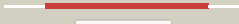



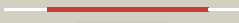














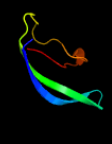

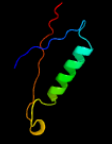



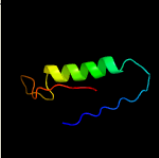

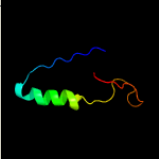
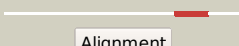
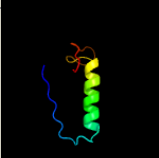
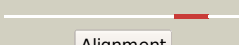
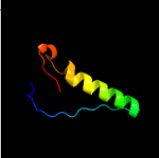
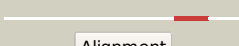
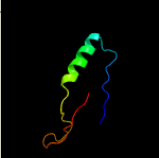
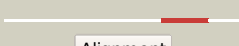
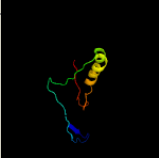

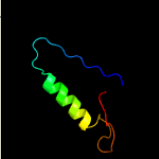

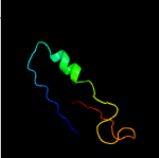




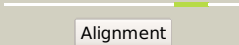
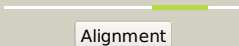
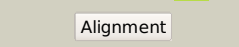
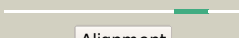


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2824c_(-)_3131780_3132724
Date	Wed Aug 7 12:50:48 BST 2019
Unique Job ID	f651b13c01be4579

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fjwA_	 Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: cas6 protein; PDBTitle: streptococcus thermophilus cas6
2	c4c97B_	 Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: cas6a; PDBTitle: cas6 (ttha0078) h37a mutant
3	c4c9dA_	 Alignment		100.0	27	PDB header: hydrolase/rna Chain: A: PDB Molecule: cas6b; PDBTitle: cas6 (tthb231) product complex
4	c4ilmH_	 Alignment		100.0	12	PDB header: hydrolase/rna Chain: H: PDB Molecule: crispr-associated endoribonuclease cas6 2; PDBTitle: crispr rna processing endoribonuclease
5	c6njyB_	 Alignment		100.0	23	PDB header: rna binding protein Chain: B: PDB Molecule: type iv crispr associated cas6 rna endonuclease; PDBTitle: type iv crispr associated rna endonuclease cas6 - apo form
6	c3i4hX_	 Alignment		99.9	20	PDB header: hydrolase Chain: X: PDB Molecule: endoribonuclease; PDBTitle: crystal structure of cas6 in pyrococcus furiosus
7	c3qjJB_	 Alignment		99.9	14	PDB header: immune system/rna Chain: B: PDB Molecule: putative uncharacterized protein ph0350; PDBTitle: one ramp protein binding different rna substrates
8	c5yi6A_	 Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: crispr-associated endoribonuclease cas6 1; PDBTitle: crispr associated protein cas6
9	c6dd5B_	 Alignment		98.1	18	PDB header: hydrolase Chain: B: PDB Molecule: mmb-1 cas6 fused to maltose binding protein,crispr- PDBTitle: crystal structure of the cas6 domain of marinomonas mediterranea mmb-12 cas6-rt-cas1 fusion protein
10	c4z7IB_	 Alignment		96.2	19	PDB header: hydrolase/rna Chain: B: PDB Molecule: cas6b; PDBTitle: crystal structure of cas6b
11	c6ae2B_	 Alignment		95.3	17	PDB header: rna binding protein Chain: B: PDB Molecule: csn3; PDBTitle: crystal structure of csn3 of the type iii-a crispr-cas effector2 complex

12	c4l6uB_	 Alignment		94.8	21	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of af1868: cmr1 subunit of the cmr rna silencing2 complex
13	c4n0lB_	 Alignment		94.7	21	PDB header: rna binding protein Chain: B: PDB Molecule: predicted component of a thermophile-specific dna repair PDBTitle: methanopyrus kandleri csm3 crystal structure
14	c5yjdB_	 Alignment		94.7	13	PDB header: hydrolase Chain: B: PDB Molecule: csm3; PDBTitle: structural insights into the crispr-cas-associated ribonuclease2 activity of staphylococcus epidermidis csm3
15	c4qtsC_	 Alignment		94.0	18	PDB header: rna binding protein Chain: C: PDB Molecule: crispr type iii-associated ramp protein csm3; PDBTitle: crystal structure of csm3-csm4 subcomplex in the type iii-a crispr-cas2 interference complex
16	c4w8vA_	 Alignment		93.3	15	PDB header: rna binding protein Chain: A: PDB Molecule: crispr system cmr subunit cmr6; PDBTitle: crystal structure of cmr6 from pyrococcus furiosus
17	c4w8wB_	 Alignment		93.3	24	PDB header: hydrolase Chain: B: PDB Molecule: crispr system cmr subunit cmr4; PDBTitle: crystal structure of oligomeric cmr4 from pyrococcus furiosus
18	c6muuE_	 Alignment		93.1	23	PDB header: rna binding protein/rna Chain: E: PDB Molecule: uncharacterized protein csm4; PDBTitle: cryo-em structure of larger csm-crrna binary complex in type iii-a crispr-cas2 system
19	c6ifnF_	 Alignment		92.9	18	PDB header: rna binding protein Chain: F: PDB Molecule: type iii-a crispr-associated ramp protein csm3; PDBTitle: crystal structure of type iii-a crispr csm complex
20	c6musK_	 Alignment		92.8	23	PDB header: rna binding protein/rna Chain: K: PDB Molecule: uncharacterized protein csm3; PDBTitle: cryo-em structure of larger csm-crrna-target rna ternary complex in2 type iii-a crispr-cas system
21	c4w8xA_	 Alignment	not modelled	92.0	12	PDB header: rna binding protein Chain: A: PDB Molecule: crispr system cmr subunit cmr1-1; PDBTitle: crystal structure of cmr1 from pyrococcus furiosus bound to a2 nucleotide
22	c3x1lH_	 Alignment	not modelled	87.6	24	PDB header: rna binding protein/rna/dna Chain: H: PDB Molecule: cmr6; PDBTitle: crystal structure of the crispr-cas rna silencing cmr complex bound to2 a target analog
23	c4qtsB_	 Alignment	not modelled	82.1	10	PDB header: rna binding protein Chain: B: PDB Molecule: crispr type iii-associated ramp protein csm4; PDBTitle: crystal structure of csm3-csm4 subcomplex in the type iii-a crispr-cas2 interference complex
24	c3x1lE_	 Alignment	not modelled	77.3	20	PDB header: rna binding protein/rna/dna Chain: E: PDB Molecule: cmr4; PDBTitle: crystal structure of the crispr-cas rna silencing cmr complex bound to2 a target analog
25	c6ig0B_	 Alignment	not modelled	65.8	24	PDB header: rna binding protein Chain: B: PDB Molecule: type iii-a crispr-associated ramp protein csm4; PDBTitle: type iii-a csm complex, cryo-em structure of csm-ctr1, atp bound
26	c3qrgA_	 Alignment	not modelled	62.2	21	PDB header: rna binding protein/rna Chain: A: PDB Molecule: putative uncharacterized protein tthb192; PDBTitle: structure of thermus thermophilus cse3 bound to an rna representing a2 pre-cleavage complex
27	c4dzdA_	 Alignment	not modelled	61.3	35	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ygch; PDBTitle: crystal structure of the crispr-associated protein cas6e from2 escherichia coli str. k-12
28	c1wi0A_	 Alignment	not modelled	48.5	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: crispr-associated protein;

