Resource Summary Report

Generated by dkNET on Apr 30, 2025

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

Funding:

Resource Name: SSRLocator

Resource ID: SCR_010766

Alternate IDs: OMICS_00114

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250420T014508+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.

Ka?uková 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, Im3, 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.