

Resource Summary Report

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GeMoMa

RRID:SCR_017646

Type: Tool

Proper Citation

GeMoMa (RRID:SCR_017646)

Resource Information

URL: <http://www.jstacs.de/index.php/GeMoMa>

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Description: Software tool as homology based gene prediction program that predicts gene models in target species based on gene models in evolutionary related reference species. Utilizes amino acid sequence conservation, intron position conservation, and RNA-seq data to accurately predict protein-coding transcripts. Supports combination of predictions based on several reference species allowing to transfer high quality annotation of different reference species to target species.

Synonyms: Gene Model Mapper

Resource Type: simulation software, software application, software resource

Defining Citation: [PMID:31020559](#)

Keywords: Homology, based, gene, prediction, model, target, evolutionary, related, reference, species, sequence, conservation, intron, position, RNAseq, data, protein, coding, transcript, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: GeMoMa

Resource ID: SCR_017646

Alternate IDs: biotools:gemoma

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

License: GNU General Public License version 3.0

Record Creation Time: 20220129T080336+0000

Ratings and Alerts

No rating or validation information has been found for GeMoMa.

No alerts have been found for GeMoMa.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 158 mentions in open access literature.

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

Aoyagi YB, et al. (2026) Chromosome-level genome assembly of the Gerbera (*Gerbera hybrida*) using HiFi long-read and Hi-C technologies. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 33(1).

Nie Y, et al. (2026) Identification of sex chromosome, sex-biased gene expression and dosage compensation in the pygmy mole cricket *Xya riparia* (Orthoptera: Tridactyloidea). *BMC genomics*, 27(1).

Lu D, et al. (2026) An annotated genome of freshwater amphipod (*Gammarus nekkensis*). *Scientific data*, 13(1).

Huang X, et al. (2026) Pangenome Analysis Reveals Structural Variations Associated With Citric Acid Accumulation in *Prunus mume*. *Plant biotechnology journal*, 24(4), 2623.

Wolf M, et al. (2026) The genome of the relict earless monitor lizard, *Lanthanotus borneensis*, and the Toxicofera hypothesis. *BMC biology*, 24(1).

Wang J, et al. (2026) The chromosomal-level genome assembly and annotation of *Phyllospadix iwatensis* (Surfgrass). *Scientific data*, 13(1).

Zhong CY, et al. (2026) Near complete telomere-to-telomere level genome assembly of blackchin tilapia (*Sarotherodon melanotheron*). *Scientific data*, 13(1).

Liu Z, et al. (2026) Genomic contraction of the LOX gene family limits jasmonic acid biosynthesis and contributes to delayed flower bud opening in honeysuckle (*Lonicera japonica*). *Horticulture research*, 13(6), uhag078.

Pfeifer M, et al. (2026) High-quality haplotype-resolved genome assembly and annotation of *Malus baccata* 'Jackii'. *Scientific data*, 13(1), 14.

Cheng Z, et al. (2026) A chromosome-level reference genome of an endangered plant *Craigia yunnanensis*. *Scientific data*, 13(1).

Chen YZ, et al. (2026) Whole-Genome Sequencing of Pathogenic *Nigrospora musae* ST1 Causing Leaf Spot Disease in *Idesia polycarpa*. *Journal of fungi* (Basel, Switzerland), 12(3).

Wang J, et al. (2026) The chromosome-level genome assembly of *Sitobion avenae* Fabricius (Hemiptera: Aphididae). *Scientific data*, 13(1).

Perdon DM, et al. (2026) Genomic analysis reveals recent population decline and exceptionally low genome-wide heterozygosity of the critically endangered Philippine eagle, *Pithecophaga jefferyi* (Aves: Accipitridae). *BMC genomics*, 27(1).

Liu G, et al. (2026) Extraordinary diversity of antiviral immune-related gene families across 38 bat species. *BMC biology*, 24(1).

Robbins MD, et al. (2026) Haplotype-resolved chromosome-level genome assembly of creeping bentgrass, *Agrostis stolonifera*. *Scientific data*, 13(1), 241.

Du J, et al. (2026) Chromosome-level genome assembly of the dwarf cattail *Typha minima*. *Scientific data*, 13(1), 231.

Zhou P, et al. (2026) The telomere-to-telomere haplotype genome provides in-depth insights into the molecular mechanisms of the anthocyanin deficiency phenotype in *Prunus mume*. *Molecular horticulture*, 6(1), 8.

Plasil M, et al. (2026) A chromosome-level genome assembly of the snow leopard, *Panthera uncia*. *The Journal of heredity*, 117(2), 272.

Al Khazal FJ, et al. (2026) Unbiased CRISPR synthetic lethal screening for genetic vulnerabilities in a succinate dehydrogenase-loss model of paraganglioma. *iScience*, 29(6), 115885.

Shen X, et al. (2025) A chromosomal-level genome assembly of *Omiodes indicata* Fabricius (Lepidoptera: Crambidae). *Scientific data*, 12(1), 1514.