
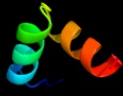
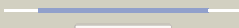










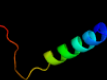











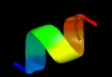


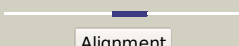

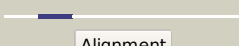

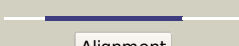

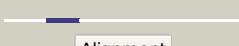






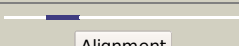

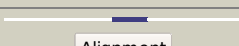

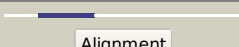


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0229Ac\_(RVBD0229Ac)\_274710\_274904  
 Date Tue Jul 23 14:50:28 BST 2019  
 Unique Job ID aea8bf94c151fe3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6a7vU_</a>	 Alignment		67.8	33	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> U; <b>PDB Molecule:</b> antitoxin vappb11; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
2	<a href="#">d1puga_</a>	 Alignment		26.0	20	<b>Fold:</b> YbaB-like <b>Superfamily:</b> YbaB-like <b>Family:</b> YbaB-like
3	<a href="#">c6izlB_</a>	 Alignment		19.3	64	<b>PDB header:</b> virus <b>Chain:</b> B; <b>PDB Molecule:</b> mud crab tombus-like virus; <b>PDBTitle:</b> cryo-em structure of mud crab tombus-like virus at 3.3 angstroms2 resolution
4	<a href="#">d1qx8a_</a>	 Alignment		14.0	100	<b>Fold:</b> ROP-like <b>Superfamily:</b> ROP protein <b>Family:</b> ROP protein
5	<a href="#">d1gtoa_</a>	 Alignment		12.1	100	<b>Fold:</b> ROP-like <b>Superfamily:</b> ROP protein <b>Family:</b> ROP protein
6	<a href="#">d2ijka1</a>	 Alignment		11.9	100	<b>Fold:</b> ROP-like <b>Superfamily:</b> ROP protein <b>Family:</b> ROP protein
7	<a href="#">c2w7nA_</a>	 Alignment		11.6	37	<b>PDB header:</b> transcription/dna <b>Chain:</b> A; <b>PDB Molecule:</b> trfb transcriptional repressor protein; <b>PDBTitle:</b> crystal structure of kora bound to operator dna: insight into2 repressor cooperation in rp4 gene regulation
8	<a href="#">d1pu6a_</a>	 Alignment		11.0	33	<b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> 3-Methyladenine DNA glycosylase III (MagIII)
9	<a href="#">d1f4nb_</a>	 Alignment		11.0	83	<b>Fold:</b> ROP-like <b>Superfamily:</b> ROP protein <b>Family:</b> ROP protein
10	<a href="#">d1f4na_</a>	 Alignment		10.5	83	<b>Fold:</b> ROP-like <b>Superfamily:</b> ROP protein <b>Family:</b> ROP protein
11	<a href="#">c5kgzA_</a>	 Alignment		10.5	63	<b>PDB header:</b> virulence factor <b>Chain:</b> A; <b>PDB Molecule:</b> modulin beta2; <b>PDBTitle:</b> phenol-soluble modulin beta2

12	<a href="#">c3cl3E_</a>		Alignment		9.9	63	<b>PDB header:</b> viral protein/signaling protein <b>Chain:</b> E: <b>PDB Molecule:</b> nf-kappa-b essential modulator; <b>PDBTitle:</b> crystal structure of a vflip-ikkgamma complex: insights into viral2 activation of the ikk signalosome
13	<a href="#">c3cl3D_</a>		Alignment		9.8	63	<b>PDB header:</b> viral protein/signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> nf-kappa-b essential modulator; <b>PDBTitle:</b> crystal structure of a vflip-ikkgamma complex: insights into viral2 activation of the ikk signalosome
14	<a href="#">c4jw1B_</a>		Alignment		9.4	63	<b>PDB header:</b> hydrolase activator <b>Chain:</b> B: <b>PDB Molecule:</b> effector protein b; <b>PDBTitle:</b> crystal structure of n-terminal 618-residue fragment of lepb from2 legionella pneumophila
15	<a href="#">c5yl1A_</a>		Alignment		9.2	55	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein; <b>PDBTitle:</b> t=1 subviral particle of penaeus vannamei nodavirus capsid protein2 deletion mutant (delta 1-37 & 251-368)
16	<a href="#">c4il0D_</a>		Alignment		8.8	63	<b>PDB header:</b> protein transport/hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> lepb; <b>PDBTitle:</b> crystal structure of the legionella pneumophila gap domain of lepb in2 complex with rab1b bound to gdp and bef3
17	<a href="#">d1wjta_</a>		Alignment		8.6	26	<b>Fold:</b> N-cbl like <b>Superfamily:</b> Conserved domain common to transcription factors TFII5, elongin A, CRSP70 <b>Family:</b> Conserved domain common to transcription factors TFII5, elongin A, CRSP70
18	<a href="#">d1nkda_</a>		Alignment		7.0	100	<b>Fold:</b> ROP-like <b>Superfamily:</b> ROP protein <b>Family:</b> ROP protein
19	<a href="#">c5e3eA_</a>		Alignment		6.1	23	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> cdii immunity protein; <b>PDBTitle:</b> crystal structure of cdia-ct/cdii complex from y. kristensenii 33638
20	<a href="#">c5xauC_</a>		Alignment		6.0	26	<b>PDB header:</b> cell adhesion <b>Chain:</b> C: <b>PDB Molecule:</b> laminin subunit gamma-1; <b>PDBTitle:</b> crystal structure of integrin binding fragment of laminin-511
21	<a href="#">c5ly0B_</a>		Alignment	not modelled	6.0	26	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> lob family transfactor ramosa2.1; <b>PDBTitle:</b> crystal structure of lob domain of ramosa2 from wheat
22	<a href="#">c1yo7A_</a>		Alignment	not modelled	5.8	100	<b>PDB header:</b> replication regulator <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein rop; <b>PDBTitle:</b> re-engineering topology of the homodimeric rop protein into a single-2 chain 4-helix bundle
23	<a href="#">c1motA_</a>		Alignment	not modelled	5.7	60	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine receptor alpha-1 chain; <b>PDBTitle:</b> nmr structure of extended second transmembrane domain of2 glycine receptor alpha1 subunit in sds micelles
24	<a href="#">c6ab6A_</a>		Alignment	not modelled	5.5	55	<b>PDB header:</b> virus like particle <b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein; <b>PDBTitle:</b> cryo-em structure of t=3 penaeus vannamei nodavirus
25	<a href="#">c3bc1F_</a>		Alignment	not modelled	5.3	40	<b>PDB header:</b> signaling protein/transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> synaptotagmin-like protein 2; <b>PDBTitle:</b> crystal structure of the complex rab27a-slp2a
26	<a href="#">c5ok8A_</a>		Alignment	not modelled	5.2	47	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lpp20 lipoprotein; <b>PDBTitle:</b> crystal structure of protein lpp20 (hp1456) from helicobacter pylori