



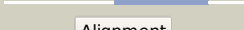
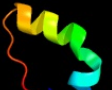
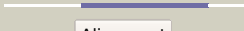





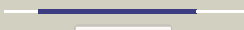
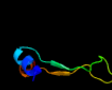


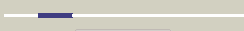


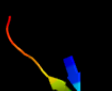


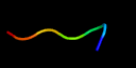
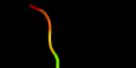
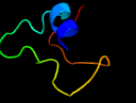


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD2231B\_(RVBD2231B)\_2506215\_2506391  
 Date Mon Aug 5 13:25:36 BST 2019  
 Unique Job ID 8915102f1ef591af

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2odka1</a>	 Alignment		70.5	30	<b>Fold:</b> YefM-like <b>Superfamily:</b> YefM-like <b>Family:</b> YefM-like
2	<a href="#">c2odkD</a>	 Alignment		62.2	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> putative prevent-host-death protein from nitrosomonas europaea
3	<a href="#">c3hryA</a>	 Alignment		23.9	28	<b>PDB header:</b> antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> prevent host death protein; <b>PDBTitle:</b> crystal structure of phd in a trigonal space group and partially2 disordered
4	<a href="#">c2mkxA</a>	 Alignment		17.6	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> autolysin; <b>PDBTitle:</b> solution structure of lysm the peptidoglycan binding domain of2 autolysin atla from enterococcus faecalis
5	<a href="#">c3hs2H</a>	 Alignment		11.5	30	<b>PDB header:</b> antitoxin <b>Chain:</b> H: <b>PDB Molecule:</b> prevent host death protein; <b>PDBTitle:</b> crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
6	<a href="#">c2lxeA</a>	 Alignment		10.6	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase suvr4; <b>PDBTitle:</b> s4wyild
7	<a href="#">c4xruE</a>	 Alignment		8.3	23	<b>PDB header:</b> protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> rnl; <b>PDBTitle:</b> structure of pnkp1/rnl/hen1 complex
8	<a href="#">c5twaC</a>	 Alignment		7.9	63	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> bak-2 protein; <b>PDBTitle:</b> crystal structure of geodia cydonium bhp2 in complex with lubomirskia2 baicalensis bak-2
9	<a href="#">c5twaD</a>	 Alignment		7.9	63	<b>PDB header:</b> apoptosis <b>Chain:</b> D: <b>PDB Molecule:</b> bak-2 protein; <b>PDBTitle:</b> crystal structure of geodia cydonium bhp2 in complex with lubomirskia2 baicalensis bak-2
10	<a href="#">c4wfwA</a>	 Alignment		7.4	17	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> general secretion pathway protein b; <b>PDBTitle:</b> the crystal structure of dickeya dadantii gpsb from the type 22 secretion system
11	<a href="#">c5an5J</a>	 Alignment		7.0	46	<b>PDB header:</b> cell cycle <b>Chain:</b> J: <b>PDB Molecule:</b> cell cycle protein gpsb; <b>PDBTitle:</b> b. subtilis gpsb c-terminal domain

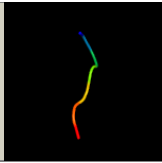
12	<a href="#">d1auya_</a>	Alignment		6.4	57	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Tymoviridae-like VP
13	<a href="#">d1auyb_</a>	Alignment		6.2	57	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Tymoviridae-like VP
14	<a href="#">c2l9yA_</a>	Alignment		6.2	28	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cvnh-lysm lectin; <b>PDBTitle:</b> solution structure of the mocvnh-lysm module from the rice blast2 fungus magnaporthe oryzae protein (mgg_03307)

15

[d1ddla\\_](#)



Alignment



5.6

43

**Fold:** Nucleoplasmin-like/VP (viral coat and capsid proteins)  
**Superfamily:** Positive stranded ssRNA viruses  
**Family:** Tymoviridae-like VP