

# Resource Summary Report

Generated by NIF on Apr 29, 2025

## assembly-stats

RRID:SCR\_023963

Type: Tool

### Proper Citation

assembly-stats (RRID:SCR\_023963)

### Resource Information

**URL:** <https://github.com/sanger-pathogens/assembly-stats>

**Proper Citation:** assembly-stats (RRID:SCR\_023963)

**Description:** Software to get assembly statistics from FASTA and FASTQ files.

**Resource Type:** source code, software resource

**Keywords:** assembly statistics, FASTA file, FASTQ files,

**Funding:**

**Availability:** Free, Available for download, Freely available

**Resource Name:** assembly-stats

**Resource ID:** SCR\_023963

**Alternate URLs:** <https://sources.debian.org/src/assembly-stats/>

**License:** GPLv3

**Record Creation Time:** 20230824T050210+0000

**Record Last Update:** 20250428T054403+0000

### Ratings and Alerts

No rating or validation information has been found for assembly-stats.

No alerts have been found for assembly-stats.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Watt AE, et al. (2025) Parameters for one health genomic surveillance of Escherichia coli from Australia. *Nature communications*, 16(1), 17.

Hirsch AM, et al. (2025) Complete genomes of *Mucilaginibacter sabulilitoris* SNA2 and *Mucilaginibacter* sp. cycad4: microbes with the potential for plant growth promotion. *Microbiology resource announcements*, 14(1), e0062624.

Flack N, et al. (2024) The genome of Przewalski's horse (*Equus ferus przewalskii*). *bioRxiv* : the preprint server for biology.

Kileeg Z, et al. (2024) Chromosome-Scale Assembly and Annotation of Eight *Arabidopsis thaliana* Ecotypes. *Genome biology and evolution*, 16(8).

Zhang Y, et al. (2024) Transcription factor PagMYB31 positively regulates cambium activity and negatively regulates xylem development in poplar. *The Plant cell*, 36(5), 1806.

Wang D, et al. (2024) Improved assembly of the *Pungitius pungitius* reference genome. *G3* (Bethesda, Md.), 14(8).

Costa AR, et al. (2024) Accumulation of defense systems in phage-resistant strains of *Pseudomonas aeruginosa*. *Science advances*, 10(8), eadj0341.

Hirsch AM, et al. (2024) Complete genomes of two *Variovorax* endophytes isolated from surface-sterilized alfalfa nodules. *Microbiology resource announcements*, 13(8), e0033624.

Zhang X, et al. (2024) Temporal genomics in Hawaiian crickets reveals compensatory intragenomic coadaptation during adaptive evolution. *Nature communications*, 15(1), 5001.

Rissi DV, et al. (2024) Comparative Genomics of Different Lifestyle Fungi in Helotiales (Leotiomycetes) Reveals Temperature and Ecosystem Adaptations. *Journal of fungi* (Basel, Switzerland), 10(12).

Wang T, et al. (2024) Genomic Anatomy of Homozygous XX Females and YY Males Reveals Early Evolutionary Trajectory of Sex-determining Gene and Sex Chromosomes in Silurus Fishes. *Molecular biology and evolution*, 41(8).

Sterzi L, et al. (2024) Genetic barriers more than environmental associations explain *Serratia marcescens* population structure. *Communications biology*, 7(1), 468.

McHugh MP, et al. (2024) Consideration of within-patient diversity highlights transmission pathways and antimicrobial resistance gene variability in vancomycin-resistant *Enterococcus faecium*. *The Journal of antimicrobial chemotherapy*, 79(3), 656.

Flack N, et al. (2024) The genome of Przewalski's horse (*Equus ferus przewalskii*). *G3 (Bethesda, Md.)*, 14(8).

Morales AE, et al. (2024) Distinct Genes with Similar Functions Underlie Convergent Evolution in Myotis Bat Ecomorphs. *Molecular biology and evolution*, 41(9).

Wy S, et al. (2024) A chromosome-level genome assembly of the Korean minipig (*Sus scrofa*). *Scientific data*, 11(1), 840.

Santos AJDC, et al. (2024) Genomic analysis of *Oceanotoga teriensis* strain UFV\_LIMV02, a multidrug-resistant thermophilic bacterium isolated from an offshore oil reservoir. *Access microbiology*, 6(8).

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.

Wiersma AT, et al. (2024) k-mer genome-wide association study for anthracnose and BCMV resistance in a *Phaseolus vulgaris* Andean Diversity Panel. *The plant genome*, 17(4), e20523.

Hirsch AM, et al. (2024) Complete genome of *Variovorax* sp. EBFNA2, isolated from a surface-sterilized fava bean nodule. *Microbiology resource announcements*, 13(12), e0076224.