

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://fdi-lab.org) on Jul 4, 2024

## MCScan

RRID:SCR\_017650

Type: Tool

---

### Proper Citation

MCScan (RRID:SCR\_017650)

---

### Resource Information

**URL:** <https://github.com/tanghaibao/mcscan>

**Proper Citation:** MCScan (RRID:SCR\_017650)

**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, software toolkit, software application, sequence analysis software, software resource

**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:** 20240704T054350+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 25 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

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

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.

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.

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

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

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).

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.

Rai A, et al. (2022) Chromosome-scale genome assembly of *Glycyrrhiza uralensis* revealed

metabolic gene cluster centred specialized metabolites biosynthesis. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 29(6).

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).

Wang H, et al. (2022) Chromosome-level assembly and annotation of the blue catfish *Ictalurus furcatus*, an aquaculture species for hybrid catfish reproduction, epigenetics, and heterosis studies. *GigaScience*, 11.

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

Xi H, et al. (2022) Chromosome-level assembly of the common vetch (*Vicia sativa*) reference genome. *GigaByte (Hong Kong, China)*, 2022, gigabyte38.

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.

Smit SJ, et al. (2021) Seeing the Forest through the (Phylogenetic) Trees: Functional Characterisation of Grapevine Terpene Synthase (VviTPS) Paralogues and Orthologues. *Plants (Basel, Switzerland)*, 10(8).

Lu J, et al. (2021) The *Physalis floridana* genome provides insights into the biochemical and morphological evolution of *Physalis* fruits. *Horticulture research*, 8(1), 244.

Yu H, et al. (2021) A route to de novo domestication of wild allotetraploid rice. *Cell*, 184(5), 1156.

Jin S, et al. (2021) A chromosome-level genome assembly of the oriental river prawn, *Macrobrachium nipponense*. *GigaScience*, 10(1).

Ayala-Usma DA, et al. (2021) A whole genome duplication drives the genome evolution of *Phytophthora betacei*, a closely related species to *Phytophthora infestans*. *BMC genomics*, 22(1), 795.