28	c1wj9A_	Alignment	not modelled	48.5	24	PDBTitle: crystal structure of a crispr-associated protein from2 thermus thermophilus
29	d1wj9a2	Alignment	not modelled	47.8	24	Fold: Ferredoxin-like Superfamily: CRISPR-associated protein Family: CRISPR-associated protein
30	c5u0aA_	Alignment	not modelled	32.1	20	PDB header: immune system Chain: A: PDB Molecule: crispr-associated protein, cse3 family; PDBTitle: crispr rna-guided surveillance complex
31	d1cuka2	Alignment	not modelled	30.1	16	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
32	d1ixra1	Alignment	not modelled	26.8	24	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
33	d1bvsa2	Alignment	not modelled	26.3	28	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
34	c5xe3F_	Alignment	not modelled	22.5	37	PDB header: hydrolase/antitoxin Chain: F: PDB Molecule: probable antitoxin maze4; PDBTitle: endoribonuclease in complex with its cognate antitoxin from2 mycobacterial species
35	c5xe3E_	Alignment	not modelled	22.5	37	PDB header: hydrolase/antitoxin Chain: E: PDB Molecule: probable antitoxin maze4; PDBTitle: endoribonuclease in complex with its cognate antitoxin from2 mycobacterial species
36	d1pzqa_	Alignment	not modelled	21.2	22	Fold: Dimerisation interlock Superfamily: Docking domain A of the erythromycin polyketide synthase (DEBS) Family: Docking domain A of the erythromycin polyketide synthase (DEBS)
37	c1xmeB_	Alignment	not modelled	20.2	33	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: structure of recombinant cytochrome ba3 oxidase from thermus2 thermophilus
38	c1ixrB_	Alignment	not modelled	19.5	22	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
39	c2h5xA_	Alignment	not modelled	19.5	22	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
40	c1d8IA_	Alignment	not modelled	18.7	15	PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
41	c5gmkj_	Alignment	not modelled	17.2	36	PDB header: rna binding protein/rna Chain: J: PDB Molecule: pre-mrna-splicing factor cwc21; PDBTitle: cryo-em structure of the catalytic step i spliceosome (c complex) at2 3.4 angstrom resolution
42	c6iczU_	Alignment	not modelled	14.2	31	PDB header: splicing Chain: U: PDB Molecule: serine/arginine repetitive matrix protein 2; PDBTitle: cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
43	c1ixrA_	Alignment	not modelled	13.9	22	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
44	c6bk8K_	Alignment	not modelled	13.2	31	PDB header: rna binding protein Chain: K: PDB Molecule: pre-mrna-splicing factor cwc21; PDBTitle: s. cerevisiae spliceosomal post-catalytic p complex
45	c1y6uA_	Alignment	not modelled	12.9	8	PDB header: dna binding protein Chain: A: PDB Molecule: excisionase from transposon tn916; PDBTitle: the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
46	c3btpA_	Alignment	not modelled	12.7	30	PDB header: dna binding protein, chaperone Chain: A: PDB Molecule: single-strand dna-binding protein; PDBTitle: crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
47	c2wg7B_	Alignment	not modelled	12.6	31	PDB header: hydrolase Chain: B: PDB Molecule: putative phospholipase a2; PDBTitle: structure of oryza sativa (rice) pla2
48	c1hjpA_	Alignment	not modelled	12.1	15	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
49	d2bcqa2	Alignment	not modelled	11.6	28	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
50	d2vana1	Alignment	not modelled	11.6	17	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
51	c3tadB_	Alignment	not modelled	10.9	23	PDB header: protein binding Chain: B: PDB Molecule: liprin-alpha-2; PDBTitle: crystal structure of the liprin-alpha/liprin-beta complex
52	c5mqfS_	Alignment	not modelled	10.7	31	PDB header: splicing Chain: S: PDB Molecule: serine/arginine repetitive matrix protein 2; PDBTitle: cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
53	d1ux5a_	Alignment	not modelled	10.3	19	Fold: Formin homology 2 domain (FH2 domain) Superfamily: Formin homology 2 domain (FH2 domain) Family: Formin homology 2 domain (FH2 domain)
						PDB header: structural protein

