



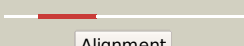

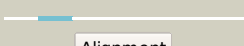
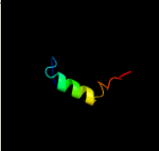

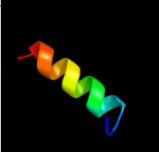






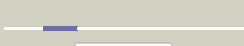







# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2827c_(-)_3134606_3135493
Date	Wed Aug 7 12:50:49 BST 2019
Unique Job ID	fd83c4c55053cd4f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1zela_</a>	 Alignment		100.0	100	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rv2827c; <b>PDBTitle:</b> crystal structure of rv2827c protein from mycobacterium tuberculosis
2	<a href="#">d1zela2</a>	 Alignment		100.0	100	<b>Fold:</b> Rv2827c C-terminal domain-like <b>Superfamily:</b> Rv2827c C-terminal domain-like <b>Family:</b> Rv2827c C-terminal domain-like
3	<a href="#">d1zela1</a>	 Alignment		100.0	100	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Rv2827c N-terminal domain-like
4	<a href="#">d1d8ca_</a>	 Alignment		33.6	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Malate synthase G <b>Family:</b> Malate synthase G
5	<a href="#">c5es2A_</a>	 Alignment		33.1	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein lpg0634; <b>PDBTitle:</b> the crystal structure of a functionally uncharacterized protein2 lpg0634 from legionella pneumophila subsp. pneumophila str.3 philadelphia 1
6	<a href="#">c3rnlA_</a>	 Alignment		21.8	43	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfotransferase; <b>PDBTitle:</b> crystal structure of sulfotransferase from alicyclobacillus2 acidocaldarius
7	<a href="#">c5z5mB_</a>	 Alignment		20.7	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> crystal structure of (s)-allantoin synthase
8	<a href="#">d1aoya_</a>	 Alignment		17.7	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
9	<a href="#">c5vmoB_</a>	 Alignment		14.2	78	<b>PDB header:</b> viral protein/apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2 interacting mediator of cell death; <b>PDBTitle:</b> crystal structure of grouper iridovirus giv66:bim complex
10	<a href="#">c2kztA_</a>	 Alignment		13.7	19	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 4; <b>PDBTitle:</b> structure of the tandem ma-3 region of pdcd4
11	<a href="#">d1ug7a_</a>	 Alignment		10.4	43	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Domain from hypothetical 2610208m17rik protein <b>Family:</b> Domain from hypothetical 2610208m17rik protein

12	<a href="#">c1atiA_</a>	Alignment		9.8	23	<b>PDB header:</b> protein biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> glycyl-trna synthetase; <b>PDBTitle:</b> crystal structure of glycyl-trna synthetase from thermus thermophilus
13	<a href="#">c5oold_</a>	Alignment		9.8	27	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 39s ribosomal protein l2, mitochondrial; <b>PDBTitle:</b> structure of a native assembly intermediate of the human mitochondrial l2 ribosome with unfolded interfacial rna
14	<a href="#">c1ggmB_</a>	Alignment		9.3	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> glycine--trna ligase; <b>PDBTitle:</b> glycyl-trna synthetase from thermus thermophilus complexed with 2 glycyl-adenylate
15	<a href="#">c3qd7X_</a>	Alignment		8.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> uncharacterized protein ydal; <b>PDBTitle:</b> crystal structure of ydal, a stand-alone small muts-related protein 2 from escherichia coli
16	<a href="#">c4rhzA_</a>	Alignment		8.5	15	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> cry23aa1; <b>PDBTitle:</b> crystal structure of cry23aa1 and cry37aa1 binary protein complex
17	<a href="#">c2bcwC_</a>	Alignment		8.3	19	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> coordinates of the n-terminal domain of ribosomal protein l11, c-2 terminal domain of ribosomal protein l7/l12 and a portion of the g'3 domain of elongation factor g, as fitted into cryo-em map of an 4 escherichia coli 70s*ef-g*gdp*fusidic acid complex
18	<a href="#">c4wqkA_</a>	Alignment		7.6	6	<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
19	<a href="#">c5zz5D_</a>	Alignment		7.6	23	<b>PDB header:</b> gene regulation <b>Chain:</b> D: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> redox-sensing transcriptional repressor rex
20	<a href="#">c1bqfA_</a>	Alignment		7.0	73	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> protein (growth-blocking peptide); <b>PDBTitle:</b> growth-blocking peptide (gpb) from pseudaletia separata
21	<a href="#">d1r7la_</a>	Alignment	not modelled	6.9	58	<b>Fold:</b> Bacillus phage protein <b>Superfamily:</b> Bacillus phage protein <b>Family:</b> Bacillus phage protein
22	<a href="#">c4kr3A_</a>	Alignment	not modelled	6.7	22	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glycine--trna ligase; <b>PDBTitle:</b> glycyl-trna synthetase mutant e71g in complex with trna-gly
23	<a href="#">c2g57A_</a>	Alignment	not modelled	6.7	67	<b>PDB header:</b> oncoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> beta-catenin; <b>PDBTitle:</b> structure of the phosphorylation motif of the oncogenic 2 protein beta-catenin recognized by a selective monoclonal 3 antibody
24	<a href="#">c2pqkB_</a>	Alignment	not modelled	6.5	53	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bim bh3 peptide; <b>PDBTitle:</b> x-ray crystal structure of human mcl-1 in complex with bim bh3
25	<a href="#">d1b4aa1</a>	Alignment	not modelled	6.0	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
26	<a href="#">c4wv4A_</a>	Alignment	not modelled	5.9	36	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 10; <b>PDBTitle:</b> heterodimer of taf8/taf10
27	<a href="#">c3jcuJ_</a>	Alignment	not modelled	5.8	43	<b>PDB header:</b> membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom 2 resolution
28	<a href="#">d2p5ka1</a>	Alignment	not modelled	5.7	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
						<b>Fold:</b> DNA/RNA-binding 3-helical bundle

29	<a href="#">d1f9na1</a>	Alignment	not modelled	5.7	14	<b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
30	<a href="#">c5unkA</a>	Alignment	not modelled	5.6	31	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sleeping beauty transposase; <b>PDBTitle:</b> nmr structure of the red subdomain of the sleeping beauty transposase
31	<a href="#">d1ohfa</a>	Alignment	not modelled	5.5	26	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Tetraviridae-like VP
32	<a href="#">c4o1hA</a>	Alignment	not modelled	5.4	33	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator glnr; <b>PDBTitle:</b> crystal structure of the regulatory domain of ameglnr
33	<a href="#">d1t6sa2</a>	Alignment	not modelled	5.1	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ScpB/YpuH-like