

























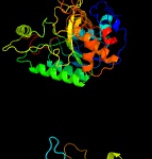
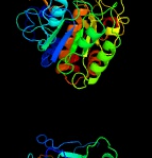





Phyre2

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|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3883c_mycP1_4363595_4364935 |
| Date | Sat Aug 10 22:05:06 BST 2019 |
| Unique Job ID | 171f7c8ebef196df |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c4j94A_ |  Alignment |  | 100.0 | 75 | PDB header: hydrolase Chain: A: PDB Molecule: membrane-anchored mycosin mycp1; PDBTitle: crystal structure of mycp1 from the esx-1 type vii secretion system |
| 2 | d1r6va_ |  Alignment |  | 100.0 | 30 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 3 | c4tr2A_ |  Alignment |  | 100.0 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: subtilisin-like 1 serine protease; PDBTitle: crystal structure of pvsu1 |
| 4 | c4kg7A_ |  Alignment |  | 100.0 | 48 | PDB header: hydrolase Chain: A: PDB Molecule: peptidase s8 and s53, subtilisin, kexin, sedolisin; PDBTitle: structure of mycp3 protease from the type vii (esx-3) secretion2 system. |
| 5 | c2oxaA_ |  Alignment |  | 100.0 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: extracellular serine protease; PDBTitle: crystal structure of serine protease of aeromonas sobria |
| 6 | c1p8jB_ |  Alignment |  | 100.0 | 22 | PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: furin precursor; PDBTitle: crystal structure of the proprotein convertase furin |
| 7 | c3vtaB_ |  Alignment |  | 100.0 | 26 | PDB header: hydrolase Chain: B: PDB Molecule: cucumisin; PDBTitle: crystal structure of cucumisin, a subtilisin-like endoprotease from2 cucumis melo l |
| 8 | c1r64A_ |  Alignment |  | 100.0 | 20 | PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: kexin; PDBTitle: the 2.2 a crystal structure of kex2 protease in complex with ac-arg-2 glu-lys-boroarg peptidyl boronic acid inhibitor |
| 9 | c3i74B_ |  Alignment |  | 100.0 | 36 | PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: subtilisin-like protease; PDBTitle: crystal structure of the plant subtilisin-like protease sbt3 in2 complex with a chloromethylketone inhibitor |
| 10 | c3qfhE_ |  Alignment |  | 100.0 | 24 | PDB header: hydrolase Chain: E: PDB Molecule: epidermin leader peptide processing serine protease epip; PDBTitle: 2.05 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) from staphylococcus aureus. |
| 11 | c1xf1A_ |  Alignment |  | 100.0 | 30 | PDB header: hydrolase Chain: A: PDB Molecule: c5a peptidase; PDBTitle: structure of c5a peptidase- a key virulence factor from2 streptococcus |

