
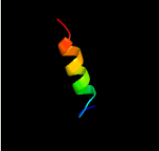
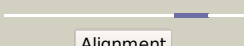
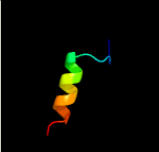
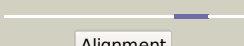

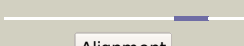




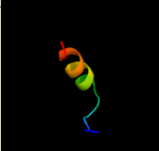

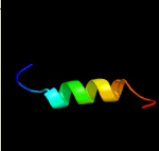




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3281_(-)_3663686_3664219
Date	Thu Aug 8 16:20:48 BST 2019
Unique Job ID	daffe695d9391cba

Detailed template information

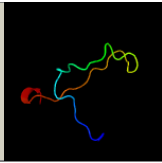
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2x3bB_</a>	 Alignment		15.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> toxic extracellular endopeptidase; <b>PDBTitle:</b> asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
2	<a href="#">d1eb6a_</a>	 Alignment		13.6	26	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Fungal zinc peptidase
3	<a href="#">c3r66A_</a>	 Alignment		11.6	75	<b>PDB header:</b> viral protein/antiviral protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 1; <b>PDBTitle:</b> crystal structure of human isg15 in complex with ns1 n-terminal region2 from influenza virus b, northeast structural genomics consortium3 target ids hx6481, hr2873, and or2
4	<a href="#">d1xeqa1</a>	 Alignment		10.6	75	<b>Fold:</b> S15/NS1 RNA-binding domain <b>Superfamily:</b> S15/NS1 RNA-binding domain <b>Family:</b> N-terminal, RNA-binding domain of nonstructural protein NS1
5	<a href="#">c4pwaA_</a>	 Alignment		9.6	25	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome c; <b>PDBTitle:</b> crystal structure of the c-type cytochrome soru from sinorhizobium2 meliloti
6	<a href="#">d1g12a_</a>	 Alignment		9.0	17	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Fungal zinc peptidase
7	<a href="#">d1cota_</a>	 Alignment		8.1	21	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
8	<a href="#">c3oa8A_</a>	 Alignment		7.9	12	<b>PDB header:</b> heme-binding protein/heme-binding protei <b>Chain:</b> A: <b>PDB Molecule:</b> soxa; <b>PDBTitle:</b> diheme soxax

9

[d1f00i3](#)



Alignment



6.5

26

**Fold:**C-type lectin-like  
**Superfamily:**C-type lectin-like  
**Family:**Invasin/intimin cell-adhesion fragment, C-terminal domain