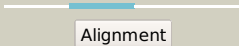





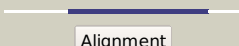

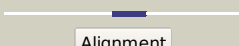

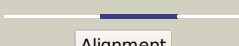

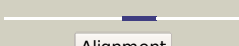











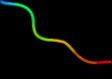
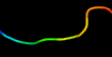
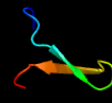


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2706c (-) _3020210_3020467
Date	Wed Aug 7 12:50:36 BST 2019
Unique Job ID	7abe79076824f863

Detailed template information

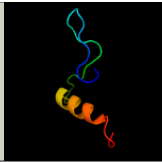
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2rtyA_</a>	 Alignment		30.9	42	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> navitoxin; <b>PDBTitle:</b> solution structure of navitoxin
2	<a href="#">d1vb0a_</a>	 Alignment		10.8	36	<b>Fold:</b> Snake toxin-like <b>Superfamily:</b> Snake toxin-like <b>Family:</b> Snake venom toxins
3	<a href="#">c3hh7A_</a>	 Alignment		9.1	24	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> muscarinic toxin-like protein 3 homolog; <b>PDBTitle:</b> structural and functional characterization of a novel homodimeric2 three-finger neurotoxin from the venom of ophiophagus hannah (king3 cobra)
4	<a href="#">c4lb0B_</a>	 Alignment		7.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a hydroxyproline epimerase from agrobacterium2 vitis, target efi-506420, with bound trans-4-oh-l-proline
5	<a href="#">c5j9hA_</a>	 Alignment		6.9	38	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelopment polyprotein; <b>PDBTitle:</b> crystal structure of glycoprotein c from puumala virus in the post-2 fusion conformation (ph 8.0)
6	<a href="#">d1g6ma_</a>	 Alignment		6.8	34	<b>Fold:</b> Snake toxin-like <b>Superfamily:</b> Snake toxin-like <b>Family:</b> Snake venom toxins
7	<a href="#">c1z8yF_</a>	 Alignment		6.8	29	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> spike glycoprotein e1; <b>PDBTitle:</b> mapping the e2 glycoprotein of alphaviruses
8	<a href="#">d2v33a1</a>	 Alignment		6.7	43	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Class II viral fusion proteins C-terminal domain
9	<a href="#">c4c1oA_</a>	 Alignment		6.4	41	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylosidase; <b>PDBTitle:</b> geobacillus thermoglucosidasius gh family 52 xylosidase
10	<a href="#">c6hjgB_</a>	 Alignment		6.2	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> proline racemase a; <b>PDBTitle:</b> trypanosoma cruzi proline racemase in complex with inhibitor oxopa
11	<a href="#">c3do6B_</a>	 Alignment		6.0	40	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> formate--tetrahydrofolate ligase; <b>PDBTitle:</b> crystal structure of putative formyltetrahydrofolate synthetase2 (tm1766) from thermotoga maritima at 1.85 a resolution

12	<a href="#">d1o70a1</a>	Alignment		5.6	31	<b>Fold:</b> FAS1 domain <b>Superfamily:</b> FAS1 domain <b>Family:</b> FAS1 domain
13	<a href="#">d1eg7a_</a>	Alignment		5.3	50	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
14	<a href="#">c2pr1B_</a>	Alignment		5.2	71	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized n-acetyltransferase ylbp; <b>PDBTitle:</b> crystal structure of the bacillus subtilis n-acetyltransferase ylbp2 protein in complex with coenzyme-a
15	<a href="#">c5a4jC_</a>	Alignment		5.2	60	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> formate--tetrahydrofolate ligase; <b>PDBTitle:</b> crystal structure of fthfs1 from t.acetoxydans re1
16	<a href="#">d1cta1</a>	Alignment		5.2	56	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain

17

[c4cvwD](#)

Alignment



5.1

15

**PDB header:**hydrolase/hydrolase inhibitor  
**Chain:** D: **PDB Molecule:**limit dextrinase inhibitor;  
**PDBTitle:** structure of the barley limit dextrinase-limit dextrinase2 inhibitor complex