

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: software application, simulation software, 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 135 mentions in open access literature.

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

Faulk C, et al. (2025) The genome sequence and genomic diversity of soybean tentiform leafminer (*Macrosaccus morrisella*). *G3* (Bethesda, Md.), 15(4).

Yang J, et al. (2025) Genomic Analysis of *Penicillium griseofulvum* CF3 Reveals Potential for Plant Growth Promotion and Disease Resistance. *Journal of fungi* (Basel, Switzerland), 11(2).

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Faulk C, et al. (2025) De novo whole-genome assembly of the critically endangered southern muriqui (*Brachyteles arachnoides*). *G3* (Bethesda, Md.), 15(4).

Montandon SA, et al. (2025) Regulatory and disruptive variants in the *CLCN2* gene are associated with modified skin color pattern phenotypes in the corn snake. *Genome biology*, 26(1), 73.

Yang P, et al. (2025) Multiomic Analysis Provided Insights into the Responses of Carbon Sources by Wood-Rotting Fungi *Daldinia carpinicola*. *Journal of fungi* (Basel, Switzerland), 11(2).

Lee S, et al. (2025) Chromosome-scale genome assembly of Korean goosegrass (*Eleusine indica*). *Scientific data*, 12(1), 156.

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *GigaScience*, 14.

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

Kudo SN, et al. (2025) Evolution of gene expression in seasonal environments. *eLife*, 14.

- Zhang G, et al. (2025) Genomic and transcriptomic analyses of *Heteropoda venatoria* reveal the expansion of P450 family for starvation resistance in spiders. *GigaScience*, 14.
- Huang C, et al. (2025) A comparative genomic analysis at the chromosomal-level reveals evolutionary patterns of aphid chromosomes. *Communications biology*, 8(1), 427.
- Wang R, et al. (2025) Combining whole genome and transcriptome sequencing to analyze the pathogenic mechanism of *Diplodia sapinea* blight in *Pinus sylvestris* var. *mongolica* Litv. *Virulence*, 16(1), 2490216.
- Yuan J, et al. (2025) A telomere-to-telomere genome assembly of koi carp (*Cyprinus carpio*) using long reads and Hi-C technology. *GigaScience*, 14.
- Hu X, et al. (2025) A Chromosome-scale Genome Assembly for the Broad-leaved Bamboo *Indocalamus tessellatus*. *Scientific data*, 12(1), 1706.
- Kileeg Z, et al. (2025) A species-wide inventory of receptor-like kinases in *Arabidopsis thaliana*. *BMC biology*, 23(1), 266.
- Yang K, et al. (2025) Characterization and Genome Analysis of *Mycocentrospora acerina*, the Causal Agent of *Panax notoginseng* Round Spot Disease in China. *Journal of fungi* (Basel, Switzerland), 11(11).
- Zhang X, et al. (2025) A telomere-to-telomere gap-free genome assembly of the striped catfish (*Pangasianodon hypophthalmus*). *Scientific data*, 12(1), 1890.
- Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.
- Zhang L, et al. (2025) Chromosome-scale genome assembly of *Phyllanthus emblica* L. 'Yingyu'. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(2).