

Resource Summary Report

Generated by [NIF](#) on Aug 25, 2026

shovill

RRID:SCR_017077

Type: Tool

Proper Citation

shovill (RRID:SCR_017077)

Resource Information

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

Proper Citation: shovill (RRID:SCR_017077)

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 analysis software, data processing software, sequence analysis software, software application, software resource

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: 20260821T194103+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 587 mentions in open access literature.

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

Lu Q, et al. (2026) Genomic characterization and pathogenicity validation of *Mycoplasma ovipneumoniae* strains from diseased sheep: insights into potential pathogenic mechanisms of GSWW364. *Veterinary research*, 57(1).

Swiatek L-S, et al. (2026) Genomic and functional characterization of the L?sorbose phosphotransferase system in high-risk *Escherichia coli* lineages. *mSystems*, 11(1), e0127425.

Raro OHF, et al. (2026) In vitro selection of cefiderocol-resistant mutants in *Acinetobacter baumannii* harbouring the most common carbapenemase genes. *The Journal of antimicrobial chemotherapy*, 81(1).

Neumann T, et al. (2026) Draft genome sequences of three multidrug-resistant *Klebsiella pneumoniae* strains isolated from alfalfa sprouts in Germany. *Microbiology resource announcements*, 15(2), e0127025.

Costa LRM, et al. (2026) Five-decade global expansion of *Staphylococcus argenteus* ST2250 shapes antimicrobial resistance dynamics. *npj antimicrobials and resistance*, 4(1).

Eilers T, et al. (2026) Pangenome-based design of strain-specific primers enables precise monitoring of bacteria in human microbiome intervention trials. *Scientific reports*, 16(1).

Mataseje LF, et al. (2026) Mechanisms of fosfomycin resistance observed in clinical isolates of *Escherichia coli* from Canada: CANWARD 2007-2022. *JAC-antimicrobial resistance*, 8(1), dlag020.

Wang C, et al. (2026) Taxonomic landscape of the *Mycobacterium* "Fortuitum-Vaccae" clade: a genome study. *Frontiers in microbiology*, 17, 1728622.

Ni H, et al. (2026) Enhanced Spread of Carbapenem-Resistant *Pseudomonas aeruginosa* in ICU Environment During a COVID-19 Upsurge Period in China. *Infection and drug resistance*, 19, 562352.

Beh JQ, et al. (2026) Global dissemination of *optrA*-mediated linezolid resistance in enterococci. *The Journal of antimicrobial chemotherapy*, 81(4).

Silcocks M, et al. (2026) Dormancy regulon reduction was pivotal to the evolution of *Mycobacterium tuberculosis*. *Nature communications*, 17(1).

Bao D, et al. (2026) Genomic characterization of extended-spectrum β -Lactamases (ESBLs)-producing *Escherichia coli* recovered from bloodstream infections in China. *BMC microbiology*, 26(1).

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.

Mboowa G, et al. (2026) Multicountry genomic analysis underscores regional cholera spread in Africa. *Nature communications*, 17(1).

Yuan B, et al. (2026) Rapid Detection of *Vibrio vulnificus* with Recombinase Polymerase Amplification Assays Based on Specific Sequence Tags of Core Genome. *Microorganisms*, 14(2).

Projahn M, et al. (2026) Draft genomes of two *Escherichia marmotae* strains isolated from animal feces from a grain field in Germany. *Microbiology resource announcements*, 15(5), e0136525.

Mondéjar L, et al. (2026) Characterizing *Aeromonas* spp. as a Potential Sentinel Organism for Antimicrobial Resistance Dissemination in Wastewater and Drinking Water Treatment Systems: A Case Study in the Barcelona Metropolitan Area, Spain. *Antibiotics* (Basel, Switzerland), 15(3).

Chihara K, et al. (2026) Phage homing endonuclease amplifies anti-defense genes to evade bacterial immunity. *Nature communications*, 17(1).

Maqbool M, et al. (2026) Exploration of the genomic diversity of third-generation cephalosporin-resistant *Escherichia coli* in Australian clinical settings. *Microbial genomics*, 12(1).

Bernier A-M, et al. (2026) Complete genome of a *Corynebacterium ulcerans* clinical isolate with two novel toxin gene alleles isolated from a leg ulcer. *Microbiology resource announcements*, 15(1), e0085725.