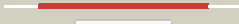



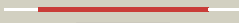







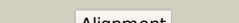


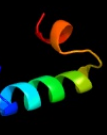
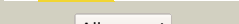
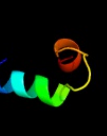


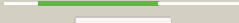

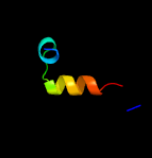
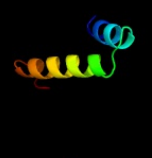

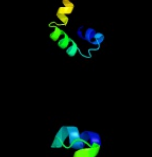




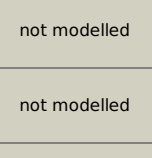


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0300 (-) _363826_364047
Date	Tue Jul 23 14:50:36 BST 2019
Unique Job ID	73fd121ba558b6c8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h87D_	 Alignment		100.0	100	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
2	c2h1oH_	 Alignment		91.6	19	PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
3	d2bsqe1	 Alignment		91.6	19	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
4	c2k5jB_	 Alignment		88.6	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
5	d2bj7a1	 Alignment		79.5	40	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
6	c2bj3D_	 Alignment		77.3	40	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
7	c1q5vB_	 Alignment		76.8	44	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
8	d2hzab1	 Alignment		76.1	44	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
9	d2hzaa1	 Alignment		75.1	44	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
10	c2ca9B_	 Alignment		68.1	32	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
11	c2k29A_	 Alignment		51.6	28	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb

12	d2phcb1	Alignment		48.0	22	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like
13	c4qoyC_	Alignment		40.4	25	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase e1 component; PDBTitle: novel binding motif and new flexibility revealed by structural2 analysis of a pyruvate dehydrogenase-dihydrolipoyl acetyltransferase3 sub-complex from the escherichia coli pyruvate dehydrogenase multi-4 enzyme complex
14	c2zp2B_	Alignment		40.3	26	PDB header: transferase inhibitor Chain: B: PDB Molecule: kinase a inhibitor; PDBTitle: c-terminal domain of kipi from bacillus subtilis
15	c5chhA_	Alignment		35.3	22	PDB header: transcription Chain: A: PDB Molecule: arac family transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
16	d3proc1	Alignment		33.4	17	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
17	c2phcB_	Alignment		33.1	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein ph0987; PDBTitle: crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
18	c5dudB_	Alignment		32.8	26	PDB header: unknown function Chain: B: PDB Molecule: ybgj; PDBTitle: crystal structure of e. coli ybgjk
19	c3mmlD_	Alignment		29.7	17	PDB header: hydrolase Chain: D: PDB Molecule: allophanate hydrolase subunit 1; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
20	c6ajnF_	Alignment		22.9	21	PDB header: toxin Chain: F: PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atar bound with accoa
21	c6gtsC_	Alignment	not modelled	22.4	21	PDB header: transcription Chain: C: PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna
22	c2mdvB_	Alignment	not modelled	20.4	39	PDB header: de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: nmr structure of beta alpha alpha 38
23	c6qeqD_	Alignment	not modelled	18.7	4	PDB header: dna binding protein Chain: D: PDB Molecule: pcf;f; PDBTitle: pcf from enterococcus faecalis pcf10
24	c4me7E_	Alignment	not modelled	18.6	36	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: antitoxin endoai; PDBTitle: crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze
25	c6humN_	Alignment	not modelled	18.4	50	PDB header: proton transport Chain: N: PDB Molecule: nad(p)h-quinone oxidoreductase subunit n; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
26	c1zgwA_	Alignment	not modelled	17.0	22	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ada polyprotein; PDBTitle: nmr structure of e. coli ada protein in complex with dna
27	c4q2uM_	Alignment	not modelled	14.5	22	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
28	d2csba5	Alignment	not modelled	13.8	69	Fold: Topoisomerase V catalytic domain-like Superfamily: Topoisomerase V catalytic domain-like Family: Topoisomerase V catalytic domain-like

