Resource Summary Report

Generated by Kravitz on Sep 10, 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: 20260905T133437+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 50 mentions in open access literature.

Listed below are recent publications. The full list is available at Kravitz .

Zeng Z, et al. (2026) Highly heterozygous Citrus changshan-huyou Y. B. Chang originated from ancient hybridization between mandarin and pummelo and displayed distinct tissue-specific allelic imbalance. The plant genome, 19(2), e70232.

Ha SM, et al. (2026) Genomes of Syntrophomonas erecta GB4-38T and Syntrophomonas erecta subsp. sporosyntropha 5-3-ZT that degrade C4-8 short-chain fatty acids. Microbiology resource announcements, 15(3), e0141925.

Dias GR, et al. (2026) Gems From the Caves: Genomic Insights Into the Biosynthetic Potential of Antimicrobial-Producing Bacteria Associated With Tropical Cave-Dwelling Sponges. Environmental microbiology, 28(1), e70244.

Körnig J, et al. (2026) Genetic Variation in Chemical Defence Affects Protection of an Herbivorous Insect Against Predation. Molecular ecology, 35(9), e70363.

Möllmann JS, et al. (2026) A Chromosome-Level Genome Assembly and Resequencing Data Reveal Low DNA Methylation and Reduced Diversity in the Solitary Bee Pollinator Osmia cornuta. Genome biology and evolution, 18(1).

Humm E, et al. (2026) Whole genome sequence of the syntrophic fatty acid-degrading bacterium Syntrophomonas curvata GB8-1T. Microbiology resource announcements, 15(3), e0152525.

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.

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

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

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).

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.

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.

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

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). bioRxiv : the preprint server for biology.