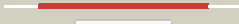



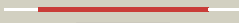

















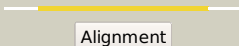

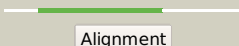

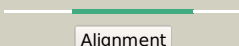
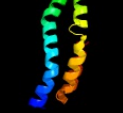
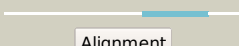

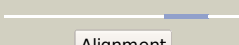

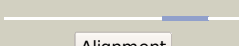

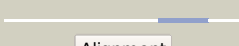




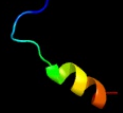

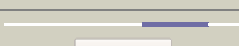

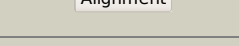

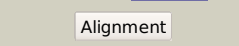




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2533c_nusB_2858264_2858734
Date	Wed Aug 7 12:50:16 BST 2019
Unique Job ID	b56a68ede8f792c6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jr0A_	 Alignment		100.0	27	PDB header: transcription Chain: A: PDB Molecule: n utilization substance protein b homolog; PDBTitle: solution structure of nusB from aquifex aeolicus
2	c1eyvA_	 Alignment		100.0	100	PDB header: transcription Chain: A: PDB Molecule: n-utilizing substance protein b homolog; PDBTitle: the crystal structure of nusB from mycobacterium tuberculosis
3	d1eyva_	 Alignment		100.0	100	Fold: NusB-like Superfamily: NusB-like Family: Antitermination factor NusB
4	c6cckqA_	 Alignment		100.0	28	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusB; PDBTitle: solution structure of the burkholderia thailandensis transcription2 antitermination protein nusB (bth_i1529) - seattle structural3 genomics center for infectious disease target butha.17903.a
5	d1tzva_	 Alignment		100.0	32	Fold: NusB-like Superfamily: NusB-like Family: Antitermination factor NusB
6	d1ey1a_	 Alignment		100.0	31	Fold: NusB-like Superfamily: NusB-like Family: Antitermination factor NusB
7	d1sqqal	 Alignment		100.0	18	Fold: NusB-like Superfamily: NusB-like Family: RmsB N-terminal domain-like
8	c1sqqA_	 Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: sun protein; PDBTitle: the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution
9	c2yx1A_	 Alignment		99.8	17	PDB header: transferase Chain: A: PDB Molecule: 450aa long hypothetical fmu protein; PDBTitle: crystal structure of ph0851
10	c5wwrA_	 Alignment		97.0	20	PDB header: transferase/rna Chain: A: PDB Molecule: putative methyltransferase nsun6; PDBTitle: crystal structure of human nsun6/trna/sfg
11	d1q8ca_	 Alignment		81.0	17	Fold: NusB-like Superfamily: NusB-like Family: Hypothetical protein MG027

