

# Resource Summary Report

Generated by [NIF](#) on Apr 23, 2025

## GMATo

RRID:SCR\_000165

Type: Tool

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### Proper Citation

GMATo (RRID:SCR\_000165)

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### Resource Information

**URL:** <http://sourceforge.net/projects/gmato/files/?source=navbar>

**Proper Citation:** GMATo (RRID:SCR\_000165)

**Description:** A software tool used for simple sequence repeats (SSR) or microsatellite characterization. It also facilitates SSR marker design on a genomic scale, microsatellite mining at any length, and comprehensive statistical analysis for DNA sequences in any genome at any size. Analysis parameters are customizable.

**Synonyms:** Genome-wide Microsatellite Analyzing Tool, Genome Microsatellite Analyzing Tool, Genome-wide Microsatellite Analyzing Tool (GMATo)

**Resource Type:** software application, data processing software, sequence analysis software, data analysis software, software resource

**Defining Citation:** [PMID:23861572](#)

**Keywords:** simple sequence repeat, ssr, microsatellite, genomic, marker design, sequence analysis software

**Funding:**

**Availability:** Open source, Free, Available for download

**Resource Name:** GMATo

**Resource ID:** SCR\_000165

**Alternate IDs:** OMICS\_00106

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**Record Creation Time:** 20220129T080159+0000

**Record Last Update:** 20250423T055911+0000

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## Ratings and Alerts

No rating or validation information has been found for GMATo.

No alerts have been found for GMATo.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Hodel RG, et al. (2016) The report of my death was an exaggeration: A review for researchers using microsatellites in the 21st century. Applications in plant sciences, 4(6).