
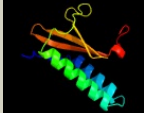

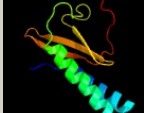
















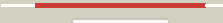



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1959c_(-)_2203688_2203984
Date	Mon Aug 5 13:25:05 BST 2019
Unique Job ID	9b1c94f909820280

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5cegB_</a>	 Alignment		99.9	28	<b>PDB header:</b> toxin <b>Chain:</b> B; <b>PDB Molecule:</b> plasmid stabilization system; <b>PDBTitle:</b> x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
2	<a href="#">c3kxeB_</a>	 Alignment		99.9	43	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> toxin protein pare-1; <b>PDBTitle:</b> a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
3	<a href="#">c5cw7H_</a>	 Alignment		99.9	21	<b>PDB header:</b> toxin <b>Chain:</b> H; <b>PDB Molecule:</b> plasmid stabilization protein pare; <b>PDBTitle:</b> crystal structure of the paaa2-pare2 antitoxin-toxin complex
4	<a href="#">d1wmia1</a>	 Alignment		98.4	13	<b>Fold:</b> RelE-like <b>Superfamily:</b> RelE-like <b>Family:</b> RelE-like
5	<a href="#">c2kheA_</a>	 Alignment		98.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> toxin-like protein; <b>PDBTitle:</b> solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
6	<a href="#">c3g5oC_</a>	 Alignment		98.1	19	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> C; <b>PDB Molecule:</b> uncharacterized protein rv2866; <b>PDBTitle:</b> the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
7	<a href="#">c3oeiH_</a>	 Alignment		98.0	16	<b>PDB header:</b> toxin, protein binding <b>Chain:</b> H; <b>PDB Molecule:</b> relk (toxin rv3358); <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
8	<a href="#">d2a6sa1</a>	 Alignment		97.8	14	<b>Fold:</b> RelE-like <b>Superfamily:</b> RelE-like <b>Family:</b> YoeB/Txe-like
9	<a href="#">c3bpgD_</a>	 Alignment		97.4	22	<b>PDB header:</b> toxin <b>Chain:</b> D; <b>PDB Molecule:</b> toxin rele3; <b>PDBTitle:</b> crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
10	<a href="#">c3kixy_</a>	 Alignment		96.9	24	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of rele nuclease bound to the 70s ribosome (postcleavage2 state; part 3 of 4)
11	<a href="#">c2otrA_</a>	 Alignment		95.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein hp0892; <b>PDBTitle:</b> solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori

12	<a href="#">c5ja9D_</a>	Alignment		91.8	21	<b>PDB header:</b> toxin <b>Chain:</b> D: <b>PDB Molecule:</b> toxin higb-2; <b>PDBTitle:</b> crystal structure of the higb2 toxin in complex with nb6
13	<a href="#">d1z8ma1</a>	Alignment		87.9	16	<b>Fold:</b> RelE-like <b>Superfamily:</b> RelE-like <b>Family:</b> RelE-like
14	<a href="#">c4q2uH_</a>	Alignment		38.7	16	<b>PDB header:</b> toxin/toxin repressor <b>Chain:</b> H: <b>PDB Molecule:</b> mrna interferase yafq; <b>PDBTitle:</b> crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
15	<a href="#">c2apnA_</a>	Alignment		38.5	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein hi1723; <b>PDBTitle:</b> hi1723 solution structure
16	<a href="#">c2dbhA_</a>	Alignment		37.9	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily <b>PDBTitle:</b> solution structure of the carboxyl-terminal card-like2 domain in human tnfr-related death receptor-6
17	<a href="#">c4mctD_</a>	Alignment		18.9	13	<b>PDB header:</b> toxin <b>Chain:</b> D: <b>PDB Molecule:</b> killer protein; <b>PDBTitle:</b> p. vulgaris higba structure, crystal form 1
18	<a href="#">c3w8hB_</a>	Alignment		16.7	15	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase 25; <b>PDBTitle:</b> crystal structure of ccm3 in complex with the c-terminal regulatory2 domain of stk25
19	<a href="#">d1pmma_</a>	Alignment		15.1	21	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Pyridoxal-dependent decarboxylase
20	<a href="#">d1legxa_</a>	Alignment		13.9	15	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
21	<a href="#">c4gehB_</a>	Alignment	not modelled	13.8	12	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase mst4; <b>PDBTitle:</b> crystal structure of mst4 dimerization domain complex with pdcd10
22	<a href="#">d1evha_</a>	Alignment	not modelled	13.3	16	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
23	<a href="#">c2kruA_</a>	Alignment	not modelled	13.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> solution nmr structure of the pcp_red domain of light-independent2 protochlorophyllide reductase subunit b from chlorobium tepidum.3 northeast structural genomics consortium target ctr69a
24	<a href="#">c4wvrB_</a>	Alignment	not modelled	11.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like protein 4a; <b>PDBTitle:</b> crystal structure of bag6-ubl4a dimerization domain
25	<a href="#">c2jp2A_</a>	Alignment	not modelled	10.9	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sprouty-related, evh1 domain-containing protein <b>PDBTitle:</b> solution structure and resonance assignment of the n-2 terminal evh1 domain from the human spred2 protein3 (sprouty-related protein with evh1 domain isoform 2)
26	<a href="#">c4lh9A_</a>	Alignment	not modelled	10.6	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> heterocyst differentiation control protein; <b>PDBTitle:</b> crystal structure of the refolded hood domain (asp256-gly295) of hetr
27	<a href="#">c6gcsH_</a>	Alignment	not modelled	10.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> 24-kda subunit (nuhm); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica

28	<a href="#">c2l09A_</a>	Alignment	not modelled	10.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> asr4154 protein; <b>PDBTitle:</b> solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
29	<a href="#">d1ofda1</a>	Alignment	not modelled	10.1	11	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> Alpha subunit of glutamate synthase, C-terminal domain <b>Family:</b> Alpha subunit of glutamate synthase, C-terminal domain
30	<a href="#">c4wwrD_</a>	Alignment	not modelled	9.8	21	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> ubiquitin-like protein 4a; <b>PDBTitle:</b> crystal structure of bag6-ubl4a dimerization domain
31	<a href="#">c4u1dA_</a>	Alignment	not modelled	9.4	10	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit a; <b>PDBTitle:</b> structure of the pci domain of translation initiation factor eif3a
32	<a href="#">c2x7pA_</a>	Alignment	not modelled	9.0	7	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> possible thiamine biosynthesis enzyme; <b>PDBTitle:</b> the conserved candida albicans ca3427 gene product defines a new2 family of proteins exhibiting the generic periplasmic binding3 protein structural fold
33	<a href="#">c2l4mA_</a>	Alignment	not modelled	8.2	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of the zbeta domain of human dai and its binding2 modes to b- and z-dna
34	<a href="#">d1ayia_</a>	Alignment	not modelled	7.9	13	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> Colicin E immunity proteins <b>Family:</b> Colicin E immunity proteins
35	<a href="#">c3j38T_</a>	Alignment	not modelled	7.8	29	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> 40s ribosomal protein s19a; <b>PDBTitle:</b> structure of the d. melanogaster 40s ribosomal proteins
36	<a href="#">c2q00B_</a>	Alignment	not modelled	7.5	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> orf c02003 protein; <b>PDBTitle:</b> crystal structure of the p95883 sulso protein from sulfobolus2 solfataricus. nescg target ssr10.
37	<a href="#">c4b6aC_</a>	Alignment	not modelled	7.3	27	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> 60s ribosomal protein l4-a; <b>PDBTitle:</b> cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
38	<a href="#">d2v7fa1</a>	Alignment	not modelled	7.3	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Rps19E-like
39	<a href="#">c3eyiB_</a>	Alignment	not modelled	7.0	27	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> z-dna-binding protein 1; <b>PDBTitle:</b> the crystal structure of the second z-dna binding domain of2 human dai (zbp1) in complex with z-dna
40	<a href="#">c3nqjA_</a>	Alignment	not modelled	6.1	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> histone h3-like centromeric protein a; <b>PDBTitle:</b> crystal structure of (cenp-a/h4)2 heterotetramer
41	<a href="#">c4esxA_</a>	Alignment	not modelled	6.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine biosynthesis enzyme thi13; <b>PDBTitle:</b> crystal structure of c. albicans thi5 complexed with plp
42	<a href="#">c3hbxB_</a>	Alignment	not modelled	5.7	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate decarboxylase 1; <b>PDBTitle:</b> crystal structure of gad1 from arabidopsis thaliana
43	<a href="#">c2ncxA_</a>	Alignment	not modelled	5.6	14	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> pseudin-2; <b>PDBTitle:</b> solution structure of pseudin-2 isolated from the skin of paradoxical2 frog, pseudis paradoxa
44	<a href="#">c3k1iA_</a>	Alignment	not modelled	5.5	9	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein; <b>PDBTitle:</b> crystal strcture of flis-hp1076 complex in h. pylori
45	<a href="#">d1gxha_</a>	Alignment	not modelled	5.5	11	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> Colicin E immunity proteins <b>Family:</b> Colicin E immunity proteins
46	<a href="#">c3o10D_</a>	Alignment	not modelled	5.2	10	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> sacsin; <b>PDBTitle:</b> crystal structure of the hepn domain from human sacsin
47	<a href="#">d2ga5a1</a>	Alignment	not modelled	5.2	14	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> Frataxin/Nqo15-like <b>Family:</b> Frataxin-like