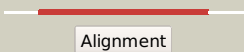

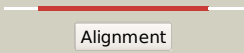



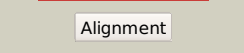



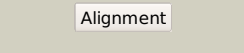

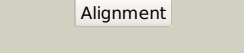



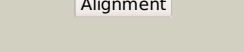

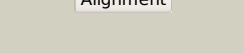

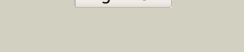

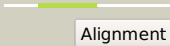
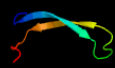
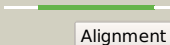

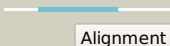

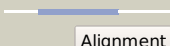
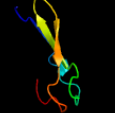
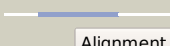
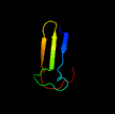
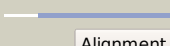

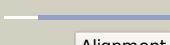

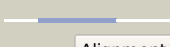
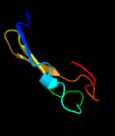
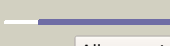


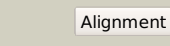
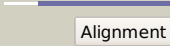
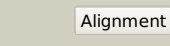
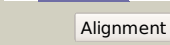
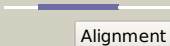
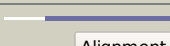
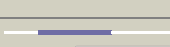


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2801c_(-)_3110177_3110533
Date	Wed Aug 7 12:50:46 BST 2019
Unique Job ID	d7bfe077deef8d6b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5hjzA_	 Alignment		99.9	98	PDB header: hydrolase/rna Chain: A: PDB Molecule: endoribonuclease mazf9; PDBTitle: structure of m. tuberculosis mazf-mt1 (rv2801c) in complex with rna
2	c4mzpC_	 Alignment		99.9	30	PDB header: hydrolase Chain: C: PDB Molecule: mazf mrna interferase; PDBTitle: mazf from s. aureus crystal form iii, c2221, 2.7 a
3	d1ne8a_	 Alignment		99.9	31	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
4	d1m1fa_	 Alignment		99.9	33	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
5	c5hk3B_	 Alignment		99.9	34	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
6	c5xe3B_	 Alignment		99.9	23	PDB header: hydrolase/antitoxin Chain: B: PDB Molecule: endoribonuclease mazf4; PDBTitle: endoribonuclease in complex with its cognate antitoxin from2 mycobacterial species
7	d1ub4a_	 Alignment		99.9	38	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
8	c5wygC_	 Alignment		99.9	35	PDB header: hydrolase Chain: C: PDB Molecule: probable endoribonuclease mazf7; PDBTitle: the crystal structure of the apo form of mtb mazf
9	c5ccaA_	 Alignment		99.7	24	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease mazf3; PDBTitle: crystal structure of mtb toxin
10	c3jrzA_	 Alignment		92.3	16	PDB header: toxin Chain: A: PDB Molecule: ccdb; PDBTitle: ccdbvfi-formii-ph5.6
11	d3vuBa_	 Alignment		89.4	17	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: CcdB

12	c5ikjA	 Alignment		61.7	33	PDB header: transcription Chain: A: PDB Molecule: cryptic loci regulator 2; PDBTitle: structure of clr2 bound to the clr1 c-terminus
13	c6n1bA	 Alignment		52.5	14	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate-binding protein; PDBTitle: crystal structure of an n-acetylgalactosamine deacetylase from f.2 plautii in complex with blood group b trisaccharide
14	c3mxuA	 Alignment		36.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from bartonella2 henselae
15	d1onla	 Alignment		28.4	23	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
16	c2edgA	 Alignment		27.8	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: solution structure of the gcv_h domain from mouse glycine
17	c3llrA	 Alignment		24.0	10	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
18	d1h3za	 Alignment		21.3	13	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
19	c3a8jF	 Alignment		20.8	21	PDB header: transferase/transport protein Chain: F: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of et-ehred complex
20	c5vc8B	 Alignment		19.8	9	PDB header: dna binding protein Chain: B: PDB Molecule: histone-lysine n-methyltransferase nsd2; PDBTitle: crystal structure of the whsc1 pwwp1 domain
21	c3iftA	 Alignment	not modelled	19.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
22	d1ex0a1	 Alignment	not modelled	19.3	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
23	c2l89A	 Alignment	not modelled	18.9	12	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
24	d1okja2	 Alignment	not modelled	17.2	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
25	d1cxqa	 Alignment	not modelled	16.5	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
26	d1hpca	 Alignment	not modelled	16.0	23	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
27	c4rmoA	 Alignment	not modelled	16.0	15	PDB header: toxin/rna Chain: A: PDB Molecule: cptn toxin; PDBTitle: crystal structure of the cptn type iii toxin-antitoxin system from2 eubacterium rectale
28	c1ssfA	 Alignment	not modelled	14.8	26	PDB header: cell cycle Chain: A: PDB Molecule: transformation related protein 53 binding PDBTitle: solution structure of the mouse 53bp1 fragment (residues2 1463-1617)

29	c2jysA	Alignment	not modelled	13.2	0	PDB header: hydrolase Chain: A: PDB Molecule: protease/reverse transcriptase; PDBTitle: solution structure of simian foamy virus (mac) protease
30	c5a35A	Alignment	not modelled	13.0	7	PDB header: transport protein Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage protein h-like (gcvh-l)2 from streptococcus pyogenes
31	c4mnoA	Alignment	not modelled	13.0	29	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 1a; PDBTitle: crystal structure of aif1a from pyrococcus abyssi
32	c2zkrT	Alignment	not modelled	12.9	18	PDB header: ribosomal protein/rna Chain: T: PDB Molecule: rna expansion segment es39 part iii; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
33	c2fqpD	Alignment	not modelled	12.2	14	PDB header: metal binding protein Chain: D: PDB Molecule: hypothetical protein bp2299; PDBTitle: crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohama i at 1.80 a resolution
34	c2dgyA	Alignment	not modelled	11.9	40	PDB header: translation Chain: A: PDB Molecule: mgc11102 protein; PDBTitle: solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
35	d2daq1	Alignment	not modelled	11.9	17	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
36	c3c19A	Alignment	not modelled	11.6	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mk0293; PDBTitle: crystal structure of protein mk0293 from methanopyrus kandleri av19
37	c6bwqB	Alignment	not modelled	11.2	16	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
38	c2ka7A	Alignment	not modelled	10.7	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: nmr solution structure of tm0212 at 40 c
39	d1rz4a1	Alignment	not modelled	10.6	19	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
40	c1cffB	Alignment	not modelled	10.5	40	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
41	c3bxpA	Alignment	not modelled	9.7	8	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase/esterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcfs1 at 1.70 a resolution
42	c4l3uA	Alignment	not modelled	9.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf3571 family protein (abaye3784) from2 acinetobacter baumannii aye at 1.95 a resolution
43	c4eyzB	Alignment	not modelled	9.6	25	PDB header: hydrolase Chain: B: PDB Molecule: cellulosome-related protein module from ruminococcus PDBTitle: crystal structure of an uncommon cellulosome-related protein module2 from ruminococcus flavefaciens that resembles papain-like cysteine3 peptidases
44	c2of3A	Alignment	not modelled	9.3	16	PDB header: structural protein, cell cycle Chain: A: PDB Molecule: zyg-9; PDBTitle: tog domain structure from c.elegans zyg9
45	c2oqkA	Alignment	not modelled	8.8	27	PDB header: translation Chain: A: PDB Molecule: putative translation initiation factor eif-1a; PDBTitle: crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
46	c5ofxF	Alignment	not modelled	8.8	24	PDB header: sugar binding protein Chain: F: PDB Molecule: plla; PDBTitle: plla lectin, trisaccharide complex
47	c6fosE	Alignment	not modelled	8.5	23	PDB header: photosynthesis Chain: E: PDB Molecule: photosystem i iron-sulfur center subunit vii; PDBTitle: cyanidioschyzon merolae photosystem i
48	c5zc2B	Alignment	not modelled	7.7	16	PDB header: flavoprotein Chain: B: PDB Molecule: p-hydroxyphenylacetate 3-hydroxylase, reductase component; PDBTitle: acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
49	c3j8l1	Alignment	not modelled	7.6	29	PDB header: ribosome Chain: I: PDB Molecule: es8; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
50	c4xxlA	Alignment	not modelled	7.1	30	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c class i; PDBTitle: crystal structure of class 1 cytochrome mtod from sideroxydans2 lithotrophicus es-1
51	c3d55A	Alignment	not modelled	7.0	25	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
52	c5cz1B	Alignment	not modelled	6.7	19	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase
53	d1zaka2	Alignment	not modelled	6.7	24	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain

						Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
54	d1e5ra	Alignment	not modelled	6.4	32	Fold: Double-stranded beta-helix Superfamily: Clavaminate synthase-like Family: Type II Proline 3-hydroxylase (proline oxidase)
55	d1jt8a	Alignment	not modelled	6.4	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
56	d2uubm1	Alignment	not modelled	6.3	20	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
57	c5o5jM	Alignment	not modelled	6.2	8	PDB header: ribosome Chain: M: PDB Molecule: 30s ribosomal protein s13; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
58	c6gu1B	Alignment	not modelled	6.2	38	PDB header: unknown function Chain: B: PDB Molecule: secreted rxlr effector peptide protein, putative; PDBTitle: sfi3 effector protein from the oomycete plant pathogen phytophthora2 infestans
59	d1kt0a3	Alignment	not modelled	6.1	38	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
60	c3bcxA	Alignment	not modelled	6.1	10	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; PDBTitle: e1 dehydrase
61	c3pfsA	Alignment	not modelled	6.1	10	PDB header: protein binding Chain: A: PDB Molecule: bromodomain and phd finger-containing protein 3; PDBTitle: pwwp domain of human bromodomain and phd finger-containing protein 3
62	c4p7xA	Alignment	not modelled	6.1	43	PDB header: oxidoreductase Chain: A: PDB Molecule: l-proline cis-4-hydroxylase; PDBTitle: l-pipecolic acid-bound l-proline cis-4-hydroxylase
63	c3oeiB	Alignment	not modelled	6.0	25	PDB header: toxin, protein binding Chain: B: PDB Molecule: relj (antitoxin rv3357); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
64	d2nlua1	Alignment	not modelled	6.0	10	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
65	c4bpp0	Alignment	not modelled	5.9	18	PDB header: ribosome Chain: 0: PDB Molecule: translation initiation factor eif-1a family protein; PDBTitle: the crystal structure of the eukaryotic 40s ribosomal subunit in2 complex with eif1 and eif1a - complex 4
66	d1xgsa2	Alignment	not modelled	5.9	18	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
67	c4z8aA	Alignment	not modelled	5.8	44	PDB header: rim-binding protein Chain: A: PDB Molecule: rim-binding protein, isoform f; PDBTitle: sh3-iii of drosophila rim-binding protein bound to a cacophony derived2 peptide
68	d1qp3a	Alignment	not modelled	5.8	14	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Photosystem I accessory protein E (PsaE)
69	c6g25A	Alignment	not modelled	5.8	13	PDB header: oncoprotein Chain: A: PDB Molecule: histone-lysine n-methyltransferase nsd3; PDBTitle: x-ray structure of nsd3-pwwp1 in complex with compound 4
70	c4ipaC	Alignment	not modelled	5.6	18	PDB header: hydrolase Chain: C: PDB Molecule: putative curved dna-binding protein; PDBTitle: structure of a thermophilic arx1
71	c1fxzC	Alignment	not modelled	5.5	31	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
72	c2jnsA	Alignment	not modelled	5.5	13	PDB header: unknown function Chain: A: PDB Molecule: bromodomain-containing protein 4; PDBTitle: solution structure of the bromodomain-containing protein 42 et domain
73	c2lfeA	Alignment	not modelled	5.4	15	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase hecw2; PDBTitle: solution nmr structure of n-terminal domain of human e3 ubiquitin-2 protein ligase hecw2, northeast structural genomics consortium (nesg)3 target ht6306a
74	d1k1va	Alignment	not modelled	5.4	21	Fold: A DNA-binding domain in eukaryotic transcription factors Superfamily: A DNA-binding domain in eukaryotic transcription factors Family: A DNA-binding domain in eukaryotic transcription factors
75	d1b6aa2	Alignment	not modelled	5.3	18	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
76	c4yknA	Alignment	not modelled	5.3	18	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha, PDBTitle: pi3k alpha lipid kinase with active site inhibitor
77	d2q3za1	Alignment	not modelled	5.2	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
78	d1c0ma2	Alignment	not modelled	5.2	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
						PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel

79	c2ovcA_	Alignment	not modelled	5.1	17	subfamily kqt member 4; PDBTitle: crystal structure of a coiled-coil tetramerization domain from kv7.42 channels
80	c2odmA_	Alignment	not modelled	5.1	20	PDB header: unknown function Chain: A: PDB Molecule: upf0358 protein mw0995; PDBTitle: crystal structure of s. aureus ylan, an essential leucine rich protein2 involved in the control of cell shape
81	d1kp0a2	Alignment	not modelled	5.1	25	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase