

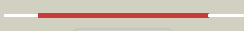




















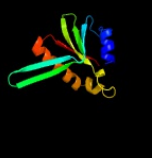
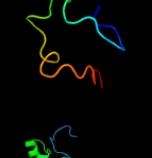
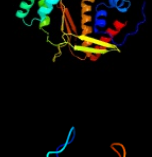
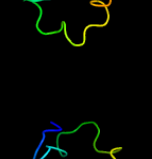

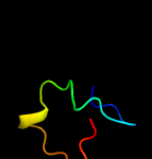

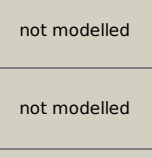


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2119 (-)_2378394_2379230
Date	Mon Aug 5 13:25:23 BST 2019
Unique Job ID	295bf79d52057816

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3u44B_	 Alignment		100.0	19	PDB header: hydrolase/dna Chain: B; PDB Molecule: atp-dependent helicase/deoxyribonuclease subunit b; PDBTitle: crystal structure of addab-dna complex
2	c4ic1D_	 Alignment		99.8	19	PDB header: structural genomics, unknown function Chain: D; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of sso0001
3	c5eaxB_	 Alignment		99.8	14	PDB header: hydrolase/dna Chain: B; PDB Molecule: dna replication atp-dependent helicase/nuclease dna2; PDBTitle: crystal structure of dna2 in complex with an ssdna
4	c4onbA_	 Alignment		99.8	27	PDB header: hydrolase Chain: A; PDB Molecule: crispr-associated exonuclease, cas4 family; PDBTitle: crystal structure of crispr-associated exonuclease (cas4 family) from2 pyrobaculum calidifontis jcm 11548
5	c3l0aA_	 Alignment		99.7	20	PDB header: hydrolase Chain: A; PDB Molecule: putative exonuclease; PDBTitle: crystal structure of putative exonuclease (rer070207002219) from2 eubacterium rectale at 2.19 a resolution
6	c3h4rA_	 Alignment		99.6	19	PDB header: hydrolase Chain: A; PDB Molecule: exodeoxyribonuclease 8; PDBTitle: crystal structure of e. coli rece exonuclease
7	c3u4qA_	 Alignment		99.5	15	PDB header: hydrolase/dna Chain: A; PDB Molecule: atp-dependent helicase/nuclease subunit a; PDBTitle: structure of addab-dna complex at 2.8 angstroms
8	c5zyuA_	 Alignment		99.2	17	PDB header: dna binding protein/dna Chain: A; PDB Molecule: mitochondrial genome maintenance exonuclease 1; PDBTitle: the crytal struture of humanmgme1 with single strand dna2
9	c1w36F_	 Alignment		99.0	16	PDB header: recombination Chain: F; PDB Molecule: exodeoxyribonuclease v gamma chain; PDBTitle: recbcd:dna complex
10	c1w36E_	 Alignment		98.8	16	PDB header: recombination Chain: E; PDB Molecule: exodeoxyribonuclease v beta chain; PDBTitle: recbcd:dna complex
11	d1w36b3	 Alignment		98.4	18	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Exodeoxyribonuclease V beta chain (RecB), C-terminal domain

12	c5gkeB_	Alignment		89.8	22	PDB header: hydrolase/dna Chain: B: PDB Molecule: endonuclease endoms; PDBTitle: structure of endoms-dsdna1 complex
13	c2vldA_	Alignment		84.8	23	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease nucs; PDBTitle: crystal structure of a repair endonuclease from pyrococcus abyssi
14	d1rrqa1	Alignment		80.0	30	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
15	d1w36c3	Alignment		72.4	15	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Exodeoxyribonuclease V beta chain (RecC), C-terminal domain
16	d1kq2a_	Alignment		71.5	30	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
17	c4unfA_	Alignment		64.1	20	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-1; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-1
18	c1rrqA_	Alignment		55.1	31	PDB header: hydrolase/dna Chain: A: PDB Molecule: muty; PDBTitle: muty adenine glycosylase in complex with dna containing an2 a:oxog pair
19	d2abka_	Alignment		54.6	12	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
20	d1orna_	Alignment		49.6	23	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Endonuclease III
21	d1keaa_	Alignment	not modelled	47.4	13	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: Mismatch glycosylase
22	c3n5nX_	Alignment	not modelled	47.3	27	PDB header: hydrolase Chain: X: PDB Molecule: a/g-specific adenine dna glycosylase; PDBTitle: crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
23	c4uobA_	Alignment	not modelled	39.4	30	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-3; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-3
24	c1klrA_	Alignment	not modelled	35.5	22	PDB header: transcription Chain: A: PDB Molecule: zinc finger y-chromosomal protein; PDBTitle: nmr structure of the zfy-6[y10f] zinc finger
25	d1klra_	Alignment	not modelled	35.5	22	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
26	c6hz9N_	Alignment	not modelled	33.6	14	PDB header: dna binding protein Chain: N: PDB Molecule: protein mcrc; PDBTitle: structure of mcrcb without dna binding domains (class 5)
27	d1luzka3	Alignment	not modelled	32.9	30	Fold: TB module/8-cys domain Superfamily: TB module/8-cys domain Family: TB module/8-cys domain
28	c5znfA_	Alignment	not modelled	32.6	22	PDB header: zinc finger dna binding domain Chain: A: PDB Molecule: zinc finger; PDBTitle: alternating zinc fingers in the human male associated2 protein zfy: 2d nmr structure of an even finger and3 implications for "jumping-linker" dna recognition

29	c1klsA	Alignment	not modelled	30.8	22	PDB header: transcription Chain: A: PDB Molecule: zinc finger y-chromosomal protein; PDBTitle: nmr structure of the zfy-6[y10] zinc finger
30	c7znfA	Alignment	not modelled	28.2	22	PDB header: zinc finger dna binding domain Chain: A: PDB Molecule: zinc finger; PDBTitle: alternating zinc fingers in the human male associated2 protein zfy: 2d nmr structure of an even finger and3 implications for "jumping-linker" dna recognition
31	d7znfa	Alignment	not modelled	28.2	22	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
32	d2h28a1	Alignment	not modelled	24.8	16	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
33	c3hkpP	Alignment	not modelled	24.7	14	PDB header: transferase Chain: P: PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
34	d2ea9a1	Alignment	not modelled	24.2	27	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
35	d1js2a	Alignment	not modelled	23.9	31	Fold: HIPIP (high potential iron protein) Superfamily: HIPIP (high potential iron protein) Family: HIPIP (high potential iron protein)
36	d2inwa1	Alignment	not modelled	23.3	16	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
37	c3ks8D	Alignment	not modelled	22.8	14	PDB header: viral protein/rna Chain: D: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of reston ebolavirus vp35 rna binding domain in2 complex with 18bp dsrna
38	c4r33A	Alignment	not modelled	21.0	20	PDB header: lyase Chain: A: PDB Molecule: nosl; PDBTitle: x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
39	d1b0ya	Alignment	not modelled	20.9	31	Fold: HIPIP (high potential iron protein) Superfamily: HIPIP (high potential iron protein) Family: HIPIP (high potential iron protein)
40	c6c8vA	Alignment	not modelled	20.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
41	c4gh9A	Alignment	not modelled	20.6	6	PDB header: viral protein,rna binding protein Chain: A: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of marburg virus vp35 rna binding domain
42	c6f40P	Alignment	not modelled	19.8	5	PDB header: transcription Chain: P: PDB Molecule: dna-directed rna polymerase iii subunit rpc6; PDBTitle: rna polymerase iii open complex
43	d1x5wa2	Alignment	not modelled	17.6	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
44	c2liyA	Alignment	not modelled	16.9	24	PDB header: hormone Chain: A: PDB Molecule: epidermal patterning factor-like protein 9; PDBTitle: plant peptide hormone regulating stomatal density
45	d1apja	Alignment	not modelled	16.1	29	Fold: TB module/8-cys domain Superfamily: TB module/8-cys domain Family: TB module/8-cys domain
46	c2elpA	Alignment	not modelled	16.1	29	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
47	c3fkeB	Alignment	not modelled	16.0	17	PDB header: rna binding protein Chain: B: PDB Molecule: polymerase cofactor vp35; PDBTitle: structure of the ebola vp35 interferon inhibitory domain
48	c6dkuA	Alignment	not modelled	15.0	9	PDB header: unknown function Chain: A: PDB Molecule: vp35; PDBTitle: crystal structure of myotis vp35 mutant of interferon inhibitory2 domain
49	c5fj9P	Alignment	not modelled	14.3	13	PDB header: transcription Chain: P: PDB Molecule: dna-directed rna polymerase iii subunit rpc6; PDBTitle: cryo-em structure of yeast apo rna polymerase iii at 4.6 a
50	d2dmda1	Alignment	not modelled	13.8	20	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
51	d2dmda3	Alignment	not modelled	13.7	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
52	d3hipa	Alignment	not modelled	12.8	28	Fold: HIPIP (high potential iron protein) Superfamily: HIPIP (high potential iron protein) Family: HIPIP (high potential iron protein)
53	d1dan3	Alignment	not modelled	12.7	29	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
54	d2c4fl3	Alignment	not modelled	12.5	29	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
55	c5wggA	Alignment	not modelled	11.0	36	PDB header: peptide binding protein Chain: A: PDB Molecule: radical sam domain protein; PDBTitle: structural insights into thioether bond formation in the

