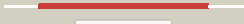






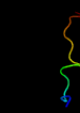

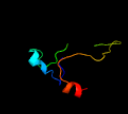

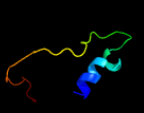
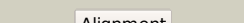


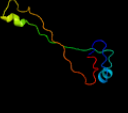




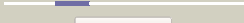
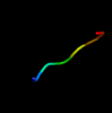
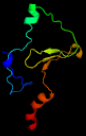


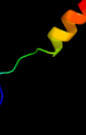

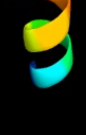
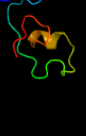

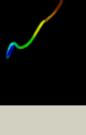


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1989c (-) _2232747_2233307
Date	Mon Aug 5 13:25:09 BST 2019
Unique Job ID	bdf577cc9190c1f8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fkqB_	 Alignment		100.0	100	PDB header: toxin Chain: B: PDB Molecule: rv1989c (mbct); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
2	c6d0hA_	 Alignment		98.7	31	PDB header: toxin Chain: A: PDB Molecule: part: cog5654 (res domain) toxin; PDBTitle: part: prs adp-ribosylating toxin bound to cognate antitoxin pars
3	c6gw6A_	 Alignment		98.6	28	PDB header: toxin Chain: A: PDB Molecule: res toxin; PDBTitle: structure of the pseudomonas putida res-xre toxin-antitoxin complex
4	c2l4wA_	 Alignment		40.8	44	PDB header: protein transport Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the xanthomonas virb7
5	c4tv4C_	 Alignment		30.7	20	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 burkholderia pseudomallei
6	c4okmA_	 Alignment		24.4	26	PDB header: transferase Chain: A: PDB Molecule: terpene synthase metal-binding domain-containing protein; PDBTitle: selinadiene synthase apo and in complex with diphosphate
7	c1dsjA_	 Alignment		24.1	55	PDB header: viral peptide Chain: A: PDB Molecule: vpr protein; PDBTitle: nmr solution structure of vpr50_75, 20 structures
8	d1y12a1	 Alignment		16.9	18	Fold: Hcp1-like Superfamily: Hcp1-like Family: Hcp1-like
9	d1hpia_	 Alignment		13.2	47	Fold: HIPIP (high potential iron protein) Superfamily: HIPIP (high potential iron protein) Family: HIPIP (high potential iron protein)
10	c3hf3A_	 Alignment		12.4	34	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
11	d1od6a_	 Alignment		11.3	25	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenyltransferase

12	d1fn9a_	Alignment		10.6	31	Fold: Outer capsid protein sigma 3 Superfamily: Outer capsid protein sigma 3 Family: Outer capsid protein sigma 3
13	d2ebfx3	Alignment		10.2	60	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: PMT C-terminal domain like
14	d1js2a_	Alignment		9.8	42	Fold: HIPIP (high potential iron protein) Superfamily: HIPIP (high potential iron protein) Family: HIPIP (high potential iron protein)
15	c5ajaB_	Alignment		9.3	32	PDB header: viral protein Chain: B: PDB Molecule: vpx protein; PDBTitle: crystal structure of mandrill samhd1 (amino acid residues 1-114)2 bound to vpx isolated from mandrill and human dcaf1 (amino3 acid residues 1058-1396)
16	c3eaaB_	Alignment		9.3	14	PDB header: unknown function Chain: B: PDB Molecule: evpc; PDBTitle: structure of a type six secretion system protein
17	c5zkeA_	Alignment		8.9	70	PDB header: ligase Chain: A: PDB Molecule: aminoacyl trna synthetase complex-interacting PDBTitle: crystal structure of n-terminal domain of plasmodium vivax p43 in2 space group p212121
18	c2kuoA_	Alignment		8.9	25	PDB header: metal binding protein Chain: A: PDB Molecule: aprataxin and pnk-like factor; PDBTitle: structure and identification of adp-ribose recognition motifs of aplf2 and role in the dna damage response
19	c3q3jA_	Alignment		8.7	45	PDB header: membrane protein/protein binding Chain: A: PDB Molecule: plexin-a2; PDBTitle: crystal structure of plexin a2 rbd in complex with rnd1
20	c3f3mA_	Alignment		8.7	25	PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: six crystal structures of two phosphopantetheine adenylyltransferases2 reveal an alternative ligand binding mode and an associated3 structural change
21	c3x2dM_	Alignment	not modelled	8.5	57	PDB header: viral protein/immune system Chain: M: PDB Molecule: envelope glycoprotein gp1; PDBTitle: crystal structure of marburg virus gp in complex with the human2 survivor antibody mr78 PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
22	c3gr7A_	Alignment	not modelled	8.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
23	d1z41a1	Alignment	not modelled	8.2	30	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
24	c3ikzA_	Alignment	not modelled	8.1	25	PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of phosphopantetheine adenylyltransferase from2 burkholderia pseudomallei
25	d1vlha_	Alignment	not modelled	7.8	25	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
26	c4j8qA_	Alignment	not modelled	7.8	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a nigd-like protein (bf0700) from bacteroides2 fragilis nctc 9343 at 2.50 a resolution PDB header: transferase Chain: C: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: structure of phosphopantetheine adenylyltransferase (cbu_0288) from2 coxiella burnetii
27	c4f3rC_	Alignment	not modelled	7.5	25	PDB header: transferase Chain: C: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: structure of phosphopantetheine adenylyltransferase (cbu_0288) from2 coxiella burnetii
28	c3csyK_	Alignment	not modelled	7.3	71	PDB header: immune system/viral protein Chain: K: PDB Molecule: envelope glycoprotein gp1; PDBTitle: crystal structure of the trimeric prefusion ebola virus glycoprotein2 in complex with a neutralizing antibody from a human survivor

29	d1o6ba_	Alignment	not modelled	6.9	25	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
30	c3s88l_	Alignment	not modelled	6.8	71	PDB header: immune system/viral protein Chain: I: PDB Molecule: envelope glycoprotein; PDBTitle: crystal structure of sudan ebolavirus glycoprotein (strain gulu) bound to 16f6
31	c6cgvW_	Alignment	not modelled	6.8	50	PDB header: virus Chain: W: PDB Molecule: pre-protein vi; PDBTitle: revised crystal structure of human adenovirus
32	c4ew7A_	Alignment	not modelled	6.7	60	PDB header: transcription Chain: A: PDB Molecule: conjugative transfer: regulation; PDBTitle: the crystal structure of conjugative transfer pas_like domain from 2 salmonella enterica subsp. enterica serovar typhimurium
33	c4e86L_	Alignment	not modelled	6.7	67	PDB header: antimicrobial protein Chain: L: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
34	c4e86D_	Alignment	not modelled	6.7	67	PDB header: antimicrobial protein Chain: D: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
35	c4e86H_	Alignment	not modelled	6.7	67	PDB header: antimicrobial protein Chain: H: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
36	c3k0yA_	Alignment	not modelled	6.7	35	PDB header: toxin Chain: A: PDB Molecule: putative toxin related protein; PDBTitle: crystal structure of putative toxin related protein (yp_001303978.1)2 from parabacteroides distazonis atcc 8503 at 2.16 a resolution
37	c6qkgB_	Alignment	not modelled	6.5	38	PDB header: flavoprotein Chain: B: PDB Molecule: ncr a; PDBTitle: 2-naphthoyl-coa reductase(ncr)
38	c4e86F_	Alignment	not modelled	6.5	67	PDB header: antimicrobial protein Chain: F: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
39	c4e86C_	Alignment	not modelled	6.5	67	PDB header: antimicrobial protein Chain: C: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
40	c4e83B_	Alignment	not modelled	6.5	67	PDB header: antimicrobial protein Chain: B: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29nle mutant)
41	c4e86G_	Alignment	not modelled	6.5	67	PDB header: antimicrobial protein Chain: G: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
42	c4e86E_	Alignment	not modelled	6.5	67	PDB header: antimicrobial protein Chain: E: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
43	c4e86A_	Alignment	not modelled	6.5	67	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
44	c4e83A_	Alignment	not modelled	6.5	67	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29nle mutant)
45	c2mitB_	Alignment	not modelled	6.5	67	PDB header: antimicrobial protein Chain: B: PDB Molecule: defensin-5; PDBTitle: solution structure of oxidized dimeric form of human defensin 5
46	d1u69a_	Alignment	not modelled	6.4	22	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: 3-demethylubiquinone-9 3-methyltransferase
47	c4e86B_	Alignment	not modelled	6.4	67	PDB header: antimicrobial protein Chain: B: PDB Molecule: defensin-5; PDBTitle: crystal structure of human alpha-defensin 5, hd5 (leu29aba mutant)
48	c4hkhA_	Alignment	not modelled	6.4	11	PDB header: protein binding Chain: A: PDB Molecule: putative type vi secretion protein; PDBTitle: structure of the hcp1 protein from e. coli eaec 042 pathovar, mutants 2 n93w-s158w
49	c5cujA_	Alignment	not modelled	6.3	67	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 y27a mutant crystal form 2.
50	c5cumA_	Alignment	not modelled	6.3	67	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 y27a mutant crystal form 1.
51	c5cujD_	Alignment	not modelled	6.3	67	PDB header: antimicrobial protein Chain: D: PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 y27a mutant crystal form 2.
52	c5cujF_	Alignment	not modelled	6.3	67	PDB header: antimicrobial protein Chain: F: PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 y27a mutant crystal form 2.
53	c5cujE_	Alignment	not modelled	6.3	67	PDB header: antimicrobial protein Chain: E: PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 y27a mutant crystal form 2.
						PDB header: antimicrobial protein