29	c4proD_	Alignment	not modelled	13.7	11	PDB header: serine protease Chain: D: PDB Molecule: alpha-lytic protease; PDBTitle: alpha-lytic protease complexed with pro region
30	c3fmtF_	Alignment	not modelled	13.6	23	PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein seqa; PDBTitle: crystal structure of seqa bound to dna
31	d2auwa1	Alignment	not modelled	13.1	54	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
32	d2cyya1	Alignment	not modelled	12.5	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
33	d1b28a_	Alignment	not modelled	12.4	35	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
34	d1xrxa1	Alignment	not modelled	11.7	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like
35	c1xrxD_	Alignment	not modelled	11.7	21	PDB header: replication inhibitor Chain: D: PDB Molecule: seqa protein; PDBTitle: crystal structure of a dna-binding protein
36	c3m6zA_	Alignment	not modelled	11.5	69	PDB header: isomerase Chain: A: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of an n-terminal 44 kda fragment of topoisomerase v2 in the presence of guanidium hydrochloride
37	c1ojlD_	Alignment	not modelled	11.4	29	PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
38	d1rfma_	Alignment	not modelled	10.8	32	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
39	c5l33A_	Alignment	not modelled	10.7	88	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
40	c5z7iC_	Alignment	not modelled	10.7	43	PDB header: dna binding protein/dna Chain: C: PDB Molecule: cell cycle regulatory protein gcra; PDBTitle: caulobacter crescentus gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna
41	c4fxeB_	Alignment	not modelled	10.1	28	PDB header: toxin/toxin inhibitor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex
42	d1vbga1	Alignment	not modelled	9.7	43	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
43	c6c5rF_	Alignment	not modelled	9.1	60	PDB header: cytosolic protein Chain: F: PDB Molecule: calcium uniporter; PDBTitle: crystal structure of the soluble domain of the mitochondrial calcium2 uniporter
44	c2rgoA_	Alignment	not modelled	8.4	34	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
45	c3oepA_	Alignment	not modelled	8.1	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha0988; PDBTitle: crystal structure of ttha0988 in space group p43212
46	c3oq9C_	Alignment	not modelled	8.1	16	PDB header: apoptosis Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: structure of the fas/fadd death domain assembly
47	c5k57A_	Alignment	not modelled	7.7	45	PDB header: hydrolase Chain: A: PDB Molecule: protein ddi1 homolog 2; PDBTitle: hdd domain from human ddi2
48	c2kz3A_	Alignment	not modelled	7.7	34	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein rad51l3; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
49	d1g2ha_	Alignment	not modelled	7.5	43	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
50	c1g2hA_	Alignment	not modelled	7.5	43	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein tyrr homolog; PDBTitle: solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
51	d1vz0a1	Alignment	not modelled	7.5	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
52	d1fipa_	Alignment	not modelled	7.3	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
53	c1vw42_	Alignment	not modelled	7.1	24	PDB header: ribosome Chain: 2: PDB Molecule: 54s ribosomal protein l28, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
54	d1y9ba1	Alignment	not modelled	7.0	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like

55	d1myla_	Alignment	not modelled	7.0	23	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
56	d1mylb_	Alignment	not modelled	6.9	30	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
57	c6g1nB_	Alignment	not modelled	6.9	29	PDB header: antitoxin Chain: B: PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the burkholderia pseudomallei antitoxin hicb
58	c2hwgA_	Alignment	not modelled	6.7	32	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
59	c2q9lA_	Alignment	not modelled	6.7	21	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of imazg from vibrio dat 722: ctag-imazg (p43212)
60	d1zj8a1	Alignment	not modelled	6.7	42	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
61	c2auwB_	Alignment	not modelled	6.6	54	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
62	d1ntca_	Alignment	not modelled	6.5	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
63	c2ph0A_	Alignment	not modelled	6.5	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the q6d2t7_erwct protein from erwinia carotovora.2 nesg target ewr41.
64	c2w48D_	Alignment	not modelled	6.5	28	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
65	d1whza_	Alignment	not modelled	6.4	25	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: YcfA-like
66	d1lga1	Alignment	not modelled	6.4	37	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
67	c2csdB_	Alignment	not modelled	6.2	69	PDB header: isomerase Chain: B: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
68	c1umqA_	Alignment	not modelled	6.1	36	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
69	d1umqa_	Alignment	not modelled	6.1	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
70	d1r71a_	Alignment	not modelled	5.9	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
71	d3bwga1	Alignment	not modelled	5.9	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
72	d1bl0a1	Alignment	not modelled	5.8	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
73	d2oiea1	Alignment	not modelled	5.8	32	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
74	c2fhwA_	Alignment	not modelled	5.7	42	PDB header: signaling protein Chain: A: PDB Molecule: relaxin 3 (prorelaxin h3) (insulin-like peptide PDBTitle: solution structure of human relaxin-3
75	d2gtaa1	Alignment	not modelled	5.7	39	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
76	c3iacA_	Alignment	not modelled	5.7	42	PDB header: isomerase Chain: A: PDB Molecule: glucuronate isomerase; PDBTitle: 2.2 angstrom crystal structure of glucuronate isomerase from2 salmonella typhimurium.
77	c4o6xA_	Alignment	not modelled	5.6	24	PDB header: protein binding Chain: A: PDB Molecule: ankyrin-3; PDBTitle: crystal structure of human ankyrin g death domain
78	d1kbla1	Alignment	not modelled	5.5	40	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
79	d1h6za1	Alignment	not modelled	5.5	36	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
80	c4ifdE_	Alignment	not modelled	5.2	35	PDB header: hydrolase/rna Chain: E: PDB Molecule: exosome complex component rrp42; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna PDB header: isomerase

81	c4gfjA_	Alignment	not modelled	5.1	69	Chain: A: PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topo-78, an n-terminal 78kda fragment of2 topoisomerase v
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