

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

Defining Citation: [PMID:22217600](#)

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

Funding: NIAID R01 AI068908;
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: 20260905T132950+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 345 mentions in open access literature.

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

Li Y, et al. (2026) Chromatin Topology Reconfiguration Orchestrates Thermotolerant Male Fertility via GhAL5 in Cotton. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(14), e07766.

Mu D, et al. (2026) The genome of the medicinal plant *Uncaria rhynchophylla* provides new insights into monoterpenoid indole alkaloid metabolism and its molecular regulatory mechanism. *Molecular horticulture*, 6(1), 9.

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Zhang H, et al. (2026) Identification and Characterization of Cuticular Proteins in the Miridae Insect *Apolygus lucorum*. *International journal of molecular sciences*, 27(7).

Xie X, et al. (2026) Ancient Whole-Genome Duplication and Lineage-Specific Retention Shape the Diversification of bZIP Transcription Factors in Pooideae. *Plants* (Basel, Switzerland), 15(11).

Matthews A, et al. (2026) Genetic and Pathogenic Differentiation of *Fusarium oxysporum* Isolates from Ginger. *Journal of fungi* (Basel, Switzerland), 12(6).

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. *GigaScience*, 15.

Gao J, et al. (2026) Genome-wide identification of HXK gene families in cucumber and watermelon: CsHXK1 and ClHXK6 play key roles in responding to multiple stresses. *BMC plant biology*, 26(1), 200.

Wu L, et al. (2026) High-quality genome assembly and annotation of the white-cheeked goby, *Rhinogobius duospilus* (Herre, 1935) (Gobiiformes: Oxudercidae). *G3* (Bethesda, Md.), 16(2).

Hou C, et al. (2026) Pan-genome-wide characterization of the ascorbate peroxidase gene family reveals evolutionary dynamics and salt-responsive mechanisms in *Fraxinus*. *BMC plant biology*, 26(1).

Hu W, et al. (2026) Genome-wide identification and expression analysis of the maize ZmWOX gene family reveal its critical role in callus formation. BMC genomics, 27(1).

Liu P, et al. (2026) Telomere-to-telomere genome of *Stylosanthes guianensis* uncovers symbiotic adaptation to phosphorus-deficient soils. Genome biology, 27(1).

Fan Y, et al. (2026) Identification of SmNAC28 Transcription Factor and Its Mechanism of Regulating Salt Tolerance in Eggplant via S-Palmitoylation. Current issues in molecular biology, 48(4).

Childers IR, et al. (2026) Comparative Genomics Reveals the Ancestral Recombination Landscape of Placental Mammals. bioRxiv : the preprint server for biology.

Ba G, et al. (2026) Genome-Wide Identification, Expression, and Functional Analysis of UDP-Glucose Dehydrogenase Family Genes in *Rhus chinensis*. Genes, 17(6).

Chen Y, et al. (2026) Identification and expression analysis of the Xyloglucan Transglycosylase/Hydrolase (XTH) gene family under salt stress in cowpea (*Vigna unguiculata* L.). BMC genomics, 27(1), 187.

Wang C, et al. (2026) Identification, Characterization and Expression Profiles of Xylogen-like Gene Family in Kiwifruit in Different Developmental Tissues and Under Various Abiotic Stresses. Biology, 15(3).

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

Deng X, et al. (2026) Conserved and divergent gene regulatory networks for crop drought resistance. Nature communications, 17(1).

Liu J, et al. (2026) Transcriptome-based identification of the WRKY gene family in *Polygala tenuifolia* Willd. and their response to cold stress. BMC plant biology, 26(1).