

Resource Summary Report

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Genome Annotation Generator

RRID:SCR_016053

Type: Tool

Proper Citation

Genome Annotation Generator (RRID:SCR_016053)

Resource Information

URL: <https://github.com/genomeannotation/GAG>

Proper Citation: Genome Annotation Generator (RRID:SCR_016053)

Description: Command line program to read, modify, annotate and generate genomic data. Can write files to .gff3 or to the NCBI's .tbl format.

Abbreviations: GAG

Synonyms: gag.py

Resource Type: data processing software, sequence analysis software, data analysis software, source code, software resource, software application

Keywords: genome, annotation, tbl, ncbi, command, line, code, modify, read, annotate, gff3, bio.tools

Availability: Free, Available for download

Resource Name: Genome Annotation Generator

Resource ID: SCR_016053

Alternate IDs: biotools:gag

Alternate URLs: <https://bio.tools/gag>

License: MIT License

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260731T043006+0000

Ratings and Alerts

No rating or validation information has been found for Genome Annotation Generator.

No alerts have been found for Genome Annotation Generator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Stankiewicz KH, et al. (2025) Genomic comparison of the temperate coral *Astrangia poculata* with tropical corals yields insights into winter quiescence, innate immunity, and sexual reproduction. *G3* (Bethesda, Md.), 15(4).

Lee SJ, et al. (2024) Chromosome-level genome assembly and annotation of the Patagonian toothfish *Dissostichus eleginoides*. *Scientific data*, 11(1), 1240.

Cho M, et al. (2024) An Antarctic lichen isolate (*Cladonia borealis*) genome reveals potential adaptation to extreme environments. *Scientific reports*, 14(1), 1342.

Schultz DT, et al. (2024) Acceleration of genome rearrangement in clitellate annelids. *bioRxiv : the preprint server for biology*.

Li JX, et al. (2023) Genomic virulence features of *Beauveria bassiana* as a biocontrol agent for the mountain pine beetle population. *BMC genomics*, 24(1), 390.

Lee SJ, et al. (2023) A chromosome-level reference genome of the Antarctic blackfin icefish *Chaenocephalus aceratus*. *Scientific data*, 10(1), 657.

Li J, et al. (2022) Foster thy young: enhanced prediction of orphan genes in assembled genomes. *Nucleic acids research*, 50(7), e37.

Gostin?ar C, et al. (2022) Clonality, inbreeding, and hybridization in two extremotolerant black yeasts. *GigaScience*, 11.

Sottolano CJ, et al. (2022) Nebulous without white: annotated long-read genome assembly and CRISPR/Cas9 genome engineering in *Drosophila nebulosa*. *G3* (Bethesda, Md.), 12(11).

Zajc J, et al. (2022) From Glaciers to Refrigerators: the Population Genomics and Biocontrol Potential of the Black Yeast *Aureobasidium subglaciale*. *Microbiology spectrum*, 10(4), e0145522.

Ghosh Dasgupta M, et al. (2021) Draft genome of *Korthalsia laciniosa* (Griff.) Mart., a climbing rattan elucidates its phylogenetic position. *Genomics*, 113(4), 2010.

Kioukis A, et al. (2020) Intraspecific diversification of the crop wild relative *Brassica cretica* Lam. using demographic model selection. *BMC genomics*, 21(1), 48.

Fouret J, et al. (2020) Sequencing the Genome of Indian Flying Fox, Natural Reservoir of Nipah Virus, Using Hybrid Assembly and Conservative Secondary Scaffolding. *Frontiers in microbiology*, 11, 1807.

Nguyen HDT, et al. (2019) Genome sequencing and comparison of five *Tilletia* species to identify candidate genes for the detection of regulated species infecting wheat. *IMA fungus*, 10, 11.

Gostin?ar C, et al. (2019) Fifty *Aureobasidium pullulans* genomes reveal a recombining polyextremotolerant generalist. *Environmental microbiology*, 21(10), 3638.

Geib SM, et al. (2018) Genome Annotation Generator: a simple tool for generating and correcting WGS annotation tables for NCBI submission. *GigaScience*, 7(4), 1.

Moore GG, et al. (2018) Genome sequence of an aflatoxigenic pathogen of Argentinian peanut, *Aspergillus arachidicola*. *BMC genomics*, 19(1), 189.