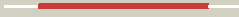
















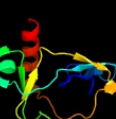




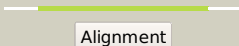

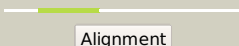
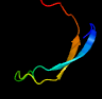
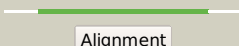

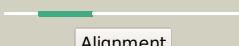

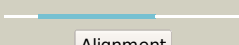
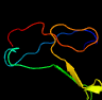
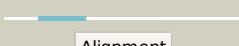
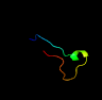
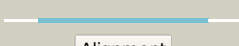


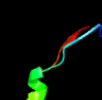

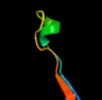

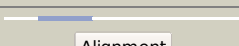

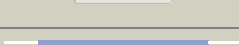
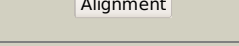
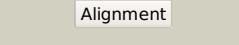

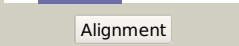



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1991c (-)_2234313_2234657
Date	Mon Aug 5 13:25:09 BST 2019
Unique Job ID	da8ce54e3be939a2

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ne8a_	 Alignment		99.9	37	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
2	c4mzpC_	 Alignment		99.9	37	PDB header: hydrolase Chain: C: PDB Molecule: mazf mrna interferase; PDBTitle: mazf from s. aureus crystal form iii, c2221, 2.7 a
3	c5hjzA_	 Alignment		99.9	30	PDB header: hydrolase/rna Chain: A: PDB Molecule: endoribonuclease mazf9; PDBTitle: structure of m. tuberculosis mazf-mt1 (rv2801c) in complex with rna
4	c5hk3B_	 Alignment		99.9	98	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	d1m1fa_	 Alignment		99.9	26	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
6	c5wygC_	 Alignment		99.9	22	PDB header: hydrolase Chain: C: PDB Molecule: probable endoribonuclease mazf7; PDBTitle: the crystal structure of the apo form of mtb mazf
7	d1ub4a_	 Alignment		99.9	20	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Kid/PemK
8	c5xe3B_	 Alignment		99.9	29	PDB header: hydrolase/antitoxin Chain: B: PDB Molecule: endoribonuclease mazf4; PDBTitle: endoribonuclease in complex with its cognate antitoxin from2 mycobacterial species
9	c5ccaA_	 Alignment		99.8	22	PDB header: hydrolase Chain: A: PDB Molecule: endoribonuclease mazf3; PDBTitle: crystal structure of mtb toxin
10	c3jrzA_	 Alignment		95.0	12	PDB header: toxin Chain: A: PDB Molecule: ccdb; PDBTitle: ccdbvfi-formii-ph5.6
11	d3vuba_	 Alignment		92.9	9	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: CcdB

12	d1h3za_	 Alignment		62.3	7	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
13	c5ikjA_	 Alignment		60.4	19	PDB header: transcription Chain: A: PDB Molecule: cryptic loci regulator 2; PDBTitle: structure of clr2 bound to the clr1 c-terminus
14	c5vc8B_	 Alignment		54.4	10	PDB header: dna binding protein Chain: B: PDB Molecule: histone-lysine n-methyltransferase nsd2; PDBTitle: crystal structure of the whsc1 pwwp1 domain
15	c3mxuA_	 Alignment		42.5	25	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from bartonella2 henselae
16	d1ex0a1	 Alignment		39.9	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
17	c2edgA_	 Alignment		37.0	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: solution structure of the gcv_h domain from mouse glycine
18	c2l89A_	 Alignment		36.3	10	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
19	c3a8jF_	 Alignment		32.3	23	PDB header: transferase/transport protein Chain: F: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of et-ehred complex
20	d1onla_	 Alignment		28.2	25	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
21	c3iftA_	 Alignment	not modelled	24.5	14	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	d1hpca_	 Alignment	not modelled	22.4	21	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
23	c2fqpD_	 Alignment	not modelled	22.1	10	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
24	c3llrA_	 Alignment	not modelled	20.1	18	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
25	d2daqal	 Alignment	not modelled	19.2	19	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
26	d2q3za1	 Alignment	not modelled	16.9	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
27	d2zjrh1	 Alignment	not modelled	16.2	13	Fold: Ribosomal protein L14 Superfamily: Ribosomal protein L14 Family: Ribosomal protein L14
28	c2jysA_	 Alignment	not modelled	16.0	10	PDB header: hydrolase Chain: A: PDB Molecule: protease/reverse transcriptase; PDBTitle: solution structure of simian foamy virus (mac) protease
		 Alignment				PDB header: toxin/rna

29	c4rmoA_	Alignment	not modelled	16.0	10	Chain: A: PDB Molecule: cptn toxin; PDBTitle: crystal structure of the cptn type iii toxin-antitoxin system from 2 eubacterium rectale
30	c3u5gB_	Alignment	not modelled	15.9	18	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein s1-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
31	c4mnoA_	Alignment	not modelled	14.7	10	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 1a; PDBTitle: crystal structure of aif1a from pyrococcus abyssi
32	d1whia_	Alignment	not modelled	14.6	17	Fold: Ribosomal protein L14 Superfamily: Ribosomal protein L14 Family: Ribosomal protein L14
33	c6g25A_	Alignment	not modelled	14.6	10	PDB header: oncoprotein Chain: A: PDB Molecule: histone-lysine n-methyltransferase nsd3; PDBTitle: x-ray structure of nsd3-pwwp1 in complex with compound 4
34	d2j01o1	Alignment	not modelled	14.1	13	Fold: Ribosomal protein L14 Superfamily: Ribosomal protein L14 Family: Ribosomal protein L14
35	d1fxza1	Alignment	not modelled	13.7	10	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
36	c3bboM_	Alignment	not modelled	13.2	19	PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein l14; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
37	c3zey0_	Alignment	not modelled	12.4	6	PDB header: ribosome Chain: 0: PDB Molecule: 40s ribosomal protein s3a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
38	d1rz4a1	Alignment	not modelled	12.0	11	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
39	c5xyiB_	Alignment	not modelled	11.6	5	PDB header: ribosome Chain: B: PDB Molecule: ribosomal protein s3ae, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
40	c2dgyA_	Alignment	not modelled	11.6	30	PDB header: translation Chain: A: PDB Molecule: mgc11102 protein; PDBTitle: solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
41	c1cffB_	Alignment	not modelled	11.4	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
42	c2oziA_	Alignment	not modelled	11.1	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rpa4178; PDBTitle: structural genomics, the crystal structure of a putative2 protein rpa4178 from rhodospseudomonas palustris cga009
43	c1fxzC_	Alignment	not modelled	11.0	10	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
44	c5cuzA_	Alignment	not modelled	11.0	41	PDB header: chaperone Chain: A: PDB Molecule: methylmalonic aciduria and homocystinuria type d protein, PDBTitle: crystal structure of semet-substituted n-terminal truncated human b12-2 chaperone cbld (108-296)
45	d1okja2	Alignment	not modelled	10.8	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
46	c6n1bA_	Alignment	not modelled	10.6	22	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
47	c3c19A_	Alignment	not modelled	10.4	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mk0293; PDBTitle: crystal structure of protein mk0293 from methanopyrus kandleri av19
48	c3bxaA_	Alignment	not modelled	10.3	25	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase/esterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_2923) from 2 lactobacillus plantarum wcfs1 at 1.70 a resolution
49	d1jt8a_	Alignment	not modelled	10.2	10	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
50	d2et1a1	Alignment	not modelled	10.0	10	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Germin/Seed storage 7S protein
51	c3j3aB_	Alignment	not modelled	9.8	17	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein s3a; PDBTitle: structure of the human 40s ribosomal proteins
52	c4yknA_	Alignment	not modelled	9.4	21	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: phosphatidylinositol 3-kinase regulatory subunit alpha, PDBTitle: pi3k alpha lipid kinase with active site inhibitor
53	c3kscD_	Alignment	not modelled	9.4	14	PDB header: plant protein Chain: D: PDB Molecule: lega class; PDBTitle: crystal structure of pea prolegumin, an 11s seed globulin from pismus2 sativum l.
54	c2zkrt_	Alignment	not modelled	9.4	21	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

55	c6bwqB	Alignment	not modelled	9.2	21	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
56	c5ofxF	Alignment	not modelled	9.1	20	PDB header: sugar binding protein Chain: F: PDB Molecule: plla; PDBTitle: plla lectin, trisaccharide complex
57	c3bcxA	Alignment	not modelled	8.9	10	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; PDBTitle: e1 dehydrase
58	c3j81i	Alignment	not modelled	8.7	12	PDB header: ribosome Chain: I: PDB Molecule: es8; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
59	d1b6aa2	Alignment	not modelled	8.3	22	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
60	c3w1hB	Alignment	not modelled	8.1	14	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	c3d55A	Alignment	not modelled	8.1	13	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
62	c2eaaB	Alignment	not modelled	8.0	11	PDB header: plant protein Chain: B: PDB Molecule: 7s globulin-3; PDBTitle: crystal structure of adzuki bean 7s globulin-3
63	c1ssfA	Alignment	not modelled	8.0	17	PDB header: cell cycle Chain: A: PDB Molecule: transformation related protein 53 binding PDBTitle: solution structure of the mouse 53bp1 fragment (residues2 1463-1617)
64	c3pfsA	Alignment	not modelled	7.9	15	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
65	d1xgsa2	Alignment	not modelled	7.9	17	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
66	c2oqkA	Alignment	not modelled	7.7	18	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
67	c2ka7A	Alignment	not modelled	7.6	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: nmr solution structure of tm0212 at 40 c
68	c2gfuA	Alignment	not modelled	7.6	15	PDB header: dna binding protein Chain: A: PDB Molecule: dna mismatch repair protein msh6; PDBTitle: nmr solution structure of the pwwp domain of mismatch2 repair protein hmsh6
69	c3ehkC	Alignment	not modelled	7.4	10	PDB header: plant protein Chain: C: PDB Molecule: prunin; PDBTitle: crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
70	c5dfzC	Alignment	not modelled	7.1	27	PDB header: transferase Chain: C: PDB Molecule: phosphatidylinositol 3-kinase vps34; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
71	c5a35A	Alignment	not modelled	7.1	15	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
72	d1qxva	Alignment	not modelled	7.0	17	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
73	c4ipaC	Alignment	not modelled	6.9	22	PDB header: hydrolase Chain: C: PDB Molecule: putative curved dna-binding protein; PDBTitle: structure of a thermophilic arx1
74	c1f13A	Alignment	not modelled	6.8	11	PDB header: coagulation factor Chain: A: PDB Molecule: cellular coagulation factor xiii zymogen; PDBTitle: recombinant human cellular coagulation factor xiii
75	c5o60V	Alignment	not modelled	6.8	10	PDB header: ribosome Chain: V: PDB Molecule: 50s ribosomal protein l24; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
76	c3oeiB	Alignment	not modelled	6.8	13	PDB header: toxin, protein binding Chain: B: PDB Molecule: relj (antitoxin rv3357); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
77	c6mrfA	Alignment	not modelled	6.7	11	PDB header: hydrolase Chain: A: PDB Molecule: methionine aminopeptidase; PDBTitle: crystal structure of a methionine aminopeptidase metap from2 acinetobacter baumannii
78	c5hbaA	Alignment	not modelled	6.7	8	PDB header: immune system Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: globular domain of zebrafish complement 1qa protein
79	d1zaka2	Alignment	not modelled	6.7	27	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
80	c1zx4B	Alignment	not modelled	6.6	25	PDB header: cell cycle Chain: B: PDB Molecule: plasmid partition par b protein; PDBTitle: structure of parb bound to dna

81	c2of3A_	Alignment	not modelled	6.5	12	PDB header: structural protein, cell cycle Chain: A: PDB Molecule: zyg-9; PDBTitle: tog domain structure from c.elegans zyg9
82	c5wpwA_	Alignment	not modelled	6.4	13	PDB header: allergen Chain: A: PDB Molecule: 11s globulin isoform 1; PDBTitle: crystal structure of coconut allergen cocosin
83	d1kp0a2	Alignment	not modelled	6.4	23	Fold: Creatinase/aminopeptidase Superfamily: Creatinase/aminopeptidase Family: Creatinase/aminopeptidase
84	d1ov3a1	Alignment	not modelled	6.3	9	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
85	c3c3vA_	Alignment	not modelled	6.3	7	PDB header: allergen Chain: A: PDB Molecule: arachin arah3 isoform; PDBTitle: crystal structure of peanut major allergen ara h 3
86	d1uija2	Alignment	not modelled	6.3	11	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
87	c4bpp0_	Alignment	not modelled	6.2	26	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
88	d1vcoa2	Alignment	not modelled	6.1	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
89	c2lfeA_	Alignment	not modelled	6.0	25	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
90	c6b4sB_	Alignment	not modelled	6.0	7	PDB header: allergen Chain: B: PDB Molecule: 11s globulin; PDBTitle: crystal structure of brazil nut (bertholletia excelsa) allergen ber e2 2
91	d1c3ha_	Alignment	not modelled	5.9	9	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
92	d1ckaa_	Alignment	not modelled	5.8	9	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
93	d1wlpb2	Alignment	not modelled	5.8	9	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
94	c5xevA_	Alignment	not modelled	5.8	17	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro dipeptidase,peptidase-related protein; PDBTitle: crystal structure of a novel xaa-pro dipeptidase from deinococcus2 radiodurans
95	d1opka1	Alignment	not modelled	5.7	18	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
96	c4eyzB_	Alignment	not modelled	5.7	27	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
97	c2eyxA_	Alignment	not modelled	5.7	9	PDB header: signaling protein Chain: A: PDB Molecule: v-crk sarcoma virus ct10 oncogene homolog PDBTitle: c-terminal sh3 domain of ct10-regulated kinase
98	c2jnsA_	Alignment	not modelled	5.6	17	PDB header: unknown function Chain: A: PDB Molecule: bromodomain-containing protein 4; PDBTitle: solution structure of the bromodomain-containing protein 42 et domain
99	c4lejA_	Alignment	not modelled	5.6	8	PDB header: allergen, plant protein Chain: A: PDB Molecule: viciilin; PDBTitle: crystal structure of the korean pine (pinus koraiensis) viciilin