

Resource Summary Report

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BRAKER

RRID:SCR_018964

Type: Tool

Proper Citation

BRAKER (RRID:SCR_018964)

Resource Information

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

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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 resource, software application

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: NHGRI HG000783;
German Research Foundation

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: 20260803T040754+0000

Ratings and Alerts

No rating or validation information has been found for BRAKER.

No alerts have been found for BRAKER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 458 mentions in open access literature.

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

Bekavac M, et al. (2026) De novo genome assembly of Ansell's mole-rat (*Fukomys anelli*). *G3* (Bethesda, Md.), 16(1).

Fogg LG, et al. (2026) The visual system of the longest-living vertebrate, the Greenland shark. *Nature communications*, 17(1), 39.

Li Z, et al. (2025) High-quality sika deer omics data and integrative analysis reveal genic and cellular regulation of antler regeneration. *Genome research*, 35(1), 188.

Polinski JM, et al. (2025) Chromosome-level reference genome for the Jonah crab, *Cancer borealis*. *G3* (Bethesda, Md.), 15(1).

Omufwoko KS, et al. (2025) Developmental transcriptomes predict adult social behaviours in the socially flexible sweat bee, *Lasioglossum baleicum*. *Molecular ecology*, 34(15), e17244.

Dong Z, et al. (2025) Chromosome-level genome sequencing and assembly of the parasitoid wasp *Leptopilina myrica*. *Scientific data*, 12(1), 235.

Plewka J, et al. (2025) Metagenomic analysis of pristine oil sheds new light on the global distribution of microbial genetic repertoire in hydrocarbon-associated ecosystems. *microLife*, 6, uqae027.

Zhang Y, et al. (2025) Metabolic enhancement contributed by horizontal gene transfer is essential for dietary specialization in leaf beetles. *Proceedings of the National Academy of Sciences of the United States of America*, 122(1), e2415717122.

Krawczyk K, et al. (2025) Chromosome-scale telomere to telomere genome assembly of common crystalwort (*Riccia sorocarpa* Bisch.). *Scientific data*, 12(1), 77.

Darragh K, et al. (2025) The Convergent Evolution of Hummingbird Pollination Results in Repeated Floral Scent Loss Through Gene Downregulation. *Molecular biology and evolution*, 42(2).

Song Y, et al. (2025) Haplotype-Phased Chromosome-Level Genome Assembly of *Cryptoporus qinlingensis*, a Typical Traditional Chinese Medicine Fungus. *Journal of fungi* (Basel, Switzerland), 11(2).

Javier MCF, et al. (2025) Draft genome of the endangered visayan spotted deer (*Rusa alfredi*), a Philippine endemic species. *GigaByte* (Hong Kong, China), 2025, gigabyte150.

Zhou X, et al. (2025) Chromosome-level genome assembly of *Phytoseiulus persimilis* Athias-Henriot. *Scientific data*, 12(1), 293.

Wang F, et al. (2025) A telomere-to-telomere genome assembly of Chinese grain sorghum 654. *Scientific data*, 12(1), 460.

Cai Y, et al. (2025) A chromosome-level genome assembly of the polyembryonic endoparasitoid *Macrocentrus cingulum*. *Scientific data*, 12(1), 670.

Kobayashi Y, et al. (2025) ???Whole-genome based phylogeny and comparative genomics of *Sporidiobolales* and related taxa of *Basidiomycetes*. *IMA fungus*, 16, e141626.

Wang LY, et al. (2025) A chromosomal-level genome assembly of *Araneus marmoreus* Schenkel, 1953 (Araneae: Araneidae). *Scientific data*, 12(1), 859.

Zhu M, et al. (2025) A chromosomal-level genome assembly of *Kibakoganea sinica*, Bouchard, 2005 (Coleoptera: Scarabaeidae). *Scientific data*, 12(1), 1012.

Dong Z, et al. (2025) A rare, evolutionarily conserved venom protein benefits endoparasitism across parasitoids. *Cell genomics*, 5(8), 100920.

Paudel D, et al. (2025) A chromosome-scale and haplotype-resolved genome assembly of tetraploid blackberry (*Rubus* L. subgenus *Rubus* Watson). *Horticulture research*, 12(6), uhaf052.