

Resource Summary Report

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MISA

RRID:SCR_010765

Type: Tool

Proper Citation

MISA (RRID:SCR_010765)

Resource Information

URL: <http://pgrc.ipk-gatersleben.de/misa/>

Proper Citation: MISA (RRID:SCR_010765)

Description: Software tool that allows the identification and localization of perfect microsatellites as well as compound microsatellites which are interrupted by a certain number of bases.

Abbreviations: MISA

Synonyms: MISA - MicroSatellite identification tool

Resource Type: software resource

Keywords: bio.tools

Funding:

Resource Name: MISA

Resource ID: SCR_010765

Alternate IDs: OMICS_00110, biotools:misa

Alternate URLs: <https://bio.tools/misa>

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250519T203622+0000

Ratings and Alerts

No rating or validation information has been found for MISA.

No alerts have been found for MISA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 868 mentions in open access literature.

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

Yang X, et al. (2025) Genome-wide characterization of the MADS-box gene family in *Paeonia ostii* and expression analysis of genes related to floral organ development. *BMC genomics*, 26(1), 49.

Yao J, et al. (2025) Chloroplast Genome Sequencing and Comparative Analysis of Six Medicinal Plants of *Polygonatum*. *Ecology and evolution*, 15(1), e70831.

Li J, et al. (2025) Full-length transcriptome analysis of male and female gonads in Japanese Eel (*Anguilla japonica*). *BMC genomics*, 26(1), 89.

Jung S, et al. (2025) Rare Variant Analyses in Ancestrally Diverse Cohorts Reveal Novel ADHD Risk Genes. *medRxiv : the preprint server for health sciences*.

Nie L, et al. (2025) Plastome data provides new insights into population differentiation and evolution of *Ginkgo* in the Sichuan Basin of China. *BMC plant biology*, 25(1), 48.

Yang H, et al. (2025) Population Genetics of *Haliotis discus hannai* in China Inferred Through EST-SSR Markers. *Genes*, 16(1).

He C, et al. (2025) Analysis of full length transcriptome and resistance characteristics of *Atraphaxis bracteata* under drought. *Scientific reports*, 15(1), 807.

Xu D, et al. (2025) Comparative analysis of mitochondrial genomes of *Stemona tuberosa* Lour. reveals heterogeneity in structure, syntenic, intercellular gene transfer, and RNA editing. *BMC plant biology*, 25(1), 23.

Zhou G, et al. (2025) De novo assembly of the mitochondrial genome of *Glycyrrhiza glabra* and identification of two types of homologous recombination configurations caused by repeat sequences. *BMC genomics*, 26(1), 13.

Xiao Z, et al. (2025) De novo assembly of the complete mitochondrial genomes of two

Camellia-oil tree species reveals their multibranch conformation and evolutionary relationships. *Scientific reports*, 15(1), 2899.

Yao Z, et al. (2024) The complete chloroplast genome sequence of a cultivar of *Chrysanthemum*, *Chrysanthemum* × *morifolium* 'Hangbaiju' (Asteraceae). *Mitochondrial DNA. Part B, Resources*, 9(3), 403.

Wang Y, et al. (2024) Phylogenomics analysis of *Scutellaria* (Lamiaceae) of the world. *BMC biology*, 22(1), 185.

Zhang J, et al. (2024) The first high-quality genome assembly and annotation of *Anthocidaris crassispina*. *Scientific data*, 11(1), 866.

Pham MP, et al. (2024) Characterisation of the *Cinnamomum parthenoxylon* (Jack) Meisn (Lauraceae) transcriptome using Illumina paired-end sequencing and EST-SSR markers development for population genetics. *Biodiversity data journal*, 12, e123405.

Hajibarat Z, et al. (2024) Genotyping-by-sequencing and weighted gene co-expression network analysis of genes responsive against Potato virus Y in commercial potato cultivars. *PloS one*, 19(5), e0303783.

Xu L, et al. (2024) Characterizing complete mitochondrial genome of *Aquilegia amurensis* and its evolutionary implications. *BMC plant biology*, 24(1), 142.

Wang R, et al. (2024) The complete Chloroplast genome of *Stachys geobombycis* and comparative analysis with related *Stachys* species. *Scientific reports*, 14(1), 8523.

Li Z, et al. (2024) De novo assembly of the complete mitochondrial genome of pepino (*Solanum muricatum*) using PacBio HiFi sequencing: insights into structure, phylogenetic implications, and RNA editing. *BMC plant biology*, 24(1), 361.

Yang L, et al. (2024) A high-quality chromosome-scale genome assembly of blood orange, an important pigmented sweet orange variety. *Scientific data*, 11(1), 460.

Liu J, et al. (2024) Genomic insights into the clonal reproductive *Opuntia cochenillifera*: mitochondrial and chloroplast genomes of the cochineal cactus for enhanced understanding of structural dynamics and evolutionary implications. *Frontiers in plant science*, 15, 1347945.