

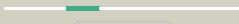












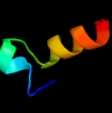





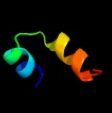






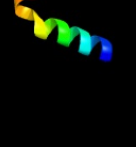

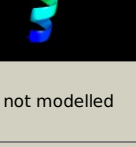


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3771c_(-)_4216582_4216908
Date	Fri Aug 9 18:20:47 BST 2019
Unique Job ID	0892894ae05c6b9a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1k78a1</a>	 Alignment		49.0	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
2	<a href="#">d2oeba1</a>	 Alignment		46.4	38	<b>Fold:</b> ATPD N-terminal domain-like <b>Superfamily:</b> AF1862-like <b>Family:</b> Cas Cmr5-like
3	<a href="#">c2zopA_</a>	 Alignment		45.1	50	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein tthb164; <b>PDBTitle:</b> x-ray crystal structure of a crispr-associated cmr5 family2 protein from thermus thermophilus hb8
4	<a href="#">c4gkfA_</a>	 Alignment		42.1	63	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> crispr system cmr subunit cmr5; <b>PDBTitle:</b> crystal structure and characterization of cmr5 protein from pyrococcus2 furiosus
5	<a href="#">d1pdnc_</a>	 Alignment		37.0	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
6	<a href="#">d6paxa1</a>	 Alignment		34.7	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
7	<a href="#">c6paxA_</a>	 Alignment		26.5	24	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein pax-6; <b>PDBTitle:</b> crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
8	<a href="#">c2rn7A_</a>	 Alignment		24.3	32	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> is629 orfa; <b>PDBTitle:</b> nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
9	<a href="#">d1iufa2</a>	 Alignment		23.7	56	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
10	<a href="#">c1sy9B_</a>	 Alignment		23.5	63	<b>PDB header:</b> calcium-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cyclic-nucleotide-gated olfactory channel; <b>PDBTitle:</b> structure of calmodulin complexed with a fragment of the2 olfactory cng channel
11	<a href="#">c1u78A_</a>	 Alignment		22.2	13	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element tc3 transposase; <b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna

12	<a href="#">c3hefB_</a>	Alignment		21.2	17	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gene 1 protein; <b>PDBTitle:</b> crystal structure of the bacteriophage sf6 terminase small subunit
13	<a href="#">c1iufA_</a>	Alignment		18.4	56	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> centromere abp1 protein; <b>PDBTitle:</b> low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
14	<a href="#">c2kwtA_</a>	Alignment		18.4	64	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protease ns2-3; <b>PDBTitle:</b> solution structure of ns2 [27-59]
15	<a href="#">d1hlva2</a>	Alignment		18.2	60	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
16	<a href="#">d2ikba1</a>	Alignment		15.1	56	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> NMB1012-like
17	<a href="#">c1hlvA_</a>	Alignment		12.0	60	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> major centromere autoantigen b; <b>PDBTitle:</b> crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
18	<a href="#">c5kn4B_</a>	Alignment		11.7	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pavine n-methyltransferase; <b>PDBTitle:</b> pavine n-methyltransferase apoenzyme ph 6.0
19	<a href="#">c6m8nA_</a>	Alignment		10.4	62	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> p5afcna; <b>PDBTitle:</b> endo-fucoidan hydrolase p5afcna from glycoside hydrolase family 107
20	<a href="#">c6gkvB_</a>	Alignment		7.9	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> coclaurine n-methyltransferase; <b>PDBTitle:</b> crystal structure of coclaurine n-methyltransferase (cnmt) bound to n-2 methylheliamine and sah
21	<a href="#">c5uumD_</a>	Alignment	not modelled	7.8	43	<b>PDB header:</b> apoptosis <b>Chain:</b> D: <b>PDB Molecule:</b> bfl-1 specific peptide fs2; <b>PDBTitle:</b> human mcl-1 in complex with a bfl-1-specific selected peptide
22	<a href="#">c5uumC_</a>	Alignment	not modelled	7.8	43	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> bfl-1 specific peptide fs2; <b>PDBTitle:</b> human mcl-1 in complex with a bfl-1-specific selected peptide
23	<a href="#">c4b6xB_</a>	Alignment	not modelled	7.4	54	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> avirulence protein; <b>PDBTitle:</b> crystal structure of in planta processed avrrps4
24	<a href="#">c3l52A_</a>	Alignment	not modelled	7.3	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> crystal structure of putative orotidine 5'-phosphate decarboxylase2 from streptomyces avermitilis ma-4680
25	<a href="#">c3bd1B_</a>	Alignment	not modelled	7.3	24	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> cro protein; <b>PDBTitle:</b> structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
26	<a href="#">c6bqcA_</a>	Alignment	not modelled	7.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclopropane-fatty-acyl-phospholipid synthase; <b>PDBTitle:</b> cyclopropane fatty acid synthase from e. coli
27	<a href="#">d2jn6a1</a>	Alignment	not modelled	7.2	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
28	<a href="#">c4czdA_</a>	Alignment	not modelled	6.8	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator, asnc family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that

					is part of the3 alternative haem biosynthesis pathway.
29	<a href="#">d1hlva1</a>	Alignment	not modelled	6.5	21 <b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Centromere-binding
30	<a href="#">c4r11D</a>	Alignment	not modelled	6.5	100 <b>PDB header:</b> cell adhesion/protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> cadherin-related hmr-1; <b>PDBTitle:</b> a conserved phosphorylation switch controls the interaction between2 cadherin and beta-catenin in vitro and in vivo
31	<a href="#">c5ejoA</a>	Alignment	not modelled	6.5	42 <b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> chromatin assembly factor 1 subunit p90; <b>PDBTitle:</b> crystal structure of the winged helix domain in chromatin assembly2 factor 1 subunit p90
32	<a href="#">c5uukB</a>	Alignment	not modelled	6.4	53 <b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bfl-1-specific selected peptide; <b>PDBTitle:</b> human bfl-1 in complex with a bfl-1-specific selected peptide
33	<a href="#">c5oetB</a>	Alignment	not modelled	6.4	29 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione synthetase-like effector 30 (gpa-gss30-apo); <b>PDBTitle:</b> the structure of a glutathione synthetase like-effector (gss30) from2 globodera pallida in apoform.
34	<a href="#">c2elhA</a>	Alignment	not modelled	6.1	39 <b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cg11849-pa; <b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
35	<a href="#">c3pvsA</a>	Alignment	not modelled	5.8	21 <b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> replication-associated recombination protein a; <b>PDBTitle:</b> structure and biochemical activities of escherichia coli mgsa
36	<a href="#">c2yskA</a>	Alignment	not modelled	5.7	38 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha1432; <b>PDBTitle:</b> crystal structure of a hypothetical protein ttha1432 from thermus2 thermophilus
37	<a href="#">c2jqtA</a>	Alignment	not modelled	5.6	78 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> h-ns/stpa-binding protein 2; <b>PDBTitle:</b> structure of the bacterial replication origin-associated2 protein cnu