










# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0055\_(rpsR\_59119\_59373)  
 Date Tue Jul 23 14:50:08 BST 2019  
 Unique Job ID 58dcab322dc08309

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3j0xU_</a>	Alignment		100.0	42	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 30s ribosomal protein s18; <b>PDBTitle:</b> structural characterization of mrna-trna translocation intermediates2 (30s ribosome of class 4b of the six classes)
2	<a href="#">c5o5jR_</a>	Alignment		100.0	92	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 30s ribosomal protein s18 2; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
3	<a href="#">c6dzkr_</a>	Alignment		100.0	54	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> <b>PDBTitle:</b> cryo-em structure of mycobacterium smegmatis c(minus) 30s ribosomal2 subunit with mpy
4	<a href="#">c5aj3p_</a>	Alignment		100.0	26	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> mitoribosomal protein bs16m, mrps16; <b>PDBTitle:</b> structure of the small subunit of the mammalian mitoribosome
5	<a href="#">c3j6vR_</a>	Alignment		100.0	29	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 28s ribosomal protein s18a, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
6	<a href="#">d1i94r_</a>	Alignment		99.9	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein S18 <b>Family:</b> Ribosomal protein S18
7	<a href="#">c5aj3R_</a>	Alignment		99.9	31	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> mitoribosomal protein bs18m, mrps18c; <b>PDBTitle:</b> structure of the small subunit of the mammalian mitoribosome
8	<a href="#">d2uubr1</a>	Alignment		99.9	36	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein S18 <b>Family:</b> Ribosomal protein S18
9	<a href="#">c3bbnR_</a>	Alignment		99.9	42	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> ribosomal protein s18; <b>PDBTitle:</b> homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
10	<a href="#">d2qalr1</a>	Alignment		99.9	49	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein S18 <b>Family:</b> Ribosomal protein S18
11	<a href="#">c3df1R_</a>	Alignment		99.9	49	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 30s ribosomal protein s18; <b>PDBTitle:</b> crystal structure of the bacterial ribosome from escherichia coli in2 complex with hygromycin b. this file contains the 30s subunit of the3 first 70s ribosome, with hygromycin b bound. the entire crystal4 structure contains two 70s ribosomes.

12	<a href="#">d1g1xc_</a>	Alignment		99.8	41	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein S18 <b>Family:</b> Ribosomal protein S18
13	<a href="#">c6drdA_</a>	Alignment		21.6	28	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> dna-directed rna polymerase ii subunit rpb1; <b>PDBTitle:</b> rna pol ii(g)
14	<a href="#">c2aamA_</a>	Alignment		21.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein tm1410; <b>PDBTitle:</b> crystal structure of a putative glycosidase (tm1410) from thermotoga2 maritima at 2.20 a resolution
15	<a href="#">d2aama1</a>	Alignment		21.3	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> TM1410-like
16	<a href="#">c2wb1Y_</a>	Alignment		18.0	15	<b>PDB header:</b> transcription <b>Chain:</b> Y; <b>PDB Molecule:</b> dna-directed rna polymerase rpo1c subunit; <b>PDBTitle:</b> the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
17	<a href="#">c2pmzG_</a>	Alignment		17.3	14	<b>PDB header:</b> translation, transferase <b>Chain:</b> G; <b>PDB Molecule:</b> dna-directed rna polymerase subunit a"; <b>PDBTitle:</b> archaeal rna polymerase from sulfolobus solfataricus
18	<a href="#">c5tcbA_</a>	Alignment		15.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> pela; <b>PDBTitle:</b> structure of the glycoside hydrolase domain of pela from pseudomonas2 aeruginosa
19	<a href="#">d1wiia_</a>	Alignment		14.4	41	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Putative zinc binding domain
20	<a href="#">c2k6xA_</a>	Alignment		13.7	14	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> rna polymerase sigma factor rpod; <b>PDBTitle:</b> autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
21	<a href="#">c3h0gA_</a>	Alignment	not modelled	13.2	24	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> dna-directed rna polymerase ii subunit rpb1; <b>PDBTitle:</b> rna polymerase ii from schizosaccharomyces pombe
22	<a href="#">c4epoL_</a>	Alignment	not modelled	13.0	21	<b>PDB header:</b> protein binding/ligase <b>Chain:</b> L; <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rnf8; <b>PDBTitle:</b> crystal structure of rnf8 bound to the ubc13/mms2 heterodimer
23	<a href="#">d1twfa_</a>	Alignment	not modelled	10.4	18	<b>Fold:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase <b>Superfamily:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase <b>Family:</b> RNA-polymerase beta-prime
24	<a href="#">c4om3D_</a>	Alignment	not modelled	9.6	32	<b>PDB header:</b> transcription, dna binding <b>Chain:</b> D; <b>PDB Molecule:</b> transducin-like enhancer protein 1; <b>PDBTitle:</b> crystal structure of human tie1 q-domain residues 20-156
25	<a href="#">c4qiWC_</a>	Alignment	not modelled	9.4	17	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> dna-directed rna polymerase subunit a"; <b>PDBTitle:</b> crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
26	<a href="#">d3orca_</a>	Alignment	not modelled	9.4	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
27	<a href="#">c1d2vD_</a>	Alignment	not modelled	8.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> myeloperoxidase; <b>PDBTitle:</b> crystal structure of bromide-bound human myeloperoxidase isoform c at2 ph 5.5
28	<a href="#">c4zemB_</a>	Alignment	not modelled	7.7	17	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> translation initiation factor eif2b-like protein, <b>PDBTitle:</b> crystal structure of eif2b beta from chaetomium

