


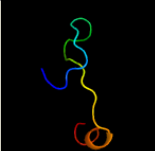

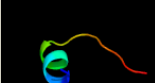



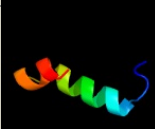

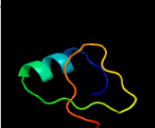





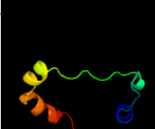






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1829_(-)_2073950_2074444
Date	Fri Aug 2 13:30:44 BST 2019
Unique Job ID	0e1d91b439d32cad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1vjla_</a>	 Alignment		100.0	33	<b>Fold:</b> Hypothetical protein TM0160 <b>Superfamily:</b> Hypothetical protein TM0160 <b>Family:</b> Hypothetical protein TM0160
2	<a href="#">c5fr7B_</a>	 Alignment		32.3	18	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> amyr; <b>PDBTitle:</b> erwinia amylovora amyr amylovoran repressor, a member of the ybjn2 protein family
3	<a href="#">d3orca_</a>	 Alignment		21.6	20	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
4	<a href="#">c3op6B_</a>	 Alignment		18.2	21	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an oligo-nucleotide binding protein (lpg1207)2 from legionella pneumophila subsp. pneumophila str. philadelphia 1 at3 2.00 a resolution
5	<a href="#">d1j2jb_</a>	 Alignment		18.1	23	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> GAT-like domain <b>Family:</b> GAT domain
6	<a href="#">d1b7go1</a>	 Alignment		15.5	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
7	<a href="#">c3btzA_</a>	 Alignment		14.7	20	<b>PDB header:</b> oxidoreductase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-ketoglutarate-dependent dioxygenase alkB homolog 2; <b>PDBTitle:</b> crystal structure of human abh2 cross-linked to dsdna
8	<a href="#">c5wtqB_</a>	 Alignment		13.7	13	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> proteasome assembly chaperone 4; <b>PDBTitle:</b> crystal structure of human proteasome-assembling chaperone pac4
9	<a href="#">c6conF_</a>	 Alignment		12.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> coa-transferase subunit beta; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis ipdab
10	<a href="#">d1o12a1</a>	 Alignment		10.3	28	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> N-acetylglucosamine-6-phosphate deacetylase, NagA
11	<a href="#">c3nr7A_</a>	 Alignment		9.0	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein h-ns; <b>PDBTitle:</b> crystal structure of s. typhimurium h-ns 1-83

12	<a href="#">c2cx5B_</a>	Alignment		8.1	13	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> a putative trans-editing enzyme; <b>PDBTitle:</b> crystal structure of a putative trans-editing enzyme for2 prolyl trna synthetase
13	<a href="#">c2dxaA_</a>	Alignment		7.9	11	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> protein ybak; <b>PDBTitle:</b> crystal structure of trans editing enzyme prox from e.coli
14	<a href="#">c3jrtA_</a>	Alignment		7.8	50	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> integron cassette protein vpc_cass2; <b>PDBTitle:</b> structure from the mobile metagenome of v. paracholerae: integron2 cassette protein vpc_cass2
15	<a href="#">c4acrB_</a>	Alignment		7.6	8	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glypican-1; <b>PDBTitle:</b> crystal structure of n-glycosylated, c-terminally truncated human2 glypican-1
16	<a href="#">d1f3ua_</a>	Alignment		6.8	25	<b>Fold:</b> triple barrel <b>Superfamily:</b> Rap30/74 interaction domains <b>Family:</b> Rap30/74 interaction domains
17	<a href="#">d1dbxa_</a>	Alignment		6.7	9	<b>Fold:</b> YbaK/ProRS associated domain <b>Superfamily:</b> YbaK/ProRS associated domain <b>Family:</b> YbaK/ProRS associated domain
18	<a href="#">c2n92A_</a>	Alignment		6.2	46	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> cecropin-p1; <b>PDBTitle:</b> solution structure of cecropin p1 with lps
19	<a href="#">d1khua_</a>	Alignment		6.2	10	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> SMAD domain
20	<a href="#">d1fo0a_</a>	Alignment		6.2	29	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
21	<a href="#">c6n7xH_</a>	Alignment	not modelled	5.7	10	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> H: <b>PDB Molecule:</b> u1 small nuclear ribonucleoprotein component snu71; <b>PDBTitle:</b> s. cerevisiae u1 snrnp
22	<a href="#">d2dsya1</a>	Alignment	not modelled	5.7	11	<b>Fold:</b> TTHA1013/TTHA0281-like <b>Superfamily:</b> TTHA1013/TTHA0281-like <b>Family:</b> TTHA0281-like
23	<a href="#">c6j0eB_</a>	Alignment	not modelled	5.6	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> arsenic responsive repressor arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
24	<a href="#">c2pijB_</a>	Alignment	not modelled	5.6	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> prophage pfl 6 cro; <b>PDBTitle:</b> structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
25	<a href="#">d3eeqa2</a>	Alignment	not modelled	5.6	20	<b>Fold:</b> CbiG N-terminal domain-like <b>Superfamily:</b> CbiG N-terminal domain-like <b>Family:</b> CbiG N-terminal domain-like
26	<a href="#">c6abfC_</a>	Alignment	not modelled	5.5	28	<b>PDB header:</b> viral protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> polymerase pb2; <b>PDBTitle:</b> structure of influenza d virus polymerase bound to vrna promoter in2 mode b conformation (class b1)
27	<a href="#">c4ep5A_</a>	Alignment	not modelled	5.5	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crossover junction endodeoxyribonuclease ruvc; <b>PDBTitle:</b> thermus thermophilus ruvc structure
28	<a href="#">c2l69A_</a>	Alignment	not modelled	5.3	26	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> rossmann 2x3 fold protein; <b>PDBTitle:</b> solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28

29	<a href="#">c5zt3A_</a>	Alignment	not modelled	5.3	27	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> wa352; <b>PDBTitle:</b> crystal structure of wa352 from oryza sativa
30	<a href="#">d1d8ba_</a>	Alignment	not modelled	5.3	19	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> HRDC domain from helicases