

Resource Summary Report

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

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

Availability: Free, Available for download, 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: 20260912T195855+0000

Ratings and Alerts

No rating or validation information has been found for MCSan.

No alerts have been found for MCSan.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 42 mentions in open access literature.

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

Zhang Z, et al. (2026) Haplotype-resolved chromosome-level genome assembly of an autohexaploid oil camellia tree *Camellia osmantha*. *Scientific data*, 13(1).

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

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

Huang C, et al. (2025) Impacts of parental genomic divergence in non-syntenic regions on cotton heterosis. *Journal of advanced research*, 73, 15.

Mochales-Riaño G, et al. (2025) Chromosome-level reference genome for the medically important Arabian horned viper (*Cerastes gasperettii*). *GigaScience*, 14.

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

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

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.

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

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.

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.

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

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.

Huang L, et al. (2022) Genome-wide identification, molecular characterization, and gene expression analyses of honeysuckle NHX antiporters suggest their involvement in salt stress adaptation. *PeerJ*, 10, e13214.

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.