



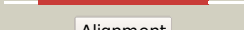

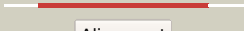









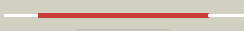






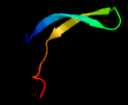



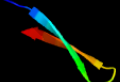
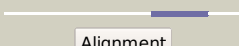

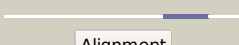
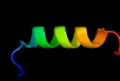
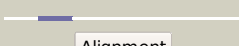
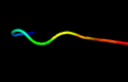
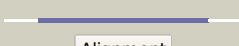









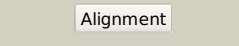


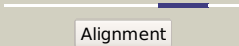


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0659c_(-)_754688_754996
Date	Fri Jul 26 01:50:22 BST 2019
Unique Job ID	c648518bc8ac81a2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ub4a_	 Alignment		100.0	21	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
2	c5xe3B_	 Alignment		99.9	25	PDB header: hydrolase/antitoxin Chain: B: PDB Molecule: endoribonuclease mazf4; PDBTitle: endoribonuclease in complex with its cognate antitoxin from2 mycobacterial species
3	c4mzpC_	 Alignment		99.9	28	PDB header: hydrolase Chain: C: PDB Molecule: mazf mrna interferase; PDBTitle: mazf from s. aureus crystal form iii, c2221, 2.7 a
4	c5hk3B_	 Alignment		99.9	31	PDB header: hydrolase/dna Chain: B: PDB Molecule: endoribonuclease mazf6; PDBTitle: crystal structure of m. tuberculosis mazf-mt3 t52d-f62d mutant in2 complex with dna
5	c5hja_	 Alignment		99.9	26	PDB header: hydrolase/rna Chain: A: PDB Molecule: endoribonuclease mazf9; PDBTitle: structure of m. tuberculosis mazf-mt1 (rv2801c) in complex with rna
6	c5wygC_	 Alignment		99.9	27	PDB header: hydrolase Chain: C: PDB Molecule: probable endoribonuclease mazf7; PDBTitle: the crystal structure of the apo form of mtb mazf
7	d1ne8a_	 Alignment		99.9	28	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
8	d1m1fa_	 Alignment		99.9	27	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
9	c5ccaA_	 Alignment		99.9	30	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease mazf3; PDBTitle: crystal structure of mtb toxin
10	d3vuba_	 Alignment		96.5	14	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: CcdB
11	c3jrza_	 Alignment		95.8	12	PDB header: toxin Chain: A: PDB Molecule: ccdb; PDBTitle: ccdbvfi-formii-ph5.6

12	c5ikjA	 Alignment		64.8	19	PDB header: transcription Chain: A: PDB Molecule: cryptic loci regulator 2; PDBTitle: structure of clr2 bound to the clr1 c-terminus
13	c6bwqB	 Alignment		21.1	33	PDB header: metal binding protein Chain: B: PDB Molecule: pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel PDBTitle: larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
14	c3c19A	 Alignment		20.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mk0293; PDBTitle: crystal structure of protein mk0293 from methanopyrus kandleri av19
15	d1rz4a1	 Alignment		17.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Eukaryotic translation initiation factor 3 subunit 12, eIF3k, C-terminal domain
16	c3vdoB	 Alignment		13.8	9	PDB header: dna binding protein/protein binding Chain: B: PDB Molecule: anti-sigma-k factor rska; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis
17	d1okja2	 Alignment		12.5	50	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
18	c4p7xA	 Alignment		12.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: l-proline cis-4-hydroxylase; PDBTitle: l-pipecolic acid-bound l-proline cis-4-hydroxylase
19	c3llrA	 Alignment		10.8	17	PDB header: transferase Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 3a; PDBTitle: crystal structure of the pwwp domain of human dna (cytosine-5-)-2 methyltransferase 3 alpha
20	c1cffB	 Alignment		10.5	38	PDB header: calmodulin Chain: B: PDB Molecule: calcium pump; PDBTitle: nmr solution structure of a complex of calmodulin with a binding2 peptide of the ca2+-pump
21	c5fmzB	 Alignment	not modelled	9.8	17	PDB header: transcription Chain: B: PDB Molecule: rna-directed rna polymerase catalytic subunit; PDBTitle: crystal structure of influenza b polymerase with bound 5' vrna
22	c4wsaB	 Alignment	not modelled	9.6	17	PDB header: transferase/rna Chain: B: PDB Molecule: rna-directed rna polymerase catalytic subunit; PDBTitle: crystal structure of influenza b polymerase bound to the vrna promoter2 (flub1 form)
23	c4nohA	 Alignment	not modelled	9.4	14	PDB header: lipid binding protein Chain: A: PDB Molecule: lipoprotein, putative; PDBTitle: 1.5 angstrom crystal structure of putative lipoprotein from bacillus2 anthracis.
24	c2l89A	 Alignment	not modelled	9.2	17	PDB header: protein binding Chain: A: PDB Molecule: pwwp domain-containing protein 1; PDBTitle: solution structure of pdp1 pwwp domain reveals its unique binding2 sites for methylated h4k20 and dna
25	d1cxqa	 Alignment	not modelled	9.1	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
26	c2dkkA	 Alignment	not modelled	8.2	32	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: structure/function studies of cytochrome p450 158a1 from streptomyces2 coelicolor a3(2)
27	c2z3tD	 Alignment	not modelled	8.1	9	PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome p450; PDBTitle: crystal structure of substrate free cytochrome p450 stap2 (cyp245a1)
28	c2jnsA	 Alignment	not modelled	7.8	13	PDB header: unknown function Chain: A: PDB Molecule: bromodomain-containing protein 4; PDBTitle: solution structure of the bromodomain-containing protein

						42 et domain
29	c4bedA	Alignment	not modelled	7.2	17	PDB header: oxygen transport Chain: A: PDB Molecule: hemocyanin klh1; PDBTitle: keyhole limpet hemocyanin (klh): 9a cryoem structure and molecular2 model of the klh1 didecamer reveal the interfaces and intricate3 topology of the 160 functional units
30	d2dexx3	Alignment	not modelled	6.8	15	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Peptidylarginine deiminase Pad4, catalytic C-terminal domain
31	c5cz1B	Alignment	not modelled	6.8	19	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase
32	c2jysA	Alignment	not modelled	6.7	7	PDB header: hydrolase Chain: A: PDB Molecule: protease/reverse transcriptase; PDBTitle: solution structure of simian foamy virus (mac) protease
33	d1lm8v	Alignment	not modelled	6.7	14	Fold: Prealbumin-like Superfamily: VHL Family: VHL
34	c4bkwA	Alignment	not modelled	6.6	15	PDB header: receptor Chain: A: PDB Molecule: zinc finger fyve domain-containing protein 9; PDBTitle: crystal structure of the c-terminal region of human zfyve9
35	d1s1fa	Alignment	not modelled	6.5	27	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
36	c2qnhv	Alignment	not modelled	6.4	47	PDB header: ribosome Chain: V: PDB Molecule: PDBTitle: interactions and dynamics of the shine-dalgarno helix in the 70s2 ribosome. this file, 2qnh, contains the 30s ribosome subunit, two3 trna, and mrna molecules. 50s ribosome subunit is in the file 1vsp.
37	c3v28U	Alignment	not modelled	6.0	47	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of hpf bound to the 70s ribosome. this pdb entry2 contains coordinates for the 30s subunit with bound hpf of the 2nd3 ribosome in the asu
38	c4dv2U	Alignment	not modelled	5.9	47	PDB header: ribosome Chain: U: PDB Molecule: ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 30s ribosomal subunit2 with a 16s rrna mutation, c912a
39	c3ohdU	Alignment	not modelled	5.9	47	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: structure of the thermus thermophilus ribosome complexed with2 erythromycin. this file contains the 30s subunit of one 70s ribosome.3 the entire crystal structure contains two 70s ribosomes.
40	c3ohcU	Alignment	not modelled	5.9	47	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: structure of the thermus thermophilus ribosome complexed with2 erythromycin. this file contains the 30s subunit of one 70s ribosome.3 the entire crystal structure contains two 70s ribosomes.
41	c3d55A	Alignment	not modelled	5.9	7	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
42	d1uyra1	Alignment	not modelled	5.8	35	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
43	c4dv1U	Alignment	not modelled	5.5	47	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 30s ribosomal subunit2 with a 16s rrna mutation, u20g, bound with streptomycin
44	c1zx4B	Alignment	not modelled	5.5	18	PDB header: cell cycle Chain: B: PDB Molecule: plasmid partition par b protein; PDBTitle: structure of parb bound to dna
45	d1c0ma2	Alignment	not modelled	5.4	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
46	c3v22U	Alignment	not modelled	5.4	47	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of rmf bound to the 70s ribosome. this pdb entry2 contains coordinates for the 30s subunit with bound rmf of the 1st3 ribosome in the asu
47	c1n34V	Alignment	not modelled	5.4	47	PDB header: ribosome Chain: V: PDB Molecule: 30s ribosomal protein thx; PDBTitle: structure of the thermus thermophilus 30s ribosomal subunit2 in the presence of codon and crystallographically3 disordered near-cognate transfer rna anticodon stem-loop4 mismatched at the first codon position
48	c3ohyU	Alignment	not modelled	5.3	47	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: structure of the thermus thermophilus 70s ribosome complexed with2 azithromycin. this file contains the 30s subunit of one 70s ribosome.3 the entire crystal structure contains two 70s ribosomes.
49	c3oi0U	Alignment	not modelled	5.3	47	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: structure of the thermus thermophilus 70s ribosome complexed with2 azithromycin. this file contains the 30s subunit of one 70s ribosome.3 the entire crystal structure contains two 70s ribosomes.
50	c2ow8v	Alignment	not modelled	5.2	47	PDB header: ribosome Chain: V: PDB Molecule: PDBTitle: crystal structure of a 70s ribosome-trna complex reveals functional2 interactions and rearrangements. this file, 2ow8,

					contains the 30s3 ribosome subunit, two trna, and mrna molecules. 50s ribosome subunit4 is in the file 1vsa.
51	d1h3za_	Alignment	not modelled	5.1	10 Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
52	c1i97U_	Alignment	not modelled	5.1	47 PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the 30s ribosomal subunit from thermus2 thermophilus in complex with tetracycline
53	c3otoU_	Alignment	not modelled	5.0	47 PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the 30s ribosomal subunit from a ksga mutant of2 thermus thermophilus (hb8)
54	c4dv5U_	Alignment	not modelled	5.0	47 PDB header: ribosome/antibiotic Chain: U: PDB Molecule: ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 30s ribosomal subunit2 with a 16s rrna mutation, a914g, bound with streptomycin