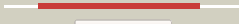



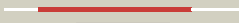

















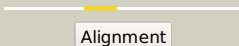

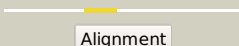

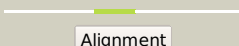
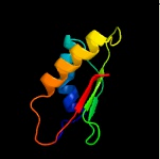
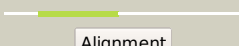
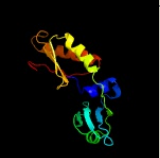
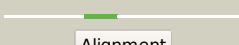
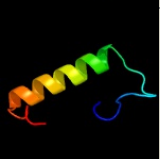
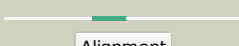
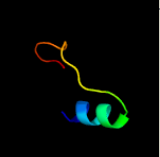



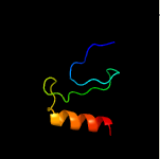

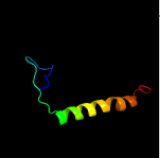



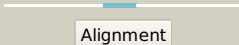
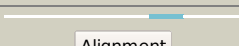


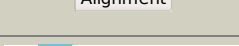


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0269c_(-)_323338_324531
Date	Tue Jul 23 14:50:33 BST 2019
Unique Job ID	d0551e2d16b93bae

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5op0B_	 Alignment		100.0	48	PDB header: transferase Chain: B: PDB Molecule: dna polymerase ligd, polymerase domain; PDBTitle: structure of prim-polc from mycobacterium smegmatis
2	c5dmuA_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: nhej polymerase; PDBTitle: structure of the nhej polymerase from methanocella paludicola
3	c2faoB_	 Alignment		100.0	27	PDB header: hydrolase/transferase Chain: B: PDB Molecule: probable atp-dependent dna ligase; PDBTitle: crystal structure of pseudomonas aeruginosa ligd polymerase2 domain
4	c2iruA_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: putative dna ligase-like protein rv0938/mt0965; PDBTitle: crystal structure of the polymerase domain from mycobacterium2 tuberculosis ligase d
5	d1zt2a1	 Alignment		97.8	23	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
6	d1v33a_	 Alignment		97.1	22	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
7	c4bpxC_	 Alignment		96.8	17	PDB header: transferase Chain: C: PDB Molecule: dna primase small subunit; PDBTitle: crystal structure of human primase in complex with the primase-2 binding motif of dna polymerase alpha
8	c4limA_	 Alignment		96.6	27	PDB header: transferase Chain: A: PDB Molecule: dna primase small subunit; PDBTitle: crystal structure of the catalytic subunit of yeast primase
9	d1g71a_	 Alignment		95.7	20	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
10	d1k1sa2	 Alignment		82.7	13	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
11	d1im4a_	 Alignment		77.7	13	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain

12	d1ro0a_	 Alignment		76.1	14	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: Bifunctional DNA primase/polymerase N-terminal domain
13	c6a9wA_	 Alignment		71.9	20	PDB header: replication Chain: A: PDB Molecule: primase; PDBTitle: structure of the bifunctional dna primase-polymerase from phage nrs-1
14	c5gl6A_	 Alignment		67.9	6	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosome maturation factor rimp; PDBTitle: msmeg rimp
15	d1jx4a2	 Alignment		63.8	15	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
16	c2xj9B_	 Alignment		54.4	24	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
17	c5yrzD_	 Alignment		47.3	30	PDB header: antitoxin/hydrolase Chain: D: PDB Molecule: hica; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
18	c5yrzB_	 Alignment		47.0	30	PDB header: antitoxin/hydrolase Chain: B: PDB Molecule: hica; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
19	d2r7ka2	 Alignment		46.0	31	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
20	c5kodA_	 Alignment		44.6	12	PDB header: ligase Chain: A: PDB Molecule: indole-3-acetic acid-amido synthetase gh3.5; PDBTitle: crystal structure of gh3.5 acyl acid amido synthetase from arabidopsis2 thaliana
21	c3m1mA_	 Alignment	not modelled	43.7	17	PDB header: replication Chain: A: PDB Molecule: orf904; PDBTitle: crystal structure of the primase-polymerase from sulfolobus islandicus
22	c2bf9A_	 Alignment	not modelled	42.0	21	PDB header: hormone Chain: A: PDB Molecule: pancreatic hormone; PDBTitle: anisotropic refinement of avian (turkey) pancreatic polypeptide at 0.2 99 angstroms resolution.
23	c1tz5A_	 Alignment	not modelled	41.0	26	PDB header: hormone/growth factor Chain: A: PDB Molecule: chimera of pancreatic hormone and neuropeptide y; PDBTitle: [pnpy19-23]-hpp bound to dpc micelles
24	c4ep1A_	 Alignment	not modelled	39.3	15	PDB header: ligase Chain: A: PDB Molecule: jasmonic acid-amido synthetase jar1; PDBTitle: crystal structure of arabidopsis thaliana gh3.11 (jar1) in complex2 with ja-ile
25	c5lnkn_	 Alignment	not modelled	38.5	50	PDB header: oxidoreductase Chain: N: PDB Molecule: mitochondrial complex i, nd2 subunit; PDBTitle: entire ovine respiratory complex i
26	c1ronA_	 Alignment	not modelled	38.5	26	PDB header: neuropeptide Chain: A: PDB Molecule: neuropeptide y; PDBTitle: nmr solution structure of human neuropeptide y
27	c3ebkA_	 Alignment	not modelled	37.3	32	PDB header: allergen Chain: A: PDB Molecule: allergen bla g 4; PDBTitle: crystal structure of major allergens, bla g 4 from cockroaches
28	c2dezA_	 Alignment	not modelled	36.0	21	PDB header: neuropeptide Chain: A: PDB Molecule: peptide yy; PDBTitle: structure of human pyy
						PDB header: fluorescent protein, transport protein

29	c3osrA	Alignment	not modelled	35.9	9	Chain: A: PDB Molecule: maltose-binding periplasmic protein, green fluorescent PDBTitle: maltose-bound maltose sensor engineered by insertion of circularly2 permuted green fluorescent protein into e. coli maltose binding3 protein at position 311
30	c3k6gA	Alignment	not modelled	34.4	37	PDB header: protein binding Chain: A: PDB Molecule: telomeric repeat-binding factor 2-interacting protein 1; PDBTitle: crystal structure of rap1 and trf2 complex
31	c4rq9A	Alignment	not modelled	28.5	17	PDB header: signaling protein Chain: A: PDB Molecule: photoreceptor-histidine kinase bphp; PDBTitle: crystal structure of the chromophore-binding domain of stigmatella2 aurantiaca bacteriophytochrome (thr289his mutant) in the pr state
32	c3dclC	Alignment	not modelled	25.4	22	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: tm1086; PDBTitle: crystal structure of tm1086
33	c4fugD	Alignment	not modelled	24.1	17	PDB header: ligase Chain: D: PDB Molecule: malonyl coa synthetase; PDBTitle: crystal structure of apo matb from rhodospseudomonas palustris
34	c4ki0A	Alignment	not modelled	24.0	19	PDB header: calcium binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the effector protein xoo4466
35	c4euV	Alignment	not modelled	23.8	16	PDB header: signaling protein Chain: A: PDB Molecule: peld; PDBTitle: crystal structure of peld 158-ct from pseudomonas aeruginosa pao1, in2 complex with c-di-gmp, form 1
36	c5f4zB	Alignment	not modelled	23.3	16	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus
37	c4kx0A	Alignment	not modelled	22.9	24	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yhfx; PDBTitle: crystal structure of the pyridoxal-5'-phosphate dependent protein yhfx2 from escherichia coli
38	c4dezA	Alignment	not modelled	22.3	14	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iv 1; PDBTitle: structure of msdpo4
39	c4b2gB	Alignment	not modelled	21.4	9	PDB header: signaling protein Chain: B: PDB Molecule: gh3-1 auxin conjugating enzyme; PDBTitle: crystal structure of an indole-3-acetic acid amido synthase from vitis2 vinifera involved in auxin homeostasis
40	c4g9iA	Alignment	not modelled	21.1	19	PDB header: transferase Chain: A: PDB Molecule: hydrogenase maturation protein hypf; PDBTitle: crystal structure of t.kodakarensis hypf
41	d2r85a2	Alignment	not modelled	17.8	11	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
42	c3kd4A	Alignment	not modelled	17.6	16	PDB header: hydrolase Chain: A: PDB Molecule: putative protease; PDBTitle: crystal structure of a putative protease (bdi_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
43	c3menC	Alignment	not modelled	17.4	25	PDB header: hydrolase Chain: C: PDB Molecule: acetylpolymine aminohydrolase; PDBTitle: crystal structure of acetylpolymine aminohydrolase from burkholderia2 pseudomallei, iodide soak
44	d2fhzb1	Alignment	not modelled	16.6	15	Fold: Colicin D/E5 nuclease domain Superfamily: Colicin D/E5 nuclease domain Family: Colicin E5 nuclease domain
45	c3p42D	Alignment	not modelled	16.6	9	PDB header: unknown function Chain: D: PDB Molecule: predicted protein; PDBTitle: structure of gfcc (ymcb), protein encoded by the e. coli group 42 capsule operon
46	d2g0ta1	Alignment	not modelled	16.5	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
47	c3p6iA	Alignment	not modelled	16.1	6	PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
48	c3nezA	Alignment	not modelled	16.0	12	PDB header: fluorescent protein Chain: A: PDB Molecule: mrojao; PDBTitle: mrojao
49	c3zqbB	Alignment	not modelled	15.6	23	PDB header: cell invasion Chain: B: PDB Molecule: protein prgi, cell invasion protein sipd; PDBTitle: prgi-sipd from salmonella typhimurium
50	c1ceuA	Alignment	not modelled	15.4	42	PDB header: viral protein Chain: A: PDB Molecule: protein (hiv-1 regulatory protein n-terminal) PDBTitle: nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
51	c4cabA	Alignment	not modelled	15.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase; PDBTitle: the refined structure of catalase dr1998 from deinococcus radiodurans2 at 2.6 a resolution
52	d1ib8a2	Alignment	not modelled	15.2	9	Fold: Alpha-lytic protease prodomain-like Superfamily: YhbC-like, N-terminal domain Family: YhbC-like, N-terminal domain
53	d1xhna1	Alignment	not modelled	15.2	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
54	c3k1iA	Alignment	not modelled	14.7	38	PDB header: ligase Chain: A: PDB Molecule: fanc1;