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|----|-------------------------|-----------|---|-------|----|--|
| 12 | c5xxzB_ | Alignment |  | 100.0 | 24 | PDB header: lyase Chain: B; PDB Molecule: chemokine protease c; PDBTitle: crystal structure of a serine protease from streptococcus species |
| 13 | c3t41B_ | Alignment |  | 100.0 | 23 | PDB header: hydrolase Chain: B; PDB Molecule: epidermin leader peptide processing serine protease epip; PDBTitle: 1.95 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) s393a mutant from staphylococcus3 aureus |
| 14 | c5xyrA_ | Alignment |  | 100.0 | 26 | PDB header: lyase Chain: A; PDB Molecule: chemokine protease c; PDBTitle: crystal structure of a serine protease from streptococcus species |
| 15 | c6mw4A_ | Alignment |  | 100.0 | 21 | PDB header: signaling protein Chain: A; PDB Molecule: putative germination-specific protease; PDBTitle: structure of pseudoprotease cspc from clostridioides difficile |
| 16 | c4mzdA_ | Alignment |  | 100.0 | 25 | PDB header: hydrolase Chain: A; PDB Molecule: nisin leader peptide-processing serine protease nisp; PDBTitle: high resolution crystal structure of the nisin leader peptidase nisp2 from lactococcus lactis |
| 17 | d1p8ja2 | Alignment |  | 100.0 | 21 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 18 | c2iy9A_ | Alignment |  | 100.0 | 22 | PDB header: toxin Chain: A; PDB Molecule: suba; PDBTitle: crystal structure of the a-subunit of the ab5 toxin from e.2 coli |
| 19 | c3bpsA_ | Alignment |  | 100.0 | 26 | PDB header: hydrolase/lipid transport Chain: A; PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: pcsk9:egf-a complex |
| 20 | d2id4a2 | Alignment |  | 100.0 | 21 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 21 | c4lvnA_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase/inhibitor/immune system Chain: A; PDB Molecule: subtilisin-like serine protease; PDBTitle: crystal structure of pfsb1-prodomain-nimp.m7 fab complex |
| 22 | c1wmeA_ | Alignment | not modelled | 100.0 | 26 | PDB header: hydrolase Chain: A; PDB Molecule: protease; PDBTitle: crystal structure of alkaline serine protease kp-43 from bacillus sp.2 ksm-kp43 (1.50 angstrom, 293 k) |
| 23 | c4aktB_ | Alignment | not modelled | 100.0 | 27 | PDB header: hydrolase/peptide Chain: B; PDB Molecule: thiazoline oxidase/subtilisin-like protease; PDBTitle: patg macrocylase in complex with peptide |
| 24 | c5vlpA_ | Alignment | not modelled | 100.0 | 31 | PDB header: hydrolase Chain: A; PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: pcsk9 complex with lldr antagonist peptide and fab7g7 |
| 25 | c4i0wB_ | Alignment | not modelled | 100.0 | 24 | PDB header: hydrolase Chain: B; PDB Molecule: protease cspb; PDBTitle: structure of the clostridium perfringens cspb protease |
| 26 | c2pmwB_ | Alignment | not modelled | 100.0 | 30 | PDB header: hydrolase Chain: B; PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: the crystal structure of proprotein convertase subtilisin2 kexin type 9 (pcsk9) |
| 27 | d1meeA_ | Alignment | not modelled | 100.0 | 31 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 28 | d1to2e_ | Alignment | not modelled | 100.0 | 30 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |

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| 29 | d1v6ca_ | Alignment | not modelled | 100.0 | 32 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 30 | c3whiA_ | Alignment | not modelled | 100.0 | 30 | PDB header: hydrolase Chain: A: PDB Molecule: subtilisin e; PDBTitle: crystal structure of unautoprocessed form of is1-inserted pro-2 subtilisin e |
| 31 | c3afgA_ | Alignment | not modelled | 100.0 | 30 | PDB header: hydrolase Chain: A: PDB Molecule: subtilisin-like serine protease; PDBTitle: crystal structure of pron-tk-sp from thermococcus kodakaraensis |
| 32 | d1bh6a_ | Alignment | not modelled | 100.0 | 30 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 33 | c4zoqM_ | Alignment | not modelled | 100.0 | 27 | PDB header: hydrolase Chain: M: PDB Molecule: intracellular serine protease; PDBTitle: crystal structure of a lanthipeptide protease |
| 34 | d1r0re_ | Alignment | not modelled | 100.0 | 29 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 35 | d1gcia_ | Alignment | not modelled | 100.0 | 34 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 36 | c5vIIA_ | Alignment | not modelled | 100.0 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: short pcsk9 delta-p' complex with peptide pep3 |
| 37 | d1dbia_ | Alignment | not modelled | 100.0 | 32 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 38 | c3vv3B_ | Alignment | not modelled | 100.0 | 26 | PDB header: hydrolase Chain: B: PDB Molecule: deseasin mcp-01; PDBTitle: crystal structure of deseasin mcp-01 from pseudoalteromonas sp. sm9913 |
| 39 | d1wmda2 | Alignment | not modelled | 100.0 | 23 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 40 | c5yl7A_ | Alignment | not modelled | 100.0 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: pseudoalteromonas arctica pamc 21717; PDBTitle: proteases from pseudoalteromonas arctica pamc 21717 (pro21717) |
| 41 | d1gnsa_ | Alignment | not modelled | 100.0 | 30 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 42 | d1thma_ | Alignment | not modelled | 100.0 | 30 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 43 | c3lpcA_ | Alignment | not modelled | 100.0 | 31 | PDB header: hydrolase Chain: A: PDB Molecule: aprb2; PDBTitle: crystal structure of a subtilisin-like protease |
| 44 | c2z2zA_ | Alignment | not modelled | 100.0 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: tk-subtilisin precursor; PDBTitle: crystal structure of unautoprocessed form of tk-subtilisin soaked by 2 10mm cacl2 |
| 45 | c2z2yC_ | Alignment | not modelled | 100.0 | 23 | PDB header: hydrolase Chain: C: PDB Molecule: tk-subtilisin; PDBTitle: crystal structure of autoprocessed form of tk-subtilisin |
| 46 | c2w2qA_ | Alignment | not modelled | 100.0 | 25 | PDB header: hydrolase/receptor Chain: A: PDB Molecule: proprotein convertase subtilisin/kexin type 9; PDBTitle: pcsk9-delta c d374h mutant bound to wt egf-a of ldlr |
| 47 | c3f7oB_ | Alignment | not modelled | 100.0 | 25 | PDB header: hydrolase Chain: B: PDB Molecule: serine protease; PDBTitle: crystal structure of cuticle-degrading protease from paecilomyces2 lilacinus (pl646) |
| 48 | c5z6oA_ | Alignment | not modelled | 100.0 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: protease; PDBTitle: crystal structure of penicillium cyclopium protease |
| 49 | c4aksA_ | Alignment | not modelled | 100.0 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: thiazoline oxidase/subtilisin-like protease; PDBTitle: patg macrocyclase domain |
| 50 | c4h6wB_ | Alignment | not modelled | 100.0 | 29 | PDB header: hydrolase Chain: B: PDB Molecule: n-terminal cyanobactin protease; PDBTitle: structure of prenylagaramide maturation protease paga |
| 51 | c4dzta_ | Alignment | not modelled | 100.0 | 30 | PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: aqualysin-1; PDBTitle: aqualysin i: the crystal structure of a serine protease from an2 extreme thermophile, thermus aquaticus yt-1 |
| 52 | c3lxuX_ | Alignment | not modelled | 100.0 | 31 | PDB header: hydrolase Chain: X: PDB Molecule: tripeptidyl-peptidase 2; PDBTitle: crystal structure of tripeptidyl peptidase 2 (tpp ii) |
| 53 | d2ixta1 | Alignment | not modelled | 100.0 | 24 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 54 | d2pwaa1 | Alignment | not modelled | 100.0 | 25 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Subtilases |
| 55 | c6f9mA_ | Alignment | not modelled | 100.0 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: serine protease; PDBTitle: the lipy/f-motif in an intracellular subtilisin protease is involved2 in inhibition |

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| 56 | d1sioa_ | Alignment | not modelled | 100.0 | 21 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Serine-carboxyl proteinase, SCP |
| 57 | c2x8jB_ | Alignment | not modelled | 100.0 | 22 | PDB header: hydrolase Chain: B: PDB Molecule: intracellular subtilisin protease; PDBTitle: intracellular subtilisin precursor from b. clausii |
| 58 | c2b6nA_ | Alignment | not modelled | 100.0 | 28 | PDB header: hydrolase Chain: A: PDB Molecule: proteinase k; PDBTitle: the 1.8 a crystal structure of a proteinase k like enzyme from a2 psychrotroph serratia species |
| 59 | c1s2nB_ | Alignment | not modelled | 100.0 | 30 | PDB header: hydrolase Chain: B: PDB Molecule: extracellular subtilisin-like serine proteinase; PDBTitle: crystal structure of a cold adapted subtilisin-like serine proteinase |
| 60 | c3zxxA_ | Alignment | not modelled | 100.0 | 31 | PDB header: hydrolase Chain: A: PDB Molecule: subtilisin-like protein; PDBTitle: structure of self-cleaved protease domain of pata |
| 61 | d1t1ga_ | Alignment | not modelled | 100.0 | 17 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Serine-carboxyl proteinase, SCP |
| 62 | d1ga6a_ | Alignment | not modelled | 100.0 | 19 | Fold: Subtilisin-like Superfamily: Subtilisin-like Family: Serine-carboxyl proteinase, SCP |
| 63 | c3zxyA_ | Alignment | not modelled | 100.0 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: subtilisin-like protein; PDBTitle: structure of s218a mutant of the protease domain of pata |
| 64 | c1t1eA_ | Alignment | not modelled | 100.0 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: kumamolisin; PDBTitle: high resolution crystal structure of the intact pro-2 kumamolisin, a sedolisin type proteinase (previously3 called kumamolysin or kscp) |
| 65 | c3ee6A_ | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: tripeptidyl-peptidase 1; PDBTitle: crystal structure analysis of tripeptidyl peptidase -i |
| 66 | c3edyA_ | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: tripeptidyl-peptidase 1; PDBTitle: crystal structure of the precursor form of human tripeptidyl-peptidase2 1 |
| 67 | d1k78a2 | Alignment | not modelled | 76.7 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain |
| 68 | d6paxa2 | Alignment | not modelled | 72.2 | 23 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain |
| 69 | d1mzga_ | Alignment | not modelled | 58.0 | 36 | Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like |
| 70 | d1ni7a_ | Alignment | not modelled | 57.4 | 28 | Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like |
| 71 | c2k27A_ | Alignment | not modelled | 44.1 | 19 | PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain |
| 72 | c1wloA_ | Alignment | not modelled | 33.0 | 30 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sufe protein; PDBTitle: solution structure of the hypothetical protein from thermus2 thermophilus hb8 |
| 73 | d2ga1a1 | Alignment | not modelled | 21.7 | 22 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Alr1493-like |
| 74 | d1pdnc_ | Alignment | not modelled | 15.8 | 7 | Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain |
| 75 | d1b74a1 | Alignment | not modelled | 14.9 | 30 | Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase |
| 76 | c3uhfB_ | Alignment | not modelled | 14.1 | 40 | PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from campylobacter jejuni2 subsp. jejuni |
| 77 | c1b74A_ | Alignment | not modelled | 13.0 | 30 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus |
| 78 | c3sjrB_ | Alignment | not modelled | 13.0 | 33 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved unknwn function protein cv_1783 from2 chromobacterium violaceum atcc 12472 |
| 79 | d1p3qr_ | Alignment | not modelled | 12.0 | 36 | Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain |
| 80 | c5a49l_ | Alignment | not modelled | 10.2 | 17 | PDB header: protein binding Chain: I: PDB Molecule: maternal effect protein oskar; PDBTitle: crystal structure of the lotus domain (aa 139-222) of2 drosophila oskar in c222 |
| 81 | c2jfzB_ | Alignment | not modelled | 10.0 | 40 | PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor |
| 82 | d1wglA_ | Alignment | not modelled | 8.5 | 21 | Fold: RuvA C-terminal domain-like Superfamily: UBA-like |

| | | | | Family:CUE domain | | |
|----|------------------------|-----------|--------------|-------------------|----|---|
| 83 | c6paxA | Alignment | not modelled | 8.4 | 21 | PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions |
| 84 | c4plaA | Alignment | not modelled | 8.3 | 26 | PDB header: transferase,hydrolase Chain: A: PDB Molecule: chimera protein of phosphatidylinositol 4-kinase type 2- PDBTitle: crystal structure of phosphatidyl inositol 4-kinase ii alpha in2 complex with atp |
| 85 | c2pe4A | Alignment | not modelled | 8.0 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase-1; PDBTitle: structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis |
| 86 | c1fcuA | Alignment | not modelled | 7.5 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: crystal structure (trigonal) of bee venom hyaluronidase |
| 87 | c2dhyA | Alignment | not modelled | 6.5 | 17 | PDB header: immune system Chain: A: PDB Molecule: cue domain-containing protein 1; PDBTitle: solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1) |
| 88 | d1ixsa | Alignment | not modelled | 6.4 | 17 | Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain |
| 89 | c5ijwA | Alignment | not modelled | 6.0 | 38 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase (muri) from mycobacterium smegmatis with bound d-2 glutamate, 1.8 angstrom resolution, x-ray diffraction |
| 90 | d1p3qq | Alignment | not modelled | 5.9 | 41 | Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain |
| 91 | c2dwuA | Alignment | not modelled | 5.8 | 50 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis |
| 92 | d1fcqa | Alignment | not modelled | 5.8 | 11 | Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Bee venom hyaluronidase |
| 93 | c5w16D | Alignment | not modelled | 5.7 | 50 | PDB header: isomerase Chain: D: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from thermus thermophilus in2 complex with d-glutamate |
| 94 | c2jfnA | Alignment | not modelled | 5.6 | 67 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala |
| 95 | c3hfrA | Alignment | not modelled | 5.3 | 50 | PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from listeria monocytogenes |