Resource Summary Report

Generated by RRID on Apr 28, 2025

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

Funding:

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

Record Last Update: 20250428T054057+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 96 mentions in open access literature.

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

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

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.

Wang Y, et al. (2025) A high-quality chromosome-scale genome assembly of the Cherokee rose (Rosa laevigata). Scientific data, 12(1), 132.

Cao J, et al. (2024) Chromosome-level genome assembly and characterization of the Calophaca sinica genome. DNA research : an international journal for rapid publication of reports on genes and genomes, 31(3).

Gatins R, et al. (2024) Whole genome assembly and annotation of the King Angelfish (Holacanthus passer) gives insight into the evolution of marine fishes of the Tropical Eastern Pacific. GigaByte (Hong Kong, China), 2024, gigabyte115.

Wang C, et al. (2024) Chromosome-level genome assemblies reveal genome evolution of an invasive plant Phragmites australis. Communications biology, 7(1), 1007.

Zhu X, et al. (2024) An expanded odorant-binding protein mediates host cue detection in the parasitic wasp Baryscapus dioryctriae basis of the chromosome-level genome assembly analysis. BMC biology, 22(1), 196.

Zhao L, et al. (2024) Chromosome-level genome and population genomics of the intermediate horseshoe bat (Rhinolophus affinis) reveal the molecular basis of virus tolerance in Rhinolophus and echolocation call frequency variation. Zoological research, 45(5), 1147.

Ye M, et al. (2024) A chromosome-level genome assembly of Serangium japonicum Chapin, 1940 (Coleoptera: Coccinellidae). Scientific data, 11(1), 1421.

Zhao Q, et al. (2024) Genome Sequencing and Analysis of Nigrospora oryzae, a Rice Leaf Disease Fungus. Journal of fungi (Basel, Switzerland), 10(2).

Chen X, et al. (2024) Telomere-to-Telomere Haplotype-Resolved Genomes of Agrocybe chaxingu Reveals Unique Genetic Features and Developmental Insights. Journal of fungi (Basel, Switzerland), 10(9).

Lyu ZY, et al. (2024) The first high-altitude autotetraploid haplotype-resolved genome assembled (Rhododendron nivale subsp. boreale) provides new insights into mountaintop adaptation. GigaScience, 13.

Wang Y, et al. (2024) Insights into the adaptive evolution of chromosome and essential traits through chromosome-level genome assembly of Gekko japonicus. iScience, 27(1), 108445.

Duan M, et al. (2024) Chromosome-level genome assembly and annotation of the Rhabdophis nuchalis (Hubei keelback). Scientific data, 11(1), 850.

Shi CY, et al. (2024) A high-quality chromosome-level genome assembly of the endangered tree Kmeria septentrionalis. Scientific data, 11(1), 775.

Zhang H, et al. (2024) The High-Quality Genome Sequencing and Analysis of Red Raspberry (Rubus idaeus L.). International journal of genomics, 2024, 9271183.

Masson F, et al. (2024) Pathogen-specific social immunity is associated with erosion of individual immune function in an ant. Nature communications, 15(1), 9260.

Yin D, et al. (2024) Telomere-to-telomere gap-free genome assembly of the endangered Yangtze finless porpoise and East Asian finless porpoise. GigaScience, 13.

Huang X, et al. (2024) The genome of African manatee Trichechus senegalensis reveals secondary adaptation to the aquatic environment. iScience, 27(7), 110394.

Ge X, et al. (2024) Chromosome-scale genome assemblies of Himalopsyche anomala and Eubasilissa splendida (Insecta: Trichoptera). Scientific data, 11(1), 267.