

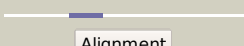
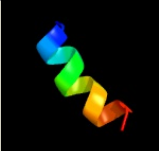
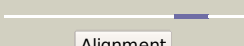

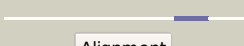


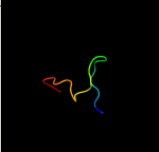





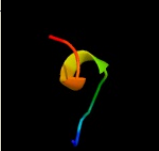



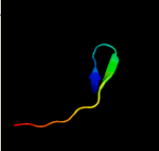




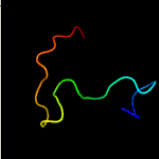
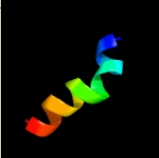
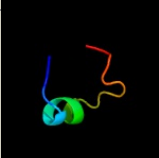
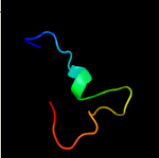





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0745 (-) _835157_835684
Date	Fri Jul 26 01:50:32 BST 2019
Unique Job ID	8f8e8b544ffd99ba

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2mvoA_</a>	 Alignment		22.0	75	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> solution structure of the lantibiotic self-resistance lipoprotein mlbq2 from microbispora atcc pta-5024
2	<a href="#">c6adql_</a>	 Alignment		19.4	43	<b>PDB header:</b> electron transport <b>Chain:</b> I; <b>PDB Molecule:</b> cytochrome c oxidase subunit ctaj; <b>PDBTitle:</b> respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
3	<a href="#">c5llyA_</a>	 Alignment		15.3	58	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> envelopment polyprotein; <b>PDBTitle:</b> structure of hantavirus envelope glycoprotein gc in complex with scfv2 a5
4	<a href="#">c2ec3A_</a>	 Alignment		15.3	38	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> fibronectin; <b>PDBTitle:</b> solution structure of the 11th fn1 domain from human2 fibronectin 1
5	<a href="#">c2kw0A_</a>	 Alignment		14.3	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ccmh protein; <b>PDBTitle:</b> solution structure of n-terminal domain of ccmh from escherichia.coli
6	<a href="#">c2hl7A_</a>	 Alignment		13.6	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> cytochrome c-type biogenesis protein ccmh; <b>PDBTitle:</b> crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
7	<a href="#">c5lk1A_</a>	 Alignment		12.0	58	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> envelopment polyprotein; <b>PDBTitle:</b> structure of hantavirus envelope glycoprotein gc in postfusion2 conformation in presence of 200 mm kcl
8	<a href="#">c2hlgA_</a>	 Alignment		10.9	64	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> fruit-specific protein; <b>PDBTitle:</b> nmr solution structure of a new tomato peptide
9	<a href="#">c6hwhR_</a>	 Alignment		9.1	55	<b>PDB header:</b> electron transport <b>Chain:</b> R; <b>PDB Molecule:</b> msmeg_4693; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
10	<a href="#">c3ejhB_</a>	 Alignment		8.9	25	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> fibronectin; <b>PDBTitle:</b> crystal structure of the fibronectin 8-9fni domain pair in complex2 with a type-i collagen peptide
11	<a href="#">c2fe1A_</a>	 Alignment		8.5	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> conserved hypothetical protein pae0151; <b>PDBTitle:</b> crystal structure of pae0151 from pyrobaculum aerophilum

12	<a href="#">d2fe1a1</a>	Alignment		8.5	16	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> PIN domain
13	<a href="#">c2n2cA</a>	Alignment		7.9	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> tar dna-binding protein 43; <b>PDBTitle:</b> nmr structure of tdp-43 prion-like hydrophobic helix in dpc
14	<a href="#">c5c2wF</a>	Alignment		7.5	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> hypothetical (di heme) protein; <b>PDBTitle:</b> kueningenia stuttgartiensis hydrazine synthase pressurized with 20 bar2 xenon
15	<a href="#">c2n3xA</a>	Alignment		7.2	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> tar dna-binding protein 43; <b>PDBTitle:</b> solution structure of tdp-43 amyloidogenic core region
16	<a href="#">c5lxyH</a>	Alignment		6.9	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> H; <b>PDB Molecule:</b> zinc finger cchc domain-containing protein 8; <b>PDBTitle:</b> structure of the minimal rbm7 - zchc8 complex
17	<a href="#">d1iqca1</a>	Alignment		6.8	20	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Di-heme cytochrome c peroxidase
18	<a href="#">c6hwhB</a>	Alignment		6.5	30	<b>PDB header:</b> electron transport <b>Chain:</b> B; <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
19	<a href="#">d2j8ba1</a>	Alignment		6.4	23	<b>Fold:</b> Snake toxin-like <b>Superfamily:</b> Snake toxin-like <b>Family:</b> Extracellular domain of cell surface receptors
20	<a href="#">d1j98a</a>	Alignment		6.4	13	<b>Fold:</b> LuxS/MPP-like metallohydrolase <b>Superfamily:</b> LuxS/MPP-like metallohydrolase <b>Family:</b> Autoinducer-2 production protein LuxS
21	<a href="#">c4d6ul</a>	Alignment	not modelled	6.3	48	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I; <b>PDB Molecule:</b> cytochrome b-c1 complex subunit rieske, mitochondrial; <b>PDBTitle:</b> cytochrome bc1 bound to the 4(1h)-pyridone gsk932121
22	<a href="#">d1j6wa</a>	Alignment	not modelled	5.7	20	<b>Fold:</b> LuxS/MPP-like metallohydrolase <b>Superfamily:</b> LuxS/MPP-like metallohydrolase <b>Family:</b> Autoinducer-2 production protein LuxS
23	<a href="#">c3j38V</a>	Alignment	not modelled	5.4	83	<b>PDB header:</b> ribosome <b>Chain:</b> V; <b>PDB Molecule:</b> 40s ribosomal protein s21; <b>PDBTitle:</b> structure of the d. melanogaster 40s ribosomal proteins
24	<a href="#">c4dapA</a>	Alignment	not modelled	5.4	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> sugar fermentation stimulation protein a; <b>PDBTitle:</b> the structure of escherichia coli sfsa
25	<a href="#">c6e1cB</a>	Alignment	not modelled	5.4	25	<b>PDB header:</b> metal binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> di-heme enzyme; <b>PDBTitle:</b> crystal structure of a maug-like protein associated with microbial2 copper homeostasis
26	<a href="#">c2vhdB</a>	Alignment	not modelled	5.3	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> cytochrome c551 peroxidase; <b>PDBTitle:</b> crystal structure of the di-haem cytochrome c peroxidase from2 pseudomonas aeruginosa - mixed valence form
27	<a href="#">c4xchB</a>	Alignment	not modelled	5.1	20	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> s-ribosylhomocysteine lyase; <b>PDBTitle:</b> s-ribosylhomocysteinase from streptococcus suis