor (spi)
32	<a href="#">d2cp5a1</a>	Alignment	not modelled	9.9	25	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
33	<a href="#">c6fmlI_</a>	Alignment	not modelled	9.7	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> ies6; <b>PDBTitle:</b> cryoem structure ino80core nucleosome complex
34	<a href="#">c2xzm8_</a>	Alignment	not modelled	9.5	26	<b>PDB header:</b> ribosome <b>Chain:</b> 8: <b>PDB Molecule:</b> rps25e,; <b>PDBTitle:</b> 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
35	<a href="#">c4ivvA_</a>	Alignment	not modelled	9.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> autolysin; <b>PDBTitle:</b> catalytic amidase domain of the major autolysin lyta from2 streptococcus pneumoniae
36	<a href="#">d1nj1a2</a>	Alignment	not modelled	8.8	11	<b>Fold:</b> IF3-like <b>Superfamily:</b> C-terminal domain of ProRS <b>Family:</b> C-terminal domain of ProRS
37	<a href="#">c3j3aZ_</a>	Alignment	not modelled	8.7	26	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 40s ribosomal protein s25; <b>PDBTitle:</b> structure of the human 40s ribosomal proteins
38	<a href="#">c3iz6V_</a>	Alignment	not modelled	8.7	26	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 40s ribosomal protein s25 (s25e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
39	<a href="#">c1qw1A_</a>	Alignment	not modelled	8.6	21	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> solution structure of the c-terminal domain of dtxr2 residues 110-226
40	<a href="#">d1n10a2</a>	Alignment	not modelled	8.2	17	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> Barwin-like endoglucanases <b>Family:</b> Pollen allergen PHL P 1 N-terminal domain
41	<a href="#">c1z4hA_</a>	Alignment	not modelled	8.1	18	<b>PDB header:</b> protein binding, dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tor inhibition protein; <b>PDBTitle:</b> the response regulator tori belongs to a new family of2 atypical excisionase
42	<a href="#">c4r4eA_</a>	Alignment	not modelled	8.0	19	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator glnr; <b>PDBTitle:</b> structure of glnr-dna complex
43	<a href="#">c4qoyC_</a>	Alignment	not modelled	7.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate dehydrogenase e1 component; <b>PDBTitle:</b> novel binding motif and new flexibility revealed by structural2 analysis of a pyruvate dehydrogenase-dihydrolipoyl acetyltransferase3 sub-complex from the escherichia coli pyruvate dehydrogenase multi-4 enzyme complex
44	<a href="#">c3bboY_</a>	Alignment	not modelled	7.6	13	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> ribosomal protein l28; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
45	<a href="#">c6dzpy_</a>	Alignment	not modelled	7.2	25	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> <b>PDBTitle:</b> cryo-em structure of mycobacterium smegmatis c(minus) 50s ribosomal2 subunit
46	<a href="#">c3hh0C_</a>	Alignment	not modelled	7.0	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
47	<a href="#">d1kcfal</a>	Alignment	not modelled	6.6	21	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> SAP domain <b>Family:</b> SAP domain
48	<a href="#">d2qamz1</a>	Alignment	not modelled	6.6	13	<b>Fold:</b> L28p-like <b>Superfamily:</b> L28p-like <b>Family:</b> Ribosomal protein L28
49	<a href="#">c2fugC_</a>	Alignment	not modelled	6.6	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 3; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
50	<a href="#">d1e0ea_</a>	Alignment	not modelled	6.4	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> N-terminal Zn binding domain of HIV integrase <b>Family:</b> N-terminal Zn binding domain of HIV integrase
51	<a href="#">d1whha_</a>	Alignment	not modelled	6.3	20	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
52	<a href="#">c5xxuZ_</a>	Alignment	not modelled	6.3	33	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> ribosomal protein es25; <b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
53	<a href="#">d1wg2a_</a>	Alignment	not modelled	6.2	27	<b>Fold:</b> AN1-like Zinc finger <b>Superfamily:</b> AN1-like Zinc finger <b>Family:</b> AN1-like Zinc finger
54	<a href="#">c4uj3B_</a>	Alignment	not modelled	5.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> rab-3a-interacting protein; <b>PDBTitle:</b> crystal structure of human rab11-rabin8-fip3

55	<a href="#">c4jcwB</a>	Alignment	not modelled	5.9	21	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cellulose binding protein; <b>PDBTitle:</b> crystal structure of clavibacter michiganensis expansin in complex2 with cellopentaose
56	<a href="#">d1s7za</a>	Alignment	not modelled	5.8	17	<b>Fold:</b> Another 3-helical bundle <b>Superfamily:</b> B-form DNA mimic Ocr <b>Family:</b> B-form DNA mimic Ocr
57	<a href="#">c6ddgJ</a>	Alignment	not modelled	5.7	25	<b>PDB header:</b> ribosome/antibiotic <b>Chain:</b> J: <b>PDB Molecule:</b> 50s ribosomal protein l28; <b>PDBTitle:</b> structure of the 50s ribosomal subunit from methicillin resistant2 staphylococcus aureus in complex with the oxazolidinone antibiotic3 lzd-6
58	<a href="#">c2hr5B</a>	Alignment	not modelled	5.6	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> rubrerythrin; <b>PDBTitle:</b> pf1283- rubrerythrin from pyrococcus furiosus iron bound form
59	<a href="#">c2k0aA</a>	Alignment	not modelled	5.5	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-splicing factor rds3; <b>PDBTitle:</b> 1h, 15n and 13c chemical shift assignments for rds3 protein
60	<a href="#">c5h1nB</a>	Alignment	not modelled	5.4	19	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> upf0253 protein yaep; <b>PDBTitle:</b> crystal structure of sf173 from shigella flexneri
61	<a href="#">d1whka</a>	Alignment	not modelled	5.3	7	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
62	<a href="#">d1whja</a>	Alignment	not modelled	5.3	40	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
63	<a href="#">d2coza1</a>	Alignment	not modelled	5.3	30	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
64	<a href="#">c3qaoA</a>	Alignment	not modelled	5.3	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> merr-like transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
65	<a href="#">d1k6ya1</a>	Alignment	not modelled	5.1	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> N-terminal Zn binding domain of HIV integrase <b>Family:</b> N-terminal Zn binding domain of HIV integrase
66	<a href="#">d2coya1</a>	Alignment	not modelled	5.1	28	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
67	<a href="#">c3zf7n</a>	Alignment	not modelled	5.1	23	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 60s ribosomal protein l13; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome