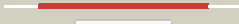


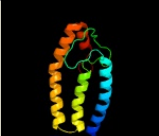
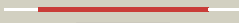








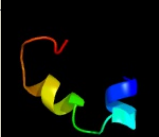

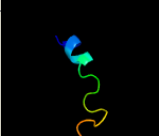

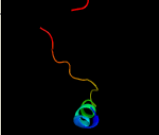






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2437 (-) _2734386_2734805
Date	Wed Aug 7 12:50:06 BST 2019
Unique Job ID	b63b15de2c1a8a35

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5v7pA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-s-isoprenylcysteine o-methyltransferase; <b>PDBTitle:</b> atomic structure of the eukaryotic intramembrane ras methyltransferase2 icmt (isoprenylcysteine carboxyl methyltransferase), in complex with3 a monobody
2	<a href="#">c4a2nB_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> isoprenylcysteine carboxyl methyltransferase; <b>PDBTitle:</b> crystal structure of ma-icmt
3	<a href="#">c4quvB_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase, membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> delta(14)-sterol reductase; <b>PDBTitle:</b> structure of an integral membrane delta(14)-sterol reductase
4	<a href="#">d1nu9c1</a>	 Alignment		41.6	24	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Staphylocoagulase <b>Family:</b> Staphylocoagulase
5	<a href="#">c2jp3A_</a>	 Alignment		37.1	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
6	<a href="#">c4y9iA_</a>	 Alignment		35.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mycobacterium tuberculosis paralogous family 11; <b>PDBTitle:</b> structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
7	<a href="#">c3r5yC_</a>	 Alignment		24.1	23	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of a deazaflavin-dependent nitroreductase from nocardia farcinica, with co-factor f420
8	<a href="#">c5e8jC_</a>	 Alignment		19.1	13	<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
9	<a href="#">d2fug11</a>	 Alignment		17.3	16	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Nqo1C-terminal domain-like <b>Family:</b> Nqo1C-terminal domain-like
10	<a href="#">c3r5wO_</a>	 Alignment		16.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> deazaflavin-dependent nitroreductase; <b>PDBTitle:</b> structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420
11	<a href="#">d1e7la1</a>	 Alignment		14.3	25	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> Recombination endonuclease VII, C-terminal and dimerization domains <b>Family:</b> Recombination endonuclease VII, C-terminal and dimerization domains

12	<a href="#">c1p58E_</a>	Alignment		13.9	37	<b>PDB header:</b> virus <b>Chain:</b> E; <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by 2 9.5 angstrom cryo-em reconstruction
13	<a href="#">c1p58F_</a>	Alignment		13.1	46	<b>PDB header:</b> virus <b>Chain:</b> F; <b>PDB Molecule:</b> envelope protein m; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by 2 9.5 angstrom cryo-em reconstruction
14	<a href="#">c5ht7A_</a>	Alignment		11.2	27	<b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a transition-metal-ion-binding betagamma-2 crystallin from methanosaeta thermophila
15	<a href="#">c3h96B_</a>	Alignment		10.6	23	<b>PDB header:</b> flavoprotein <b>Chain:</b> B; <b>PDB Molecule:</b> f420-h2 dependent reductase a; <b>PDBTitle:</b> msmeg_3358 f420 reductase
16	<a href="#">c3r5zB_</a>	Alignment		10.3	18	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
17	<a href="#">d1xyqa_</a>	Alignment		8.9	23	<b>Fold:</b> Prion-like <b>Superfamily:</b> Prion-like <b>Family:</b> Prion-like
18	<a href="#">c4b03D_</a>	Alignment		8.2	29	<b>PDB header:</b> virus <b>Chain:</b> D; <b>PDB Molecule:</b> dengue virus 1 prm protein; <b>PDBTitle:</b> 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
19	<a href="#">c4ct7A_</a>	Alignment		7.0	31	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> ccr4-not transcription complex subunit 1; <b>PDBTitle:</b> cnot9-cnot1 complex with bound tryptophan
20	<a href="#">c6em5v_</a>	Alignment		6.7	23	<b>PDB header:</b> ribosome <b>Chain:</b> V; <b>PDB Molecule:</b> 60s ribosomal protein l23-a; <b>PDBTitle:</b> state d architectural model (nsa1-tap flag-ytm1) - visualizing the 2 assembly pathway of nucleolar pre-60s ribosomes
21	<a href="#">d2e74g1</a>	Alignment	not modelled	6.6	25	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetG subunit of the cytochrome b6f complex <b>Family:</b> PetG subunit of the cytochrome b6f complex
22	<a href="#">c1vf5G_</a>	Alignment	not modelled	6.3	21	<b>PDB header:</b> photosynthesis <b>Chain:</b> G; <b>PDB Molecule:</b> protein pet g; <b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus
23	<a href="#">d1vf5g_</a>	Alignment	not modelled	6.3	21	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetG subunit of the cytochrome b6f complex <b>Family:</b> PetG subunit of the cytochrome b6f complex
24	<a href="#">c5o60g_</a>	Alignment	not modelled	6.1	67	<b>PDB header:</b> ribosome <b>Chain:</b> G; <b>PDB Molecule:</b> 50s ribosomal protein l6; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
25	<a href="#">c2m76A_</a>	Alignment	not modelled	5.3	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> carnitine o-palmitoyltransferase 1, brain isoform; <b>PDBTitle:</b> structure of the regulatory domain of human brain carnitine2 palmitoyltransferase 1
26	<a href="#">d1rgoa2</a>	Alignment	not modelled	5.3	67	<b>Fold:</b> CCCH zinc finger <b>Superfamily:</b> CCCH zinc finger <b>Family:</b> CCCH zinc finger