
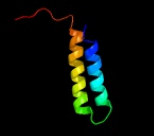



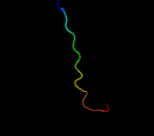



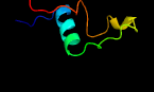



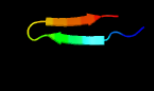



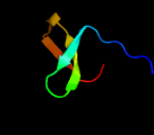






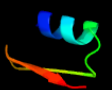
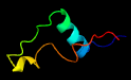


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0513 (-) _605607_606155
Date	Fri Jul 26 01:50:06 BST 2019
Unique Job ID	9d86ecfe2fc614c4

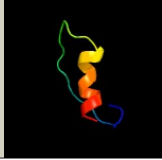
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6hwhX_</a>	 Alignment		28.9	14	<b>PDB header:</b> electron transport <b>Chain:</b> X: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 4; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
2	<a href="#">c3enoC_</a>	 Alignment		24.8	27	<b>PDB header:</b> hydrolase/unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein pf2011; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
3	<a href="#">c3x2dN_</a>	 Alignment		18.8	26	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> N: <b>PDB Molecule:</b> virion spike glycoprotein gp2; <b>PDBTitle:</b> crystal structure of marburg virus gp in complex with the human2 survivor antibody mr78
4	<a href="#">c2esyA_</a>	 Alignment		18.5	55	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lung surfactant protein c; <b>PDBTitle:</b> structure and influence on stability and activity of the n-2 terminal propetide part of lung surfactant protein c
5	<a href="#">d1ohfa_</a>	 Alignment		11.1	32	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Tetraviridae-like VP
6	<a href="#">d1pm4a_</a>	 Alignment		8.7	50	<b>Fold:</b> Superantigen (mitogen) Ypm <b>Superfamily:</b> Superantigen (mitogen) Ypm <b>Family:</b> Superantigen (mitogen) Ypm
7	<a href="#">d1lmia_</a>	 Alignment		8.2	31	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Antigen MPT63/MPB63 (immunoprotective extracellular protein) <b>Family:</b> Antigen MPT63/MPB63 (immunoprotective extracellular protein)
8	<a href="#">c2oznB_</a>	 Alignment		8.1	24	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> hyaluronoglucosaminidase; <b>PDBTitle:</b> the cohesin-dockerin complex of nagj and nagh from clostridium2 perfringens
9	<a href="#">c3le4A_</a>	 Alignment		8.1	17	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> microprocessor complex subunit dgcr8; <b>PDBTitle:</b> crystal structure of the dgcr8 dimerization domain
10	<a href="#">c1a87A_</a>	 Alignment		8.0	27	<b>PDB header:</b> bacteriocin <b>Chain:</b> A: <b>PDB Molecule:</b> colicin n; <b>PDBTitle:</b> colicin n
11	<a href="#">d1a87a_</a>	 Alignment		8.0	27	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin

12	<a href="#">d1q1ra3</a>	Alignment		7.7	13	<p><b>Fold:</b>CO dehydrogenase flavoprotein C-domain-like</p> <p><b>Superfamily:</b>FAD/NAD-linked reductases, dimerisation (C-terminal) domain</p> <p><b>Family:</b>FAD/NAD-linked reductases, dimerisation (C-terminal) domain</p>
13	<a href="#">c4uf7A_</a>	Alignment		7.3	29	<p><b>PDB header:</b>viral protein/immune system</p> <p><b>Chain:</b> A: <b>PDB Molecule:</b>glycoprotein;</p> <p><b>PDBTitle:</b> ghanaian henipavirus (gh-m74a) attachment glycoprotein in complex with2 human ephrinb2</p>
14	<a href="#">d2ibge1</a>	Alignment		6.8	23	<p><b>Fold:</b>Hedgehog/DD-peptidase</p> <p><b>Superfamily:</b>Hedgehog/DD-peptidase</p> <p><b>Family:</b>Hedgehog (development protein), N-terminal signaling domain</p>
15	<a href="#">d1ohfc_</a>	Alignment		5.6	32	<p><b>Fold:</b>Nucleoplasmin-like/VP (viral coat and capsid proteins)</p> <p><b>Superfamily:</b>Positive stranded ssRNA viruses</p> <p><b>Family:</b>Tetraviridae-like VP</p>

16 [dlwxma1](#)

Alignment



5.3

14

**Fold:**beta-Grasp (ubiquitin-like)  
**Superfamily:**Ubiquitin-like  
**Family:**Ras-binding domain, RBD