# **Resource Summary Report**

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# <u>shovill</u>

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

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

Funding:

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

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## **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 354 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Negrete-Méndez H, et al. (2025) A Lambda-evo (?evo) phage platform for Zika virus EDIII protein display. Applied microbiology and biotechnology, 109(1), 8.

Horsman S, et al. (2025) Molecular Epidemiological Characteristics of Staphylococcus pseudintermedius, Staphylococcus coagulans, and Coagulase-Negative Staphylococci Cultured from Clinical Canine Skin and Ear Samples in Queensland. Antibiotics (Basel, Switzerland), 14(1).

Tang PYP, et al. (2025) Draft genomes of two Roseibium spp. isolated from the coral Pachyseris speciosa from a Singaporean reef. Microbiology resource announcements, 14(1), e0076524.

Li C, et al. (2025) Naturally occurring influenza reassortment in pigs facilitates the emergence of intrahost virus subpopulations with distinct genotypes and replicative fitness. mBio, 16(1), e0192424.

Brodíková K, et al. (2025) Clonal Complex 398 Methicillin-Resistant Staphylococcus aureus Producing Panton-Valentine Leukocidin, Czech Republic, 2023. Emerging infectious diseases, 31(1), 174.

Larsen AL, et al. (2025) Hospital toilets and drainage systems as a reservoir for a long-term polyclonal outbreak of clinical infections with multidrug-resistant Klebsiella oxytoca species complex. Infection prevention in practice, 7(1), 100430.

Olagoke O, et al. (2025) Whole-genome automated assembly pipeline for Chlamydia trachomatis strains from reference, in vitro and clinical samples using the integrated CtGAP

pipeline. NAR genomics and bioinformatics, 7(1), Iqae187.

Tamura A, et al. (2024) Synthetic phage-based approach for sensitive and specific detection of Escherichia coli O157. Communications biology, 7(1), 535.

Ba X, et al. (2024) Global emergence of a hypervirulent carbapenem-resistant Escherichia coli ST410 clone. Nature communications, 15(1), 494.

Findlay J, et al. (2024) Molecular analysis of metallo-beta-lactamase-producing Pseudomonas aeruginosa in Switzerland 2022-2023. European journal of clinical microbiology & infectious diseases : official publication of the European Society of Clinical Microbiology, 43(3), 551.

Silva EC, et al. (2024) Molecular Characterization and Genome Mechanical Features of Two Newly Isolated Polyvalent Bacteriophages Infecting Pseudomonas syringae pv. garcae. Genes, 15(1).

Urso A, et al. (2024) Staphylococcus aureus adapts to exploit collagen-derived proline during chronic infection. Nature microbiology, 9(10), 2506.

Sánchez-Osuna M, et al. (2024) Genomic analysis of Staphylococcus aureus isolates from bacteremia reveals genetic features associated with the COVID-19 pandemic. iScience, 27(8), 110402.

Saidenberg ABS, et al. (2024) Escherichia coli ST117: exploring the zoonotic hypothesis. Microbiology spectrum, 12(10), e0046624.

Chong SKT, et al. (2024) Analysis of global Aeromonas caviae genomes revealed that strains carrying T6SS are more common in human gastroenteritis than in environmental sources and are often phylogenetically related. Microbial genomics, 10(5).

Khawaja T, et al. (2024) Deep sequencing of Escherichia coli exposes colonisation diversity and impact of antibiotics in Punjab, Pakistan. Nature communications, 15(1), 5196.

Soro O, et al. (2024) Complete genome sequences of 12 lytic phages against multidrugresistant Enterococcus faecalis. Microbiology resource announcements, 13(10), e0068724.

Gélinas V, et al. (2024) Whole-genome-based taxonomy as the most accurate approach to identify Flavobacterium species. FEMS microbiology letters, 371.

Bao D, et al. (2024) Genomic epidemiology of ceftriaxone-resistant non-typhoidal Salmonella enterica strain in China. BMC genomics, 25(1), 974.

Loh AAR, et al. (2024) Draft genome of a Pseudovibrio sp. isolated from the skeleton of Pachyseris speciosa from a Singaporean reef. Microbiology resource announcements, 13(11), e0076324.