

Resource Summary Report

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shovill

RRID:SCR_017077

Type: Tool

Proper Citation

shovill (RRID:SCR_017077)

Resource Information

URL: <https://github.com/tseemann/shovill>

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Description: Software tool to assemble bacterial isolate genomes from Illumina paired end reads. Used for isolate data only, primarily small haploid organisms. Supports assemblers like SKESA, Velvet and Megahit.

Resource Type: data processing software, sequence analysis software, data analysis software, software resource, software application

Keywords: assembly, bacteria, isolate, genome, Illumina, paired, end, read, data, haploid, organism, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: shovill

Resource ID: SCR_017077

Alternate IDs: , biotools:shovill, BioTools:shovill

Alternate URLs: <https://bio.tools/shovill>, <https://sources.debian.org/src/shovill/>

License: GNU GPL v3

License URLs: <https://github.com/tseemann/shovill/blob/master/LICENSE>

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260731T043009+0000

Ratings and Alerts

No rating or validation information has been found for shovill.

No alerts have been found for shovill.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 445 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Buiatte ABG, et al. (2026) Genomic epidemiology reveals statewide dispersal of clinical Shiga toxin-producing *Escherichia coli* and their antimicrobial resistome. *Microbiology spectrum*, 14(1), e0095625.

Kumar V, et al. (2025) Whole genome sequencing and assembly of the house sparrow, *Passer domesticus*. *GigaByte (Hong Kong, China)*, 2025, gigabyte161.

D??ndar T, et al. (2025) Antimicrobial resistance in coagulase negative staphylococci: Genome analysis and role of horizontal gene transfer. *Research in microbiology*, 176(5-6), 104298.

Nothdurfter S, et al. (2025) Epidemiology of Tularemia among Humans and Animals, Baden-Wuerttemberg, Germany, 2012-2022. *Emerging infectious diseases*, 31(4), 678.

Alam JM, et al. (2025) Unique North American isolates of severe metastatic hypervirulent *Klebsiella pneumoniae* strain infections with hepatic abscesses seen in young patients within Texas. *PloS one*, 20(2), e0308305.

Jin Q-Y, et al. (2025) Population structure of *Helicobacter pylori* and antibiotic resistance-associated variants in a high-risk area of gastric cancer. *Journal of clinical microbiology*, 63(5), e0003325.

Krause AL, et al. (2025) Comparative and functional genomic analysis of foreign DNA defense mechanisms in *Enterococcus faecium*. *Microbiology spectrum*, 13(8), e0028925.

Luk HC, et al. (2025) Draft genomes of two *Vibrio* spp. isolated from the brown alga *Sargassum ilicifolium* in Singapore. *Microbiology resource announcements*, 14(6), e0032825.

Phumthanakorn N, et al. (2025) Prevalence and antimicrobial resistance of methicillin-resistant and methicillin-susceptible *Staphylococcus* in small- to medium-scale and large-scale dairy farms in Thailand. *Translational animal science*, 9, txaf081.

Serna C, et al. (2025) Global dissemination of *npmA* mediated pan-aminoglycoside resistance via a mobile genetic element in Gram-positive bacteria. *Nature communications*, 16(1), 6360.

Olowo-Okere A, et al. (2025) Draft genome sequence of an *Acinetobacter courvalinii* isolate from Africa. *Microbiology resource announcements*, 14(8), e0050125.

Bosica S, et al. (2025) Genomic epidemiology of a *Bacillus cereus* bacteraemia outbreak linked to contaminated hospital laundry. *Microbial genomics*, 11(9).

Miller H, et al. (2025) Development and validation of a core-genome multilocus sequence typing scheme for *Legionella longbeachae*. *Microbial genomics*, 11(9).

Cheng HR, et al. (2025) Genomic analysis of the *Streptococcus pneumoniae* in Taiwan: a nationwide study from 2006 to 2022. *Microbial genomics*, 11(9).

Morohoshi T, et al. (2025) Draft genome sequences of two strains of *Pseudomonas fluorescens sensu stricto* isolated from strawberry in Japan. *Microbiology resource announcements*, 14(10), e0062025.

Dziegiel AH, et al. (2025) Metagenomic identification of disease-causing *Salmonella enterica* serovars and antimicrobial resistance genes from paediatric faecal samples. *Microbial genomics*, 11(10).

Kaestli M, et al. (2025) High genomic diversity of *Vibrio parahaemolyticus* from underexplored tropical northern Australia: a baseline for future surveillance. *Microbial genomics*, 11(10).

Batista CSP, et al. (2025) Community-Onset Fungemias: Epidemiology and Genomic Characterization at a Tertiary-Care Hospital in Barcelona, Spain. *Journal of fungi (Basel, Switzerland)*, 11(11).

Melzer F, et al. (2025) Genomic epidemiology of *Brucella suis* biovar 2 in German swine and wildlife, 2003-2023. *Frontiers in veterinary science*, 12, 1611681.

Free M, et al. (2025) Evolution of strain diversity and virulence factor repertoire in pediatric *Staphylococcus aureus* isolates. *PloS one*, 20(7), e0326353.