

Resource Summary Report

Generated by RRID on Aug 2, 2026

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

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: 20260801T190417+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 941 mentions in open access literature.

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

Peng Y, et al. (2025) Chemical composition and transcriptomic analysis revealed the dynamic changes of saponins during the growth of *Panax japonicus* var. major. *AoB PLANTS*, 17(4), plaf034.

Xu C, et al. (2025) Assembly and comparative analysis of the complete mitochondrial of *Spodiopogon sagittifolius*, an endemic and protective species from Yunnan, China. *BMC plant biology*, 25(1), 373.

He X, et al. (2025) Combined genomic, transcriptomic, and metabolomic analyses provide insights into the fruit development of bottle gourd (*Lagenaria siceraria*). *Horticulture research*, 12(3), uhae335.

Hu Q, et al. (2025) Assembly and analysis of the complete mitochondrial genome of *Leonurus japonicus* (Lamiaceae). *Scientific reports*, 15(1), 13372.

Li J, et al. (2025) Comparative Genomics and Phylogenetic Analyses of *Aquarius macrophyllus* and Related Genera in Alismataceae Based on Plastome Data. *Ecology and evolution*, 15(6), e71568.

Emeriewen OF, et al. (2025) Chromosome-scale genome assembly of the fire blight resistant *Malus fusca* accession MAL0045, donor of FB_Mfu10. *Scientific data*, 12(1), 873.

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.

Xu Y, et al. (2025) Genome-wide development of SSR molecular markers for modern sugarcane cultivars. *Frontiers in plant science*, 16, 1573967.

Shao C, et al. (2025) Integrating phylogenomic and morphological evidence to solve the taxonomy of *Phoebe legendrei* (Lauraceae) and closely related species. *BMC plant biology*, 25(1), 1736.

Liu J, et al. (2025) Analysis of EST-SSR characteristics of prickly ash transcriptome and development of molecular markers. *Scientific reports*, 15(1), 43545.

Xu S, et al. (2025) Convergent subgenome dominance but with lineage-specific functional divergence of homoeologs during cave adaptation: insights from full-length transcriptomes of *Sinocyclocheilus* species. *Frontiers in zoology*, 23(1), 1.

Nishio S, et al. (2025) Pear scab resistance gene Rvn1 from Ussurian pear is located in a cluster of receptor-like protein ethylene-inducing Xylanase (EIX) genes. BMC plant biology, 25(1), 1191.

Li Z, et al. (2025) Plastomic insights into the genetic variation and phylogenetic relationships of Macadamia. Scientific reports, 15(1), 37579.

Li C, et al. (2025) Chloroplast genome, an effective strategy for identifying hybrid species, using Dendrobium 'Black Gold' as an example. BMC plant biology, 25(1), 1257.

Zhou LN, et al. (2025) Phylogenomic Analyses and DNA Barcoding Development Within Moraceae: Insights Into Genomic Features, Mutational Hotspots, and Adaptive Evolution. Ecology and evolution, 15(11), e72399.

Xi Y, et al. (2025) Comparative mitochondrial genome analysis of Panax ginseng reveals structural variation and genetic diversity. Scientific reports, 15(1), 44760.

Peng L, et al. (2025) ?The rediscovery of Ohwialuteola (Fabaceae, Papilionoideae) after 50 years and comparative analysis of Ohwia species in plastid genome sequence. PhytoKeys, 253, 177.

Gaikwad AB, et al. (2025) Chromosome-scale genome assembly of Trigonella corniculata (L.)L. (Nagauri pan /Kasuri methi), an important spice. Scientific data, 12(1), 509.

Chen X, et al. (2025) The complete mitochondrial genome and phylogenetic analysis of Lotus corniculatus (Fabaceae, Papilionoideae). Frontiers in plant science, 16, 1555595.

Kim Y, et al. (2025) Revisiting Phryma leptostachya L.: phylogenetic relationships and biogeographical patterns from complete plastome. BMC plant biology, 25(1), 278.