























Phyre2

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 Description RVBD2450c_(rpfE)_2751672_2752190
 Date Wed Aug 7 12:50:07 BST 2019
 Unique Job ID 420d965ba43873e3

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c4ow1A_ |  Alignment |  | 100.0 | 65 | PDB header: hydrolase Chain: A: PDB Molecule: resuscitation-promoting factor rpfC; PDBTitle: crystal structure of resuscitation promoting factor c |
| 2 | c5e27B_ |  Alignment |  | 100.0 | 58 | 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 |
| 3 | c1xsfA_ |  Alignment |  | 100.0 | 53 | 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 |
| 4 | d1xsfal |  Alignment |  | 100.0 | 64 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: RPF-like |
| 5 | c3eo5A_ |  Alignment |  | 100.0 | 58 | PDB header: cell adhesion Chain: A: PDB Molecule: resuscitation-promoting factor rpfB; PDBTitle: crystal structure of the resuscitation promoting factor rpfB |
| 6 | d1yroal |  Alignment |  | 97.8 | 23 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 7 | d1fkqa_ |  Alignment |  | 97.6 | 26 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 8 | d1hfxa_ |  Alignment |  | 97.6 | 22 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 9 | c2z2fA_ |  Alignment |  | 97.6 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: lysozyme c-2; PDBTitle: x-ray crystal structure of bovine stomach lysozyme |
| 10 | c2fbdB_ |  Alignment |  | 97.6 | 24 | 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. |
| 11 | d1iiza_ |  Alignment |  | 97.5 | 18 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |

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|----|-------------------------|-----------|--------------|------|----|---|
| 12 | d1b9oa_ | Alignment | | 97.5 | 22 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 13 | d1f6sa_ | Alignment | | 97.5 | 23 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 14 | d1alca_ | Alignment | | 97.5 | 20 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 15 | d1gd6a_ | Alignment | | 97.4 | 22 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 16 | d1jsea_ | Alignment | | 97.3 | 26 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 17 | c2goiC_ | Alignment | | 97.2 | 19 | 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 | d1hhla_ | Alignment | | 97.2 | 30 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 19 | d1lsga1 | Alignment | | 97.1 | 30 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 20 | d1juga_ | Alignment | | 97.1 | 31 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 21 | d2vb1a1 | Alignment | not modelled | 97.1 | 30 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 22 | c3w6dB_ | Alignment | not modelled | 97.0 | 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 |
| 23 | d1qqya_ | Alignment | not modelled | 97.0 | 28 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 24 | d1ghla_ | Alignment | not modelled | 97.0 | 28 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 25 | d2nwdx1 | Alignment | not modelled | 97.0 | 35 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 26 | d1ivma_ | Alignment | not modelled | 96.9 | 36 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 27 | d2eqla_ | Alignment | not modelled | 96.9 | 27 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 28 | d1lmqa_ | Alignment | not modelled | 96.9 | 27 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: C-type lysozyme |
| 29 | c3hbkA | Alignment | not modelled | 96.8 | 27 | PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase; |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c3ukrA | Alignment | not modelled | 96.8 | 27 | PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144 |
| 30 | d1qsa2 | Alignment | not modelled | 96.7 | 28 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Bacterial muramidase, catalytic domain |
| 31 | d1gbsa | Alignment | not modelled | 96.5 | 27 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: G-type lysozyme |
| 32 | c4oz9A | Alignment | not modelled | 96.4 | 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 |
| 33 | c2y8pA | Alignment | not modelled | 96.3 | 32 | 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 |
| 34 | c4cfoB | Alignment | not modelled | 95.9 | 20 | 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 | c3gxkB | Alignment | not modelled | 95.9 | 25 | 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 |
| 36 | c3mgwA | Alignment | not modelled | 95.4 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: lysozyme g; PDBTitle: thermodynamics and structure of a salmon cold-active goose-type2 lysozyme |
| 37 | c4xp8A | Alignment | not modelled | 95.1 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: etga protein; PDBTitle: structure of etga d60n mutant |
| 38 | c6cfcA | Alignment | not modelled | 93.2 | 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 | c1slyA | Alignment | not modelled | 92.9 | 28 | 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 | 92.3 | 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 | c4anrA | Alignment | not modelled | 90.1 | 23 | PDB header: lyase Chain: A: PDB Molecule: soluble lytic transglycosylase b; PDBTitle: crystal structure of soluble lytic transglycosylase sltb12 from pseudomonas aeruginosa |
| 42 | d1qusa | Alignment | not modelled | 88.5 | 20 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Bacterial muramidase, catalytic domain |
| 43 | c5anzA | Alignment | not modelled | 87.8 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: soluble lytic transglycosylase b3; PDBTitle: crystal structure of sltb3 from pseudomonas aeruginosa. |
| 44 | c3ct5A | Alignment | not modelled | 79.4 | 18 | 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 |
| 45 | d1am7a | Alignment | not modelled | 78.2 | 22 | Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Lambda lysozyme |
| 46 | d1eh9a2 | Alignment | not modelled | 74.1 | 28 | Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain |
| 47 | c4nooA | Alignment | not modelled | 44.0 | 50 | PDB header: immune system Chain: A: PDB Molecule: vgrg protein; PDBTitle: molecular mechanism for self-protection against type vi secretion2 system in vibrio cholerae |
| 48 | c3csqC | Alignment | not modelled | 43.6 | 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 | c1fuiB | Alignment | not modelled | 29.7 | 33 | PDB header: isomerase Chain: B: PDB Molecule: l-fucose isomerase; PDBTitle: l-fucose isomerase from escherichia coli |
| 50 | c4fdyA | Alignment | not modelled | 29.3 | 26 | 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 | d1y2ta | Alignment | not modelled | 27.4 | 50 | Fold: Cytolysin/lectin Superfamily: Cytolysin/lectin Family: Fungal fruit body lectin |
| 52 | c4dq5B | Alignment | not modelled | 25.1 | 32 | PDB header: membrane protein Chain: B: PDB Molecule: membrane protein phi6 p5wt; PDBTitle: structural investigation of bacteriophage phi6 lysin (wt) |
| 53 | c2kukA | Alignment | not modelled | 24.1 | 60 | PDB header: antiviral protein Chain: A: PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2 |
| | | | | | | PDB header: hydrolase |

