

# Resource Summary Report

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## **BRAKER**

RRID:SCR\_018964

Type: Tool

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### Proper Citation

BRAKER (RRID:SCR\_018964)

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### Resource Information

**URL:** <https://github.com/Gaius-Augustus/BRAKER>

**Proper Citation:** BRAKER (RRID:SCR\_018964)

**Description:** Software tool as pipeline for accurate and automated gene prediction in novel eukaryotic genomes. Automated gene prediction training and gene prediction pipeline. BRAKER1 is eukaryotic genome annotation pipeline. BRAKER2 is extension of BRAKER1 which allows for fully automated training of gene prediction tools GeneMark EX R14, R15, R17, F1 and AUGUSTUS from RNA Seq and/or protein homology information, and that integrates extrinsic evidence from RNA-Seq and protein homology information into prediction.

**Synonyms:** BRAKER2, BRAKER1

**Resource Type:** simulation software, software application, software resource

**Defining Citation:** [PMID:31020555](#), [DOI:10.1101/2020.08.10.245134](#)

**Keywords:** Automated gene prediction, novel eukaryotic genomes, gene prediction training, gene prediction pipeline, protein coding gene structure, gene structure prediction, eukaryotic genome, RNA-Seq, protein homology

**Funding:** German Research Foundation ;  
NHGRI HG000783

**Availability:** Free, Available for download, Freely available

**Resource Name:** BRAKER

**Resource ID:** SCR\_018964

**Alternate IDs:** OMICS\_10582

**Alternate URLs:** <https://sources.debian.org/src/braker/>

**Record Creation Time:** 20220129T080342+0000

**Record Last Update:** 20260829T182617+0000

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## Ratings and Alerts

No rating or validation information has been found for BRAKER.

No alerts have been found for BRAKER.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 531 mentions in open access literature.

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

Zhang J, et al. (2026) A Set of Novel Venom Proteins Enables Parasitoid Wasps to Exploit Older Hosts and Coexist with Competitors. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(4), e12654.

Sedaghatkish A, et al. (2026) A contamination-reduced genome of *Plasmodiophora brassicae* with comprehensive functional annotation. *BMC microbiology*, 26(1), 118.

Cortolezzis Y, et al. (2026) RPA hyperphosphorylation hinders the resolution of R-loops and G-quadruplex-associated R-loops during RAS-driven senescence. *Nucleic acids research*, 54(7).

Mao X, et al. (2026) Sex chromosome evolution mediated by a large inversion and a possible switch of the sex determination gene. *Genome biology*, 27(1).

Yang M, et al. (2026) Chromosome-level genome assemblies of the pink snow mold pathogens *Microdochium majus* and *Microdochium nivale*. *Scientific data*, 13(1).

Stephens TG, et al. (2026) Cosmopolitan Gene Families With Known Functions Are Hotspots for the Evolution of Novel Genes in Stony Corals. *Genome biology and evolution*, 18(4).

Krüsemer R, et al. (2026) Experimental *Sodalis* infection eliminates ancient insect symbiont. *Nature communications*, 17(1).

Holt CI, et al. (2026) Gene regulation in response to host sex and infection route in *Brugia pahangi* with new genome annotation. *G3* (Bethesda, Md.), 16(6).

Fiesinger A, et al. (2026) The genome of the reef-building coral *Porites harrisoni* from the southern Persian/Arabian Gulf. *GigaByte* (Hong Kong, China), 2026, gigabyte174.

Kippes N, et al. (2026) Layer-specific genetic variation unlocks secondary metabolite diversity in long-lived clonal peppermint. *Proceedings of the National Academy of Sciences of the United States of America*, 123(21), e2532794123.

Kudoh A, et al. (2026) Whole-genome sequencing reveals a possible molecular basis of sex determination in the dioecious wild yam *Dioscorea tokoro*. *PLoS genetics*, 22(4), e1012123.

Horá?ek N, et al. (2026) Expansion of the geranylgeranyl pyrophosphate synthase gene family underlies the evolution of terpenoid biosynthesis in termites. *PLoS biology*, 24(4), e3003648.

Kataoka K, et al. (2026) Temporal orchestration of transcriptional and epigenomic programming underlying maternal embryonic diapause in a cricket model. *Communications biology*, 9(1).

Jones ARC, et al. (2026) *Cryptocercus* Genomes Expand Knowledge of Adaptations to Xylophagy and Termite Sociality. *Genome biology and evolution*, 18(2).

Hu Y, et al. (2026) The reference genome sequence of the scarlet follicle, *Sterculia lanceolata*, reveals a paleo-polyploidization and its impact on fruit quality and fruit dehiscence. *Functional & integrative genomics*, 26(1), 46.

Hu QL, et al. (2026) Chromosome-level genome assembly of the predatory stink bug, *Eocanthecona furcellata* (Wolff). *Scientific data*, 13(1), 6.

Saenko S, et al. (2026) Annotation of 200 Insect Genomes with BRAKER for Consistent Comparisons across Species. *Scientific data*, 13(1).

Bates S, et al. (2026) OMAannotator: a novel approach to building an annotated consensus genome sequence. *Bioinformatics advances*, 6(1), vbag015.

Li X, et al. (2026) A chromosome-level genome assembly of two-spotted cricket, *Gryllus bimaculatus* (Orthoptera: Grylloidea). *Scientific data*, 13(1).

Nagy NA, et al. (2026) Draft genomes of two *Lethrus* species. *Scientific data*, 13(1).