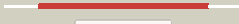



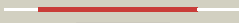

















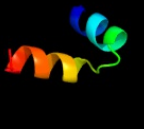
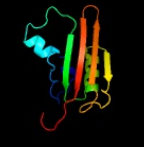



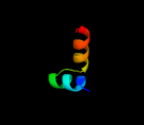





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1045_(-)_1167677_1168558
Date	Wed Jul 31 22:05:12 BST 2019
Unique Job ID	f2d50067e274ae9f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ok0B_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative; <b>PDBTitle:</b> crystal structure of putative nucleotidyltransferase from h. pylori
2	<a href="#">c5uvdA_</a>	 Alignment		98.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotidyltransferase-like protein; <b>PDBTitle:</b> crystal structure of an antigenic nucleotidyltransferase-like protein2 from paracoccidioides brasiliensis
3	<a href="#">c4wqkA_</a>	 Alignment		98.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2"-aminoglycoside nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of aminoglycoside nucleotidyltransferase ant(2")-2 ia, apo form
4	<a href="#">c4e8iA_</a>	 Alignment		98.1	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lincosamide resistance protein; <b>PDBTitle:</b> crystal structure of lincosamide antibiotic adenylyltransferase lina,2 apo
5	<a href="#">c1vfgB_</a>	 Alignment		85.3	19	<b>PDB header:</b> transferase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> crystal structure of trna nucleotidyltransferase complexed2 with a primer trna and an incoming atp analog
6	<a href="#">d1vfga2</a>	 Alignment		69.4	18	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly A polymerase head domain-like
7	<a href="#">c3h37B_</a>	 Alignment		51.2	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna nucleotidyl transferase-related protein; <b>PDBTitle:</b> the structure of cca-adding enzyme apo form i
8	<a href="#">c3wfrE_</a>	 Alignment		48.8	18	<b>PDB header:</b> transferase/rna <b>Chain:</b> E: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 2
9	<a href="#">c4x4wB_</a>	 Alignment		44.4	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cca trna nucleotidyltransferase 1, mitochondrial; <b>PDBTitle:</b> crystal structure of the full-length human mitochondrial cca-adding2 enzyme
10	<a href="#">c3wfpA_</a>	 Alignment		41.5	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme (apo form 2)
11	<a href="#">d1qb2a_</a>	 Alignment		41.0	25	<b>Fold:</b> Signal peptide-binding domain <b>Superfamily:</b> Signal peptide-binding domain <b>Family:</b> Signal peptide-binding domain

12	<a href="#">d1dula_</a>	Alignment		38.4	17	<b>Fold:</b> Signal peptide-binding domain <b>Superfamily:</b> Signal peptide-binding domain <b>Family:</b> Signal peptide-binding domain
13	<a href="#">c3wfsD_</a>	Alignment		37.8	11	<b>PDB header:</b> transferase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 3
14	<a href="#">c2jqeA_</a>	Alignment		36.9	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> soution structure of af54 m-domain
15	<a href="#">c3wfrG_</a>	Alignment		34.9	11	<b>PDB header:</b> transferase/rna <b>Chain:</b> G: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 2
16	<a href="#">c3wfgG_</a>	Alignment		34.8	18	<b>PDB header:</b> transferase/rna <b>Chain:</b> G: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 1
17	<a href="#">d1hq1a_</a>	Alignment		34.3	16	<b>Fold:</b> Signal peptide-binding domain <b>Superfamily:</b> Signal peptide-binding domain <b>Family:</b> Signal peptide-binding domain
18	<a href="#">c4ue4C_</a>	Alignment		32.2	17	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> structural basis for targeting and elongation arrest of bacillus2 signal recognition particle
19	<a href="#">d2ffha2</a>	Alignment		30.5	17	<b>Fold:</b> Signal peptide-binding domain <b>Superfamily:</b> Signal peptide-binding domain <b>Family:</b> Signal peptide-binding domain
20	<a href="#">d1qzxa2</a>	Alignment		30.2	17	<b>Fold:</b> Signal peptide-binding domain <b>Superfamily:</b> Signal peptide-binding domain <b>Family:</b> Signal peptide-binding domain
21	<a href="#">c3wfrH_</a>	Alignment	not modelled	29.0	11	<b>PDB header:</b> transferase/rna <b>Chain:</b> H: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 2
22	<a href="#">c4xcoC_</a>	Alignment	not modelled	24.8	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition particle 54 kda protein,signal sequence; <b>PDBTitle:</b> signal-sequence induced conformational changes in the signal2 recognition particle
23	<a href="#">c3c66B_</a>	Alignment	not modelled	21.6	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> poly(a) polymerase; <b>PDBTitle:</b> yeast poly(a) polymerase in complex with fip1 residues 80-105
24	<a href="#">c5oetB_</a>	Alignment	not modelled	19.3	9	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione synthetase-like effector 30 (gpa-gss30-apo); <b>PDBTitle:</b> the structure of a glutathione synthetase like-effector from2 globodera pallida in apoform.
25	<a href="#">c3wfsC_</a>	Alignment	not modelled	19.0	18	<b>PDB header:</b> transferase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 3
26	<a href="#">c3h4rA_</a>	Alignment	not modelled	18.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exodeoxyribonuclease 8; <b>PDBTitle:</b> crystal structure of e. coli rece exonuclease
27	<a href="#">d1miwa2</a>	Alignment	not modelled	17.7	19	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly A polymerase head domain-like
28	<a href="#">c3wfgE_</a>	Alignment	not modelled	17.5	17	<b>PDB header:</b> transferase/rna <b>Chain:</b> E: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 1

