

Resource Summary Report

Generated by [RRID](#) on Aug 2, 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: source code, software resource

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: 20260801T191248+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 [RRID](#) .

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.