




















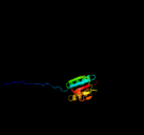

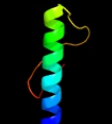
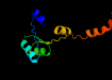
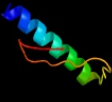


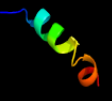
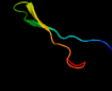
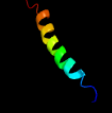


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3484_(cpsA)_3903257_3904795
Date	Fri Aug 9 18:20:16 BST 2019
Unique Job ID	ef5d8db2a6e7d641

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3okzB_</a>	 Alignment		100.0	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> putative uncharacterized protein gbs0355; <b>PDBTitle:</b> crystal structure of protein gbs0355 from streptococcus agalactiae,2 northeast structural genomics consortium target sar127
2	<a href="#">c4de8A_</a>	 Alignment		100.0	24	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> cps2a; <b>PDBTitle:</b> lytr-cps2a-psr family protein with bound octaprenyl monophosphate2 lipid
3	<a href="#">c3pe5B_</a>	 Alignment		100.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> three-dimensional structure of protein a7vv38_9clot from clostridium2 leptum dsm 753, northeast structural genomics consortium target3 qlr103
4	<a href="#">c5v8cA_</a>	 Alignment		100.0	23	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> lytr-csp2a-psr enzyme from actinomyces oris
5	<a href="#">c3qfiA_</a>	 Alignment		100.0	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> x-ray crystal structure of transcriptional regulator (ef0465) from2 enterococcus faecalis, northeast structural genomics consortium3 target efr190
6	<a href="#">c3owqB_</a>	 Alignment		100.0	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> lin1025 protein; <b>PDBTitle:</b> x-ray structure of lin1025 protein from listeria innocua, northeast2 structural genomics consortium target lkr164
7	<a href="#">c3nroA_</a>	 Alignment		100.0	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> lmo1026 protein; <b>PDBTitle:</b> crystal structure of putative transcriptional factor lmo1026 from2 listeria monocytogenes (fragment 52-321), northeast structural3 genomics consortium target lmr194
8	<a href="#">c3mejA_</a>	 Alignment		100.0	25	<b>PDB header:</b> transcriptional regulator <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator ywtf; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator ywtf from2 bacillus subtilis, northeast structural genomics consortium target3 sr736
9	<a href="#">c4obmA_</a>	 Alignment		100.0	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative transcription regulator (eubsir_01389)2 from eubacterium siraeum dsm 15702 at 2.15 a resolution
10	<a href="#">c3nxhA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A; <b>PDB Molecule:</b> transcriptional regulator yvhj; <b>PDBTitle:</b> crystal structure of the transcriptional regulator yvhj from bacillus2 subtilis, northeast structural genomics consortium target sr735.
11	<a href="#">c2m5yA_</a>	 Alignment		99.4	22	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative tuberculin related peptide; <b>PDBTitle:</b> solution structure of the c-terminal domain of rv0431

12	<a href="#">c5j5vC_</a>	Alignment		43.2	27	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> immunity protein cdii; <b>PDBTitle:</b> cdia-ct from uropathogenic escherichia coli in complex with cognate2 immunity protein and cysk
13	<a href="#">c4ddpA_</a>	Alignment		36.2	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> beclin-1; <b>PDBTitle:</b> crystal structure of beclin 1 evolutionarily conserved domain(ecd)
14	<a href="#">c2pjuD_</a>	Alignment		31.4	16	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> propionate catabolism operon regulatory protein; <b>PDBTitle:</b> crystal structure of propionate catabolism operon regulatory protein2 prpr
15	<a href="#">c3vp7A_</a>	Alignment		25.2	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 30; <b>PDBTitle:</b> crystal structure of the beta-alpha repeated, autophagy-specific2 (bara) domain of vps30/atg6
16	<a href="#">c6dfdB_</a>	Alignment		20.1	33	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> metal transporter cnm3; <b>PDBTitle:</b> crystal structure of cnm3 cyclic nucleotide-binding homology domain
17	<a href="#">c5z5bA_</a>	Alignment		18.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-tyrosine phosphatase; <b>PDBTitle:</b> crystal structure of tk-ptp in the g95a mutant form
18	<a href="#">d1ny8a_</a>	Alignment		15.0	24	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> BolA-like <b>Family:</b> BolA-like
19	<a href="#">c2fgyA_</a>	Alignment		14.7	57	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxysome shell polypeptide; <b>PDBTitle:</b> beta carbonic anhydrase from the carboxysomal shell of2 halothiobacillus neapolitanus (csosca)
20	<a href="#">c6f0kA_</a>	Alignment		14.2	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> alternative complex iii
21	<a href="#">c3txsC_</a>	Alignment	not modelled	13.4	18	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> terminase dna packaging enzyme small subunit; <b>PDBTitle:</b> crystal structure of phage 44rr small terminase gp16
22	<a href="#">c3tr3A_</a>	Alignment	not modelled	13.0	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bola; <b>PDBTitle:</b> structure of a bola protein homologue from coxiella burnetii
23	<a href="#">c5dfzD_</a>	Alignment	not modelled	11.8	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 30; <b>PDBTitle:</b> structure of vps34 complex ii from s. cerevisiae.
24	<a href="#">c4puiA_</a>	Alignment	not modelled	11.4	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> sufo-like protein, chloroplastic; <b>PDBTitle:</b> bola domain of sufe1 from arabidopsis thaliana
25	<a href="#">c2nclA_</a>	Alignment	not modelled	10.2	10	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> bola-like protein 3; <b>PDBTitle:</b> solution structure of bola3 from homo sapiens
26	<a href="#">c3o2eA_</a>	Alignment	not modelled	10.0	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bola-like protein; <b>PDBTitle:</b> crystal structure of a bol-like protein from babesia bovis
27	<a href="#">c2dhmA_</a>	Alignment	not modelled	9.4	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein bola; <b>PDBTitle:</b> solution structure of the bola protein from escherichia coli
28	<a href="#">c4pugA_</a>	Alignment	not modelled	9.1	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> bola like protein; <b>PDBTitle:</b> bola1 from arabidopsis thaliana
29	<a href="#">c4gn9A_</a>	Alignment	not modelled	8.2	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acyl-phosphatidylethanolamine-