54	c5cuiB_	Alignment	not modelled	6.3	67	Chain: B; PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 y27a mutant crystal form 2.
55	c5cumB_	Alignment	not modelled	6.3	67	PDB header: antimicrobial protein Chain: B; PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 y27a mutant crystal form 1.
56	c5cumC_	Alignment	not modelled	6.3	67	PDB header: antimicrobial protein Chain: C; PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 y27a mutant crystal form 1.
57	c5cuiC_	Alignment	not modelled	6.3	67	PDB header: antimicrobial protein Chain: C; PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 y27a mutant crystal form 2.
58	d1oyaa_	Alignment	not modelled	6.3	10	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
59	d1tfua_	Alignment	not modelled	6.3	25	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
60	c2gezE_	Alignment	not modelled	6.2	15	PDB header: hydrolase Chain: E; PDB Molecule: l-asparaginase alpha subunit; PDBTitle: crystal structure of potassium-independent plant asparaginase
61	c2mitA_	Alignment	not modelled	6.2	67	PDB header: antimicrobial protein Chain: A; PDB Molecule: defensin-5; PDBTitle: solution structure of oxidized dimeric form of human defensin 5
62	d1vqqa1	Alignment	not modelled	6.2	22	Fold: Cystatin-like Superfamily: NTF2-like Family: Penicillin binding protein 2a (PBP2A), N-terminal domain
63	c5cuiC_	Alignment	not modelled	6.2	67	PDB header: antimicrobial protein Chain: C; PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 r28a mutant.
64	c5cuiF_	Alignment	not modelled	6.2	67	PDB header: antimicrobial protein Chain: F; PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 r28a mutant.
65	c5cuiA_	Alignment	not modelled	6.2	67	PDB header: antimicrobial protein Chain: A; PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 r28a mutant.
66	c5cuiD_	Alignment	not modelled	6.2	67	PDB header: antimicrobial protein Chain: D; PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 r28a mutant.
67	c5cuiB_	Alignment	not modelled	6.2	67	PDB header: antimicrobial protein Chain: B; PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 r28a mutant.
68	c1t3mA_	Alignment	not modelled	6.2	30	PDB header: hydrolase Chain: A; PDB Molecule: putative l-asparaginase; PDBTitle: structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
69	c4e82B_	Alignment	not modelled	6.2	67	PDB header: antimicrobial protein Chain: B; PDB Molecule: defensin-5; PDBTitle: crystal structure of monomeric variant of human alpha-defensin 5, hd52 (glu21eme mutant)
70	c4e82A_	Alignment	not modelled	6.2	67	PDB header: antimicrobial protein Chain: A; PDB Molecule: defensin-5; PDBTitle: crystal structure of monomeric variant of human alpha-defensin 5, hd52 (glu21eme mutant)
71	c5cuiE_	Alignment	not modelled	6.2	67	PDB header: antimicrobial protein Chain: E; PDB Molecule: defensin-5; PDBTitle: crystal structure of human defensin-5 r28a mutant.
72	c1zmpC_	Alignment	not modelled	6.1	67	PDB header: antimicrobial protein Chain: C; PDB Molecule: defensin 5; PDBTitle: crystal structure of human defensin-5
73	c2lxzA_	Alignment	not modelled	6.1	67	PDB header: antimicrobial protein Chain: A; PDB Molecule: defensin-5; PDBTitle: solution structure of the antimicrobial peptide human defensin 5
74	c1zmpA_	Alignment	not modelled	6.1	67	PDB header: antimicrobial protein Chain: A; PDB Molecule: defensin 5; PDBTitle: crystal structure of human defensin-5
75	c1zmpB_	Alignment	not modelled	6.1	67	PDB header: antimicrobial protein Chain: B; PDB Molecule: defensin 5; PDBTitle: crystal structure of human defensin-5
76	c4tmcB_	Alignment	not modelled	6.0	8	PDB header: flavoprotein Chain: B; PDB Molecule: old yellow enzyme; PDBTitle: crystal structure of old yellow enzyme from candida macedoniensis2 aku4588 complexed with p-hydroxybenzaldehyde
77	c5ej0A_	Alignment	not modelled	5.9	43	PDB header: viral protein Chain: A; PDB Molecule: envelope protein h3; PDBTitle: the vaccinia virus h3 envelope protein, a major target of neutralizing2 antibodies, exhibits a glycosyltransferase fold and binds udp-glucose
78	c4pu6A_	Alignment	not modelled	5.9	10	PDB header: hydrolase Chain: A; PDB Molecule: l-asparaginase alpha subunit; PDBTitle: crystal structure of potassium-dependent plant-type l-asparaginase2 from phaseolus vulgaris in complex with k+ cations
79	d1qjca_	Alignment	not modelled	5.9	25	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
80	d1hlqa_	Alignment	not modelled	5.8	39	Fold: HIPIP (high potential iron protein) Superfamily: HIPIP (high potential iron protein) Family: HIPIP (high potential iron protein)

