Resource Summary Report

Generated by RRID on Apr 28, 2025

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

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

Funding:

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: 20250428T053940+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 16 mentions in open access literature.

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

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

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

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

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

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.

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

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.

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).

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

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.

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

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.