
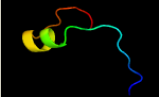

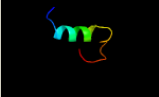
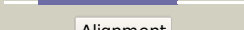
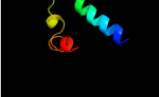
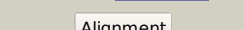
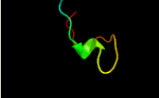
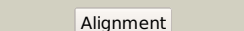





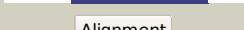

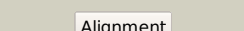




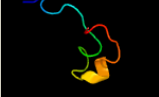


# Phyre2

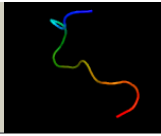
Email	mdejesus@rockefeller.edu
Description	RVBD2737A (- )_3051629_3051802
Date	Wed Aug 7 12:50:39 BST 2019
Unique Job ID	1281cc002e4b5f92

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2bs2b2</a>	 Alignment		20.8	56	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
2	<a href="#">d1kf6b2</a>	 Alignment		19.8	56	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
3	<a href="#">d2jeka1</a>	 Alignment		14.0	19	<b>Fold:</b> Rv1873-like <b>Superfamily:</b> Rv1873-like <b>Family:</b> Rv1873-like
4	<a href="#">d1nekb2</a>	 Alignment		13.8	61	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
5	<a href="#">c3hshA_</a>	 Alignment		13.2	25	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(xviii) chain; <b>PDBTitle:</b> crystal structure of human collagen xviii trimerization domain2 (tetragonal crystal form)
6	<a href="#">d1b8ta1</a>	 Alignment		9.7	63	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
7	<a href="#">c3n3fB_</a>	 Alignment		9.2	38	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-1(xv) chain; <b>PDBTitle:</b> crystal structure of the human collagen xv trimerization domain: a2 potent trimerizing unit common to multiplexin collagens
8	<a href="#">c2hd0D_</a>	 Alignment		8.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> protease ns2-3 (p23); <b>PDBTitle:</b> structure of the catalytic domain of hepatitis c virus ns2
9	<a href="#">d1fsha_</a>	 Alignment		6.9	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
10	<a href="#">c2xm5A_</a>	 Alignment		6.7	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cloq; <b>PDBTitle:</b> structural and mechanistic analysis of the magnesium-independent2 aromatic prenyltransferase cloq from the clorobiocin biosynthetic3 pathway
11	<a href="#">c5xmij_</a>	 Alignment		6.3	42	<b>PDB header:</b> electron transport <b>Chain:</b> J: <b>PDB Molecule:</b> succinate dehydrogenase iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas

12 [c3f6qB\\_](#)

Alignment



5.3

29

**PDB header:** signaling protein/signaling protein  
**Chain:** B: **PDB Molecule:** lim and senescent cell antigen-like-containing  
**PDBTitle:** crystal structure of integrin-linked kinase ankyrin repeat2 domain in complex with pinch1 lim1 domain