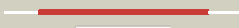
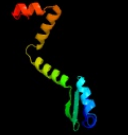

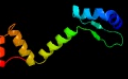

















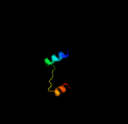


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2865_(-)_3177547_3177828
Date	Wed Aug 7 12:50:53 BST 2019
Unique Job ID	088b5eeb9a92587e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3g5oA_	 Alignment		100.0	100	PDB header: toxin/antitoxin Chain: A: PDB Molecule: uncharacterized protein rv2865; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
2	c3oeiB_	 Alignment		99.9	28	PDB header: toxin, protein binding Chain: B: PDB Molecule: relj (antitoxin rv3357); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
3	d2a6qa1	 Alignment		99.9	26	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
4	c3d55A_	 Alignment		99.9	28	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
5	d2a6qb1	 Alignment		99.8	31	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
6	c3hs2H_	 Alignment		99.6	25	PDB header: antitoxin Chain: H: PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
7	c3hryA_	 Alignment		99.5	27	PDB header: antitoxin Chain: A: PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd in a trigonal space group and partially2 disordered
8	c2odkD_	 Alignment		99.4	34	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: putative prevent-host-death protein from nitrosomonas europaea
9	d2odka1	 Alignment		99.3	34	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
10	c3k6qB_	 Alignment		94.5	13	PDB header: ligand binding protein Chain: B: PDB Molecule: putative ligand binding protein; PDBTitle: crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
11	c4q2uM_	 Alignment		37.6	19	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex

12	c2p6pB_	Alignment		32.7	16	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
13	d1n0ea_	Alignment		27.7	11	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Hypothetical protein MraZ
14	c6nkID_	Alignment		27.1	12	PDB header: antitoxin Chain: D: PDB Molecule: antitoxin vappb1; PDBTitle: 2.2 a resolution structure of vappbc-1 from nontypeable haemophilus2 influenzae
15	c2v9vA_	Alignment		26.7	4	PDB header: transcription Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: crystal structure of moorella thermoacetica selb(377-511)
16	c6ncrB_	Alignment		26.2	13	PDB header: ligase Chain: B: PDB Molecule: tryptophan--trna ligase; PDBTitle: crystal structure of tryptophan-trna ligase from chlamydia trachomatis2 with bound l-tryptophan
17	c1n0fF_	Alignment		25.7	11	PDB header: biosynthetic protein Chain: F: PDB Molecule: protein mraz; PDBTitle: crystal structure of a cell division and cell wall2 biosynthesis protein upf0040 from mycoplasma pneumoniae:3 indication of a novel fold with a possible new conserved4 sequence motif
18	d1grja1	Alignment		25.3	34	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
19	d1qbjc_	Alignment		22.8	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
20	d1ez4a2	Alignment		21.8	9	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
21	d2ovra1	Alignment	not modelled	21.7	21	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
22	c3bpqA_	Alignment	not modelled	21.7	28	PDB header: toxin Chain: A: PDB Molecule: antitoxin relb3; PDBTitle: crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
23	c1nexC_	Alignment	not modelled	21.0	19	PDB header: ligase, cell cycle Chain: C: PDB Molecule: centromere dna-binding protein complex cbf3 PDBTitle: crystal structure of scskp1-sccdc4-cpd peptide complex
24	c3ot5D_	Alignment	not modelled	20.3	20	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
25	c2qzsA_	Alignment	not modelled	19.0	7	PDB header: transferase Chain: A: PDB Molecule: glycogen synthase; PDBTitle: crystal structure of wild-type e.coli gs in complex with adp and2 glucose(wtgsb)
26	d1nexa1	Alignment	not modelled	19.0	19	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
27	d1v4va_	Alignment	not modelled	17.3	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
28	d1rzua_	Alignment	not modelled	17.2	8	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
						Fold: DNA/RNA-binding 3-helical bundle

29	d1qgpa_	Alignment	not modelled	17.2	11	Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
30	c2ovqA_	Alignment	not modelled	17.2	21	PDB header: transcription/cell cycle Chain: A: PDB Molecule: s-phase kinase-associated protein 1a; PDBTitle: structure of the skp1-fbw7-cyclinedegc complex
31	c4ochA_	Alignment	not modelled	16.9	14	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease muts2; PDBTitle: apo structure of smr domain of muts2 from deinococcus radiodurans
32	d2gxba1	Alignment	not modelled	16.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
33	c5he8J_	Alignment	not modelled	16.4	9	PDB header: protein binding Chain: J: PDB Molecule: helicase loader; PDBTitle: bacterial initiation protein
34	d1pzqa2	Alignment	not modelled	16.1	16	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
35	c2p4vA_	Alignment	not modelled	16.1	16	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor greb; PDBTitle: crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
36	c1grjA_	Alignment	not modelled	15.9	26	PDB header: transcription regulation Chain: A: PDB Molecule: grea protein; PDBTitle: grea transcript cleavage factor from escherichia coli
37	d1pkxa1	Alignment	not modelled	15.8	17	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
38	c2m4hA_	Alignment	not modelled	15.6	32	PDB header: viral protein Chain: A: PDB Molecule: feline calicivirus vpg protein; PDBTitle: solution structure of the core domain (10-76) of the feline2 calicivirus vpg protein
39	d1g8ma1	Alignment	not modelled	15.4	15	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
40	c2zqeA_	Alignment	not modelled	14.9	8	PDB header: dna binding protein Chain: A: PDB Molecule: muts2 protein; PDBTitle: crystal structure of the smr domain of thermus thermophilus muts2
41	c3bpqC_	Alignment	not modelled	14.7	28	PDB header: toxin Chain: C: PDB Molecule: antitoxin relb3; PDBTitle: crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
42	d1fs2b1	Alignment	not modelled	14.6	21	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
43	c2p1nD_	Alignment	not modelled	13.7	19	PDB header: signaling protein Chain: D: PDB Molecule: skp1-like protein 1a; PDBTitle: mechanism of auxin perception by the tir1 ubiquitin ligase
44	c2yy5C_	Alignment	not modelled	12.3	6	PDB header: ligase Chain: C: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from mycoplasma2 pneumoniae
45	c5us5B_	Alignment	not modelled	12.1	13	PDB header: structural genomics Chain: B: PDB Molecule: upf0297 protein ef_1202; PDBTitle: solution structure of the ireb homodimer
46	c6nkoA_	Alignment	not modelled	11.8	23	PDB header: unknown function Chain: A: PDB Molecule: forh; PDBTitle: crystal structure of forh
47	c2plyB_	Alignment	not modelled	11.3	23	PDB header: translation/rna Chain: B: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
48	c1lvaA_	Alignment	not modelled	11.0	4	PDB header: translation Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: crystal structure of a c-terminal fragment of moorella2 thermoacetica elongation factor selb
49	c5l87A_	Alignment	not modelled	10.5	13	PDB header: membrane protein Chain: A: PDB Molecule: peroxin 14; PDBTitle: targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiasis.
50	c1wsuA_	Alignment	not modelled	10.5	23	PDB header: translation/rna Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: c-terminal domain of elongation factor selb complexed with2 secis rna
51	d1w7pd2	Alignment	not modelled	10.1	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
52	c3wadA_	Alignment	not modelled	9.7	15	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of glycosyltransferase vinc involved in the2 biosynthesis of vicienistatin
53	c5ytpA_	Alignment	not modelled	8.9	24	PDB header: dna binding protein Chain: A: PDB Molecule: ttha0139; PDBTitle: crystal structure of ttha0139 I34a from thermus thermophilus hb8
54	c3sz3A_	Alignment	not modelled	8.7	12	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from vibrio cholerae2 with an endogenous tryptophan
55	c3s29C_	Alignment	not modelled	8.6	14	PDB header: transferase Chain: C: PDB Molecule: sucrose synthase 1; PDBTitle: the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.

56	c5yhhA	Alignment	not modelled	8.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized conserved protein yim; PDBTitle: crystal structure of yim from geobacillus stearothermophilus
57	c4rbnD	Alignment	not modelled	8.4	17	PDB header: transferase Chain: D: PDB Molecule: sucrose synthase:glycosyl transferases group 1; PDBTitle: the crystal structure of nitrosomonas europaea sucrose synthase:2 insights into the evolutionary origin of sucrose metabolism in3 prokaryotes
58	c3okaA	Alignment	not modelled	8.2	15	PDB header: transferase Chain: A: PDB Molecule: gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol PDBTitle: crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
59	d2bisa1	Alignment	not modelled	7.8	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
60	c3jvoA	Alignment	not modelled	7.5	15	PDB header: viral protein Chain: A: PDB Molecule: gp6; PDBTitle: crystal structure of bacteriophage hk97 gp6
61	c6ct6B	Alignment	not modelled	7.5	15	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate dehydrogenase; PDBTitle: crystal structure of lactate dehydrogenase from eimeria maxima with2 nadh and oxamate
62	c5d17L	Alignment	not modelled	7.4	13	PDB header: dna binding protein Chain: L: PDB Molecule: transposon tn7 transposition protein tnse; PDBTitle: structure of the c-terminal domain of tnse at 2.85 resolution
63	d1h8ba	Alignment	not modelled	7.4	25	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
64	d1sfea1	Alignment	not modelled	7.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
65	c3prhB	Alignment	not modelled	7.2	7	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase val144pro mutant from b. subtilis
66	c4q8jE	Alignment	not modelled	7.1	12	PDB header: hydrolase Chain: E: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan3; PDBTitle: structure of the saccharomyces cerevisiae pan2-pan3 core complex
67	c2do6A	Alignment	not modelled	7.0	18	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase cbl-b; PDBTitle: solution structure of rsgi ruh-065, a uba domain from human2 cdna
68	c2mqkA	Alignment	not modelled	6.7	16	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
69	c5ghaF	Alignment	not modelled	6.6	8	PDB header: transferase/transport protein Chain: F: PDB Molecule: sulfur carrier ttub; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
70	c1dpuA	Alignment	not modelled	6.6	0	PDB header: dna binding protein Chain: A: PDB Molecule: replication protein a (rpa32) c-terminal domain; PDBTitle: solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
71	d1dpua	Alignment	not modelled	6.6	0	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of RPA32
72	d1lvaa4	Alignment	not modelled	6.5	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
73	c4pu4C	Alignment	not modelled	6.5	16	PDB header: toxin/antitoxin/dna Chain: C: PDB Molecule: toxin-antitoxin system antidote transcriptional repressor PDBTitle: shewanella oneidensis mr-1 toxin antitoxin system hipa, hipb and its2 operator dna complex (space group p21)
74	c5l6mA	Alignment	not modelled	6.4	19	PDB header: hydrolase Chain: A: PDB Molecule: vapb family protein; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
75	c4d0kC	Alignment	not modelled	6.4	12	PDB header: gene regulation Chain: C: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit PDBTitle: complex of chaetomium thermophilum pan2 (wd40-cs1) with pan3 (c-term)
76	c2r60A	Alignment	not modelled	6.4	18	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
77	c3u5eL	Alignment	not modelled	6.4	29	PDB header: ribosome Chain: L: PDB Molecule: 60s ribosomal protein l13-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a
78	c4a18U	Alignment	not modelled	6.4	29	PDB header: ribosome Chain: U: PDB Molecule: rpl13; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rna and proteins of molecule 1
79	c3zf7N	Alignment	not modelled	6.2	29	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l13; PDBTitle: high-resolution cryo-electron microscopy structure of the

					trypanosoma2 brucei ribosome
80	c2jnhA_	Alignment	not modelled	6.2	18 PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase cbl-b; PDBTitle: solution structure of the uba domain from cbl-b
81	c6gneB_	Alignment	not modelled	6.2	7 PDB header: transferase Chain: B: PDB Molecule: probable starch synthase 4, chloroplastic/amyloplastic; PDBTitle: catalytic domain of starch synthase iv from arabidopsis thaliana bound2 to adp and acarbose
82	c4ghjA_	Alignment	not modelled	6.1	17 PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
83	d1b8pa2	Alignment	not modelled	6.0	14 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
84	c3zbeA_	Alignment	not modelled	5.9	17 PDB header: toxin-antitoxin Chain: A: PDB Molecule: paaa2; PDBTitle: e. coli o157 pare2-associated antitoxin 2 (paaa2)
85	c6d9tA_	Alignment	not modelled	5.6	13 PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp
86	c3bjqA_	Alignment	not modelled	5.6	19 PDB header: viral protein Chain: A: PDB Molecule: phage-related protein; PDBTitle: crystal structure of a phage-related protein (bb3626) from bordetella2 bronchiseptica rb50 at 2.05 a resolution
87	c3m05A_	Alignment	not modelled	5.6	18 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pepe_1480; PDBTitle: the crystal structure of a functionally unknown protein pepe_1480 from2 pediococcus pentosaceus atcc 25745
88	c6ejiA_	Alignment	not modelled	5.5	18 PDB header: transferase Chain: A: PDB Molecule: wlac protein; PDBTitle: structure of a glycosyltransferase
89	c3j3bL_	Alignment	not modelled	5.5	29 PDB header: ribosome Chain: L: PDB Molecule: 60s ribosomal protein l13; PDBTitle: structure of the human 60s ribosomal proteins
90	d1hlva1	Alignment	not modelled	5.2	15 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
91	c2auwB_	Alignment	not modelled	5.1	19 PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718