

Resource Summary Report

Generated by [dkNET](#) on Aug 9, 2026

SSRLocator

RRID:SCR_010766

Type: Tool

Proper Citation

SSRLocator (RRID:SCR_010766)

Resource Information

URL: <http://www.ufpel.tche.br/faem/fitotecnia/fitomelhoramento/faleconosco.html>

Proper Citation: SSRLocator (RRID:SCR_010766)

Description: A software tool for detection and characterization of micro- and minisatellites in DNA sequences.

Abbreviations: SSRLocator

Synonyms: SSR Locator, Simple Sequence Repeat Locator, SSR Locator - Simple Sequence Repeat Locator

Resource Type: software resource

Resource Name: SSRLocator

Resource ID: SCR_010766

Alternate IDs: OMICS_00114

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260808T185924+0000

Ratings and Alerts

No rating or validation information has been found for SSRLocator.

No alerts have been found for SSRLocator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Kašuková Š, et al. (2023) New Set of EST-STR Markers for Discrimination of Related *Papaver somniferum* L. Varieties. *Life* (Basel, Switzerland), 14(1).

Yang W, et al. (2021) Genetic Mapping of *ms1s*, a Recessive Gene for Male Sterility in Common Wheat. *International journal of molecular sciences*, 22(16).

Tian R, et al. (2019) A Novel Software and Method for the Efficient Development of Polymorphic SSR Loci Based on Transcriptome Data. *Genes*, 10(11).

Lemos RPM, et al. (2018) Characterization of Plastidial and Nuclear SSR Markers for Understanding Invasion Histories and Genetic Diversity of *Schinus molle* L. *Biology*, 7(3).

Wang F, et al. (2016) Characterization and Genetic Analysis of a Novel Light-Dependent Lesion Mimic Mutant, *lm3*, Showing Adult-Plant Resistance to Powdery Mildew in Common Wheat. *PloS one*, 11(5), e0155358.

Moges AD, et al. (2016) Development of Microsatellite Markers and Analysis of Genetic Diversity and Population Structure of *Colletotrichum gloeosporioides* from Ethiopia. *PloS one*, 11(3), e0151257.

Cattani AM, et al. (2016) Repetitive Elements in *Mycoplasma hyopneumoniae* Transcriptional Regulation. *PloS one*, 11(12), e0168626.

Chand SK, et al. (2015) Mining, characterization and validation of EST derived microsatellites from the transcriptome database of *Allium sativum* L. *Bioinformation*, 11(3), 145.

Ranade SS, et al. (2015) Comparative in silico analysis of SSRs in coding regions of high confidence predicted genes in Norway spruce (*Picea abies*) and Loblolly pine (*Pinus taeda*). *BMC genetics*, 16, 149.