12	c6h02A_	 Alignment		77.8	14	PDB header: transcription Chain: A: PDB Molecule: mediator of rna polymerase ii transcription subunit 23; PDBTitle: crystal structure of human mediator subunit med23
13	d3c8ga1	 Alignment		58.2	11	Fold: MtIR-like Superfamily: MtIR-like Family: MtIR-like
14	c3ls1A_	 Alignment		43.3	13	PDB header: photosynthesis Chain: A: PDB Molecule: sll1638 protein; PDBTitle: crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
15	d1xmka1	 Alignment		38.0	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
16	c2zc2A_	 Alignment		25.2	13	PDB header: replication Chain: A: PDB Molecule: dnad-like replication protein; PDBTitle: crystal structure of dnad-like replication protein from streptococcus2 mutans ua159, gi 24377835, residues 127-199
17	c3pubA_	 Alignment		23.3	18	PDB header: unknown function Chain: A: PDB Molecule: 30kda protein; PDBTitle: crystal structure of the bombyx mori low molecular weight lipoprotein2 7 (bmlp7)
18	d2i5ua1	 Alignment		22.0	12	Fold: DnaD domain-like Superfamily: DnaD domain-like Family: DnaD domain
19	c4pc4B_	 Alignment		21.4	15	PDB header: lipid binding protein Chain: B: PDB Molecule: 30k lipoprotein; PDBTitle: bombyx mori lipoprotein 6
20	c5cw9A_	 Alignment		20.6	56	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed ferredoxin-ferredoxin domain insertion PDBTitle: crystal structure of de novo designed ferredoxin-ferredoxin domain2 insertion protein
21	c4wv4B_	 Alignment	not modelled	16.5	27	PDB header: transcription Chain: B: PDB Molecule: transcription initiation factor tfiid subunit 8; PDBTitle: heterodimer of taf8/taf10
22	c6hu9r_	 Alignment	not modelled	15.9	13	PDB header: oxidoreductase/electron transport Chain: R: PDB Molecule: cytochrome b-c1 complex subunit 7; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
23	c2y69R_	 Alignment	not modelled	15.0	27	PDB header: electron transport Chain: R: PDB Molecule: cytochrome c oxidase subunit 5a; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
24	c5ybxA_	 Alignment	not modelled	14.7	38	PDB header: dna binding protein Chain: A: PDB Molecule: bouquet formation protein 4; PDBTitle: crystal structure of the n-terminal domain of bqt4 in s.pombe
25	c5lksA_	 Alignment	not modelled	13.1	5	PDB header: cell cycle Chain: A: PDB Molecule: protein mis12 homolog; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
26	c2hv8D_	 Alignment	not modelled	12.4	22	PDB header: protein transport Chain: D: PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of gtp-bound rab11 in complex with fip3
27	c5ycaA_	 Alignment	not modelled	11.1	38	PDB header: membrane protein Chain: A: PDB Molecule: ubiquitin-like protein smt3,bouquet formation protein 4; PDBTitle: crystal structure of inner membrane protein bqt4 in complex with lem2
28	c6eacC_	 Alignment	not modelled	9.8	27	PDB header: transferase Chain: C: PDB Molecule: selo; PDBTitle: pseudomonas syringae selo