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|----|-------------------------|-----------|--------------|------|-----|--|
| 54 | c2dqaA | Alignment | not modelled | 22.5 | 29 | Chain: A: PDB Molecule: lysozyme; PDBTitle: crystal structure of tapes japonica lysozyme |
| 55 | c2ofeA | Alignment | not modelled | 18.9 | 33 | 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 |
| 56 | d1ay7b | Alignment | not modelled | 15.4 | 35 | Fold: Barstar-like Superfamily: Barstar-related Family: Barstar-related |
| 57 | d1x99a | Alignment | not modelled | 13.3 | 50 | Fold: Cytolysin/lectin Superfamily: Cytolysin/lectin Family: Fungal fruit body lectin |
| 58 | d1fuia1 | Alignment | not modelled | 13.0 | 33 | Fold: Reductase/isomerase/elongation factor common domain Superfamily: Fucl/AraA C-terminal domain-like Family: L-fucose isomerase, C-terminal domain |
| 59 | c5j9hA | Alignment | not modelled | 12.4 | 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) |
| 60 | d1yarol | Alignment | not modelled | 12.0 | 35 | Fold: Four-helical up-and-down bundle Superfamily: Proteasome activator Family: Proteasome activator |
| 61 | c2lurA | Alignment | not modelled | 11.0 | 100 | PDB header: plant protein Chain: A: PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28] |
| 62 | c5bq9B | Alignment | not modelled | 11.0 | 55 | PDB header: unknown function, structural genomics Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein lpg1496 legionella2 pneumophila subsp. pneumophila |
| 63 | c2jwmA | Alignment | not modelled | 10.6 | 63 | PDB header: plant protein Chain: A: PDB Molecule: kalata-b7; PDBTitle: nmr spatial srcture of ternary complex kalata b7/mn2+/dpc2 micelle |
| 64 | c3e4hA | Alignment | not modelled | 10.4 | 75 | PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f |
| 65 | c3a9rA | Alignment | not modelled | 10.0 | 44 | PDB header: isomerase Chain: A: PDB Molecule: d-arabinose isomerase; PDBTitle: x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol |
| 66 | c4by6F | Alignment | not modelled | 10.0 | 20 | PDB header: transcription Chain: F: PDB Molecule: general negative regulator of transcription subunit 5; PDBTitle: yeast not1-not2-not5 complex |
| 67 | d1ddla | Alignment | not modelled | 10.0 | 64 | Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tymoviridae-like VP |
| 68 | c5e7tl | Alignment | not modelled | 9.8 | 48 | PDB header: viral protein Chain: I: PDB Molecule: major structural protein 1; PDBTitle: structure of the tripod (bppuct-a-I) from the baseplate of 2 bacteriophage tuc2009 |
| 69 | d1kula | Alignment | not modelled | 9.7 | 20 | Fold: Prealbumin-like Superfamily: Starch-binding domain-like Family: Starch-binding domain |
| 70 | c2wnwB | Alignment | not modelled | 9.7 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: activated by transcription factor ssrb; PDBTitle: the crystal structure of srjf from salmonella typhimurium |
| 71 | c1n1uA | Alignment | not modelled | 9.2 | 75 | PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1 |
| 72 | d1n1ua | Alignment | not modelled | 9.2 | 75 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1 |
| 73 | d2cx6a1 | Alignment | not modelled | 9.2 | 6 | Fold: Barstar-like Superfamily: Barstar-related Family: Barstar-related |
| 74 | c4oltA | Alignment | not modelled | 8.8 | 28 | PDB header: hydrolase Chain: A: PDB Molecule: chitosanase; PDBTitle: chitosanase complex structure |
| 75 | c2miiA | Alignment | not modelled | 8.6 | 21 | PDB header: protein binding Chain: A: PDB Molecule: penicillin-binding protein activator lpob; PDBTitle: nmr structure of e. coli lpob |
| 76 | c5xc2D | Alignment | not modelled | 8.5 | 28 | PDB header: hydrolase Chain: D: PDB Molecule: endo-beta-1,3-glucanase; PDBTitle: crystal structure of gh family 81 beta-1,3-glucanase from rhizomucr2 miehei complexed with laminarihexaose |
| 77 | d1pt4a | Alignment | not modelled | 8.4 | 63 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1 |
| 78 | c1nb1A | Alignment | not modelled | 8.3 | 75 | PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: high resolution solution structure of kalata b1 |
| 79 | d1nb1a | Alignment | not modelled | 8.3 | 75 | Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1 |
| 80 | c2m4IA | Alignment | not modelled | 8.2 | 31 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein bt_0846; PDBTitle: nmr structure of the protein bt_0846 from bacteroides thetaotaomicron2 vpi-5482 (np_809759.1) |
| 81 | c2wg4B | Alignment | not modelled | 7.4 | 26 | PDB header: sugar binding protein Chain: B: PDB Molecule: lectin; |

