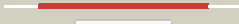

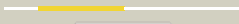
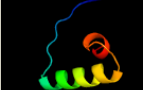







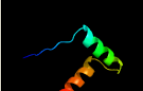





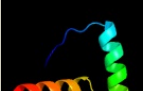






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2063 (-) _2320839_2321072
Date	Mon Aug 5 13:25:17 BST 2019
Unique Job ID	f184e6a0ff244b3d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6a6xC_</a>	 Alignment		100.0	100	<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
2	<a href="#">d2cpga_</a>	 Alignment		74.6	36	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
3	<a href="#">c1ea4K_</a>	 Alignment		74.6	36	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> K: <b>PDB Molecule:</b> transcriptional repressor copg; <b>PDBTitle:</b> transcriptional repressor copg/22bp dsdna complex
4	<a href="#">c5yrzC_</a>	 Alignment		47.2	20	<b>PDB header:</b> antitoxin/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> hicb; <b>PDBTitle:</b> toxin-antitoxin complex from streptococcus pneumoniae
5	<a href="#">c2k29A_</a>	 Alignment		46.3	20	<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
6	<a href="#">d1q9ja2</a>	 Alignment		40.6	26	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> NRPS condensation domain (amide synthase)
7	<a href="#">c6qeQD_</a>	 Alignment		39.6	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> pcff; <b>PDBTitle:</b> pcff from enterococcus faecalis pcf10
8	<a href="#">c2mdvB_</a>	 Alignment		39.3	36	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> designed protein; <b>PDBTitle:</b> nmr structure of beta alpha alpha 38
9	<a href="#">c4fxeB_</a>	 Alignment		39.3	18	<b>PDB header:</b> toxin/toxin inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin relb; <b>PDBTitle:</b> crystal structure of the intact e. coli relbe toxin-antitoxin complex
10	<a href="#">c3kk4B_</a>	 Alignment		31.9	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein bp1543; <b>PDBTitle:</b> uncharacterized protein bp1543 from bordetella pertussis tohama i
11	<a href="#">c6ajnF_</a>	 Alignment		31.8	18	<b>PDB header:</b> toxin <b>Chain:</b> F: <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> crystal structure of atatr bound with accoa

12	<a href="#">c6gtsC_</a>	Alignment		29.3	18	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> duf1778 domain-containing protein; <b>PDBTitle:</b> structure of the atat-atar complex bound dna
13	<a href="#">c3qoqC_</a>	Alignment		26.5	25	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> alginate and motility regulator z; <b>PDBTitle:</b> crystal structure of the transcription factor amrz in complex with the 218 base pair amrz1 binding site
14	<a href="#">c4q2uM_</a>	Alignment		26.1	16	<b>PDB header:</b> toxin/toxin repressor <b>Chain:</b> M: <b>PDB Molecule:</b> antitoxin dinj; <b>PDBTitle:</b> crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
15	<a href="#">c6g1nB_</a>	Alignment		24.5	18	<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
16	<a href="#">c4d8jD_</a>	Alignment		22.4	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> macrodomain ter protein; <b>PDBTitle:</b> structure of e. coli matp-mats complex
17	<a href="#">d1y9ba1</a>	Alignment		18.1	32	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> VCA0319-like
18	<a href="#">d1b3qa1</a>	Alignment		15.4	32	<b>Fold:</b> ROP-like <b>Superfamily:</b> Homodimeric domain of signal transducing histidine kinase <b>Family:</b> Homodimeric domain of signal transducing histidine kinase
19	<a href="#">c1u9pA_</a>	Alignment		15.3	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> parc; <b>PDBTitle:</b> permuted single-chain arc
20	<a href="#">d1mnta_</a>	Alignment		13.9	29	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Arc/Mnt-like phage repressors
21	<a href="#">d1gyza_</a>	Alignment	not modelled	13.3	27	<b>Fold:</b> PABP domain-like <b>Superfamily:</b> Ribosomal protein L20 <b>Family:</b> Ribosomal protein L20
22	<a href="#">c4hv0B_</a>	Alignment	not modelled	12.9	24	<b>PDB header:</b> transcription, viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> avtr; <b>PDBTitle:</b> structure and function of avtr, a novel transcriptional regulator from 2 a hyperthermophilic archaeal lipothrixvirus
23	<a href="#">c2k5jB_</a>	Alignment	not modelled	12.6	21	<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
24	<a href="#">c4jvsA_</a>	Alignment	not modelled	12.0	35	<b>PDB header:</b> hydrolase activator/protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of lepb gap domain from legionella drancourtii in2 complex with rab1-gdp and alf3
25	<a href="#">c4p7dA_</a>	Alignment	not modelled	9.3	18	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin hicb3; <b>PDBTitle:</b> antitoxin hicb3 crystal structure
26	<a href="#">c2rocB_</a>	Alignment	not modelled	9.3	43	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-binding component 3; <b>PDBTitle:</b> solution structure of mcl-1 complexed with puma
27	<a href="#">c4go1A_</a>	Alignment	not modelled	8.7	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lsrr; <b>PDBTitle:</b> crystal structure of full length transcription repressor lsrr from e.2 coli.
28	<a href="#">c5uulB_</a>	Alignment	not modelled	8.2	43	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-binding component 3; <b>PDBTitle:</b> human bfl-1 in complex with puma bh3

29	<a href="#">d2hsqa1</a>	Alignment	not modelled	8.1	23	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
30	<a href="#">d2bsqe1</a>	Alignment	not modelled	7.2	17	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> Trafficking protein A-like
31	<a href="#">c2h1oH_</a>	Alignment	not modelled	6.9	17	<b>PDB header:</b> gene regulation/dna complex <b>Chain:</b> H; <b>PDB Molecule:</b> trafficking protein a; <b>PDBTitle:</b> structure of fitab bound to ir36 dna fragment
32	<a href="#">c3fshC_</a>	Alignment	not modelled	6.3	47	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> autocrine motility factor receptor, isoform 2; <b>PDBTitle:</b> crystal structure of the ubiquitin conjugating enzyme2 ube2g2 bound to the g2br domain of ubiquitin ligase gp78
33	<a href="#">c5losA_</a>	Alignment	not modelled	6.1	53	<b>PDB header:</b> metal binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> piin_05872; <b>PDBTitle:</b> piriformospora indica piin_05872
34	<a href="#">c5b83B_</a>	Alignment	not modelled	6.1	50	<b>PDB header:</b> signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> optineurin; <b>PDBTitle:</b> crystal structure of optineurin uban in complex with linear ubiquitin
35	<a href="#">c5b83C_</a>	Alignment	not modelled	5.6	50	<b>PDB header:</b> signaling protein <b>Chain:</b> C; <b>PDB Molecule:</b> optineurin; <b>PDBTitle:</b> crystal structure of optineurin uban in complex with linear ubiquitin
36	<a href="#">d1iyb2</a>	Alignment	not modelled	5.4	86	<b>Fold:</b> BRCA2 tower domain <b>Superfamily:</b> BRCA2 tower domain <b>Family:</b> BRCA2 tower domain
37	<a href="#">c2m04B_</a>	Alignment	not modelled	5.4	43	<b>PDB header:</b> apoptosis/protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> bcl-2-binding component 3; <b>PDBTitle:</b> solution structure of bcl-xl in complex with puma bh3 peptide
38	<a href="#">d2outa1</a>	Alignment	not modelled	5.3	54	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> Rho N-terminal domain-like <b>Family:</b> YqbF C-terminal domain-like
39	<a href="#">d1luxca_</a>	Alignment	not modelled	5.2	39	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator