

Resource Summary Report

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GENSCAN

RRID:SCR_012902

Type: Tool

Proper Citation

GENSCAN (RRID:SCR_012902)

Resource Information

URL: <http://genome.dkfz-heidelberg.de/cgi-bin/GENSCAN/genscan.cgi>

Proper Citation: GENSCAN (RRID:SCR_012902)

Description: Resource out of service. Documented on February 24,2021.

Synonyms: GENSCAN

Resource Type: service resource

Availability: Resource out of service. Documented on February 24,2021.

Resource Name: GENSCAN

Resource ID: SCR_012902

Alternate IDs: nif-0000-30609

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260903T235158+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 192 mentions in open access literature.

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

Wang X, et al. (2022) Chromosome-level genome and recombination map of the male buffalo. *GigaScience*, 12.

Tian Q, et al. (2022) Whole-genome sequence of the planarian *Dugesia japonica* combining Illumina and PacBio data. *Genomics*, 114(2), 110293.

Zhao T, et al. (2021) A chromosome-level reference genome of the hazelnut, *Corylus heterophylla* Fisch. *GigaScience*, 10(4).

Suo Y, et al. (2020) A high-quality chromosomal genome assembly of *Diospyros oleifera* Cheng. *GigaScience*, 9(1).

Liang Z, et al. (2020) *Mesostigma viride* Genome and Transcriptome Provide Insights into the Origin and Evolution of Streptophyta. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 7(1), 1901850.

Jiang S, et al. (2020) Chromosome-level genome assembly and annotation of the loquat (*Eriobotrya japonica*) genome. *GigaScience*, 9(3).

Yin D, et al. (2020) Comparison of *Arachis monticola* with Diploid and Cultivated Tetraploid Genomes Reveals Asymmetric Subgenome Evolution and Improvement of Peanut. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 7(4), 1901672.

Liang P, et al. (2020) Long-read sequencing and de novo genome assembly of marine medaka (*Oryzias melastigma*). *BMC genomics*, 21(1), 640.

Rafati N, et al. (2020) Reconstruction of the birth of a male sex chromosome present in Atlantic herring. *Proceedings of the National Academy of Sciences of the United States of America*, 117(39), 24359.

Xu XW, et al. (2020) Draft genomes of female and male turbot *Scophthalmus maximus*. *Scientific data*, 7(1), 90.

Su H, et al. (2020) Effect of the selection pressure of vaccine antibodies on evolution of H9N2 avian influenza virus in chickens. *AMB Express*, 10(1), 98.

Li H, et al. (2020) A High-Quality Genome Sequence of Model Legume *Lotus japonicus* (MG-20) Provides Insights into the Evolution of Root Nodule Symbiosis. *Genes*, 11(5).

Sturtevant D, et al. (2020) The genome of jojoba (*Simmondsia chinensis*): A taxonomically isolated species that directs wax ester accumulation in its seeds. *Science advances*, 6(11), eaay3240.

Liu X, et al. (2020) Pathogenic Adaptations Revealed by Comparative Genome Analyses of Two *Colletotrichum* spp., the Causal Agent of Anthracnose in Rubber Tree. *Frontiers in microbiology*, 11, 1484.

Liang Y, et al. (2020) Chromosome Level Genome Assembly of *Andrographis paniculata*. *Frontiers in genetics*, 11, 701.

Nikaido M, et al. (2020) Comparative genomic analyses illuminate the distinct evolution of megabats within Chiroptera. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 27(4).

Guo W, et al. (2020) Origin and adaptation to high altitude of Tibetan semi-wild wheat. *Nature communications*, 11(1), 5085.

Miyatake K, et al. (2020) Fine mapping of a major locus representing the lack of prickles in eggplant revealed the availability of a 0.5-kb insertion/deletion for marker-assisted selection. *Breeding science*, 70(4), 438.

Yañez-Guerra LA, et al. (2020) Echinoderms provide missing link in the evolution of PrRP/sNPF-type neuropeptide signalling. *eLife*, 9.

Hong Z, et al. (2020) The chromosome-level draft genome of *Dalbergia odorifera*. *GigaScience*, 9(8).