

Resource Summary Report

Generated by [NIF](#) on Jul 31, 2026

[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: software resource, source code

Keywords: assembly statistics, FASTA file, FASTQ files,

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: 20260731T043153+0000

Ratings and Alerts

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

No alerts have been found for assembly-stats.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 36 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.

Lynch RC, et al. (2025) Domesticated cannabinoid synthases amid a wild mosaic cannabis pangenome. *Nature*, 643(8073), 1001.

Foysal MJ, et al. (2025) The impact of anthropogenic activities on antimicrobial and heavy metal resistance in aquatic environments. *Applied and environmental microbiology*, 91(4), e0231724.

Cheng L, et al. (2025) Leveraging a phased pangenome for haplotype design of hybrid potato. *Nature*, 640(8058), 408.

Kollar LM, et al. (2025) The Evolution of Locally Adaptive Chromosome Inversions in *Mimulus guttatus*. *Molecular ecology*, 34(20), e17708.

Gunsalus RP, et al. (2025) Whole genome sequence of the syntrophic benzoate-degrading bacterium, *Syntrophus buswellii* DSM 102354T. *Microbiology resource announcements*, 14(9), e0026625.

Marturano G, et al. (2025) SmithRNAs: A Common Feature among Metazoa. *Genome biology and evolution*, 17(11).

Chaguza C, et al. (2025) The capsule and genetic background, rather than specific individual loci, strongly influence in vitro pneumococcal growth kinetics. *eLife*, 14.

Khalaf A, et al. (2025) Forty new genomes shed light on sexual reproduction and the origin of tetraploidy in Microsporidia. *PLoS biology*, 23(10), e3003446.

Behling W, et al. (2025) Genetic basis for broad interspecific compatibility in *Solanum verrucosum*. *The Plant journal : for cell and molecular biology*, 123(4), e70426.

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.

Ritter EJ, et al. (2025) The assembly and annotation of two teinturier grapevine varieties, Dakapo and Rubired. *GigaByte (Hong Kong, China)*, 2025, gigabyte149.

Cassens J, et al. (2025) The genome of the American dog tick (*Dermacentor variabilis*). *G3 (Bethesda, Md.)*, 15(8).

Cassens J, et al. (2025) The Genome of the American Dog Tick (*Dermacentor variabilis*). *bioRxiv : the preprint server for biology*.

Humm E, et al. (2025) Complete genomes of the hydrogenotrophic methanogen species-*Methanospirillum stamsii* Pt1 and *Methanospirillum lacunae* Ki8-1. *Microbiology resource announcements*, 14(10), e0073625.

Lecomte L, et al. (2025) Chromosome-level genome assembly of a doubled haploid brook trout (*Salvelinus fontinalis*). *G3 (Bethesda, Md.)*, 15(6).

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

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

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

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