

Resource Summary Report

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MCScanX

RRID:SCR_022067

Type: Tool

Proper Citation

MCScanX (RRID:SCR_022067)

Resource Information

URL: <https://github.com/wyp1125/MCScanx>

Proper Citation: MCScanX (RRID:SCR_022067)

Description: Software toolkit for detection and evolutionary analysis of gene synteny and collinearity.

Synonyms: Multiple Collinearity Scan toolkit X version

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

Defining Citation: [PMID:22217600](#)

Keywords: gene synteny and collinearity, detection and evolutionary analysis,

Funding: NSF DBI 0849896;
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Availability: Free, Available for download, Freely available

Resource Name: MCScanX

Resource ID: SCR_022067

License: BSD

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260729T044536+0000

Ratings and Alerts

No rating or validation information has been found for MCSanX.

No alerts have been found for MCSanX.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 257 mentions in open access literature.

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

Hirase S, et al. (2026) Ancestral Origin and Structural Characteristics of Non-Syntenic Homologous Chromosomes in Abalones (*Haliotis*). *Molecular ecology resources*, 26(1), e70057.

Zhao Y, et al. (2025) Genome-Wide Identification of CONSTANS-like (COL) Gene Family and the Potential Function of ApCOL08 Under Salt Stress in *Andrographis paniculata*. *International journal of molecular sciences*, 26(2).

Song Y, et al. (2025) Haplotype-Phased Chromosome-Level Genome Assembly of *Cryptoporus qinlingensis*, a Typical Traditional Chinese Medicine Fungus. *Journal of fungi* (Basel, Switzerland), 11(2).

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. *GigaByte* (Hong Kong, China), 2025, gigabyte155.

Ludwig CD, et al. (2025) The genome of *Chenopodium ficifolium*: developing genetic resources and a diploid model system for allotetraploid quinoa. *G3* (Bethesda, Md.), 15(10).

Song WL, et al. (2025) Telomere-to-telomere genome assembly and 3D chromatin architecture of *Centella asiatica* insight into evolution and genetic basis of triterpenoid saponin biosynthesis. *Horticulture research*, 12(5), uhaf037.

Chen CC, et al. (2025) High-quality chromosome-level genome of three *Meretrix* species using Nanopore and Hi-C technologies. *Scientific data*, 12(1), 1141.

Zhang J, et al. (2025) Evolution of HD-ZIP transcription factors and their function in cabbage leafy head formation. *Frontiers in plant science*, 16, 1583110.

Wang M, et al. (2025) Chromosome-level genome assembly of a hemiparasitic plant, *Scurrula parasitica* (Loranthaceae). *Scientific data*, 12(1), 1802.

Liu L, et al. (2025) Genome-wide identification and expression analysis of the PtrUGT gene family in *Populus trichocarpa*. *BMC plant biology*, 25(1), 1527.

Radwan NS, et al. (2025) Genome-wide identification, characterization, and evolutionary analysis of the HSP70 gene family in rice (*Oryza sativa* L.). *BMC plant biology*, 25(1), 1671.

Kharte S, et al. (2025) Whole genome sequencing and functional annotation of *Fusarium oxysporum* f. sp. *lentis* to unravel virulence and secondary metabolite biosynthesis gene clusters. *Frontiers in genetics*, 16, 1585510.

Sang S, et al. (2025) Genome-wide analysis of the CBF gene family and their transcriptional response to cold stress in *Hibiscus mutabilis*. *Scientific reports*, 15(1), 23808.

Wen H, et al. (2025) Evolutionary analysis of the DHHCs in *Saccharinae*. *Scientific reports*, 15(1), 2290.

Zhang L, et al. (2025) Chromosome-level genome assembly and annotation of the gynogenetic large-scale loach (*Paramisgurnus dabryanus*). *Scientific data*, 12(1), 155.

Ali A, et al. (2025) Chromosome level genome assembly and annotation of the Swanson rainbow trout homozygous line. *Scientific data*, 12(1), 345.

Wang J, et al. (2025) Resolving floral development dynamics using genome and single-cell temporal transcriptome of *Dendrobium devonianum*. *Plant biotechnology journal*, 23(8), 2997.

Ma X, et al. (2025) Genome-wide identification and expression pattern analysis of the CPP transcription factor family in *Medicago sativa* L. *BMC plant biology*, 25(1), 1400.

Robbins MD, et al. (2025) Haplotype-resolved genome assembly of 'Manhattan' perennial ryegrass (*Lolium perenne* L.) and characterization of drought responsive late embryogenesis abundant genes. *BMC genomics*, 26(1), 1125.