
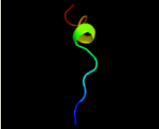
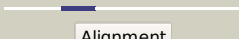
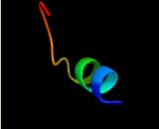
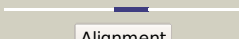


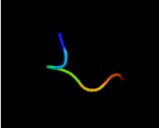



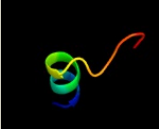

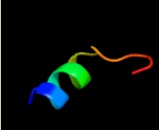



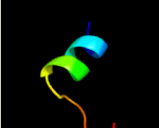



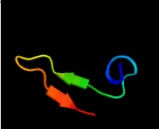








# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3861 (-) _4338124_4338450
Date	Sat Aug 10 22:05:04 BST 2019
Unique Job ID	8f819a87bed83d6e

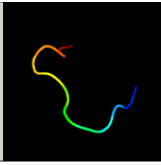
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1qb3B_</a>	 Alignment		10.3	53	<b>PDB header:</b> cell cycle <b>Chain:</b> B; <b>PDB Molecule:</b> cyclin-dependent kinases regulatory subunit; <b>PDBTitle:</b> crystal structure of the cell cycle regulatory protein cks1
2	<a href="#">d1t3qa1</a>	 Alignment		8.7	33	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
3	<a href="#">c2v51E_</a>	 Alignment		8.4	86	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> E; <b>PDB Molecule:</b> mkl/myocardin-like protein 1; <b>PDBTitle:</b> structure of mal-rpel1 complexed to actin
4	<a href="#">c2v51F_</a>	 Alignment		8.1	86	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> F; <b>PDB Molecule:</b> mkl/myocardin-like protein 1; <b>PDBTitle:</b> structure of mal-rpel1 complexed to actin
5	<a href="#">c5e8jC_</a>	 Alignment		7.8	75	<b>PDB header:</b> translation <b>Chain:</b> C; <b>PDB Molecule:</b> rnmt-activating mini protein; <b>PDBTitle:</b> crystal structure of mrna cap guanine-n7 methyltransferase in complex2 with ram
6	<a href="#">d1jroa1</a>	 Alignment		7.7	33	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
7	<a href="#">d1v97a1</a>	 Alignment		7.5	40	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
8	<a href="#">d1rm6c1</a>	 Alignment		7.3	27	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
9	<a href="#">d1zxia1</a>	 Alignment		7.0	40	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
10	<a href="#">d1dgja1</a>	 Alignment		6.4	40	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
11	<a href="#">d2gxba1</a>	 Alignment		6.3	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Z-DNA binding domain

12	<a href="#">d1n62a1</a>	Alignment		6.2	40	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
13	<a href="#">c2qkdA_</a>	Alignment		6.2	50	<b>PDB header:</b> signaling protein, cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein zpr1; <b>PDBTitle:</b> crystal structure of tandem zpr1 domains
14	<a href="#">d1ffva1</a>	Alignment		6.2	33	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
15	<a href="#">d1vlba1</a>	Alignment		5.5	47	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
16	<a href="#">d1qbjc_</a>	Alignment		5.4	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Z-DNA binding domain
17	<a href="#">c1t3qD_</a>	Alignment		5.3	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> quinoline 2-oxidoreductase small subunit; <b>PDBTitle:</b> crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86

18 [c2kctA\\_](#)

Alignment



5.3

31

**PDB header:**chaperone

**Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccme;

**PDBTitle:** solution nmr structure of the ob-fold domain of heme2 chaperone ccme from desulfovibrio vulgaris. northeast3 structural genomics target dvr115g.