81	d2bosa_	Alignment	not modelled	5.7	32	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
82	c6ivsA_	Alignment	not modelled	5.6	67	PDB header: transcription Chain: A: PDB Molecule: anti-sigma-i factor rsg1; PDBTitle: solution structure of the n-terminal domain of the anti-sigma factor2 rsg1 from clostridium thermocellum
83	d1kama_	Alignment	not modelled	5.6	63	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
84	c3nd5D_	Alignment	not modelled	5.6	38	PDB header: transferase Chain: D: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of phosphopantetheine adenylyltransferase (ppat)2 from enterococcus faecalis
85	d1miau5	Alignment	not modelled	5.5	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
86	c5h16D_	Alignment	not modelled	5.5	25	PDB header: transferase Chain: D: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of the complex of phosphopantetheine2 adenylyltransferase from acinetobacter baumannii with citrate at 2.33 a resolution.
87	c3x1mC_	Alignment	not modelled	5.4	25	PDB header: transferase Chain: C: PDB Molecule: phosphopantetheine adenylyltransferase; PDBTitle: crystal structure of phosphopantetheine adenylyltransferase/ppat from2 pseudomonas aeruginosa with coa
88	c6agzA_	Alignment	not modelled	5.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: old yellow enzyme; PDBTitle: crystal structure of old yellow enzyme from pichia sp. aku4542