

Resource Summary Report

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RepeatSeq

RRID:SCR_013235

Type: Tool

Proper Citation

RepeatSeq (RRID:SCR_013235)

Resource Information

URL: <https://github.com/adaptivegenome/repeatseq>

Proper Citation: RepeatSeq (RRID:SCR_013235)

Description: Software that determines genotypes for microsatellite repeats in high-throughput sequencing data.

Abbreviations: RepeatSeq

Resource Type: software resource

Defining Citation: [PMID:23090981](#)

Resource Name: RepeatSeq

Resource ID: SCR_013235

Alternate IDs: OMICS_00112

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260725T190746+0000

Ratings and Alerts

No rating or validation information has been found for RepeatSeq.

No alerts have been found for RepeatSeq.

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 [nidm-terms](#) .

Kinney N, et al. (2025) Short tandem repeat variants are possibly associated with RNA secondary structure and gene expression. PloS one, 20(6), e0326355.

McComish BJ, et al. (2024) Ancient and Modern Genomes Reveal Microsatellites Maintain a Dynamic Equilibrium Through Deep Time. Genome biology and evolution, 16(3).

Kinney N, et al. (2021) Ethnically biased microsatellites contribute to differential gene expression and glutathione metabolism in Africans and Europeans. PloS one, 16(3), e0249148.

Boluda CG, et al. (2021) Species Delimitation and Conservation in Taxonomically Challenging Lineages: The Case of Two Clades of Capurodendron (Sapotaceae) in Madagascar. Plants (Basel, Switzerland), 10(8).

Rajan-Babu IS, et al. (2021) Genome-wide sequencing as a first-tier screening test for short tandem repeat expansions. Genome medicine, 13(1), 126.

Pimentel JDSM, et al. (2020) Genetic evaluation of migratory fish: Implications for conservation and stocking programs. Ecology and evolution, 10(19), 10314.

Halman A, et al. (2020) Accuracy of short tandem repeats genotyping tools in whole exome sequencing data. F1000Research, 9, 200.

Li Z, et al. (2019) Effects of marker type and filtering criteria on Q ST-F ST comparisons. Royal Society open science, 6(11), 190666.

Kinney N, et al. (2019) Abundance of ethnically biased microsatellites in human gene regions. PloS one, 14(12), e0225216.

Kinney N, et al. (2019) CAGm: a repository of germline microsatellite variations in the 1000 genomes project. Nucleic acids research, 47(D1), D39.

Pimentel JSM, et al. (2018) High-Throughput Sequencing Strategy for Microsatellite Genotyping Using Neotropical Fish as a Model. Frontiers in genetics, 9, 73.

Engelbrecht J, et al. (2017) New microsatellite markers for population studies of Phytophthora cinnamomi, an important global pathogen. Scientific reports, 7(1), 17631.

Fang H, et al. (2017) Whole genome sequencing of one complex pedigree illustrates challenges with genomic medicine. BMC medical genomics, 10(1), 10.

Kinney N, et al. (2017) ZDHHC3 as a Risk and Mortality Marker for Breast Cancer in African American Women. Cancer informatics, 16, 1176935117746644.

Quilez J, et al. (2016) Polymorphic tandem repeats within gene promoters act as modifiers of gene expression and DNA methylation in humans. Nucleic acids research, 44(8), 3750.

Amambua-Ngwa A, et al. (2016) Exceptionally long-range haplotypes in *Plasmodium falciparum* chromosome 6 maintained in an endemic African population. *Malaria journal*, 15(1), 515.

Bilgin Sonay T, et al. (2015) Tandem repeat variation in human and great ape populations and its impact on gene expression divergence. *Genome research*, 25(11), 1591.

Willems T, et al. (2014) The landscape of human STR variation. *Genome research*, 24(11), 1894.