







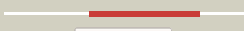












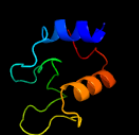


Phyre2

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 Description RVBD1884c_rpfC_2133738_2134268
 Date Fri Aug 2 13:30:50 BST 2019
 Unique Job ID 85d272def37e8fe1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ow1A_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: resuscitation-promoting factor rpfC; PDBTitle: crystal structure of resuscitation promoting factor c
2	c1xsfA_	 Alignment		100.0	48	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
3	d1xsfal	 Alignment		100.0	52	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: RPF-like
4	c3eo5A_	 Alignment		100.0	50	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	52	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	c2z2fA_	 Alignment		97.7	29	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme c-2; PDBTitle: x-ray crystal structure of bovine stomach lysozyme
7	c2fbdB_	 Alignment		97.7	25	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	d1yroal	 Alignment		97.7	26	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
9	d1hfxa_	 Alignment		97.6	20	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
10	d1b9oa_	 Alignment		97.6	23	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
11	d1iiza_	 Alignment		97.6	20	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme

12	d1fkqa_	Alignment		97.6	28	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
13	d1f6sa_	Alignment		97.4	23	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
14	d1alca_	Alignment		97.4	25	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
15	d1gd6a_	Alignment		97.4	20	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
16	d1jsea_	Alignment		97.4	28	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
17	c2goiC_	Alignment		97.3	25	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
18	d1ivma_	Alignment		97.3	35	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
19	d1lsga1	Alignment		97.3	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
20	d2nwdx1	Alignment		97.2	38	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
21	d1ghla_	Alignment	not modelled	97.2	28	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
22	d2vb1a1	Alignment	not modelled	97.2	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
23	d1hhla_	Alignment	not modelled	97.2	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
24	d1qqya_	Alignment	not modelled	97.1	30	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
25	d1juga_	Alignment	not modelled	97.1	33	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
26	d2eqla_	Alignment	not modelled	96.9	30	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
27	c3bkhA_	Alignment	not modelled	96.8	24	PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
28	d1lmqa_	Alignment	not modelled	96.8	32	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme
29	c3w6dB	Alignment	not modelled	96.5	22	PDB header: hydrolase Chain: B: PDB Molecule: lysozyme-like chitinolytic enzyme;

29	c3w00b_	Alignment	not modelled	96.3	25	PDBTitle: crystal structure of catalytic domain of chitinase from ralstonia sp.2 a-471 (e141q) in complex with tetrasaccharide
30	d1qsaa2	Alignment	not modelled	96.3	26	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Bacterial muramidase, catalytic domain
31	d1gbsa_	Alignment	not modelled	96.0	25	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: G-type lysozyme
32	c2y8pA_	Alignment	not modelled	95.7	30	PDB header: lyase Chain: A; PDB Molecule: endo-type membrane-bound lytic murein transglycosylase a; PDBTitle: crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
33	c4cfoB_	Alignment	not modelled	95.0	25	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.
34	c3mgwA_	Alignment	not modelled	94.8	22	PDB header: hydrolase Chain: A; PDB Molecule: lysozyme g; PDBTitle: thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
35	c4oz9A_	Alignment	not modelled	94.6	24	PDB header: lyase Chain: A; PDB Molecule: membrane-bound lytic murein transglycosylase f; PDBTitle: crystal structure of mltf from pseudomonas aeruginosa complexed with2 isoleucine
36	c3gxkB_	Alignment	not modelled	94.5	21	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
37	c4xp8A_	Alignment	not modelled	93.7	22	PDB header: hydrolase Chain: A; PDB Molecule: etga protein; PDBTitle: structure of etga d60n mutant
38	c6cfcA_	Alignment	not modelled	85.2	29	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	c1slyA_	Alignment	not modelled	83.4	26	PDB header: glycosyltransferase Chain: A; PDB Molecule: 70-kda soluble lytic transglycosylase; PDBTitle: complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
40	c6fcqA_	Alignment	not modelled	83.3	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
41	c3ct5A_	Alignment	not modelled	68.5	19	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	63.5	23	PDB header: lyase Chain: A; PDB Molecule: soluble lytic transglycosylase b; PDBTitle: crystal structure of soluble lytic transglycosylase sltb12 from pseudomonas aeruginosa
43	d1qusa_	Alignment	not modelled	57.4	21	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Bacterial muramidase, catalytic domain
44	c5anzA_	Alignment	not modelled	55.6	28	PDB header: hydrolase Chain: A; PDB Molecule: soluble lytic transglycosylase b3; PDBTitle: crystal structure of sltb3 from pseudomonas aeruginosa.
45	d1eh9a2	Alignment	not modelled	49.6	22	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
46	c4nooA_	Alignment	not modelled	49.5	29	PDB header: immune system Chain: A; PDB Molecule: vgrg protein; PDBTitle: molecular mechanism for self-protection against type vi secretion2 system in vibrio cholerae
47	d1am7a_	Alignment	not modelled	48.9	27	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Lambda lysozyme
48	c2kukA_	Alignment	not modelled	34.1	54	PDB header: antiviral protein Chain: A; PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2
49	c3csqC_	Alignment	not modelled	24.2	20	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
50	c2jwmA_	Alignment	not modelled	19.6	55	PDB header: plant protein Chain: A; PDB Molecule: kalata-b7; PDBTitle: nmr spatial srcture of ternary complex kalata b7/mn2+/dpc2 micelle
51	d1h72c1	Alignment	not modelled	19.4	20	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
52	c2dqaA_	Alignment	not modelled	16.0	29	PDB header: hydrolase Chain: A; PDB Molecule: lysozyme; PDBTitle: crystal structure of tapes japonica lysozyme
53	c6g67B_	Alignment	not modelled	14.2	71	PDB header: de novo protein Chain: B; PDB Molecule: cc-type2-ii; PDBTitle: crystal structure of a parallel eight-helix coiled coil cc-type2-ii
54	c6g67A_	Alignment	not modelled	14.2	71	PDB header: de novo protein Chain: A; PDB Molecule: cc-type2-ii;

