

Resource Summary Report

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[gffread](#)

RRID:SCR_018965

Type: Tool

Proper Citation

gffread (RRID:SCR_018965)

Resource Information

URL: <http://ccb.jhu.edu/software/stringtie/gff.shtml>

Proper Citation: gffread (RRID:SCR_018965)

Description: Open source software tool to manipulate files in GFF format. Used to convert, sort, filter, transform, or cluster genomic features.

Synonyms: General Feature Format Read, GFF Read

Resource Type: software resource, software application, data processing software

Defining Citation: [DOI:10.12688/f1000research.23297.1](https://doi.org/10.12688/f1000research.23297.1)

Keywords: Gene annotation, transcriptome analysis, GFF file format, convert, sort, filter, transform, cluster genomic feature

Availability: Free, Available for download, Freely available

Resource Name: gffread

Resource ID: SCR_018965

Alternate IDs: OMICS_28050

Alternate URLs: <https://github.com/gpertea/gffread>,
<https://sources.debian.org/src/gffread/>

License: MIT License

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260801T190850+0000

Ratings and Alerts

No rating or validation information has been found for gffread .

No alerts have been found for gffread .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Fu Y, et al. (2025) Evidence for evolution of a new sex chromosome within the haploid-dominant Marchantiales plant lineage. *Journal of integrative plant biology*, 67(6), 1533.

Movilli A, et al. (2025) Long-read detection of transposable element mobilization in the soma of hypomethylated *Arabidopsis thaliana* individuals. *Genome biology*, 26(1), 231.

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

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

Chen M, et al. (2025) The genome of *Hippophae salicifolia* provides new insights into the sexual differentiation of sea buckthorn. *GigaScience*, 14.

Yuan X, et al. (2025) BBSome deficiency in *Lotmaria passim* reveals divergent functions in trypanosomatid parasites. *Parasites & vectors*, 18(1), 60.

Bacchetti R, et al. (2025) *Cryptosporidium* oocyst wall proteins are true components of the oocyst wall and COWP8 is not required for parasite transmission. *PLoS pathogens*, 21(10), e1013561.

Willis CRG, et al. (2025) Chronic alcohol intake elicits distinct multi-omic profiles in the liver versus skeletal muscle of mice. *bioRxiv : the preprint server for biology*.

Song G, et al. (2024) Identification and Expression Analysis of R2R3-MYB Transcription Factors Associated with Flavonoid Biosynthesis in *Panax quinquefolius*. *International journal of molecular sciences*, 25(7).

Shippy TD, et al. (2024) Diaci v3.0: chromosome-level assembly, de novo transcriptome, and manual annotation of *Diaphorina citri*, insect vector of Huanglongbing. *GigaScience*, 13.

Mansueto L, et al. (2024) Building a community-driven bioinformatics platform to facilitate *Cannabis sativa* multi-omics research. *GigaByte (Hong Kong, China)*, 2024, gigabyte137.

Wang L, et al. (2024) Asteraceae genome database: a comprehensive platform for Asteraceae genomics. *Frontiers in plant science*, 15, 1445365.

Fernandez O, et al. (2023) The Combination of Both Heat and Water Stresses May Worsen *Botryosphaeria* Dieback Symptoms in Grapevine. *Plants (Basel, Switzerland)*, 12(4).

Bernot JP, et al. (2022) Chromosome-level genome assembly, annotation, and phylogenomics of the gooseneck barnacle *Pollicipes pollicipes*. *GigaScience*, 11.

L??tter A, et al. (2022) Haplogenome assembly reveals structural variation in *Eucalyptus* interspecific hybrids. *GigaScience*, 12.

da Silva EMG, et al. (2022) Identification of Novel Genes and Proteoforms in *Angiostrongylus costaricensis* through a Proteogenomic Approach. *Pathogens (Basel, Switzerland)*, 11(11).

Xiao C, et al. (2021) Whole-Transcriptome Analysis of Preadipocyte and Adipocyte and Construction of Regulatory Networks to Investigate Lipid Metabolism in Sheep. *Frontiers in genetics*, 12, 662143.

Tinti M, et al. (2021) Polysomal mRNA Association and Gene Expression in *Trypanosoma brucei*. *Wellcome open research*, 6, 36.

Wu Y, et al. (2021) DWV Infection in vitro Using Honey Bee Pupal Tissue. *Frontiers in microbiology*, 12, 631889.

Chen S, et al. (2021) Transcriptome Analysis Reveals Differentially Expressed Genes and Long Non-coding RNAs Associated With Fecundity in Sheep Hypothalamus With Different *FecB* Genotypes. *Frontiers in cell and developmental biology*, 9, 633747.