Resource Summary Report

Generated by NIF on May 14, 2025

MCScan

RRID:SCR_017650
Type: Tool

Proper Citation

MCScan (RRID:SCR_017650)

Resource Information

URL: https://github.com/tanghaibao/mcscan

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Description: Software package to simultaneously scan multiple genomes to identify homologous chromosomal regions and subsequently align these regions using genes as anchors.Used to identify conserved gene arrays both within same genome and across different genomes. Command line program to wrap dagchainer and combine pairwise results into multi alignments in column format.

Synonyms: Multiple Collinearity Scan

Resource Type: software application, data analysis software, software toolkit, data processing software, sequence analysis software, software resource

Keywords: Simultaneously, scan, multiple, genome, identify, homologous, chromosomal, region, align, gene, anchor, bio.tools

Funding:

Availability: Free, Available for downoad, Freely available

Resource Name: MCScan

Resource ID: SCR_017650

Alternate IDs: biotools:MCScan

Alternate URLs: http://chibba.agtec.uga.edu/duplication/mcscan/, https://bio.tools/MCScan

Record Creation Time: 20220129T080336+0000

Record Last Update: 20250514T061818+0000

Ratings and Alerts

No rating or validation information has been found for MCScan.

No alerts have been found for MCScan.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 33 mentions in open access literature.

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

Li J, et al. (2025) SoyOD: An Integrated Soybean Multi-omics Database for Mining Genes and Biological Research. Genomics, proteomics & bioinformatics, 22(6).

Li Z, et al. (2024) Intraspecific diploidization of a halophyte root fungus drives heterosis. Nature communications, 15(1), 5872.

Huang J, et al. (2024) Genome assembly provides insights into the genome evolution of Baccaurea ramiflora Lour. Scientific reports, 14(1), 4867.

Huang T, et al. (2024) A chromosome-level genome assembly and evolutionary analysis of Coregonus ussuriensis Berg. Scientific data, 11(1), 792.

Zhou B, et al. (2024) Evolutionary patterns and functional effects of 3D chromatin structures in butterflies with extensive genome rearrangements. Nature communications, 15(1), 6303.

Kobayashi Y, et al. (2024) Chromosome-level genome assemblies for two quinoa inbred lines from northern and southern highlands of Altiplano where quinoa originated. Frontiers in plant science, 15, 1434388.

Zhang Y, et al. (2024) A trade-off in evolution: the adaptive landscape of spiders without venom glands. GigaScience, 13.

, et al. (2024) Chromosomal-level genome assembly and single-nucleotide polymorphism sites of black-faced spoonbill Platalea minor. GigaByte (Hong Kong, China), 2024, 1.

Kim J, et al. (2024) Chromosome-level genome assembly and comparative genomics shed

light on Helicoverpa assulta ecology and pest management. Pest management science, 80(10), 5440.

Chen X, et al. (2023) Unraveling the complex evolutionary history of lepidopteran chromosomes through ancestral chromosome reconstruction and novel chromosome nomenclature. BMC biology, 21(1), 265.

Lei T, et al. (2023) Comparative Genomics Reveals Three Genetic Groups of the Whitefly Obligate Endosymbiont Candidatus Portiera aleyrodidarum. Insects, 14(11).

Yang Y, et al. (2023) Genome sequencing of Sitopsis species provides insights into their contribution to the B subgenome of bread wheat. Plant communications, 4(4), 100567.

Hofstatter PG, et al. (2022) Repeat-based holocentromeres influence genome architecture and karyotype evolution. Cell, 185(17), 3153.

He X, et al. (2022) The whole-genome assembly of an endangered Salicaceae species: Chosenia arbutifolia (Pall.) A. Skv. GigaScience, 11.

Zhao Q, et al. (2022) Chromosome-level genome assembly of goose provides insight into the adaptation and growth of local goose breeds. GigaScience, 12.

Zhong Y, et al. (2022) Chromosomal-level genome assembly of the orchid tree Bauhinia variegata (Leguminosae; Cercidoideae) supports the allotetraploid origin hypothesis of Bauhinia. DNA research : an international journal for rapid publication of reports on genes and genomes, 29(2).

Barros CP, et al. (2022) A new haplotype-resolved turkey genome to enable turkey genetics and genomics research. GigaScience, 12.

Wang ZF, et al. (2022) Genome assembly of Musa beccarii shows extensive chromosomal rearrangements and genome expansion during evolution of Musaceae genomes. GigaScience, 12.

Li X, et al. (2022) The Manchurian Walnut Genome: Insights into Juglone and Lipid Biosynthesis. GigaScience, 11.

Hao S, et al. (2022) Chromosomal-level genome of velvet bean (Mucuna pruriens) provides resources for L-DOPA synthetic research and development. DNA research : an international journal for rapid publication of reports on genes and genomes, 29(5).