54	c0g07A	Alignment	not modelled	14.2	71	PDBTitle: crystal structure of a parallel eight-helix coiled coil cc-type2-ii
55	c2mw0A	Alignment	not modelled	14.2	55	PDB header: protein binding Chain: A: PDB Molecule: kalata b7; PDBTitle: kalata b7 ser mutant
56	c4fdyA	Alignment	not modelled	13.5	24	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
57	c4oltA	Alignment	not modelled	11.7	25	PDB header: hydrolase Chain: A: PDB Molecule: chitosanase; PDBTitle: chitosanase complex structure
58	d1ay7b	Alignment	not modelled	11.2	31	Fold: Barstar-like Superfamily: Barstar-related Family: Barstar-related
59	c1p9cA	Alignment	not modelled	11.0	30	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
60	d1k47a1	Alignment	not modelled	10.7	11	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
61	d1y2ta	Alignment	not modelled	10.7	50	Fold: Cytolysin/lectin Superfamily: Cytolysin/lectin Family: Fungal fruit body lectin
62	c2lurA	Alignment	not modelled	10.5	80	PDB header: plant protein Chain: A: PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]
63	c4dq5B	Alignment	not modelled	10.0	42	PDB header: membrane protein Chain: B: PDB Molecule: membrane protein phi6 p5wt; PDBTitle: structural investigation of bacteriophage phi6 lysin (wt)
64	c1kalA	Alignment	not modelled	9.5	55	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: elucidation of the primary and three-dimensional structure2 of the uterotonic polypeptide kalata b1
65	c2ofeA	Alignment	not modelled	9.4	36	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
66	d1he1a	Alignment	not modelled	8.8	21	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
67	d1ss3a	Alignment	not modelled	8.0	43	Fold: Toxic hairpin Superfamily: Pollen allergen ole e 6 Family: Pollen allergen ole e 6
68	c5bq9B	Alignment	not modelled	7.7	45	PDB header: unknown function, structural genomics Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein lpg1496 legionella2 pneumophila subsp. pneumophila
69	c3e4hA	Alignment	not modelled	7.3	55	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f
70	c4wybj	Alignment	not modelled	6.8	29	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
71	c3h3mB	Alignment	not modelled	6.7	36	PDB header: structural genomics Chain: B: PDB Molecule: flagellar protein flit; PDBTitle: crystal structure of flagellar protein flit from bordetella2 bronchiseptica
72	c5j9hA	Alignment	not modelled	6.6	20	PDB header: viral protein Chain: A: PDB Molecule: envelopment polyprotein; PDBTitle: crystal structure of glycoprotein c from puumala virus in the post-2 fusion conformation (ph 8.0)
73	c2gyaZ	Alignment	not modelled	6.6	36	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
74	c3j6vU	Alignment	not modelled	6.5	27	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
75	c3noyA	Alignment	not modelled	6.4	33	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
76	c4l7zC	Alignment	not modelled	6.3	16	PDB header: lyase Chain: C: PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of chloroflexus aurantiacus maly-coa lyase
77	d1dxha2	Alignment	not modelled	6.1	42	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
78	d1dx5i3	Alignment	not modelled	5.8	50	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
79	d2cx6a1	Alignment	not modelled	5.8	7	Fold: Barstar-like Superfamily: Barstar-related Family: Barstar-related
80	c1n1uA	Alignment	not modelled	5.7	55	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1;

						PDBTitle: nmr structure of [ala1,15]kalata b1
81	d1n1ua_	Alignment	not modelled	5.7	55	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
82	d2pf1a2	Alignment	not modelled	5.6	28	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
83	c4pnbC_	Alignment	not modelled	5.6	69	PDB header: de novo protein Chain: C; PDB Molecule: cc-hex3; PDBTitle: a de novo designed hexameric coiled coil cc-hex3
84	d1x99a_	Alignment	not modelled	5.5	36	Fold: Cytolysin/lectin Superfamily: Cytolysin/lectin Family: Fungal fruit body lectin
85	c4pnbA_	Alignment	not modelled	5.5	69	PDB header: de novo protein Chain: A; PDB Molecule: cc-hex3; PDBTitle: a de novo designed hexameric coiled coil cc-hex3
86	c4pnbB_	Alignment	not modelled	5.5	69	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex3; PDBTitle: a de novo designed hexameric coiled coil cc-hex3
87	c4pnbD_	Alignment	not modelled	5.5	69	PDB header: de novo protein Chain: D; PDB Molecule: cc-hex3; PDBTitle: a de novo designed hexameric coiled coil cc-hex3
88	d1pt4a_	Alignment	not modelled	5.3	55	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
89	c1wqbA_	Alignment	not modelled	5.3	44	PDB header: toxin Chain: A; PDB Molecule: aptotoxin vii; PDBTitle: three-dimensional solution structure of aptotoxin vii, from2 the venom of a trap-door spider
90	c4wybP_	Alignment	not modelled	5.3	35	PDB header: contractile protein/protein binding Chain: P; PDB Molecule: bud site selection protein 6; PDBTitle: structure of the bud6 flank domain in complex with actin
91	d1nb1a_	Alignment	not modelled	5.2	55	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1