




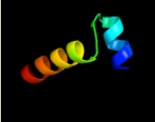


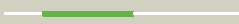




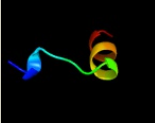

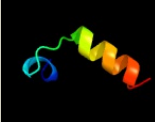

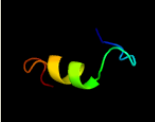



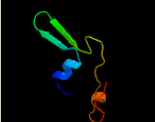
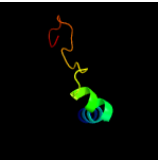
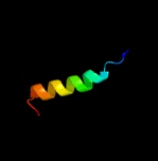

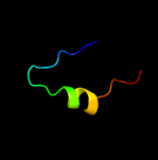

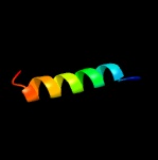

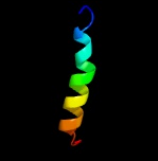
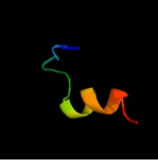


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0660c_(-)_754983_755228
Date	Fri Jul 26 01:50:22 BST 2019
Unique Job ID	c1968ebe608bb4c6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2bj7a1</a>	 Alignment		68.0	21	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
2	<a href="#">c2k5jB_</a>	 Alignment		67.8	22	<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
3	<a href="#">c2bj3D_</a>	 Alignment		57.8	21	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> nikr-apo
4	<a href="#">d2hza1</a>	 Alignment		54.7	46	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
5	<a href="#">d2hzaa1</a>	 Alignment		54.5	44	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
6	<a href="#">c1q5vB_</a>	 Alignment		50.6	44	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> apo-nikr
7	<a href="#">c2ca9B_</a>	 Alignment		50.4	50	<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
8	<a href="#">c6g1nB_</a>	 Alignment		32.5	35	<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
9	<a href="#">d2byea1</a>	 Alignment		23.5	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
10	<a href="#">c4p7dA_</a>	 Alignment		19.9	25	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin hicb3; <b>PDBTitle:</b> antitoxin hicb3 crystal structure
11	<a href="#">d1cmca_</a>	 Alignment		18.4	42	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Met repressor, Metj (MetR)

12	<a href="#">d1b4pa1</a>	Alignment		10.1	18	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
13	<a href="#">d1rqa2</a>	Alignment		10.1	29	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
14	<a href="#">d1irxa2</a>	Alignment		9.8	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
15	<a href="#">c5khqB_</a>	Alignment		9.5	26	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ras-interacting protein 1; <b>PDBTitle:</b> rasip1 ra domain
16	<a href="#">d1f3va_</a>	Alignment		9.0	42	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> TRADD, N-terminal domain <b>Family:</b> TRADD, N-terminal domain
17	<a href="#">d1f7ua2</a>	Alignment		8.8	26	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
18	<a href="#">c5yrzC_</a>	Alignment		8.5	29	<b>PDB header:</b> antitoxin/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> hicb; <b>PDBTitle:</b> toxin-antitoxin complex from streptococcus pneumoniae
19	<a href="#">d1iq0a2</a>	Alignment		8.4	43	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
20	<a href="#">d2cs4a1</a>	Alignment		8.1	40	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
21	<a href="#">c3ddcB_</a>	Alignment	not modelled	7.9	22	<b>PDB header:</b> hydrolase/apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> ras association domain-containing family protein 5; <b>PDBTitle:</b> crystal structure of nore1a in complex with ras
22	<a href="#">c2lciA_</a>	Alignment	not modelled	7.5	60	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein or36; <b>PDBTitle:</b> solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or36 (casd3 target)
23	<a href="#">c2uwqA_</a>	Alignment	not modelled	7.4	30	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> apoptosis-stimulating of p53 protein 2; <b>PDBTitle:</b> solution structure of aspp2 n-terminus
24	<a href="#">d1ll5a2</a>	Alignment	not modelled	7.1	29	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
25	<a href="#">d2vnga1</a>	Alignment	not modelled	6.7	33	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> NPCBM-like
26	<a href="#">d1wgra_</a>	Alignment	not modelled	6.7	39	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
27	<a href="#">c4jj9A_</a>	Alignment	not modelled	6.6	32	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-carboxymethyl-2-hydroxyuconate delta-isomerase; <b>PDBTitle:</b> crystal structure of 5-carboxymethyl-2-hydroxyuconate delta-isomerase
28	<a href="#">c3hl4B_</a>	Alignment	not modelled	6.1	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> choline-phosphate cytidyltransferase a; <b>PDBTitle:</b> crystal structure of a mammalian ctp:phosphocholine2 cytidyltransferase with cdp-choline

29	<a href="#">c2gp8A_</a>	Alignment	not modelled	6.1	38	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (scaffolding protein); <b>PDBTitle:</b> nmr solution structure of the coat protein-binding domain2 of bacteriophage p22 scaffolding protein
30	<a href="#">c1gp8A_</a>	Alignment	not modelled	6.1	38	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (scaffolding protein); <b>PDBTitle:</b> nmr solution structure of the coat protein-binding domain2 of bacteriophage p22 scaffolding protein
31	<a href="#">c5mz6B_</a>	Alignment	not modelled	6.0	50	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> interactor of fizzy protein; <b>PDBTitle:</b> cryo-em structure of a separase-securin complex from caenorhabditis2 elegans at 3.8 a resolution
32	<a href="#">d1duga1</a>	Alignment	not modelled	5.8	13	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
33	<a href="#">d2c4ja1</a>	Alignment	not modelled	5.7	16	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
34	<a href="#">c3kxeD_</a>	Alignment	not modelled	5.7	50	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> antitoxin protein pard-1; <b>PDBTitle:</b> a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
35	<a href="#">c3u1dA_</a>	Alignment	not modelled	5.6	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the structure of a protein with a gntr superfamily winged-helix-turn-2 helix domain from halomicrobium mukohataei.
36	<a href="#">c4q2tB_</a>	Alignment	not modelled	5.6	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> arginine--trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of arginyl-trna synthetase complexed with l-arginine