


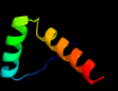
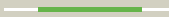






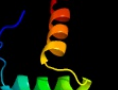



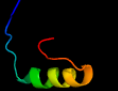

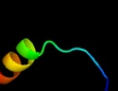



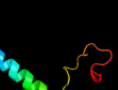
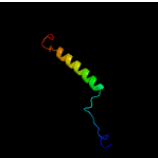

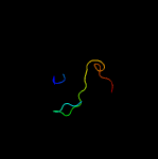
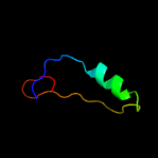
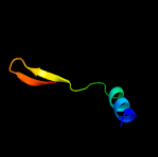
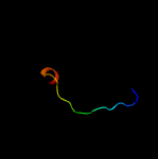
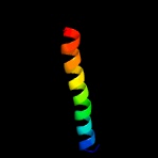
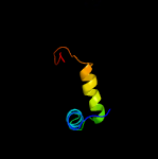
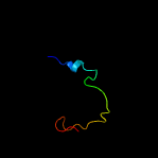


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0616A\_(RVBD0616A)\_710785\_711012  
 Date Fri Jul 26 01:50:17 BST 2019  
 Unique Job ID 06a6648e9a50493a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2k5jB_</a>	 Alignment		82.5	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yiif; <b>PDBTitle:</b> solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
2	<a href="#">d2bj7a1</a>	 Alignment		57.0	24	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
3	<a href="#">c2ca9B_</a>	 Alignment		52.9	26	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative nickel-responsive regulator; <b>PDBTitle:</b> apo-nikr from helicobacter pylori in closed trans-2 conformation
4	<a href="#">d2hzab1</a>	 Alignment		49.6	31	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
5	<a href="#">c1q5vB_</a>	 Alignment		49.4	28	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> apo-nikr
6	<a href="#">c2bj3D_</a>	 Alignment		45.8	26	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> nikr-apo
7	<a href="#">d2hzaa1</a>	 Alignment		40.0	32	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
8	<a href="#">c2k9iB_</a>	 Alignment		25.2	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein orf56; <b>PDBTitle:</b> nmr structure of plasmid copy control protein orf56 from sulfolobus2 islandicus
9	<a href="#">c6a7vU_</a>	 Alignment		22.6	28	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> U: <b>PDB Molecule:</b> antitoxin vapb11; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
10	<a href="#">c6g1nB_</a>	 Alignment		14.9	21	<b>PDB header:</b> antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin hicb; <b>PDBTitle:</b> crystal structure of the burkholderia pseudomallei antitoxin hicb
11	<a href="#">d1lbqa_</a>	 Alignment		13.7	38	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> Ferrochelatase

12	<a href="#">d1bg3a1</a>	Alignment		12.6	27	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
13	<a href="#">c4jjaA_</a>	Alignment		11.1	45	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf1343 family protein (bf0379) from2 bacteroides fragilis nctc 9343 at 1.30 a resolution
14	<a href="#">c4k05B_</a>	Alignment		8.4	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical exported protein; <b>PDBTitle:</b> crystal structure of a duf1343 family protein (bf0371) from2 bacteroides fragilis nctc 9343 at 1.65 a resolution
15	<a href="#">c2j8aA_</a>	Alignment		8.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase, h3 lysine-4 <b>PDBTitle:</b> x-ray structure of the n-terminus rrm domain of set1
16	<a href="#">d1xhna1</a>	Alignment		7.3	27	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
17	<a href="#">d2hrca1</a>	Alignment		7.2	35	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> Ferrochelatase
18	<a href="#">c2k48A_</a>	Alignment		7.1	31	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> nmr structure of the n-terminal coiled coil domain of the2 andes hantavirus nucleocapsid protein
19	<a href="#">d1mnta_</a>	Alignment		6.8	16	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
20	<a href="#">c2lnvA_</a>	Alignment		6.5	27	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> general secretion pathway protein c; <b>PDBTitle:</b> solution structure of gspc-hr of typeii secretion system
21	<a href="#">c6etxR_</a>	Alignment	not modelled	6.2	45	<b>PDB header:</b> dna binding protein <b>Chain:</b> R: <b>PDB Molecule:</b> ino80 complex subunit b; <b>PDBTitle:</b> cryo-em structure of the human ino80 complex bound to nucleosome
22	<a href="#">c4d8jD_</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> macrodomein ter protein; <b>PDBTitle:</b> structure of e. coli matp-mats complex
23	<a href="#">c3e7hA_</a>	Alignment	not modelled	5.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta; <b>PDBTitle:</b> the crystal structure of the beta subunit of the dna-directed rna2 polymerase from vibrio cholerae o1 biovar eltor
24	<a href="#">c3dnhB_</a>	Alignment	not modelled	5.3	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein atu2129; <b>PDBTitle:</b> the crystal structure of the protein atu2129 (unknown function) from2 agrobacterium tumefaciens str. c58