

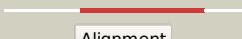






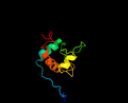






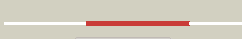







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2389c_(rpfD)_2683258_2683722
Date	Mon Aug 5 13:25:54 BST 2019
Unique Job ID	b7a8b9cdfb0de630

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1xsfA_	 Alignment		100.0	43	PDB header: cell cycle, hydrolase Chain: A: PDB Molecule: probable resuscitation-promoting factor rpfb; PDBTitle: solution structure of a resuscitation promoting factor2 domain from mycobacterium tuberculosis
2	c4ow1A_	 Alignment		100.0	60	PDB header: hydrolase Chain: A: PDB Molecule: resuscitation-promoting factor rpfC; PDBTitle: crystal structure of resuscitation promoting factor c
3	d1xsfal	 Alignment		100.0	49	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: RPF-like
4	c3eo5A_	 Alignment		100.0	46	PDB header: cell adhesion Chain: A: PDB Molecule: resuscitation-promoting factor rpfB; PDBTitle: crystal structure of the resuscitation promoting factor rpfB
5	c5e27B_	 Alignment		100.0	44	PDB header: cell adhesion Chain: B: PDB Molecule: resuscitation-promoting factor rpfB; PDBTitle: the structure of resuscitation promoting factor b from m. tuberculosis2 reveals unexpected ubiquitin-like domains
6	d1fkqa_	 Alignment		97.9	25	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
7	c2fbdB_	 Alignment		97.9	26	PDB header: hydrolase Chain: B: PDB Molecule: lysozyme 1; PDBTitle: the crystallographic structure of the digestive lysozyme 1 from musca2 domestica at 1.90 ang.
8	d1hfxa_	 Alignment		97.8	22	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
9	d1yroal	 Alignment		97.8	24	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
10	d1b9oa_	 Alignment		97.8	24	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
11	d1f6sa_	 Alignment		97.8	22	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme

12	c2z2fA_	Alignment		97.7	25	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme c-2; PDBTitle: x-ray crystal structure of bovine stomach lysozyme
13	d1iiza_	Alignment		97.7	26	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
14	d1alca_	Alignment		97.6	24	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
15	d1jsea_	Alignment		97.6	29	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
16	d1gd6a_	Alignment		97.5	25	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
17	d1lsga1	Alignment		97.5	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
18	c2goiC_	Alignment		97.5	29	PDB header: cell adhesion, sugar binding protein Chain: C: PDB Molecule: sperm lysozyme-like protein 1; PDBTitle: crystal structure of mouse sperm c-type lysozyme-like protein 1
19	d1ghla_	Alignment		97.5	29	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
20	d2vb1a1	Alignment		97.5	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
21	d1juga_	Alignment	not modelled	97.5	28	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
22	d1qqya_	Alignment	not modelled	97.5	25	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
23	d1hhla_	Alignment	not modelled	97.4	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
24	d2eqla_	Alignment	not modelled	97.2	26	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
25	d1lmqa_	Alignment	not modelled	97.2	28	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
26	d1ivma_	Alignment	not modelled	97.2	34	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
27	d2nwdx1	Alignment	not modelled	97.2	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
28	c3w6dB_	Alignment	not modelled	96.9	18	PDB header: hydrolase Chain: B: PDB Molecule: lysozyme-like chitinolytic enzyme; PDBTitle: crystal structure of catalytic domain of chitinase from ralstonia sp.2 a-471 (e141q) in complex with tetrasaccharide
29	c3hbhA_	Alignment	not modelled	96.8	21	PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase;

29	c3ukrA	Alignment	not modelled	98.8	41	PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
30	d1gbsa	Alignment	not modelled	96.7	25	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: G-type lysozyme
31	d1qsaa2	Alignment	not modelled	96.5	25	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Bacterial muramidase, catalytic domain
32	c2y8pA	Alignment	not modelled	96.2	29	PDB header: lyase Chain: A; PDB Molecule: endo-type membrane-bound lytic murein transglycosylase a; PDBTitle: crystal structure of an outer membrane-anchored endolytic 2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
33	c3gxkB	Alignment	not modelled	95.8	27	PDB header: hydrolase Chain: B; PDB Molecule: goose-type lysozyme 1; PDBTitle: the crystal structure of g-type lysozyme from atlantic cod (gadus2 morhua l.) in complex with nag oligomers sheds new light on substrate3 binding and the catalytic mechanism. native structure to 1.9
34	c4cfoB	Alignment	not modelled	95.8	29	PDB header: hydrolase Chain: B; PDB Molecule: mltc; PDBTitle: structure of lytic transglycosylase mltc from escherichia2 coli in complex with tetrasaccharide at 2.9 a resolution.
35	c3mgwA	Alignment	not modelled	95.6	16	PDB header: hydrolase Chain: A; PDB Molecule: lysozyme g; PDBTitle: thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
36	c4oz9A	Alignment	not modelled	95.4	22	PDB header: lyase Chain: A; PDB Molecule: membrane-bound lytic murein transglycosylase f; PDBTitle: crystal structure of mltf from pseudomonas aeruginosa complexed with2 isoleucine
37	c4xp8A	Alignment	not modelled	94.8	24	PDB header: hydrolase Chain: A; PDB Molecule: etga protein; PDBTitle: structure of etga d60n mutant
38	c6cfcA	Alignment	not modelled	87.9	26	PDB header: hydrolase Chain: A; PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of soluble lytic transglycosylase cj0843 of2 campylobacter jejuni in complex with bulgecin a
39	c6fcqA	Alignment	not modelled	87.6	27	PDB header: lyase Chain: A; PDB Molecule: soluble lytic murein transglycosylase; PDBTitle: the x-ray structure of lytic transglycosylase slt inactive mutant2 e503q from pseudomonas aeruginosa in complex with bulgecin a
40	c1slyA	Alignment	not modelled	87.3	25	PDB header: glycosyltransferase Chain: A; PDB Molecule: 70-kda soluble lytic transglycosylase; PDBTitle: complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
41	c3ct5A	Alignment	not modelled	77.1	15	PDB header: hydrolase Chain: A; PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
42	c4anrA	Alignment	not modelled	68.6	21	PDB header: lyase Chain: A; PDB Molecule: soluble lytic transglycosylase b; PDBTitle: crystal structure of soluble lytic transglycosylase sltb12 from pseudomonas aeruginosa
43	c4nooA	Alignment	not modelled	61.6	33	PDB header: immune system Chain: A; PDB Molecule: svrg protein; PDBTitle: molecular mechanism for self-protection against type vi secretion2 system in vibrio cholerae
44	d1qusa	Alignment	not modelled	61.4	22	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Bacterial muramidase, catalytic domain
45	d1am7a	Alignment	not modelled	59.8	27	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Lambda lysozyme
46	c5anzA	Alignment	not modelled	55.9	27	PDB header: hydrolase Chain: A; PDB Molecule: soluble lytic transglycosylase b3; PDBTitle: crystal structure of sltb3 from pseudomonas aeruginosa.
47	d1eh9a2	Alignment	not modelled	51.2	22	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
48	c3csqC	Alignment	not modelled	45.9	17	PDB header: hydrolase Chain: C; PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
49	c2dqaA	Alignment	not modelled	22.9	31	PDB header: hydrolase Chain: A; PDB Molecule: lysozyme; PDBTitle: crystal structure of tapes japonica lysozyme
50	c4fdyA	Alignment	not modelled	20.2	29	PDB header: hydrolase Chain: A; PDB Molecule: similar to lipoprotein, nlp/p60 family; PDBTitle: crystal structure of a similar to lipoprotein, nlp/p60 family2 (sav0400) from staphylococcus aureus subsp. aureus mu50 at 2.23 a3 resolution
51	c1p9cA	Alignment	not modelled	19.8	25	PDB header: ligand binding protein Chain: A; PDB Molecule: 26s proteasome non-atpase regulatory subunit 4; PDBTitle: nmr solution structure of the c-terminal ubiquitin-2 interacting motif of the proteasome subunit s5a
52	c4pwaA	Alignment	not modelled	19.8	18	PDB header: electron transport Chain: A; PDB Molecule: putative cytochrome c; PDBTitle: crystal structure of the c-type cytochrome soru from sinorhizobium2 meliloti
53	c2kukA	Alignment	not modelled	18.0	38	PDB header: antiviral protein Chain: A; PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2

