Resource Summary Report

Generated by dkNET on Apr 30, 2025

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: 20250420T014508+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 dkNET.

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.

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.

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

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, synteny, 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.

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

Koubínová D, et al. (2024) Microsatellite Content in 397 Nuclear Exons and Their Flanking Regions in the Fern Family Ophioglossaceae. Plants (Basel, Switzerland), 13(5).

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.

Ran Z, et al. (2024) Complete chloroplast genomes of 13 species of sect. Tuberculata Chang (Camellia L.): genomic features, comparative analysis, and phylogenetic relationships. BMC genomics, 25(1), 108.

Pan X, et al. (2024) Full-length transcriptome analysis of a bloom-forming dinoflagellate Prorocentrum shikokuense (Dinophyceae). Scientific data, 11(1), 430.

Wang C, et al. (2024) Chromosome-level genome assembly of Triplophysa bombifrons using PacBio HiFi sequencing and Hi-C technologies. Scientific data, 11(1), 1451.

Pan R, et al. (2024) Genome-Wide Development of InDel-SSRs and Association Analysis of Important Agronomic Traits of Taro (Colocasia esculenta) in China. Current issues in molecular biology, 46(12), 13347.

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

Zhan Z, et al. (2024) Chromosome-level genome assembly and annotation of a sea toad (Chaunax sp.). Scientific data, 11(1), 1397.

Tu XD, et al. (2024) The complete mitochondrial genome of Castanopsis carlesii and Castanea henryi reveals the rearrangement and size differences of mitochondrial DNA molecules. BMC plant biology, 24(1), 988.