

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 16, 2026

SSR pipeline

RRID:SCR_010767

Type: Tool

Proper Citation

SSR pipeline (RRID:SCR_010767)

Resource Information

URL: <http://pubs.usgs.gov/ds/778/>

Proper Citation: SSR pipeline (RRID:SCR_010767)

Description: Software for the Identification of Microsatellite Sequences from Paired-End Illumina High-Throughput DNA Sequence Data

Abbreviations: SSR_pipeline

Synonyms: SSR_pipeline: Computer Software for the Identification of Microsatellite Sequences from Paired-End Illumina High-Throughput DNA Sequence Data

Resource Type: software resource

Defining Citation: [PMID:24052535](#)

Keywords: python, next-generation dna sequencing, simple sequence repeat

Resource Name: SSR pipeline

Resource ID: SCR_010767

Alternate IDs: OMICS_00115

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260912T195723+0000

Ratings and Alerts

No rating or validation information has been found for SSR pipeline.

No alerts have been found for SSR pipeline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Martin CJ, et al. (2017) Digitally Barcoding Mycobacterium tuberculosis Reveals In Vivo Infection Dynamics in the Macaque Model of Tuberculosis. mBio, 8(3).

Neuditschko M, et al. (2017) Identification of key contributors in complex population structures. PloS one, 12(5), e0177638.

Tice AK, et al. (2016) Expansion of the molecular and morphological diversity of Acanthamoebidae (Centramoebida, Amoebozoa) and identification of a novel life cycle type within the group. Biology direct, 11(1), 69.

Ilicic T, et al. (2016) Classification of low quality cells from single-cell RNA-seq data. Genome biology, 17, 29.

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).

Rinaldi R, et al. (2016) New Insights on Eggplant/Tomato/Pepper Synteny and Identification of Eggplant and Pepper Orthologous QTL. Frontiers in plant science, 7, 1031.

De Pasquale I, et al. (2016) Spatial Distribution of the Metabolically Active Microbiota within Italian PDO Ewes' Milk Cheeses. PloS one, 11(4), e0153213.

Kozlov AM, et al. (2016) Phylogeny-aware identification and correction of taxonomically mislabeled sequences. Nucleic acids research, 44(11), 5022.

Nadler DC, et al. (2016) Rapid construction of metabolite biosensors using domain-insertion profiling. Nature communications, 7, 12266.

Li FW, et al. (2015) Phytochrome diversity in green plants and the origin of canonical plant phytochromes. Nature communications, 6, 7852.

Boni A, et al. (2015) Live imaging and modeling of inner nuclear membrane targeting reveals its molecular requirements in mammalian cells. The Journal of cell biology, 209(5), 705.

Müller S, et al. (2014) APADB: a database for alternative polyadenylation and microRNA regulation events. Database : the journal of biological databases and curation, 2014.

Karlsson E, et al. (2014) Eight new genomes and synthetic controls increase the accessibility of rapid melt-MAMA SNP typing of Coxiella burnetii. PloS one, 9(1), e85417.

Pereira-Leal JB, et al. (2014) A comprehensive assessment of the transcriptome of cork oak (*Quercus suber*) through EST sequencing. *BMC genomics*, 15(1), 371.

Luo C, et al. (2014) MyTaxa: an advanced taxonomic classifier for genomic and metagenomic sequences. *Nucleic acids research*, 42(8), e73.

Connolly LA, et al. (2013) The APSES transcription factor Efg1 is a global regulator that controls morphogenesis and biofilm formation in *Candida parapsilosis*. *Molecular microbiology*, 90(1), 36.

Riccombeni A, et al. (2012) Sequence and analysis of the genome of the pathogenic yeast *Candida orthopsilosis*. *PloS one*, 7(4), e35750.

Boerner S, et al. (2012) Computational identification and functional predictions of long noncoding RNA in *Zea mays*. *PloS one*, 7(8), e43047.