54	c3vdlB_	Alignment	not modelled	13.4	17	PDB header: cell invasion Chain: B: PDB Molecule: circumsporozoite (cs) protein; PDBTitle: crystal structure of circumsporozoite protein atsr domain, p43212 form
55	c4oltA_	Alignment	not modelled	10.9	18	PDB header: hydrolase Chain: A: PDB Molecule: chitosanase; PDBTitle: chitosanase complex structure
56	c3h3mB_	Alignment	not modelled	10.0	21	PDB header: structural genomics Chain: B: PDB Molecule: flagellar protein flit; PDBTitle: crystal structure of flagellar protein flit from bordetella2 bronchiseptica
57	d2pf1a2	Alignment	not modelled	9.0	37	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
58	c2mn1A_	Alignment	not modelled	8.8	38	PDB header: unknown function Chain: A: PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
59	c2ofeA_	Alignment	not modelled	8.7	29	PDB header: sugar binding protein Chain: A: PDB Molecule: sclerotium rolfsii lectin; PDBTitle: the crystal structure of sclerotium rolfsii lectin in complex with n-2 acetyl-d-glucosamine
60	d2hfva1	Alignment	not modelled	8.5	17	Fold: Ferredoxin-like Superfamily: GlnB-like Family: RPA1041-like
61	d1ss3a_	Alignment	not modelled	8.1	43	Fold: Toxic hairpin Superfamily: Pollen allergen ole e 6 Family: Pollen allergen ole e 6
62	c2ml7A_	Alignment	not modelled	7.7	41	PDB header: unknown function Chain: A: PDB Molecule: specific abundant protein 3; PDBTitle: ginsentides: characterization, structure and application of a new2 class of highly stable cystine knot peptides in ginseng
63	c6ch2E_	Alignment	not modelled	7.7	36	PDB header: structural protein Chain: E: PDB Molecule: flagellar hook-associated protein 2,flagellar protein flit; PDBTitle: crystal structure of the cytoplasmic domain of flha and flit-flid2 complex
64	d1ay7b_	Alignment	not modelled	7.5	25	Fold: Barstar-like Superfamily: Barstar-related Family: Barstar-related
65	c1cwvA_	Alignment	not modelled	7.3	38	PDB header: structural protein Chain: A: PDB Molecule: invasin; PDBTitle: crystal structure of invasin: a bacterial integrin-binding protein
66	c5bq9B_	Alignment	not modelled	7.1	45	PDB header: unknown function, structural genomics Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein lpg1496 legionella2 pneumophila subsp. pneumophila
67	c2guzO_	Alignment	not modelled	7.1	8	PDB header: chaperone, protein transport Chain: O: PDB Molecule: mitochondrial import inner membrane translocase subunit PDBTitle: structure of the tim14-tim16 complex of the mitochondrial protein2 import motor
68	c1wqbA_	Alignment	not modelled	7.0	26	PDB header: toxin Chain: A: PDB Molecule: aptotoxin vii; PDBTitle: three-dimensional solution strucutre of aptotoxin vii, from2 the venom of a trap-door spider
69	c1jzA_	Alignment	not modelled	6.8	50	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
70	c1k48A_	Alignment	not modelled	6.8	50	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
71	c4uf6L_	Alignment	not modelled	6.7	33	PDB header: hydrolase Chain: L: PDB Molecule: nuclear factor related to kappa-b-binding protein; PDBTitle: uch-15 in complex with ubiquitin-propargyl bound to an activating2 fragment of ino80g
72	c4ttnA_	Alignment	not modelled	6.6	50	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
73	c4ttmA_	Alignment	not modelled	6.4	50	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
74	c2lurA_	Alignment	not modelled	6.3	60	PDB header: plant protein Chain: A: PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]
75	c2khaA_	Alignment	not modelled	6.2	50	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
76	c4dq5B_	Alignment	not modelled	6.1	33	PDB header: membrane protein Chain: B: PDB Molecule: membrane protein phi6 p5wt; PDBTitle: structural investigation of bacteriophage phi6 lysin (wt)
77	c3nkzD_	Alignment	not modelled	6.0	36	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: flagellar protein flit; PDBTitle: the crystal structure of a flagella protein from yersinia2 enterocolitica subsp. enterocolitica 8081
78	c1orxA_	Alignment	not modelled	5.9	60	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
79	c3j6vU_	Alignment	not modelled	5.8	20	PDB header: ribosome Chain: U: PDB Molecule: 28s ribosomal protein s21, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian

						mitochondrial2 ribosome
80	c3a7mA_	Alignment	not modelled	5.8	33	PDB header: gene regulation, chaperone Chain: A; PDB Molecule: flagellar protein flit; PDBTitle: structure of flit, the flagellar type iii chaperone for flid
81	c2gj0A_	Alignment	not modelled	5.8	25	PDB header: plant protein Chain: A; PDB Molecule: cycloviolacin o14; PDBTitle: cycloviolacin o14
82	c4ttoA_	Alignment	not modelled	5.7	50	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1
83	c3jb9g_	Alignment	not modelled	5.7	30	PDB header: rna binding protein/rna Chain: G; PDB Molecule: small nuclear ribonucleoprotein sm d2; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
84	c3e4hA_	Alignment	not modelled	5.7	50	PDB header: plant protein Chain: A; PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f
85	d1dx5i3	Alignment	not modelled	5.7	63	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
86	c2gyaZ_	Alignment	not modelled	5.6	40	PDB header: ribosome Chain: Z; PDB Molecule: 50s ribosomal protein l32; PDBTitle: structure of the 50s subunit of a pre-translocational e. coli ribosome2 obtained by fitting atomic models for rna and protein components into3 cryo-em map emd-1056
87	c5foeA_	Alignment	not modelled	5.6	20	PDB header: transferase Chain: A; PDB Molecule: gdp-fucose protein o-fucosyltransferase 2,thrombospondin-1; PDBTitle: crystal structure of the c. elegans protein o-fucosyltransferase 22 (cepofut2) double mutant (r298k-r299k) in complex with gdp and the3 human tsr1 from thrombospondin 1
88	c1hznA_	Alignment	not modelled	5.6	14	PDB header: hormone/growth factor Chain: A; PDB Molecule: cholecystokinin type a receptor; PDBTitle: nmr solution structure of the third extracellular loop of2 the cholecystokinin a receptor
89	c3l0iA_	Alignment	not modelled	5.5	21	PDB header: protein binding/protein transport Chain: A; PDB Molecule: drira; PDBTitle: complex structure of sidm/drira with the wild type rab1
90	c5kp0A_	Alignment	not modelled	5.4	33	PDB header: chaperone Chain: A; PDB Molecule: flagellar protein flit,flagellum-specific atp synthase; PDBTitle: recognition and targeting mechanisms by chaperones in flagella2 assembly and operation
91	c4wybj_	Alignment	not modelled	5.1	19	PDB header: contractile protein/protein binding Chain: J; PDB Molecule: bud site selection protein 6; PDBTitle: structure of the bud6 flank domain in complex with actin