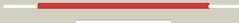
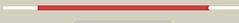
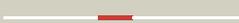
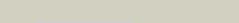
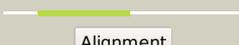
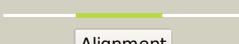
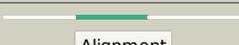
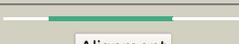
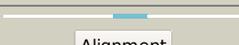
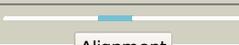


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3730c_(-)_4180858_4181898
Date	Fri Aug 9 18:20:43 BST 2019
Unique Job ID	ecd80d86922dcf99

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5op0B_	 Alignment		100.0	80	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	c2fa0B_	 Alignment		100.0	30	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	27	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		97.7	20	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
6	c4bpxC_	 Alignment		96.7	14	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
7	d1v33a_	 Alignment		96.6	31	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
8	d1g71a_	 Alignment		96.3	35	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
9	c4limA_	 Alignment		96.2	21	PDB header: transferase Chain: A: PDB Molecule: dna primase small subunit; PDBTitle: crystal structure of the catalytic subunit of yeast primase
10	c6a9wA_	 Alignment		81.6	29	PDB header: replication Chain: A: PDB Molecule: primase; PDBTitle: structure of the bifunctional dna primase-polymerase from phage nrs-1
11	d1k1sa2	 Alignment		79.7	10	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain

12	c5gl6A_	 Alignment		74.9	8	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosome maturation factor rimp; PDBTitle: msmeg rimp
13	d1ro0a_	 Alignment		72.4	19	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: Bifunctional DNA primase/polymerase N-terminal domain
14	c4baxH_	 Alignment		63.2	17	PDB header: ligase Chain: H: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from streptomyces2 coelicolor
15	d1jx4a2	 Alignment		61.7	12	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
16	c2d3aj_	 Alignment		61.4	23	PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
17	c3ebkA_	 Alignment		57.8	24	PDB header: allergen Chain: A: PDB Molecule: allergen bla g 4; PDBTitle: crystal structure of major allergens, bla g 4 from cockroaches
18	c4is4G_	 Alignment		52.7	21	PDB header: ligase Chain: G: PDB Molecule: glutamine synthetase; PDBTitle: the glutamine synthetase from the dicotyledonous plant m. truncatula2 is a decamer
19	c4ki0A_	 Alignment		51.6	18	PDB header: calcium binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the effector protein xoo4466
20	c5yrzD_	 Alignment		47.1	35	PDB header: antitoxin/hydrolase Chain: D: PDB Molecule: hica; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
21	c5yrzB_	 Alignment	not modelled	46.7	35	PDB header: antitoxin/hydrolase Chain: B: PDB Molecule: hica; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
22	c2qc8J_	 Alignment	not modelled	45.8	18	PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of human glutamine synthetase in complex with adp2 and methionine sulfoximine phosphate
23	c5kodA_	 Alignment	not modelled	41.6	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
24	c3qajL_	 Alignment	not modelled	41.2	13	PDB header: ligase Chain: L: PDB Molecule: glutamine synthetase; PDBTitle: x-ray crystal structure of glutamine synthetase from bacillus subtilis2 cocrystallized with atp
25	c3osrA_	 Alignment	not modelled	39.2	19	PDB header: fluorescent protein, transport protein 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
26	d2r7ka2	 Alignment	not modelled	38.9	23	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
27	c2bf9A_	 Alignment	not modelled	38.4	18	PDB header: hormone Chain: A: PDB Molecule: pancreatic hormone; PDBTitle: anisotropic refinement of avian (turkey) pancreatic polypeptide at 0.2 99 angstroms resolution.
28	c3m1mA_	 Alignment	not modelled	37.7	14	PDB header: replication Chain: A: PDB Molecule: orf904;

28	c3m1m1A_	Alignment	not modelled	37.7	14	PDBTitle: crystal structure of the primase-polymerase from <i>sulfolobus islandicus</i>
29	d1m4a_	Alignment	not modelled	36.8	13	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
30	c1s21A_	Alignment	not modelled	36.8	10	PDB header: chaperone Chain: A: PDB Molecule: orf2; PDBTitle: crystal structure of avrpphf orf2, a type iii effector from <i>p.2 syringae</i>
31	d1s21a_	Alignment	not modelled	36.8	10	Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: AvrPphF ORF2, a type III effector
32	c1t25A_	Alignment	not modelled	36.7	24	PDB header: hormone/growth factor Chain: A: PDB Molecule: chimera of pancreatic hormone and neuropeptide y; PDBTitle: [pnpy19-23]-hpp bound to dpc micelles
33	c3cqkB_	Alignment	not modelled	36.6	9	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
34	c4hppA_	Alignment	not modelled	35.2	19	PDB header: ligase Chain: A: PDB Molecule: probable glutamine synthetase; PDBTitle: crystal structure of novel glutamine synthase homolog
35	c5f4zB_	Alignment	not modelled	34.7	21	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from <i>streptomyces2 carzinostaticus</i> subsp. <i>neocarzinostaticus</i>
36	c2xj9B_	Alignment	not modelled	34.5	32	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
37	d2bvca2	Alignment	not modelled	34.0	8	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain
38	c4eplA_	Alignment	not modelled	33.6	13	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
39	c1ronA_	Alignment	not modelled	33.2	19	PDB header: neuropeptide Chain: A: PDB Molecule: neuropeptide y; PDBTitle: nmr solution structure of human neuropeptide y
40	c5zlpH_	Alignment	not modelled	33.0	10	PDB header: ligase Chain: H: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from <i>helicobacter pylori</i>
41	c2dezA_	Alignment	not modelled	32.3	21	PDB header: neuropeptide Chain: A: PDB Molecule: peptide yy; PDBTitle: structure of human ppy
42	c3nezA_	Alignment	not modelled	29.9	10	PDB header: fluorescent protein Chain: A: PDB Molecule: mrojoa; PDBTitle: mrojoa
43	c5lnkn_	Alignment	not modelled	29.7	44	PDB header: oxidoreductase Chain: N: PDB Molecule: mitochondrial complex i, nd2 subunit; PDBTitle: entire ovine respiratory complex i
44	c5dm3A_	Alignment	not modelled	29.2	7	PDB header: ligase Chain: A: PDB Molecule: l-glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from <i>chromohalobacter2 salexigens</i> dsm 3043(csa1_0679, target efi-550015) with bound adp
45	c4s17E_	Alignment	not modelled	28.4	11	PDB header: ligase Chain: E: PDB Molecule: glutamine synthetase; PDBTitle: the crystal structure of glutamine synthetase from <i>bifidobacterium2 adolescentis</i> atcc 15703
46	c4rq9A_	Alignment	not modelled	28.3	17	PDB header: signaling protein Chain: A: PDB Molecule: photoreceptor-histidine kinase bphp; PDBTitle: crystal structure of the chromophore-binding domain of <i>stigmatella2 aurantiaca</i> bacteriophytochrome (thr289his mutant) in the pr state
47	c5l2xA_	Alignment	not modelled	27.9	16	PDB header: transferase/dna Chain: A: PDB Molecule: dna-directed primase/polymerase protein; PDBTitle: crystal structure of human pimg1 ternary complex
48	c2icrD_	Alignment	not modelled	26.7	18	PDB header: fluorescent protein Chain: D: PDB Molecule: red fluorescent protein zoanrfp; PDBTitle: red fluorescent protein zrfp574 from <i>zoanthus</i> sp.
49	c3akoG_	Alignment	not modelled	25.5	17	PDB header: fluorescent protein Chain: G: PDB Molecule: venus; PDBTitle: crystal structure of the reassembled venus
50	c2j9iL_	Alignment	not modelled	25.0	14	PDB header: ligase Chain: L: PDB Molecule: glutamate-ammonia ligase domain-containing protein 1; PDBTitle: lengsin is a survivor of an ancient family of class i glutamine2 synthetases in eukaryotes that has undergone evolutionary re-3 engineering for a tissue-specific role in the vertebrate eye lens.
51	d1ib8a2	Alignment	not modelled	24.3	6	Fold: Alpha-lytic protease prodomain-like Superfamily: YhbC-like, N-terminal domain Family: YhbC-like, N-terminal domain
52	c1ib8A_	Alignment	not modelled	23.8	6	PDB header: nucleic acid binding protein Chain: A: PDB Molecule: conserved protein sp14.3; PDBTitle: solution structure and function of a conserved protein2 sp14.3 encoded by an essential <i>streptococcus pneumoniae3</i> gene
53	c3mazA_	Alignment	not modelled	23.4	10	PDB header: signaling protein Chain: A: PDB Molecule: signal-transducing adaptor protein 1; PDBTitle: crystal structure of the human brdg1/stap-1 sh2 domain in complex with2 the ntal ptry136 peptide

54	c3menC_	Alignment	not modelled	22.8	33	PDB header: hydrolase Chain: C: PDB Molecule: acetylpolymine aminohydrolase; PDBTitle: crystal structure of acetylpolymine aminohydrolase from burkholderia2 pseudomallei, iodide soak
55	d1i5za1	Alignment	not modelled	22.6	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
56	c3s29C_	Alignment	not modelled	22.3	18	PDB header: transferase Chain: C: PDB Molecule: sucrose synthase 1; PDBTitle: the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
57	c3vhtB_	Alignment	not modelled	22.1	18	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 complex2 with ubiquitin
58	c4g9iA_	Alignment	not modelled	21.8	23	PDB header: transferase Chain: A: PDB Molecule: hydrogenase maturation protein hypf; PDBTitle: crystal structure of t.kodakarensis hypf
59	c3ai5A_	Alignment	not modelled	21.1	18	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
60	c4jrbA_	Alignment	not modelled	20.4	18	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
61	c5dmnA_	Alignment	not modelled	20.2	7	PDB header: transferase Chain: A: PDB Molecule: homocysteine s-methyltransferase; PDBTitle: crystal structure of the homocysteine methyltransferase mmum from2 escherichia coli, apo form
62	c2d4vD_	Alignment	not modelled	20.0	13	PDB header: oxidoreductase Chain: D: PDB Molecule: isocitrate dehydrogenase; PDBTitle: crystal structure of nad dependent isocitrate dehydrogenase2 from acidithiobacillus thiooxidans
63	d1hvxa1	Alignment	not modelled	19.8	19	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
64	c4bduC_	Alignment	not modelled	19.6	18	PDB header: apoptosis Chain: C: PDB Molecule: green fluorescent protein, apoptosis regulator bax; PDBTitle: bax bh3-in-groove dimer (gfp)
65	c3nezB_	Alignment	not modelled	19.1	10	PDB header: fluorescent protein Chain: B: PDB Molecule: mrojao; PDBTitle: mrojao
66	c4i2yB_	Alignment	not modelled	18.8	10	PDB header: fluorescent protein Chain: B: PDB Molecule: rgeco1; PDBTitle: crystal structure of the genetically encoded calcium indicator rgeco1
67	d1mywa_	Alignment	not modelled	18.5	17	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
68	c2yqkA_	Alignment	not modelled	18.4	35	PDB header: transcription/apoptosis Chain: A: PDB Molecule: arginine-glutamic acid dipeptide repeats protein; PDBTitle: solution structure of the sant domain in arginine-glutamic2 acid dipeptide (re) repeats
69	c2g3dB_	Alignment	not modelled	18.2	18	PDB header: luminescent protein Chain: B: PDB Molecule: green fluorescent protein; PDBTitle: structure of s65g y66a gfp variant after spontaneous2 peptide hydrolysis
70	c2jadA_	Alignment	not modelled	18.2	18	PDB header: electron transport Chain: A: PDB Molecule: yellow fluorescent protein glutaredoxin fusion protein; PDBTitle: yellow fluorescent protein - glutaredoxin fusion protein
71	c2zo7A_	Alignment	not modelled	17.9	18	PDB header: luminescent protein Chain: A: PDB Molecule: cyan/green-emitting gfp-like protein, kusabira-cyan mutant PDBTitle: crystal structure of a kusabira-cyan mutant (kcy-r1), a cyan/green-2 emitting gfp-like protein
72	c3evpA_	Alignment	not modelled	17.9	18	PDB header: signaling protein Chain: A: PDB Molecule: green fluorescent protein,green fluorescent protein; PDBTitle: crystal structure of circular-permuted egfp
73	c4xbiA_	Alignment	not modelled	17.7	18	PDB header: chaperone Chain: A: PDB Molecule: clpb protein, putative,green fluorescent protein; PDBTitle: structure of a malarial protein involved in proteostasis
74	d1kp5a_	Alignment	not modelled	17.3	18	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
75	c3p42D_	Alignment	not modelled	17.1	11	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
76	c6efrA_	Alignment	not modelled	17.1	17	PDB header: choline-binding protein Chain: A: PDB Molecule: inicsnfr 1.0, a genetically encoded nicotine biosensor, PDBTitle: crystal structure of inicsnfr 1.0
77	c3ng0A_	Alignment	not modelled	16.8	9	PDB header: ligase Chain: A: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803
78	d2fhzb1	Alignment	not modelled	16.8	20	Fold: Colicin D/E5 nuclease domain Superfamily: Colicin D/E5 nuclease domain Family: Colicin E5 nuclease domain
79	c4h3zB_	Alignment	not modelled	16.7	11	PDB header: signaling protein Chain: B: PDB Molecule: gh3-1 auxin conjugating enzyme;

79	c6uzgB	Alignment	not modelled	16.7	11	PDBTitle: crystal structure of an indole-3-acetic acid amido synthase from vitis2 vinifera involved in auxin homeostasis
80	c6dgvA	Alignment	not modelled	16.6	17	PDB header: fluorescent protein Chain: A: PDB Molecule: fluorescent gaba sensor precursor; PDBTitle: igabasnfr fluorescent gaba sensor precursor
81	c2ddcA	Alignment	not modelled	16.5	15	PDB header: luminescent protein Chain: A: PDB Molecule: photoconvertible fluorescent protein; PDBTitle: unique behavior of a histidine responsible for an engineered green-to-2 red photoconversion process
82	c5j3nA	Alignment	not modelled	16.4	18	PDB header: hydrolase Chain: A: PDB Molecule: green fluorescent protein, hsdR; PDBTitle: c-terminal domain of ecor124i hsdR subunit fused with the ph-sensitive2 gfp variant ratiometric phluorin
83	c1k1qA	Alignment	not modelled	16.4	13	PDB header: transcription Chain: A: PDB Molecule: dbh protein; PDBTitle: crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
84	d1oxda	Alignment	not modelled	16.4	18	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
85	c3rggA	Alignment	not modelled	16.3	14	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptprt1 in complex with pi(5)p
86	c4pfeB	Alignment	not modelled	16.0	18	PDB header: fluorescent protein Chain: B: PDB Molecule: green fluorescent protein; PDBTitle: crystal structure of vsfgfp-0
87	d2oz6a1	Alignment	not modelled	15.7	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
88	c4dezA	Alignment	not modelled	15.6	18	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iv 1; PDBTitle: structure of msdp04
89	d1h6ra	Alignment	not modelled	15.5	18	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
90	c2oolA	Alignment	not modelled	15.5	16	PDB header: signaling protein Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of the chromophore-binding domain of an unusual2 bacteriophytochrome rpbph3 from r. palustris
91	d1u7pa	Alignment	not modelled	15.4	36	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
92	d2d3na1	Alignment	not modelled	15.3	10	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
93	d2gjpA1	Alignment	not modelled	15.0	10	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
94	c3k9gA	Alignment	not modelled	14.8	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: pf-32 protein; PDBTitle: crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak
95	c1bqfA	Alignment	not modelled	14.8	40	PDB header: hormone/growth factor Chain: A: PDB Molecule: protein (growth-blocking peptide); PDBTitle: growth-blocking peptide (gpb) from pseudaletia separata
96	c3ai4A	Alignment	not modelled	14.6	18	PDB header: fluorescent protein, replication protein, dna polymerase Chain: A: PDB Molecule: yeast enhanced green fluorescent protein - mouse2 polymerase iota ubiquitin binding motif fusion protein PDBTitle: crystal structure of yeast enhanced green fluorescent protein - mouse2 polymerase iota ubiquitin binding motif fusion protein
97	d1e43a1	Alignment	not modelled	14.4	10	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
98	c3evrA	Alignment	not modelled	14.3	18	PDB header: signaling protein Chain: A: PDB Molecule: myosin light chain kinase, green fluorescent protein, PDBTitle: crystal structure of calcium bound monomeric gcamp2
99	d1hc7a1	Alignment	not modelled	14.2	23	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS