

Resource Summary Report

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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: 20260801T190416+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 [ASWG](#) .

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.

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.

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

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.

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

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.

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.