						thermophilum
29	<a href="#">c2ma6A_</a>	Alignment	not modelled	7.5	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rnf123; <b>PDBTitle:</b> solution nmr structure of the ring finger domain from the kip12 ubiquitination-promoting e3 complex protein 1 (kpc1/rnf123) from homo3 sapiens, northeast structural genomics consortium (nesg) target4 hr8700a
30	<a href="#">c6ercA_</a>	Alignment	not modelled	6.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxinectin a; <b>PDBTitle:</b> peroxidase a from dictyostelium discoideum (ddpoxa)
31	<a href="#">c6i7tB_</a>	Alignment	not modelled	6.5	24	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit alpha; <b>PDBTitle:</b> eif2b:eif2 complex
32	<a href="#">c6gmlA_</a>	Alignment	not modelled	6.5	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase subunit; <b>PDBTitle:</b> structure of paused transcription complex pol ii-dsif-nelf
33	<a href="#">c2pijB_</a>	Alignment	not modelled	6.1	24	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> prophage pfl 6 cro; <b>PDBTitle:</b> structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
34	<a href="#">d1lrza2</a>	Alignment	not modelled	5.9	33	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> FemXAB nonribosomal peptidyltransferases
35	<a href="#">d1q4ga1</a>	Alignment	not modelled	5.7	29	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Myeloperoxidase-like
36	<a href="#">c5tbzD_</a>	Alignment	not modelled	5.6	9	<b>PDB header:</b> transcription/rna <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> e. coli rna polymerase complexed with nusg
37	<a href="#">c1i6hA_</a>	Alignment	not modelled	5.4	18	<b>PDB header:</b> transcription/dna-rna hybrid <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase ii largest subunit; <b>PDBTitle:</b> rna polymerase ii elongation complex
38	<a href="#">c5tw1E_</a>	Alignment	not modelled	5.4	20	<b>PDB header:</b> transcription activator/transferase/dna <b>Chain:</b> E: <b>PDB Molecule:</b> dna-directed rna polymerase subunit omega; <b>PDBTitle:</b> crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
39	<a href="#">d2nn6c2</a>	Alignment	not modelled	5.3	15	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
40	<a href="#">c5b04C_</a>	Alignment	not modelled	5.3	21	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> probable translation initiation factor eif-2b subunit beta; <b>PDBTitle:</b> crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
41	<a href="#">d4croa_</a>	Alignment	not modelled	5.3	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
42	<a href="#">d2ba0g2</a>	Alignment	not modelled	5.2	9	<b>Fold:</b> Ribonuclease PH domain 2-like <b>Superfamily:</b> Ribonuclease PH domain 2-like <b>Family:</b> Ribonuclease PH domain 2-like
43	<a href="#">c3ecsD_</a>	Alignment	not modelled	5.1	20	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit alpha; <b>PDBTitle:</b> crystal structure of human eif2b alpha