

Resource Summary Report

Generated by [RRID](#) on Aug 11, 2026

[gfastats](#)

RRID:SCR_026368

Type: Tool

Proper Citation

gfastats (RRID:SCR_026368)

Resource Information

URL: <https://github.com/vgl-hub/gfastats>

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Description: Standalone tool to compute assembly summary statistics and manipulate assembly sequences in FASTA, FASTQ or GFA [.gz] format. Gfastats stores assembly sequences internally in a GFA-like format. This feature allows gfastats to seamlessly convert FAST* to and from GFA [.gz] files. Gfastats can also build an assembly graph that can in turn be used to manipulate the underlying sequences following instructions provided by the user, while simultaneously generating key metrics for the new sequences.

Resource Type: source code, software resource

Defining Citation: [PMID:35799367](#)

Keywords: summary statistics, genome assembly file manipulation, fasta, fastq, gfa, file conversion,

Funding: Rockefeller University ;
German National Research Data Initiative

Availability: Free, Available for download, Freely available

Resource Name: gfastats

Resource ID: SCR_026368

License: MIT license

Record Creation Time: 20250204T060303+0000

Record Last Update: 20260810T040904+0000

Ratings and Alerts

No rating or validation information has been found for gfastats.

No alerts have been found for gfastats.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 55 mentions in open access literature.

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

Fletcher C, et al. (2025) The genome sequence of the European smelt, *Osmerus eperlanus* (Linnaeus, 1758). Wellcome open research, 10, 118.

Mitchell R, et al. (2025) The genome sequence of a soldier beetle, *Malthinus seriepunctatus* Kiesenwetter, 1851. Wellcome open research, 10, 80.

Hutchinson F, et al. (2025) The genome sequence of the Maple Pug moth, *Eupithecia inturbata* (Hübner, 1817). Wellcome open research, 10, 141.

Willink B, et al. (2025) The genome sequence of the Tropical Bluetail Damselfly, *Ischnura senegalensis* (Rambur, 1842). Wellcome open research, 10, 104.

Falk S, et al. (2025) The genome sequence of the Coppice Mining Bee, *Andrena helvola* (Linnaeus, 1758). Wellcome open research, 10, 102.

Boyes D, et al. (2025) The genome sequence of the Warty Knot-Horn moth, *Acrobasis repandana* Fabricius, 1798. Wellcome open research, 10, 50.

Geiser MF, et al. (2025) The genome sequence of a flea beetle, *Neocrepidodera transversa* (Marsham, 1802). Wellcome open research, 10, 62.

Crowley LM, et al. (2025) The genome sequence of a snail-killing fly, *Dichetophora oblitterata* (Fabricius, 1805). Wellcome open research, 10, 176.

Sivell D, et al. (2025) The genome sequence of a carabid beetle, *Carabus problematicus* Herbst, 1786. Wellcome open research, 10, 59.

Wangwiwatsin A, et al. (2025) The genome sequence of the liver fluke *Opisthorchis viverrini* (Poirier, 1886) Stiles & Hassall, 1896. Wellcome open research, 10, 1.

Sivell O, et al. (2025) The genome sequence of the Small Red Damselfly, *Ceragrion tenellum* (de Villers, 1789). Wellcome open research, 10, 79.

Bein B, et al. (2025) Long-read sequencing and genome assembly of natural history collection samples and challenging specimens. *Genome biology*, 26(1), 25.

Sivell D, et al. (2025) The genome sequence of the click beetle, *Ampedus sanguinolentus* (*Schrank, 1776*). Wellcome open research, 10, 96.

Volpe E, et al. (2025) The reference genome of the human diploid cell line RPE-1. *Nature communications*, 16(1), 7751.

Arshad F, et al. (2025) A comprehensive water buffalo pangenome reveals extensive structural variation linked to population-specific signatures of selection. *GigaScience*, 14.

Rammou DL, et al. (2025) The genome sequence of the European ground squirrel, *Spermophilus citellus* (*Linnaeus, 1766*). Wellcome open research, 10, 184.

Barclay MVL, et al. (2025) The genome sequence of a bark-dwelling beetle, *Silvanus unidentatus* (*Olivier, 1790*). Wellcome open research, 10, 136.

Sivell O, et al. (2025) The genome sequence of the Common Sheetweb Spider *Linyphia triangularis* (*Clerck, 1757*). Wellcome open research, 10, 92.

Hesson JC, et al. (2025) A chromosomal reference genome sequence for the northern house mosquito, *Culex pipiens form pipiens*, *Linnaeus, 1758*. Wellcome open research, 10, 107.

Falk S, et al. (2025) The genome sequence of a long-legged fly, *Scellus notatus* (*Fabricius, 1781*). Wellcome open research, 10, 117.