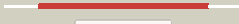



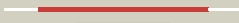










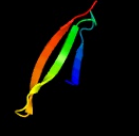





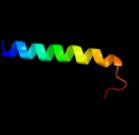


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3923c\_(rnpA)\_4410589\_4410966  
 Date Sat Aug 10 22:05:11 BST 2019  
 Unique Job ID 465668d276498176

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1d6ta_</a>	 Alignment		100.0	20	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> RNase P protein
2	<a href="#">d1a6fa_</a>	 Alignment		100.0	26	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> RNase P protein
3	<a href="#">c2ljpA_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease p protein component; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for e.coli2 ribonuclease p protein
4	<a href="#">d1nz0a_</a>	 Alignment		100.0	19	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> RNase P protein
5	<a href="#">c4oxpA_</a>	 Alignment		95.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease e; <b>PDBTitle:</b> x-ray crystal structure of the s1 and 5'-sensor domains of rnae e2 from caulobacter crescentus
6	<a href="#">c2c4rL_</a>	 Alignment		52.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> ribonuclease e; <b>PDBTitle:</b> catalytic domain of e. coli rnae e
7	<a href="#">c3b0zA_</a>	 Alignment		16.7	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar biosynthetic protein flhb; <b>PDBTitle:</b> crystal structure of cytoplasmic domain of flhb from salmonella2 typhimurium
8	<a href="#">c5aycA_</a>	 Alignment		16.2	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-o-beta-d-mannosyl-d-glucose phosphorylase; <b>PDBTitle:</b> crystal structure of ruminococcus albus 4-o-beta-d-mannosyl-d-glucose2 phosphorylase (ramp1) in complexes with sulfate and 4-o-beta-d-3 mannosyl-d-glucose
9	<a href="#">c2ml9A_</a>	 Alignment		10.7	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> yop proteins translocation protein u; <b>PDBTitle:</b> solution structure of yscucn in a micellar complex with sds
10	<a href="#">c3b1sC_</a>	 Alignment		9.9	32	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> flagellar biosynthetic protein flhb; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of flhb from aquifex2 aeolicus
11	<a href="#">c3b1sA_</a>	 Alignment		9.9	32	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar biosynthetic protein flhb; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of flhb from aquifex2 aeolicus

12	<a href="#">c3qc3B_</a>	Alignment		9.4	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> d-ribose-5-phosphate-3-epimerase; <b>PDBTitle:</b> crystal structure of a d-ribose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
13	<a href="#">c3b1sE_</a>	Alignment		9.1	32	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> flagellar biosynthetic protein flhb; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of flhb from aquifex2 aeolicus
14	<a href="#">d1vpza_</a>	Alignment		9.0	27	<b>Fold:</b> CsrA-like <b>Superfamily:</b> CsrA-like <b>Family:</b> CsrA-like
15	<a href="#">c2jppB_</a>	Alignment		8.6	27	<b>PDB header:</b> translation/rna <b>Chain:</b> B: <b>PDB Molecule:</b> translational repressor; <b>PDBTitle:</b> structural basis of rsma/csrA rna recognition: structure of2 rsme bound to the shine-dalgarno sequence of hcna mrna
16	<a href="#">c1vpzB_</a>	Alignment		8.5	27	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> carbon storage regulator homolog; <b>PDBTitle:</b> crystal structure of a putative carbon storage regulator protein2 (csrA, pa0905) from pseudomonas aeruginosa at 2.05 a resolution
17	<a href="#">c5dmbD_</a>	Alignment		8.3	19	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> carbon storage regulator homolog; <b>PDBTitle:</b> crystal structure of a translational regulator bound to a flagellar2 assembly factor
18	<a href="#">c5usrB_</a>	Alignment		8.1	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lyr motif-containing protein 4; <b>PDBTitle:</b> crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
19	<a href="#">c2kjaA_</a>	Alignment		8.0	16	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s6; <b>PDBTitle:</b> solution structure and backbone dynamics of the permutant p54-55
20	<a href="#">d2jfga2</a>	Alignment		7.0	7	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
21	<a href="#">c3t0yA_</a>	Alignment	not modelled	6.9	13	<b>PDB header:</b> transcription regulator/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the phyr anti-anti-sigma2 domain bound to the anti-sigma2 factor, nepr
22	<a href="#">c1tteA_</a>	Alignment	not modelled	6.7	9	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-conjugating enzyme e2-24 kda; <b>PDBTitle:</b> the structure of a class ii ubiquitin-conjugating enzyme,2 ubc1.
23	<a href="#">c4whnB_</a>	Alignment	not modelled	6.4	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> apxc; <b>PDBTitle:</b> structure of toxin-activating acyltransferase (taat)
24	<a href="#">c1t3oA_</a>	Alignment	not modelled	6.1	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> carbon storage regulator; <b>PDBTitle:</b> solution structure of csrA, a bacterial carbon storage2 regulatory protein
25	<a href="#">d1xxaa_</a>	Alignment	not modelled	6.1	14	<b>Fold:</b> DCoH-like <b>Superfamily:</b> C-terminal domain of arginine repressor <b>Family:</b> C-terminal domain of arginine repressor
26	<a href="#">d1gzga_</a>	Alignment	not modelled	5.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
27	<a href="#">d2c1ha1</a>	Alignment	not modelled	5.8	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
28	<a href="#">d1l6sa_</a>	Alignment	not modelled	5.8	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
						<b>Fold:</b> Secretion chaperone-like

29	<a href="#">d1k8kd1</a>	Alignment	not modelled	5.8	18	<b>Superfamily:</b> Arp2/3 complex subunits <b>Family:</b> Arp2/3 complex subunits
30	<a href="#">c3obkH</a>	Alignment	not modelled	5.7	8	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> delta-aminolevulinic acid dehydratase; <b>PDBTitle:</b> crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
31	<a href="#">d1pv8a</a>	Alignment	not modelled	5.7	4	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)