						biosynthesis2 of sactipeptides
56	d1iuaa_	Alignment	not modelled	10.8	31	Fold: HIPIP (high potential iron protein) Superfamily: HIPIP (high potential iron protein) Family: HIPIP (high potential iron protein)
57	d3fapb_	Alignment	not modelled	10.8	17	Fold: Four-helical up-and-down bundle Superfamily: FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP) Family: FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP)
58	d1hlqa_	Alignment	not modelled	9.9	34	Fold: HIPIP (high potential iron protein) Superfamily: HIPIP (high potential iron protein) Family: HIPIP (high potential iron protein)
59	d1omca_	Alignment	not modelled	9.6	40	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Conotoxin
60	c1ttiA_	Alignment	not modelled	9.6	40	PDB header: toxin Chain: A; PDB Molecule: omega-conotoxin gvia; PDBTitle: omega-conotoxin gvia, a n-type calcium channel blocker
61	c1omcA_	Alignment	not modelled	9.6	40	PDB header: presynaptic neurotoxin Chain: A; PDB Molecule: omega-conotoxin gvia; PDBTitle: solution structure of omega-conotoxin gvia using 2-d nmr spectroscopy2 and relaxation matrix analysis
62	c2ccoA_	Alignment	not modelled	9.6	40	PDB header: toxin Chain: A; PDB Molecule: omega-conotoxin gvia; PDBTitle: structure of the calcium channel blocker omega conotoxin2 gvia, nmr, 20 structures
63	c3h31A_	Alignment	not modelled	8.6	24	PDB header: electron transport Chain: A; PDB Molecule: high potential iron-sulfur protein; PDBTitle: structure of rhodothermus marinus hipip at 1.0 a resolution
64	c4k39A_	Alignment	not modelled	8.5	27	PDB header: oxidoreductase Chain: A; PDB Molecule: anaerobic sulfatase-maturing enzyme; PDBTitle: native ansmece with bound adomet and cp18cys peptide
65	d1ksqa_	Alignment	not modelled	8.0	24	Fold: TB module/8-cys domain Superfamily: TB module/8-cys domain Family: TB module/8-cys domain
66	c4rtbA_	Alignment	not modelled	7.9	11	PDB header: lyase Chain: A; PDB Molecule: hydrg protein; PDBTitle: x-ray structure of the efe-hydrogenase maturase hydrg from2 carboxythermus hydrogenofmans
67	d1u6pa_	Alignment	not modelled	7.3	18	Fold: Retrovirus zinc finger-like domains Superfamily: Retrovirus zinc finger-like domains Family: Retrovirus zinc finger-like domains
68	c1r30A_	Alignment	not modelled	7.2	33	PDB header: transferase Chain: A; PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
69	d1r30a_	Alignment	not modelled	7.2	33	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
70	c4qbnA_	Alignment	not modelled	7.0	15	PDB header: hydrolase Chain: A; PDB Molecule: nuclease; PDBTitle: vrr_nuc domain
71	c5oayA_	Alignment	not modelled	6.9	31	PDB header: signaling protein Chain: A; PDB Molecule: transcriptional regulator whib1; PDBTitle: m. tuberculosis [4fe-4s] protein whib1 is a four-helix bundle that2 forms a no-sensitive complex with sigmaa and regulates the major3 virulence factor esx-1
72	c1a6bB_	Alignment	not modelled	6.7	18	PDB header: viral protein/dna Chain: B; PDB Molecule: zinc finger protein ncp10; PDBTitle: nmr structure of the complex between the zinc finger2 protein ncp10 of moloney murine leukemia virus and a3 sequence of the psi-packaging domain of hiv-1, 204 structures
73	d2d5ba1	Alignment	not modelled	6.7	11	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
74	c2m0dA_	Alignment	not modelled	6.6	50	PDB header: transcription Chain: A; PDB Molecule: zinc finger and btb domain-containing protein 17; PDBTitle: solution structure of miz-1 zinc finger 5
75	c3cw19_	Alignment	not modelled	6.4	60	PDB header: splicing Chain: 9; PDB Molecule: u1 small nuclear ribonucleoprotein c; PDBTitle: crystal structure of human spliceosomal u1 snrnp
76	c2eluA_	Alignment	not modelled	6.3	33	PDB header: transcription Chain: A; PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 5th c2h2 zinc finger of human2 zinc finger protein 406
77	c5v1tA_	Alignment	not modelled	6.3	27	PDB header: metal binding protein Chain: A; PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suib bound to precursor2 peptide sua
78	d2yrka1	Alignment	not modelled	6.3	18	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: HkH motif-containing C2H2 finger
79	d1g72b_	Alignment	not modelled	6.3	30	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Methanol dehydrogenase subunit Family: Methanol dehydrogenase subunit
80	d1rqga1	Alignment	not modelled	6.1	15	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases

						Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
81	d1w6sb	Alignment	not modelled	6.1	40	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Methanol dehydrogenase subunit Family: Methanol dehydrogenase subunit
82	d2ad6b1	Alignment	not modelled	6.1	30	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Methanol dehydrogenase subunit Family: Methanol dehydrogenase subunit
83	c3t7vA	Alignment	not modelled	6.0	20	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
84	d2vrda1	Alignment	not modelled	5.9	60	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: HkH motif-containing C2H2 finger
85	c3hk4B	Alignment	not modelled	5.8	11	PDB header: lyase Chain: B: PDB Molecule: mlr7391 protein; PDBTitle: crystal structure of a putative snoal-like polyketide cyclase2 [carbohydrate phosphatase] (mlr7391) from mesorhizobium loti at 1.963 a resolution
86	d1brza	Alignment	not modelled	5.8	50	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Plant defensins
87	d1wjpa2	Alignment	not modelled	5.6	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
88	d1olta	Alignment	not modelled	5.5	27	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
89	c5a8lZ	Alignment	not modelled	5.5	16	PDB header: translation Chain: Z: PDB Molecule: nascent chain; PDBTitle: human erf1 and the hcmv nascent peptide in the translation termination2 complex
90	d1bboa2	Alignment	not modelled	5.5	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
91	c6c4zl	Alignment	not modelled	5.4	42	PDB header: de novo protein Chain: I: PDB Molecule: cross-alpha amyloid-like structure alphaamg - low resolution PDBTitle: cross-alpha amyloid-like structure alphaamg - low resolution
92	c6c4yM	Alignment	not modelled	5.4	42	PDB header: de novo protein Chain: M: PDB Molecule: cross-alpha amyloid-like structure alphaamg; PDBTitle: cross-alpha amyloid-like structure alphaamg
93	c6c4yD	Alignment	not modelled	5.4	42	PDB header: de novo protein Chain: D: PDB Molecule: cross-alpha amyloid-like structure alphaamg; PDBTitle: cross-alpha amyloid-like structure alphaamg
94	c6c4zR	Alignment	not modelled	5.4	42	PDB header: de novo protein Chain: R: PDB Molecule: cross-alpha amyloid-like structure alphaamg - low resolution PDBTitle: cross-alpha amyloid-like structure alphaamg - low resolution
95	c6c4zO	Alignment	not modelled	5.4	42	PDB header: de novo protein Chain: O: PDB Molecule: cross-alpha amyloid-like structure alphaamg - low resolution PDBTitle: cross-alpha amyloid-like structure alphaamg - low resolution
96	c6c4zF	Alignment	not modelled	5.4	42	PDB header: de novo protein Chain: F: PDB Molecule: cross-alpha amyloid-like structure alphaamg - low resolution PDBTitle: cross-alpha amyloid-like structure alphaamg - low resolution
97	c6c4yA	Alignment	not modelled	5.4	42	PDB header: de novo protein Chain: A: PDB Molecule: cross-alpha amyloid-like structure alphaamg; PDBTitle: cross-alpha amyloid-like structure alphaamg
98	c6c4yF	Alignment	not modelled	5.4	42	PDB header: de novo protein Chain: F: PDB Molecule: cross-alpha amyloid-like structure alphaamg; PDBTitle: cross-alpha amyloid-like structure alphaamg
99	c6c4yP	Alignment	not modelled	5.4	42	PDB header: de novo protein Chain: P: PDB Molecule: cross-alpha amyloid-like structure alphaamg; PDBTitle: cross-alpha amyloid-like structure alphaamg