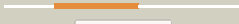

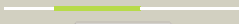


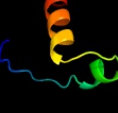




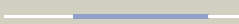


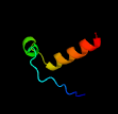

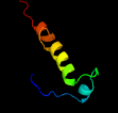

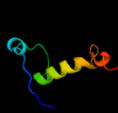

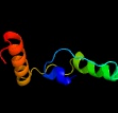


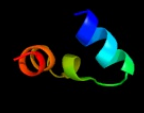
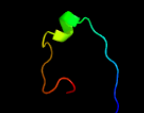





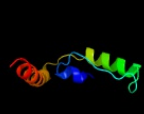



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0550c_(-)_640641_640907
Date	Fri Jul 26 01:50:10 BST 2019
Unique Job ID	d7e1e88b0afc47d4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5yrzC_</a>	 Alignment		83.8	25	<b>PDB header:</b> antitoxin/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> hicb; <b>PDBTitle:</b> toxin-antitoxin complex from streptococcus pneumoniae
2	<a href="#">c4p7dA_</a>	 Alignment		69.5	12	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin hicb3; <b>PDBTitle:</b> antitoxin hicb3 crystal structure
3	<a href="#">c6g1nB_</a>	 Alignment		62.4	27	<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
4	<a href="#">c6a6xC_</a>	 Alignment		37.9	62	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> antitoxin maze7; <b>PDBTitle:</b> the crystal structure of the mtb maze-mazf-mt9 complex
5	<a href="#">c5x3tA_</a>	 Alignment		26.8	43	<b>PDB header:</b> antitoxin/toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin vapp26; <b>PDBTitle:</b> vappc from mycobacterium tuberculosis
6	<a href="#">c3qd5B_</a>	 Alignment		24.4	23	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative ribose-5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
7	<a href="#">c2k5jB_</a>	 Alignment		23.1	27	<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
8	<a href="#">c2ca9B_</a>	 Alignment		23.0	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
9	<a href="#">c2bj3D_</a>	 Alignment		20.2	24	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> nikr-apo
10	<a href="#">d2vvpa1</a>	 Alignment		19.4	19	<b>Fold:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Superfamily:</b> Ribose/Galactose isomerase RpiB/AlsB <b>Family:</b> Ribose/Galactose isomerase RpiB/AlsB
11	<a href="#">c1q5vB_</a>	 Alignment		17.5	28	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> apo-nikr

12	<a href="#">c1b4aA_</a>	Alignment		12.6	50	<b>PDB header:</b> repressor <b>Chain:</b> A: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> structure of the arginine repressor from bacillus stearothermophilus
13	<a href="#">c2k29A_</a>	Alignment		12.4	40	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin relb; <b>PDBTitle:</b> structure of the dbd domain of e. coli antitoxin relb
14	<a href="#">c3e38A_</a>	Alignment		11.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> two-domain protein containing predicted php-like metal- <b>PDBTitle:</b> crystal structure of a two-domain protein containing predicted php-2 like metal-dependent phosphoesterase (bvu_3505) from bacteroides3 vulgatus atcc 8482 at 2.20 a resolution
15	<a href="#">d2p5ka1</a>	Alignment		10.8	39	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
16	<a href="#">c4lfnD_</a>	Alignment		10.0	22	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> galactose-6-phosphate isomerase subunit b; <b>PDBTitle:</b> crystal structure of d-galactose-6-phosphate isomerase in complex with2 d-ribose
17	<a href="#">d1v0da_</a>	Alignment		9.9	60	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> Caspase-activated DNase, CAD (DffB, DFF40)
18	<a href="#">c1v0dA_</a>	Alignment		9.9	60	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna fragmentation factor 40 kda subunit; <b>PDBTitle:</b> crystal structure of caspase-activated dnase (cad)
19	<a href="#">c6mu0A_</a>	Alignment		9.8	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable ribose-5-phosphate isomerase b; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase b from mycoplasma2 genitalium with bound ribulose-5-phosphate
20	<a href="#">c2k9iB_</a>	Alignment		8.7	40	<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
21	<a href="#">c6fxwA_</a>	Alignment	not modelled	8.6	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ribose 5-phosphate isomerase; <b>PDBTitle:</b> structure of leishmania infantum type b ribose 5-phosphate isomerase
22	<a href="#">c6ae9B_</a>	Alignment	not modelled	8.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable protein phosphatase 2c 1; <b>PDBTitle:</b> x-ray structure of the photosystem ii phosphatase pbcp
23	<a href="#">c3shgB_</a>	Alignment	not modelled	7.8	75	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> vbha; <b>PDBTitle:</b> vbht fic protein from bartonella schoenbuchensis in complex with vbha2 antitoxin
24	<a href="#">c3qgaD_</a>	Alignment	not modelled	6.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> fusion of urease beta and gamma subunits; <b>PDBTitle:</b> 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
25	<a href="#">d1ugpa_</a>	Alignment	not modelled	6.3	50	<b>Fold:</b> Nitrile hydratase alpha chain <b>Superfamily:</b> Nitrile hydratase alpha chain <b>Family:</b> Nitrile hydratase alpha chain
26	<a href="#">c3v4gA_</a>	Alignment	not modelled	6.2	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
27	<a href="#">c5aj3g_</a>	Alignment	not modelled	6.2	30	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> mitoribosomal protein us7m, mrps7; <b>PDBTitle:</b> structure of the small subunit of the mammalian mitoribosome
28	<a href="#">c4yh5B_</a>	Alignment	not modelled	6.2	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> levoglucosan kinase; <b>PDBTitle:</b> lipomyces starkeyi levoglucosan kinase bound to adp and manganese

29	<a href="#">c1e9zA_</a>	Alignment	not modelled	5.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> urease subunit alpha; <b>PDBTitle:</b> crystal structure of helicobacter pylori urease
30	<a href="#">c3skqA_</a>	Alignment	not modelled	5.4	25	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial distribution and morphology protein 38; <b>PDBTitle:</b> mdm38 is a 14-3-3-like receptor and associates with the protein2 synthesis machinery at the inner mitochondrial membrane
31	<a href="#">c3ereD_</a>	Alignment	not modelled	5.2	46	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> D: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
32	<a href="#">c3m1pA_</a>	Alignment	not modelled	5.1	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase; <b>PDBTitle:</b> structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
33	<a href="#">c3k7pA_</a>	Alignment	not modelled	5.1	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase; <b>PDBTitle:</b> structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.