54	c1y64B_	Alignment	not modelled	10.3	19	Chain: B: PDB Molecule: bni1 protein; PDBTitle: bni1p formin homology 2 domain complexed with atp-actin
55	c5nocA_	Alignment	not modelled	10.1	9	PDB header: dna binding protein Chain: A: PDB Molecule: stage 0 sporulation protein j; PDBTitle: solution nmr structure of the c-terminal domain of parb (spo0j)
56	d2o3aa1	Alignment	not modelled	9.8	45	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF0751-like
57	d1jmsa3	Alignment	not modelled	9.6	22	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
58	c5gqtA_	Alignment	not modelled	9.0	24	PDB header: plant protein Chain: A: PDB Molecule: nitrile-specifier protein 1; PDBTitle: crystal structure of a specifier protein from arabidopsis thaliana
59	c6nusA_	Alignment	not modelled	8.2	31	PDB header: viral protein Chain: A: PDB Molecule: nsp12; PDBTitle: sars-coronavirus nsp12 bound to nsp8 co-factor
60	d1bxua_	Alignment	not modelled	8.1	32	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
61	d2p19a1	Alignment	not modelled	7.8	9	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
62	c4tvxU_	Alignment	not modelled	7.7	16	PDB header: PDB COMPND:
63	c5mqcA_	Alignment	not modelled	7.5	63	PDB header: virus Chain: A: PDB Molecule: vp1; PDBTitle: structure of black queen cell virus
64	d1or7c_	Alignment	not modelled	7.5	12	Fold: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA Superfamily: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA Family: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA
65	c1or7C_	Alignment	not modelled	7.5	12	PDB header: transcription Chain: C: PDB Molecule: sigma-e factor negative regulatory protein; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
66	c2h1xB_	Alignment	not modelled	7.4	30	PDB header: hydrolase Chain: B: PDB Molecule: 5-hydroxyisourate hydrolase (formerly known as PDBTitle: crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
67	c3ggeA_	Alignment	not modelled	7.4	7	PDB header: protein binding Chain: A: PDB Molecule: pdz domain-containing protein gipc2; PDBTitle: crystal structure of the pdz domain of pdz domain-containing protein2 gipc2
68	d1oo2a_	Alignment	not modelled	7.3	32	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
69	d1b26a2	Alignment	not modelled	7.1	14	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
70	c6dxwC_	Alignment	not modelled	7.0	8	PDB header: hydrolase Chain: C: PDB Molecule: n-acylethanolamine-hydrolyzing acid amidase; PDBTitle: human n-acylethanolamine-hydrolyzing acid amidase (naaa) precursor2 (c126a)
71	c4jhdF_	Alignment	not modelled	6.8	67	PDB header: structural protein/protein binding Chain: F: PDB Molecule: protein cordon-bleu; PDBTitle: crystal structure of an actin dimer in complex with the actin2 nucleator cordon-bleu
72	c4wwwxB_	Alignment	not modelled	6.6	13	PDB header: hydrolase, ligase Chain: B: PDB Molecule: v(d)j recombination-activating protein 1; PDBTitle: crystal structure of the core rag1/2 recombinase
73	c1pggB_	Alignment	not modelled	6.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin h2 synthase-1; PDBTitle: prostaglandin h2 synthase-1 complexed with 1-(4-iodobenzoyl)-5-2 methoxy-2-methylindole-3-acetic acid (iodoindomethacin), trans model
74	c1ht8B_	Alignment	not modelled	6.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin h2 synthase-1; PDBTitle: the 2.7 angstrom resolution model of ovine cox-1 complexed with2 alclofenac
75	d1tfpa_	Alignment	not modelled	6.4	36	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
76	c6ir9W_	Alignment	not modelled	6.3	10	PDB header: transcription/rna/dna Chain: W: PDB Molecule: spt5; PDBTitle: rna polymerase ii elongation complex bound with elf1 and spt4/5,2 stalled at shl(-1) of the nucleosome
77	d1f86a_	Alignment	not modelled	6.2	30	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
78	d1kgia_	Alignment	not modelled	6.2	32	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
79	c5cdcA_	Alignment	not modelled	6.2	50	PDB header: virus Chain: A: PDB Molecule: vp1, structural polyprotein; PDBTitle: crystal structure of israel acute paralysis virus