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| 81 | c2wq4B | Alignment | not modelled | 7.4 | 20 | PDBTitle: n-terminal domain of bc2l-c lectin from burkholderia cenocepacia |
| 82 | c3l0iA | Alignment | not modelled | 7.4 | 43 | PDB header: protein binding/protein transport Chain: A; PDB Molecule: drdra; PDBTitle: complex structure of sidm/drra with the wild type rab1 |
| 83 | c3vdlB | Alignment | not modelled | 7.3 | 17 | PDB header: cell invasion Chain: B; PDB Molecule: circumsporozoite (cs) protein; PDBTitle: crystal structure of circumsporozoite protein atsr domain, p43212 form |
| 84 | c2f2iA | Alignment | not modelled | 7.1 | 50 | PDB header: antimicrobial protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1 |
| 85 | c1zxxA | Alignment | not modelled | 6.8 | 19 | PDB header: transferase Chain: A; PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii |
| 86 | c5eznA | Alignment | not modelled | 6.8 | 33 | PDB header: immune system Chain: A; PDB Molecule: cysteine-rich protective antigen; PDBTitle: crystal structure of pfcyrpa |
| 87 | d1xrsb1 | Alignment | not modelled | 6.7 | 10 | Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain |
| 88 | d1quba1 | Alignment | not modelled | 6.6 | 23 | Fold: Complement control module/SCR domain Superfamily: Complement control module/SCR domain Family: Complement control module/SCR domain |
| 89 | c3jb9g | Alignment | not modelled | 6.6 | 42 | 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 |
| 90 | d1e57a | Alignment | not modelled | 6.6 | 50 | Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tymoviridae-like VP |
| 91 | c1hznA | Alignment | not modelled | 6.5 | 38 | 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 |
| 92 | c2mn1A | Alignment | not modelled | 6.4 | 63 | PDB header: unknown function Chain: A; PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww] |
| 93 | c1k48A | Alignment | not modelled | 6.4 | 83 | PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide |
| 94 | c1jzA | Alignment | not modelled | 6.4 | 83 | PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide |
| 95 | c3noyA | Alignment | not modelled | 6.4 | 44 | PDB header: oxidoreductase Chain: A; PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe) |
| 96 | c3t8tA | Alignment | not modelled | 6.3 | 24 | PDB header: unknown function Chain: A; PDB Molecule: staphylococcus aureus cymr (oxidized form); PDBTitle: crystal structure of staphylococcus aureus cymr oxidized form |
| 97 | d1auyb | Alignment | not modelled | 6.3 | 55 | Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tymoviridae-like VP |
| 98 | d1auya | Alignment | not modelled | 6.2 | 55 | Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tymoviridae-like VP |
| 99 | c4ttnA | Alignment | not modelled | 6.2 | 83 | PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1 |