

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 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: 20260725T190702+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 [kravitz2](#) .

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 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.

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.

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.

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.

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.

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

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

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.

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.

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.

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.

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

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

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.