80	c6h3jA_	Alignment	not modelled	6.0	22	PDB header: protein transport Chain: A: PDB Molecule: protein involved in gliding motility sprA; PDBTitle: structural snapshots of the type 9 protein translocon plug-complex
81	c2n5qA_	Alignment	not modelled	6.0	27	PDB header: unknown function Chain: A: PDB Molecule: cysteine-rich peptide js1; PDBTitle: solution structure of cysteine-rich peptide js1 from <i>jasminum sambac</i>
82	d1cmwa1	Alignment	not modelled	6.0	30	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
83	c2oyuP_	Alignment	not modelled	5.8	14	PDB header: oxidoreductase Chain: P: PDB Molecule: prostaglandin g/h synthase 1; PDBTitle: indomethacin-(s)-alpha-ethyl-ethanolamide bound to cyclooxygenase-1
84	c1ddxA_	Alignment	not modelled	5.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (prostaglandin h2 synthase-2); PDBTitle: crystal structure of a mixture of arachidonic acid and prostaglandin2 bound to the cyclooxygenase active site of cox-2: prostaglandin3 structure
85	d1ttaa_	Alignment	not modelled	5.6	30	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
86	c3a0hj_	Alignment	not modelled	5.6	31	PDB header: electron transport Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: crystal structure of i-substituted photosystem ii complex
87	d2axtj1	Alignment	not modelled	5.6	31	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, Psbj Family: Psbj-like
88	d1na6a1	Alignment	not modelled	5.5	27	Fold: DNA-binding pseudobarrel domain Superfamily: DNA-binding pseudobarrel domain Family: Type II restriction endonuclease effector domain
89	c3ui3A_	Alignment	not modelled	5.5	20	PDB header: rna binding protein Chain: A: PDB Molecule: immunoglobulin g-binding protein g, virulence-associated PDBTitle: structural and biochemical characterization of hp0315 from <i>2 helicobacter pylori</i> as a vapt protein with an endoribonuclease3 activity
90	d1mc8a1	Alignment	not modelled	5.5	38	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
91	c4luqB_	Alignment	not modelled	5.5	19	PDB header: protein binding/toxin inhibitor Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of virulence effector tse3 in complex with2 neutralizer tsi3
92	d2fmpa2	Alignment	not modelled	5.4	22	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
93	c4khaE_	Alignment	not modelled	5.4	30	PDB header: transcription/replication Chain: E: PDB Molecule: protein spt16d; PDBTitle: structure of the spt16d pob3n heterodimer
94	c5ot4D_	Alignment	not modelled	5.4	47	PDB header: transport protein Chain: D: PDB Molecule: interaptin; PDBTitle: structure of the legionella pneumophila effector rid1 (1-866)
95	c6iicA_	Alignment	not modelled	5.3	25	PDB header: virus Chain: A: PDB Molecule: vp1 of mud crab dicistrovirus; PDBTitle: cryoem structure of mud crab dicistrovirus
96	c2gpzC_	Alignment	not modelled	5.3	29	PDB header: hydrolase Chain: C: PDB Molecule: transthyretin-like protein; PDBTitle: transthyretin-like protein from salmonella dublin
97	c3qvaB_	Alignment	not modelled	5.2	13	PDB header: hydrolase Chain: B: PDB Molecule: transthyretin-like protein; PDBTitle: structure of klebsiella pneumoniae 5-hydroxyisourate hydrolase
98	c6h3iA_	Alignment	not modelled	5.1	22	PDB header: protein transport Chain: A: PDB Molecule: protein involved in gliding motility sprA; PDBTitle: structural snapshots of the type 9 protein translocon
99	c4atoA_	Alignment	not modelled	5.1	29	PDB header: toxin/antitoxin Chain: A: PDB Molecule: toxin; PDBTitle: new insights into the mechanism of bacterial type iii toxin-antitoxin2 systems: selective toxin inhibition by a non-coding rna pseudoknot