29	<a href="#">c3wfgH_</a>	Alignment	not modelled	16.3	17	<b>PDB header:</b> transferase/rna <b>Chain:</b> H: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 1
30	<a href="#">c2jpfA_</a>	Alignment	not modelled	16.2	24	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> bpp3783_115-220
31	<a href="#">c3wfrF_</a>	Alignment	not modelled	15.7	18	<b>PDB header:</b> transferase/rna <b>Chain:</b> F: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 2
32	<a href="#">d1ou5a2</a>	Alignment	not modelled	13.8	16	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly A polymerase head domain-like
33	<a href="#">d2ay0a1</a>	Alignment	not modelled	13.7	18	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> PutA pre-N-terminal region-like
34	<a href="#">c2khrA_</a>	Alignment	not modelled	13.7	20	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein mbth; <b>PDBTitle:</b> solution structure of rv2377c, a mbth-like protein from mycobacterium2 tuberculosis
35	<a href="#">d1mnta_</a>	Alignment	not modelled	11.4	29	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
36	<a href="#">c5ja1B_</a>	Alignment	not modelled	9.3	10	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> enterobactin biosynthesis protein ybdz; <b>PDBTitle:</b> entf, a terminal nonribosomal peptide synthetase module bound to the2 mbth-like protein ybdz
37	<a href="#">c5wmmB_</a>	Alignment	not modelled	8.8	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> mbth homologue; <b>PDBTitle:</b> crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios
38	<a href="#">d2gpfa1</a>	Alignment	not modelled	8.5	15	<b>Fold:</b> Mbth/L9 domain-like <b>Superfamily:</b> Mbth-like <b>Family:</b> Mbth-like
39	<a href="#">c2rbfB_</a>	Alignment	not modelled	8.0	16	<b>PDB header:</b> oxidoreductase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
40	<a href="#">c3qoqC_</a>	Alignment	not modelled	7.9	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> alginate and motility regulator z; <b>PDBTitle:</b> crystal structure of the transcription factor amrz in complex with the2 18 base pair amrz1 binding site
41	<a href="#">c5gafi_</a>	Alignment	not modelled	7.8	17	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein I10; <b>PDBTitle:</b> rnc in complex with srp
42	<a href="#">d4ubpc1</a>	Alignment	not modelled	7.8	30	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> alpha-Subunit of urease
43	<a href="#">d2pstx1</a>	Alignment	not modelled	7.6	13	<b>Fold:</b> Mbth/L9 domain-like <b>Superfamily:</b> Mbth-like <b>Family:</b> Mbth-like
44	<a href="#">c1u9pA_</a>	Alignment	not modelled	7.4	29	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> parc; <b>PDBTitle:</b> permuted single-chain arc
45	<a href="#">c2j37W_</a>	Alignment	not modelled	7.3	25	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein (srp54); <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs
46	<a href="#">d1bu2a1</a>	Alignment	not modelled	7.1	9	<b>Fold:</b> Cyclin-like <b>Superfamily:</b> Cyclin-like <b>Family:</b> Cyclin
47	<a href="#">d1yt3a2</a>	Alignment	not modelled	6.7	13	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> RNase D C-terminal domains
48	<a href="#">c6q52A_</a>	Alignment	not modelled	6.4	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cca-adding enzyme; <b>PDBTitle:</b> structure of a psychrophilic cca-adding enzyme in complex with cmpcp2 at room temperature in chipx microfluidic device
49	<a href="#">d1qmha2</a>	Alignment	not modelled	6.4	24	<b>Fold:</b> IF3-like <b>Superfamily:</b> EPT/RTPC-like <b>Family:</b> RNA 3'-terminal phosphate cyclase, RTPC
50	<a href="#">d1lvaa3</a>	Alignment	not modelled	6.4	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal fragment of elongation factor SelB
51	<a href="#">c2np3A_</a>	Alignment	not modelled	6.1	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family regulator; <b>PDBTitle:</b> crystal structure of tetr-family regulator (sco0857) from streptomyces2 coelicolor a3.
52	<a href="#">c5u89B_</a>	Alignment	not modelled	6.0	23	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> mbth domain protein; <b>PDBTitle:</b> crystal structure of a cross-module fragment from the dimodular nrps2 dhbf
53	<a href="#">d1g3nc1</a>	Alignment	not modelled	5.9	9	<b>Fold:</b> Cyclin-like <b>Superfamily:</b> Cyclin-like <b>Family:</b> Cyclin
54	<a href="#">c2lpdA_</a>	Alignment	not modelled	5.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of a mbth-like protein from burkholderia2 pseudomallei, the etiological agent responsible for melioidosis,3 seattle structural genomics center for infectious disease target4 bupsa.13472.b