


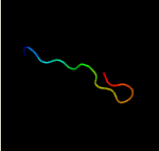
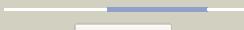
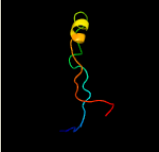

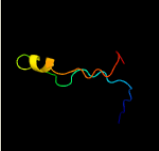

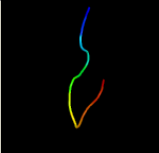

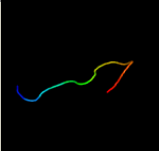

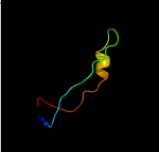

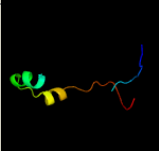

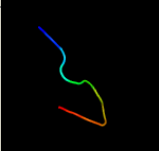

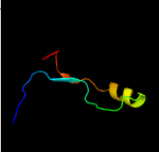

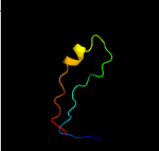
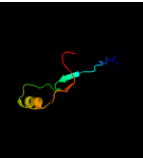
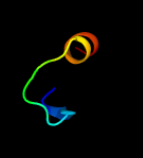
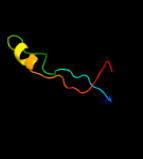


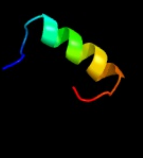
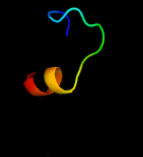




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2545_(-)_2867793_2868071
Date	Wed Aug 7 12:50:18 BST 2019
Unique Job ID	1e55d525ec7a0cf8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6a7vU_</a>	 Alignment		95.0	47	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> U: <b>PDB Molecule:</b> antitoxin vapp11; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
2	<a href="#">d1ea0a3</a>	 Alignment		28.2	47	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
3	<a href="#">d1ygpa_</a>	 Alignment		23.7	33	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
4	<a href="#">d2gj4a1</a>	 Alignment		21.4	25	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
5	<a href="#">d1ofda3</a>	 Alignment		21.2	58	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
6	<a href="#">c2vdcF_</a>	 Alignment		21.0	47	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamate synthase [nadph] large chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
7	<a href="#">c4l22A_</a>	 Alignment		18.2	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphorylase; <b>PDBTitle:</b> crystal structure of putative glycogen phosphorylase from2 streptococcus mutans
8	<a href="#">d1l5wa_</a>	 Alignment		18.0	43	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
9	<a href="#">c1lm1A_</a>	 Alignment		17.5	58	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-dependent glutamate synthase; <b>PDBTitle:</b> structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
10	<a href="#">d2atia1</a>	 Alignment		17.4	33	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
11	<a href="#">c2c4mA_</a>	 Alignment		17.3	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen phosphorylase; <b>PDBTitle:</b> starch phosphorylase: structural studies explain oxyanion-dependent2 kinetic stability and regulatory control.

12	<a href="#">c3ddsB_</a>	Alignment		17.0	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycogen phosphorylase, liver form; <b>PDBTitle:</b> crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
13	<a href="#">d1hiod_</a>	Alignment		16.1	24	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
14	<a href="#">c4bqeA_</a>	Alignment		15.6	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucan phosphorylase 2,4-glucan phosphorylase; <b>PDBTitle:</b> arabidopsis thaliana cytosolic alpha-1,4-glucan phosphorylase (phs2)
15	<a href="#">c3b0dB_</a>	Alignment		14.0	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> centromere protein t; <b>PDBTitle:</b> crystal structure of the chicken cenp-t histone fold/cenp-w complex,2 crystal form ii
16	<a href="#">d1id3b_</a>	Alignment		12.4	24	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
17	<a href="#">c5lnkn_</a>	Alignment		12.2	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N: <b>PDB Molecule:</b> mitochondrial complex i, nd2 subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
18	<a href="#">d2huec1</a>	Alignment		12.1	24	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
19	<a href="#">d1htaa_</a>	Alignment		10.4	41	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Archaeal histone
20	<a href="#">d1kx5b_</a>	Alignment		10.2	24	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
21	<a href="#">c6mzlk_</a>	Alignment	not modelled	10.1	19	<b>PDB header:</b> transcription <b>Chain:</b> K: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 8,taf8; <b>PDBTitle:</b> human tfiid canonical state
22	<a href="#">c3nquA_</a>	Alignment	not modelled	9.7	40	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> histone h3-like centromeric protein a; <b>PDBTitle:</b> crystal structure of partially trypsinized (cenp-a/h4)2 heterotetramer
23	<a href="#">c3r2cj_</a>	Alignment	not modelled	8.7	56	<b>PDB header:</b> transcription/rna <b>Chain:</b> J: <b>PDB Molecule:</b> 30s ribosomal protein s10; <b>PDBTitle:</b> crystal structure of antitermination factors nusB and nusE in complex2 with boxA rna
24	<a href="#">c3nqjA_</a>	Alignment	not modelled	8.2	40	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> histone h3-like centromeric protein a; <b>PDBTitle:</b> crystal structure of (cenp-a/h4)2 heterotetramer
25	<a href="#">c4e6fB_</a>	Alignment	not modelled	8.1	35	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf4468 family protein (bacova_04320) from bacteroides ovatus atcc 8483 at 1.49 a resolution
26	<a href="#">d1ku5a_</a>	Alignment	not modelled	8.0	35	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Archaeal histone
27	<a href="#">d2f06a1</a>	Alignment	not modelled	7.8	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> BT0572-like
28	<a href="#">c5lrbb_</a>	Alignment	not modelled	7.7	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-1,4 glucan phosphorylase; <b>PDBTitle:</b> plastidial phosphorylase from barley in complex with acarbose

29	<a href="#">c3v9rC_</a>	Alignment	not modelled	7.5	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein yol086w-a; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae mhf complex
30	<a href="#">c6e0cA_</a>	Alignment	not modelled	6.8	40	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> histone h3-like centromeric protein a; <b>PDBTitle:</b> cryo-em structure of the cenp-a nucleosome (w601) in complex with a2 single chain antibody fragment
31	<a href="#">d1a7wa_</a>	Alignment	not modelled	6.7	41	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Archaeal histone
32	<a href="#">c6mzdC_</a>	Alignment	not modelled	6.1	20	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 3; <b>PDBTitle:</b> human tfiid lobe a canonical
33	<a href="#">c1cr5B_</a>	Alignment	not modelled	6.0	24	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> B: <b>PDB Molecule:</b> sec18p (residues 22 - 210); <b>PDBTitle:</b> n-terminal domain of sec18p
34	<a href="#">d1tafa_</a>	Alignment	not modelled	5.4	57	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
35	<a href="#">c6b12B_</a>	Alignment	not modelled	5.2	44	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> tni2; <b>PDBTitle:</b> structure of tne2 in complex with tni2
36	<a href="#">c3vh5A_</a>	Alignment	not modelled	5.1	38	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cenp-s; <b>PDBTitle:</b> crystal structure of the chicken cenp-t histone fold/cenp-w/cenp-2 s/cenp-x heterotetrameric complex, crystal form i