29	d2ga1a1	Alignment	not modelled	9.8	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Alr1493-like
30	d1sxje1	Alignment	not modelled	9.4	17	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
31	c2ynqD_	Alignment	not modelled	8.3	14	PDB header: membrane protein Chain: D: PDB Molecule: essb; PDBTitle: crystal structure of geobacillus thermodenitrificans essb2 extracellular fragment
32	d1qzma_	Alignment	not modelled	8.3	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
33	c2n9rA_	Alignment	not modelled	8.0	21	PDB header: antimicrobial protein Chain: A: PDB Molecule: antimicrobial peptide padbs1r1; PDBTitle: novel antimicrobial peptide padbs1r1 designed from the ribosomal2 protein l39e from pyrobaculum aerophilum using bioinformatics
34	d1ou9a_	Alignment	not modelled	7.7	15	Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
35	d1v54e_	Alignment	not modelled	7.1	22	Fold: alpha-alpha superhelix Superfamily: Cytochrome c oxidase subunit E Family: Cytochrome c oxidase subunit E
36	c5ldwd_	Alignment	not modelled	6.8	25	PDB header: oxidoreductase Chain: D: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 2, PDBTitle: structure of mammalian respiratory complex i, class1
37	c5ldxd_	Alignment	not modelled	6.8	25	PDB header: oxidoreductase Chain: D: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 2, PDBTitle: structure of mammalian respiratory complex i, class3.
38	c5lc5d_	Alignment	not modelled	6.8	25	PDB header: oxidoreductase Chain: D: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 2, PDBTitle: structure of mammalian respiratory complex i, class2
39	c6emwD_	Alignment	not modelled	6.6	21	PDB header: chaperone Chain: D: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: structure of s.aureus clpc in complex with meca
40	c4q9vB_	Alignment	not modelled	6.4	17	PDB header: immune system Chain: B: PDB Molecule: tumor necrosis factor alpha-induced protein 8-like protein PDBTitle: crystal structure of tipe3
41	c1yodB_	Alignment	not modelled	6.1	22	PDB header: de novo protein Chain: B: PDB Molecule: water-solublized phospholamban; PDBTitle: crystal structure of a water soluble analog of phospholamban
42	c4c9yB_	Alignment	not modelled	6.0	11	PDB header: cell cycle Chain: B: PDB Molecule: spindle and kinetochore-associated protein 1; PDBTitle: structural basis for the microtubule binding of the human2 kinetochore ska complex
43	c2vckC_	Alignment	not modelled	6.0	28	PDB header: oxidoreductase Chain: C: PDB Molecule: cyanobacterial phycoerythrobilin; PDBTitle: structure of phycoerythrobilin synthase pebs from the cyanophage p-2 ssm2 in complex with the bound substrate biliverdin ixa
44	c4a56A_	Alignment	not modelled	6.0	19	PDB header: protein transport Chain: A: PDB Molecule: pullulanase secretion protein puls; PDBTitle: crystal structure of the type 2 secretion system pilotin2 from klebsiella oxytoca
45	c2mu6A_	Alignment	not modelled	6.0	18	PDB header: peptide binding Chain: A: PDB Molecule: starp antigen; PDBTitle: 3d structure determination of starp peptides implicated in p.2 falciparum invasion of hepatic cells
46	c5a9qZ_	Alignment	not modelled	5.9	12	PDB header: transport protein Chain: Z: PDB Molecule: nuclear pore complex protein nup85; PDBTitle: human nuclear pore complex
47	c6dqwD_	Alignment	not modelled	5.8	9	PDB header: oxidoreductase Chain: D: PDB Molecule: ribonucleoside-diphosphate reductase, alpha chain; PDBTitle: flavobacterium johnsoniae class id ribonucleotide reductase alpha2 subuint
48	c4auvH_	Alignment	not modelled	5.8	27	PDB header: apoptosis Chain: H: PDB Molecule: breast cancer metastasis suppressor 1; PDBTitle: crystal structure of the brms1 n-terminal region
49	d1qbjc_	Alignment	not modelled	5.8	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
50	c6cgmA_	Alignment	not modelled	5.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase; PDBTitle: x-ray crystal structure of bacillus subtilis ribonucleotide reductase2 nrde alpha subunit (nucleotide free)
51	c3utkA_	Alignment	not modelled	5.6	24	PDB header: protein transport Chain: A: PDB Molecule: lipoprotein outs; PDBTitle: structure of the pilotin of the type ii secretion system
52	c1yodA_	Alignment	not modelled	5.5	22	PDB header: de novo protein Chain: A: PDB Molecule: water-solublized phospholamban; PDBTitle: crystal structure of a water soluble analog of phospholamban
53	c4auvG_	Alignment	not modelled	5.5	32	PDB header: apoptosis Chain: G: PDB Molecule: breast cancer metastasis suppressor 1; PDBTitle: crystal structure of the brms1 n-terminal region
						Fold: DNA/RNA-binding 3-helical bundle

54	d2gxba1	Alignment	not modelled	5.5	27	Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
55	d1qgpa_	Alignment	not modelled	5.3	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
56	c3sola_	Alignment	not modelled	5.3	24	PDB header: protein transport Chain: A: PDB Molecule: type ii secretion pathway related protein; PDBTitle: crystal structure of the type 2 secretion system pilotin gsp5
57	d1s7za_	Alignment	not modelled	5.3	21	Fold: Another 3-helical bundle Superfamily: B-form DNA mimic Ocr Family: B-form DNA mimic Ocr
58	c4p4sB_	Alignment	not modelled	5.2	21	PDB header: antiviral protein/hydrolase Chain: B: PDB Molecule: interferon-induced gtp-binding protein mx1; PDBTitle: gmppcp-bound stalkless-mxa
59	c2kebA_	Alignment	not modelled	5.2	19	PDB header: dna binding protein Chain: A: PDB Molecule: dna polymerase subunit alpha b; PDBTitle: nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
60	c3w1hB_	Alignment	not modelled	5.2	11	PDB header: transferase Chain: B: PDB Molecule: l-seryl-trna(sec) selenium transferase; PDBTitle: crystal structure of the selenocysteine synthase sela from aquifex2 aeolicus
61	c5tdyD_	Alignment	not modelled	5.0	20	PDB header: motor protein Chain: D: PDB Molecule: flagellar motor switch protein flig; PDBTitle: structure of cofolded flifc:flign complex from thermotoga maritima
62	c6djqa_	Alignment	not modelled	5.0	21	PDB header: hydrolase Chain: A: PDB Molecule: vps1 gtpase-bse; PDBTitle: vps1 gtpase-bse fusion complexed with gdp.alf4-