

Resource Summary Report

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GENSCAN

RRID:SCR_013362

Type: Tool

Proper Citation

GENSCAN (RRID:SCR_013362)

Resource Information

URL: <http://genes.mit.edu/GENSCAN.html>

Proper Citation: GENSCAN (RRID:SCR_013362)

Description: Web server for identification of complete gene structures in genomic DNA. Tool for predicting locations and exon-intron structures of genes in genomic sequences from variety of organisms. Used for prediction of complete gene structures in human genomic DNA.

Abbreviations: genscan

Synonyms: GENSCAN Web Server at MIT

Resource Type: data analysis service, production service resource, service resource, analysis service resource

Defining Citation: [PMID:9149143](#)

Keywords: complete gene structures identification, genomic DNA, predicting locations, exon-intron structures, genomic sequences, bio.tools

Availability: Restricted

Resource Name: GENSCAN

Resource ID: SCR_013362

Alternate IDs: biotools:genscan, OMICS_01494

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

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260806T054600+0000

Ratings and Alerts

No rating or validation information has been found for GENSCAN.

No alerts have been found for GENSCAN.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 765 mentions in open access literature.

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

Liu F, et al. (2025) The telomere-to-telomere gapless genome of grass carp provides insights for genetic improvement. *GigaScience*, 14.

Guo J, et al. (2025) Molecular identification of a thioredoxin peroxidase in *Babesia gibsoni* with potential against oxidative stress. *Parasitology research*, 124(3), 28.

Liu J, et al. (2025) Chromosome-level genome assembly of the seasonally polyphenic scorpionfly (*Panorpa liui*). *Scientific data*, 12(1), 22.

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).

Lyu MA, et al. (2025) A dominant role of transcriptional regulation during the evolution of C4 photosynthesis in *Flaveria* species. *Nature communications*, 16(1), 1643.

Chen Y, et al. (2025) An improved chromosome-level genome assembly and annotation of Hong Kong catfish (*Clarias fuscus*). *Scientific data*, 12(1), 193.

Zou X, et al. (2025) Chromosome-level genome assembly of the pine wood nematode carrier *Arhopalus unicolor*. *Scientific data*, 12(1), 111.

Feng X, et al. (2025) Assembling the chromosome-level genome of *Arctium Lappa* L. provides new insights into carotenoid biosynthesis. *BMC plant biology*, 25(1), 1508.

Sun S, et al. (2024) Chromosomal-scale genome assembly and annotation of the land slug (*Meghimatium bilineatum*). *Scientific data*, 11(1), 35.

Wang R, et al. (2024) Dipterocarpaceae genomics reveal their demography and adaptations to Asian rainforests. *Nature communications*, 15(1), 1683.

Wang S, et al. (2024) Chromosome-level assembly and analysis of *Camelina neglecta*: a novel diploid model for *Camelina* biotechnology research. *Biotechnology for biofuels and bioproducts*, 17(1), 17.

Moawad AS, et al. (2024) Evolution of Endogenous Retroviruses in the Subfamily of Caprinae. *Viruses*, 16(3).

Cheng Y, et al. (2024) A chromosome-level genome assembly of the Echiura *Urechis unicinctus*. *Scientific data*, 11(1), 90.

He Z, et al. (2024) The whole chromosome-level genome provides resources and insights into the endangered fish *Percocypris pingi* evolution and conservation. *BMC genomics*, 25(1), 1175.

Han C, et al. (2024) Chromosome-level genome assembly and annotation of the cold-water species *Ophiura sarsii*. *Scientific data*, 11(1), 560.

Ma Y, et al. (2024) Chromosome-level genome assembly of American sweetgum (*Liquidambar styraciflua*, Altingiaceae). *Scientific data*, 11(1), 1078.

Liu G, et al. (2024) Comparative Genomics Provides Insights into Adaptive Evolution and Demographics of Bats. *Molecular biology and evolution*, 41(12).

Sun Q, et al. (2024) Integrated multi-approaches reveal unique metabolic mechanisms of Vestimentifera to adapt to deep sea. *Microbiome*, 12(1), 241.

Zhang C, et al. (2024) Genome resequencing reveals the genetic basis of population evolution, local adaptation, and rewiring of the rhizome metabolome in *Atractylodes lancea*. *Horticulture research*, 11(8), uhae167.

Hu R, et al. (2024) A Chromosomal-Level Genome of *Dermatophagoides farinae*, a Common Allergenic Mite Species. *International journal of genomics*, 2024, 3779688.