29	<a href="#">c9qn9A_</a>	Alignment	not modelled	8.5	11	hydrolyzing phospholipase <b>PDBTitle:</b> structure of human nape-pld
30	<a href="#">c4hynA_</a>	Alignment	not modelled	8.0	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> chec, inhibitor of mcp methylation / flin fusion protein; <b>PDBTitle:</b> x-ray crystal structure of thermotoga maritima fliy
31	<a href="#">c5nfmA_</a>	Alignment	not modelled	8.0	13	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> yrba; <b>PDBTitle:</b> crystal structure of yrba from sinorhizobium meliloti in complex with2 copper.
32	<a href="#">c3samB_</a>	Alignment	not modelled	7.0	25	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> rifampicin resistance protein; <b>PDBTitle:</b> structure of d13, the scaffolding protein of vaccinia virus (mutant2 d513g)
33	<a href="#">c2mm9A_</a>	Alignment	not modelled	6.9	10	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> bola2; <b>PDBTitle:</b> solution structure of reduced bola2 from arabidopsis thaliana
34	<a href="#">c1v60A_</a>	Alignment	not modelled	6.8	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> riken cdna 1810037g04; <b>PDBTitle:</b> solution structure of bola1 protein from mus musculus
35	<a href="#">c5y4bA_</a>	Alignment	not modelled	6.8	29	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> bola-like protein 2; <b>PDBTitle:</b> solution structure of yeast fra2
36	<a href="#">c6dj3B_</a>	Alignment	not modelled	6.7	36	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> metal transporter cnm2; <b>PDBTitle:</b> crystal structure of cnm2 cyclic nucleotide-binding homology domain
37	<a href="#">c1xs3A_</a>	Alignment	not modelled	5.7	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein xc975; <b>PDBTitle:</b> solution structure analysis of the xc975 protein
38	<a href="#">c1n7sB_</a>	Alignment	not modelled	5.6	17	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> syntaxin 1a; <b>PDBTitle:</b> high resolution structure of a truncated neuronal snare complex
39	<a href="#">c5iiqA_</a>	Alignment	not modelled	5.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> vacuolar transporter chaperone 4; <b>PDBTitle:</b> structure of the spx-ttm domain fragment of the yeast inorganic2 polyphosphate polymerase vtc4 (form b).
40	<a href="#">c4b96A_</a>	Alignment	not modelled	5.5	10	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> cellulose binding domain-containing protein; <b>PDBTitle:</b> family 3b carbohydrate-binding module from the biomass2 sensing system of clostridium clariflavum
41	<a href="#">c5ijjB_</a>	Alignment	not modelled	5.1	38	<b>PDB header:</b> inositol polyphosphate binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> spx domain; <b>PDBTitle:</b> structure of the spx domain of chaetomium thermophilum2 glycerophosphodiester phosphodiesterase 1 in complex with inositol3 hexakisphosphate (insp6)
42	<a href="#">d1o57a1</a>	Alignment	not modelled	5.0	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> N-terminal domain of Bacillus PurR