						PDBTitle: crystal structure of fancI
55	c2icrD_	Alignment	not modelled	14.6	19	PDB header: fluorescent protein Chain: D; PDB Molecule: red fluorescent protein zoanrfp; PDBTitle: red fluorescent protein zrfp574 from zoanthus sp.
56	c2oolA_	Alignment	not modelled	14.3	20	PDB header: signaling protein Chain: A; PDB Molecule: sensor protein; PDBTitle: crystal structure of the chromophore-binding domain of an unusual 2 bacteriophytochrome rpbphp3 from r. palustris
57	c6f2xA_	Alignment	not modelled	14.2	23	PDB header: transferase Chain: A; PDB Molecule: protein tyrosine kinase a; PDBTitle: structural characterization of the mycobacterium tuberculosis protein 2 tyrosine kinase a (ptka)
58	c3vhtB_	Alignment	not modelled	13.6	10	PDB header: fluorescent protein/protein binding Chain: B; PDB Molecule: green fluorescent protein, atpase wrnip1; PDBTitle: crystal structure of gfp-wrnip1 ubz domain fusion protein in complex 2 with ubiquitin
59	c1bqfA_	Alignment	not modelled	13.6	20	PDB header: hormone/growth factor Chain: A; PDB Molecule: protein (growth-blocking peptide); PDBTitle: growth-blocking peptide (gbp) from pseudaletia separata
60	c3fkyD_	Alignment	not modelled	13.5	14	PDB header: ligase Chain: D; PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the glutamine synthetase gln1deltaN182 from the yeast saccharomyces cerevisiae
61	d1si8a_	Alignment	not modelled	13.4	19	Fold: Heme-dependent catalase-like Superfamily: Heme-dependent catalase-like Family: Heme-dependent catalases
62	c4ir7A_	Alignment	not modelled	13.2	9	PDB header: transferase Chain: A; PDB Molecule: long chain fatty acid coa ligase fadd10; PDBTitle: crystal structure of mtb fadd10 in complex with dodecanoyl-amp
63	c2k4bA_	Alignment	not modelled	13.2	18	PDB header: dna binding protein Chain: A; PDB Molecule: transcriptional regulator; PDBTitle: copr repressor structure
64	c6humM_	Alignment	not modelled	13.1	21	PDB header: proton transport Chain: M; PDB Molecule: nad(p)h-quinone oxidoreductase subunit m; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus 2 elongatus
65	c3mr2A_	Alignment	not modelled	12.3	7	PDB header: transferase/dna Chain: A; PDB Molecule: dna polymerase eta; PDBTitle: human dna polymerase eta in complex with normal dna and incoming 2 nucleotide (nrm)
66	d1e8ga1	Alignment	not modelled	12.3	17	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
67	d2arza1	Alignment	not modelled	12.1	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
68	c4jrbA_	Alignment	not modelled	11.9	10	PDB header: lipid binding protein Chain: A; PDB Molecule: green fluorescent protein; PDBTitle: structure of cockroach allergen bla g 1 tandem repeat as a egfp fusion
69	c3ai5A_	Alignment	not modelled	11.9	10	PDB header: fluorescent protein, transcription Chain: A; PDB Molecule: yeast enhanced green fluorescent protein, ubiquitin; PDBTitle: crystal structure of yeast enhanced green fluorescent protein-2 ubiquitin fusion protein
70	d1i5za1	Alignment	not modelled	11.8	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
71	c4i2yB_	Alignment	not modelled	11.7	15	PDB header: fluorescent protein Chain: B; PDB Molecule: rgeco1; PDBTitle: crystal structure of the genetically encoded calcium indicator rgeco1
72	d1jvaa3	Alignment	not modelled	11.4	13	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
73	c2a5hC_	Alignment	not modelled	11.4	16	PDB header: isomerase Chain: C; PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from 2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine 3 external aldimine form of pyridoxal-5'-phosphate).
74	c1ib8A_	Alignment	not modelled	11.3	9	PDB header: nucleic acid binding protein Chain: A; PDB Molecule: conserved protein sp14.3; PDBTitle: solution structure and function of a conserved protein 2 sp14.3 encoded by an essential streptococcus pneumoniae 3 gene
75	c1dsjA_	Alignment	not modelled	11.2	36	PDB header: viral peptide Chain: A; PDB Molecule: vpr protein; PDBTitle: nmr solution structure of vpr50_75, 20 structures
76	d1oxda_	Alignment	not modelled	11.0	9	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
77	c4r0mA_	Alignment	not modelled	10.9	14	PDB header: ligase Chain: A; PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
78	d1snla_	Alignment	not modelled	10.9	35	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
79	c4hkmA_	Alignment	not modelled	10.8	16	PDB header: transferase Chain: A; PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: crystal structure of an anthranilate phosphoribosyltransferase (target2 id nysgrc-016600) from xanthomonas campestris

80	c2d4vD	Alignment	not modelled	10.8	16	PDB header: oxidoreductase Chain: D: PDB Molecule: isocitrate dehydrogenase; PDBTitle: crystal structure of nad dependent isocitrate dehydrogenase2 from acidithiobacillus thiooxidans
81	c3f6sl	Alignment	not modelled	10.8	15	PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin alternate2 conformers
82	c4e04B	Alignment	not modelled	10.7	23	PDB header: signaling protein Chain: B: PDB Molecule: bacteriophytochrome (light-regulated signal transduction PDBTitle: rpbphp2 chromophore-binding domain crystallized by homologue-directed2 mutagenesis.
83	d1lcia	Alignment	not modelled	10.4	15	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
84	c3akoG	Alignment	not modelled	10.4	10	PDB header: fluorescent protein Chain: G: PDB Molecule: venus; PDBTitle: crystal structure of the reassembled venus
85	c3evpA	Alignment	not modelled	10.3	10	PDB header: signaling protein Chain: A: PDB Molecule: green fluorescent protein,green fluorescent protein; PDBTitle: crystal structure of circular-permuted egfp
86	c3evrA	Alignment	not modelled	10.3	9	PDB header: signaling protein Chain: A: PDB Molecule: myosin light chain kinase, green fluorescent protein, PDBTitle: crystal structure of calcium bound monomeric gcamp2
87	c3ijdB	Alignment	not modelled	10.3	7	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: uncharacterized protein cthe_2304 from clostridium thermocellum binds2 two copies of 5-methyl-5,6,7,8-tetrahydrofolic acid
88	c4s17E	Alignment	not modelled	10.2	10	PDB header: ligase Chain: E: PDB Molecule: glutamine synthetase; PDBTitle: the crystal structure of glutamine synthetase from bifidobacterium2 adolescentis atcc 15703
89	c6h77B	Alignment	not modelled	10.1	20	PDB header: signaling protein Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: e1 enzyme for ubiquitin like protein activation in complex with ubl
90	c5d6aA	Alignment	not modelled	10.1	38	PDB header: hydrolase Chain: A: PDB Molecule: predicted atpase of the abc class; PDBTitle: 2.7 angstrom crystal structure of abc transporter atpase from vibrio2 vulnificus in complex with adenylyl-imidodiphosphate (amp-pnp)
91	c4xbiA	Alignment	not modelled	10.0	10	PDB header: chaperone Chain: A: PDB Molecule: clpb protein, putative,green fluorescent protein; PDBTitle: structure of a malarial protein involved in proteostasis
92	c2ponA	Alignment	not modelled	10.0	38	PDB header: apoptosis inhibitor Chain: A: PDB Molecule: beclin-1; PDBTitle: solution structure of the bcl-xl/beclin-1 complex
93	c3ni2A	Alignment	not modelled	9.9	13	PDB header: ligase Chain: A: PDB Molecule: 4-coumarate:coa ligase; PDBTitle: crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
94	c4lqeA	Alignment	not modelled	9.9	31	PDB header: dna binding protein Chain: A: PDB Molecule: mepb; PDBTitle: crystal structure of mepb
95	d1u7pa	Alignment	not modelled	9.8	36	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
96	c2g3dB	Alignment	not modelled	9.8	10	PDB header: luminescent protein Chain: B: PDB Molecule: green fluorescent protein; PDBTitle: structure of s65g y66a gfp variant after spontaneous2 peptide hydrolysis
97	d1ef4a	Alignment	not modelled	9.7	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: RNA polymerase subunit RPB10 Family: RNA polymerase subunit RPB10
98	c4malB	Alignment	not modelled	9.6	40	PDB header: unknown function Chain: B: PDB Molecule: motility protein fimv; PDBTitle: tpr3 of fimv from p. aeruginosa (pao1)
99	d1kp5a	Alignment	not modelled	9.5	10	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins