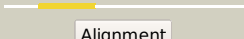
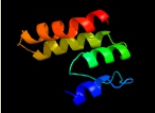
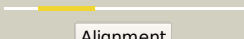

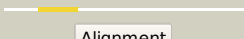
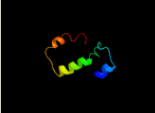


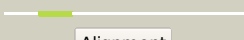
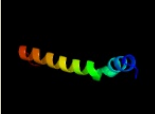

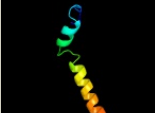





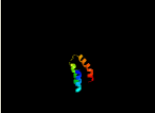










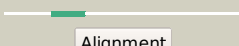

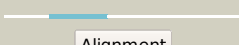

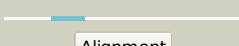

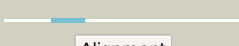






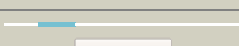

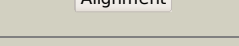

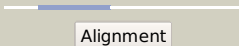
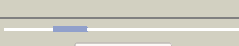
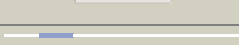


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3333c_(-)_3720108_3720953
Date	Thu Aug 8 16:20:54 BST 2019
Unique Job ID	fb5f4765300bb3a2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2y69R_	 Alignment		71.6	25	PDB header: electron transport Chain: R: PDB Molecule: cytochrome c oxidase subunit 5a; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
2	d1v54e_	 Alignment		70.9	25	Fold: alpha-alpha superhelix Superfamily: Cytochrome c oxidase subunit E Family: Cytochrome c oxidase subunit E
3	c5yysC_	 Alignment		70.4	19	PDB header: transferase Chain: C: PDB Molecule: I-fucokinase, I-fucose-1-p guanylyltransferase; PDBTitle: cryo-em structure of I-fucokinase, gdp-fucose pyrophosphorylase (fkp)2 in bacteroides fragilis
4	d1zsqaz	 Alignment		69.3	18	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Myotubularin-like phosphatases
5	c4y7iB_	 Alignment		65.8	18	PDB header: hydrolase Chain: B: PDB Molecule: myotubularin-related protein 8; PDBTitle: crystal structure of mtmr8
6	c1lw3A_	 Alignment		58.1	16	PDB header: hydrolase Chain: A: PDB Molecule: myotubularin-related protein 2; PDBTitle: crystal structure of myotubularin-related protein 22 complexed with phosphate
7	c3g2bA_	 Alignment		55.4	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: coenzyme pqq synthesis protein d; PDBTitle: crystal structure of pqqd from xanthomonas campestris
8	d1ajsa_	 Alignment		52.9	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
9	c6hu9r_	 Alignment		52.8	16	PDB header: oxidoreductase/electron transport Chain: R: PDB Molecule: cytochrome b-c1 complex subunit 7; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
10	c1zsqA_	 Alignment		52.5	15	PDB header: hydrolase Chain: A: PDB Molecule: myotubularin-related protein 2; PDBTitle: crystal structure of mtmr2 in complex with2 phosphatidylinositol 3-phosphate
11	c2yf0A_	 Alignment		51.1	21	PDB header: hydrolase Chain: A: PDB Molecule: myotubularin-related protein 6; PDBTitle: human myotubularin related protein 6 (mtmr6)

12	c5u32A_	 Alignment		44.5	24	PDB header: transferase Chain: A: PDB Molecule: trna ligase; PDBTitle: crystal structure of fungal rna kinase
13	c5sxyA_	 Alignment		43.8	31	PDB header: chaperone Chain: A: PDB Molecule: bifunctional coenzyme pqq synthesis protein c/d; PDBTitle: the solution nmr structure for the pqqd truncation of methylobacterium2 extorquens pqqcd representing a functional and stand-alone3 ribosomally synthesized and post-translational modified (ripp)4 recognition element (rre)
14	c6jx3B_	 Alignment		43.5	23	PDB header: peptide binding protein Chain: B: PDB Molecule: tfub1; PDBTitle: lasso peptide synthetase b1 complexed with the leader peptide
15	d1iqa1	 Alignment		40.8	22	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
16	c4rodA_	 Alignment		38.1	9	PDB header: transcription Chain: A: PDB Molecule: transcription factor iib 50 kda subunit; PDBTitle: human tfiib-related factor 2 (brf2) and tpb bound to trna1 promoter
17	d1j6ua3	 Alignment		37.7	16	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
18	d1sxd1	 Alignment		35.8	19	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
19	c4f43A_	 Alignment		32.7	19	PDB header: recombination/dna Chain: A: PDB Molecule: protelomerase; PDBTitle: protelomerase tela mutant r255a complexed with caag hairpin dna
20	c5vykC_	 Alignment		32.1	21	PDB header: signaling protein Chain: C: PDB Molecule: chimera protein of brs domain of braf and cc-sam domain of PDBTitle: crystal structure of the brs domain of braf in complex with the cc-sam2 domain of ksr1
21	c2lnmA_	 Alignment	not modelled	31.7	30	PDB header: protein transport Chain: A: PDB Molecule: protein tic 40, chloroplastic; PDBTitle: solution structure of the c-terminal np-repeat domain of tic40, a co-2 chaperone during protein import into chloroplasts
22	c4gduB_	 Alignment	not modelled	30.9	15	PDB header: hydrolase Chain: B: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of sulfate-bound human l-asparaginase protein
23	c3t5qA_	 Alignment	not modelled	29.5	31	PDB header: viral protein/rna Chain: A: PDB Molecule: nucleoprotein; PDBTitle: 3a structure of lassa virus nucleoprotein in complex with ssrna
24	d1sxjc1	 Alignment	not modelled	29.5	19	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
25	c3qfIA_	 Alignment	not modelled	28.5	17	PDB header: protein binding Chain: A: PDB Molecule: m1a10; PDBTitle: coiled-coil domain-dependent homodimerization of intracellular m1a2 immune receptors defines a minimal functional module for triggering3 cell death
26	c5v1uB_	 Alignment	not modelled	28.3	19	PDB header: protein binding Chain: B: PDB Molecule: tbib1; PDBTitle: tbib1 in complex with the tbia(beta) leader peptide
27	d1rp3a3	 Alignment	not modelled	27.3	19	Fold: Sigma2 domain of RNA polymerase sigma factors Superfamily: Sigma2 domain of RNA polymerase sigma factors Family: Sigma2 domain of RNA polymerase sigma factors
28	c4cmrB_	 Alignment	not modelled	27.0	28	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase/deacetylase family protein; PDBTitle: the crystal structure of novel exo-type maltose-forming2

						amylase(py04_0872) from pyrococcus sp. st04 PDB header: viral protein Chain: A: PDB Molecule: influenza a pb2 subunit; PDBTitle: crystal structure of the mid, cap-binding, mid-link and 627 domains2 from avian influenza a virus polymerase pb2 subunit bound to m7gtp
29	c5fmmA_	Alignment	not modelled	26.6	33	Fold: CH domain-like Superfamily: Calponin-homology domain, CH-domain Family: Calponin-homology domain, CH-domain
30	d1aoaa2	Alignment	not modelled	26.2	25	PDB header: viral protein/inhibitor Chain: A: PDB Molecule: polymerase basic protein 2; PDBTitle: co-crystal structure of influenza a h3n2 pb2 (241-741) bound to vx-787
31	c5wl0A_	Alignment	not modelled	24.9	33	PDB header: nuclear protein Chain: J: PDB Molecule: spc34; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
32	c6cfzj_	Alignment	not modelled	24.1	12	PDB header: transferase/transcription Chain: C: PDB Molecule: inhibitor of nuclear factor kappa-b kinase subunit beta, PDBTitle: nemo/ikk association domain structure
33	c3brtC_	Alignment	not modelled	23.6	29	PDB header: ribosome Chain: H: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
34	c4v1ah_	Alignment	not modelled	22.8	17	PDB header: rna binding protein Chain: B: PDB Molecule: serrate rna effector molecule homolog; PDBTitle: crystal structure of human ars2 residues 147-270 + 408-763 with2 deletion of loop b
35	c6f7sB_	Alignment	not modelled	22.3	20	Fold: Saposin-like Superfamily: Saposin Family: NKL-like
36	d1l9la_	Alignment	not modelled	22.0	19	PDB header: protein binding Chain: A: PDB Molecule: bud site selection protein 6; PDBTitle: crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
37	c3okqA_	Alignment	not modelled	21.8	21	PDB header: ribosome Chain: 5: PDB Molecule: 54s ribosomal protein l3, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
38	c1vw45_	Alignment	not modelled	21.2	19	PDB header: transcription Chain: E: PDB Molecule: subunit (60 kda) of tfiid and saga complexes; PDBTitle: molecular structure of promoter-bound yeast tfiid
39	c6hqaE_	Alignment	not modelled	21.0	17	PDB header: nuclear protein Chain: A: PDB Molecule: nucleoprotein; PDBTitle: lassa fever virus nucleoprotein complexed with dttp
40	c3mx2A_	Alignment	not modelled	20.7	31	PDB header: photosynthesis Chain: D: PDB Molecule: photosystem i reaction center subunit ii, chloroplast; PDBTitle: the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution
41	c2o01D_	Alignment	not modelled	20.6	35	PDB header: transferase Chain: H: PDB Molecule: 2-methylcitrate synthase; PDBTitle: crystal structure of 2-methylcitrate synthase (prpc) from salmonella2 typhimurium
42	c3o8jh_	Alignment	not modelled	20.1	17	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of yfmf, a putative dna-binding membrane2 protein from staphylococcus aureus
43	c3fymA_	Alignment	not modelled	20.0	14	PDB header: photosynthesis Chain: D: PDB Molecule: photosystem i p700 chlorophyll a apoprotein a2; PDBTitle: cyanidioschyzon merolae photosystem i
44	c6fosD_	Alignment	not modelled	19.7	27	Fold: Ntn hydrolase-like Superfamily: Archaeal IMP cyclohydrolase PurO Family: Archaeal IMP cyclohydrolase PurO
45	d2ntka1	Alignment	not modelled	18.9	25	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
46	d1sxb1	Alignment	not modelled	18.8	19	PDB header: transferase Chain: B: PDB Molecule: 378aa long hypothetical citrate synthase; PDBTitle: crystal structure of an isozyme of citrate synthase from sulfolbus2 tokodaii strain7
47	c1vgmB_	Alignment	not modelled	18.6	29	PDB header: transcription Chain: H: PDB Molecule: mediator of rna polymerase ii transcription subunit 8; PDBTitle: structure of the schizosaccharomyces pombe mediator head module
48	c4h63H_	Alignment	not modelled	18.3	10	PDB header: translation Chain: D: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: crystal structure of human erf1/erf3 complex
49	c3e1yD_	Alignment	not modelled	18.2	12	PDB header: transcription Chain: V: PDB Molecule: transcription factor iibb 70 kda subunit; PDBTitle: rna polymerase iii closed complex cc1.
50	c6f42V_	Alignment	not modelled	17.9	12	PDB header: signaling protein/dna binding protein Chain: B: PDB Molecule: anti-sigma factor nepr; PDBTitle: co-crystal structure of anti-anti-sigma factor phyr complexed with2 anti-sigma factor nepr from bartonella quintana
51	c4qicB_	Alignment	not modelled	17.8	56	PDB header: lyase Chain: A: PDB Molecule: enolase; PDBTitle: crystal structure of the t. brucei enolase complexed with2 sulphate, identification of a metal binding site iv
52	c2ptwA_	Alignment	not modelled	17.7	17	PDB header: viral protein Chain: A: PDB Molecule: tegument protein ul21; PDBTitle: crystal structure of hsv-1 ul21 c-terminal domain
53	c5ed7A_	Alignment	not modelled	17.5	21	PDB header: glycoprotein

54	c2w61A_	Alignment	not modelled	17.2	16	Chain: A; PDB Molecule: glycolipid-anchored surface protein 2; PDBTitle: saccharomyces cerevisiae gas2p apostructure (e176q mutant)
55	d1euca2	Alignment	not modelled	17.1	9	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
56	c6f1yf_	Alignment	not modelled	16.5	20	PDB header: motor protein Chain: F; PDB Molecule: dynein light intermediate chain region of the dynein2 tail/dynactin/bicdr1 complex
57	d2csua3	Alignment	not modelled	16.5	27	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
58	c6egkB_	Alignment	not modelled	16.4	14	PDB header: lyase Chain: B; PDB Molecule: cucumene synthase; PDBTitle: t181n cucumene synthase
59	d1lib_	Alignment	not modelled	16.1	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
60	d1jb0d_	Alignment	not modelled	15.9	27	Fold: Photosystem I subunit Psd Superfamily: Photosystem I subunit Psd Family: Photosystem I subunit Psd
61	c5d3aA_	Alignment	not modelled	15.9	19	PDB header: motor protein Chain: A; PDB Molecule: kinesin-like protein kif21a; PDBTitle: kif21a regulatory coiled coil
62	c6igmH_	Alignment	not modelled	15.6	18	PDB header: transcription Chain: H; PDB Molecule: helicase srcap; PDBTitle: cryo-em structure of human srcap complex
63	d1vp8a_	Alignment	not modelled	15.5	21	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
64	c3rfiA_	Alignment	not modelled	15.4	10	PDB header: hydrolase Chain: A; PDB Molecule: asp; PDBTitle: crystal structure of the saposin-like domain of plant aspartic2 protease from solanum tuberosum
65	d2nu7a2	Alignment	not modelled	15.3	20	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
66	c2wseD_	Alignment	not modelled	15.1	35	PDB header: photosynthesis Chain: D; PDB Molecule: photosystem i reaction center subunit ii, chloroplastic; PDBTitle: improved model of plant photosystem i
67	d1k47a2	Alignment	not modelled	14.8	13	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Phosphomevalonate kinase (PMK)
68	c3tb4A_	Alignment	not modelled	14.7	21	PDB header: hydrolase Chain: A; PDB Molecule: vibriobactin-specific isochorismatase; PDBTitle: crystal structure of the isc domain of vibb
69	c2h5xA_	Alignment	not modelled	14.5	16	PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
70	d2dula1	Alignment	not modelled	14.4	30	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TRM1-like
71	d2jfga3	Alignment	not modelled	14.4	20	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
72	d2p10a1	Alignment	not modelled	14.3	32	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ml19387-like
73	c6cauA_	Alignment	not modelled	14.3	24	PDB header: ligase Chain: A; PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with amppnp
74	c2wusR_	Alignment	not modelled	14.3	7	PDB header: structural protein Chain: R; PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape protein rodz
75	c5f4tA_	Alignment	not modelled	14.2	30	PDB header: cell adhesion Chain: A; PDB Molecule: sizumo sperm-egg fusion protein 1; PDBTitle: crystal structure of the human sperm izumo1 residues 22-254
76	d1ngra_	Alignment	not modelled	14.2	30	Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD
77	c5b5yA_	Alignment	not modelled	14.1	32	PDB header: metal binding protein Chain: A; PDB Molecule: ptlcib4; PDBTitle: crystal structure of ptlcib4, a homolog of the limiting co2-inducible2 protein lcib
78	c2zakB_	Alignment	not modelled	14.1	22	PDB header: hydrolase Chain: B; PDB Molecule: l-asparaginase precursor; PDBTitle: orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation
79	d1dpua_	Alignment	not modelled	14.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of RPA32
80	c1dpuA_	Alignment	not modelled	14.1	20	PDB header: dna binding protein Chain: A; PDB Molecule: replication protein a (rpa32) c-terminal domain; PDBTitle: solution structure of the c-terminal domain of human

						rpa322 complexed with ung2(73-88)
81	c6cngA_	Alignment	not modelled	14.1	14	PDB header: transferase Chain: A: PDB Molecule: fatty acid kinase (fak) b3 protein; PDBTitle: the x-ray crystal structure of the streptococcus pneumoniae fatty acid2 kinase (fak) b3 protein loaded with linoleic acid to 1.47 angstrom3 resolution
82	c3j7yf_	Alignment	not modelled	13.2	38	PDB header: ribosome Chain: F: PDB Molecule: ul4; PDBTitle: structure of the large ribosomal subunit from human mitochondria
83	c4pu6A_	Alignment	not modelled	13.2	24	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
84	d1p3da3	Alignment	not modelled	13.1	24	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
85	c1mgpA_	Alignment	not modelled	13.1	21	PDB header: lipid binding protein Chain: A: PDB Molecule: hypothetical protein tm841; PDBTitle: hypothetical protein tm841 from thermotoga maritima reveals2 fatty acid binding function
86	d1mgpa_	Alignment	not modelled	13.1	21	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DegV-like
87	d1kwma2	Alignment	not modelled	13.1	18	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
88	d1h8ua_	Alignment	not modelled	12.9	17	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
89	d1gg4a4	Alignment	not modelled	12.7	28	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
90	c4lwsB_	Alignment	not modelled	12.6	12	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
91	c2p10D_	Alignment	not modelled	12.2	32	PDB header: hydrolase Chain: D: PDB Molecule: mlI9387 protein; PDBTitle: crystal structure of a putative phosphopyruvate hydrolase (mlI9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
92	c1u0iA_	Alignment	not modelled	12.1	44	PDB header: de novo protein Chain: A: PDB Molecule: iaal-e3; PDBTitle: iaal-e3/k3 heterodimer
93	c3t76A_	Alignment	not modelled	12.0	20	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
94	c2hl7A_	Alignment	not modelled	11.9	25	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccmh; PDBTitle: crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
95	d1dlwa_	Alignment	not modelled	11.7	15	Fold: Globin-like Superfamily: Globin-like Family: Truncated hemoglobin
96	c4gwpC_	Alignment	not modelled	11.7	7	PDB header: transcription Chain: C: PDB Molecule: mediator of rna polymerase ii transcription subunit 8; PDBTitle: structure of the mediator head module from s. cerevisiae
97	d1a6db2	Alignment	not modelled	11.4	31	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain
98	d1up8a_	Alignment	not modelled	11.3	28	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Haloperoxidase (bromoperoxidase)
99	c3ke2A_	Alignment	not modelled	11.2	23	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yp_928783.1; PDBTitle: crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution