Resource Summary Report

Generated by SPARC SAWG on Jul 29, 2026

Mutascope

RRID:SCR_001265
Type: Tool

Proper Citation

Mutascope (RRID:SCR_001265)

Resource Information

URL: http://sourceforge.net/projects/mutascope/

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Description: Software suite to analyze data from high throughput sequencing of PCR amplicons, with an emphasis on normal-tumor comparison for the accurate and sensitive identification of low prevalence mutations.

Abbreviations: Mutascope

Synonyms: Mutascope - Analysis software designed for PCR-amplicon sequencing data

Resource Type: software application, software resource, data analysis software, data processing software

Defining Citation: PMID:23712659

Keywords: high throughput sequencing, pcr amplicon, pcr, mutation, amplicon, sequencing, somatic variant

Related Condition: Tumor, Normal

Availability: Free, Public

Resource Name: Mutascope

Resource ID: SCR_001265

Alternate IDs: OMICS_02074

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260729T044009+0000

Ratings and Alerts

No rating or validation information has been found for Mutascope.

No alerts have been found for Mutascope.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at SPARC SAWG .

Wang X, et al. (2022) Single-cell profiling reveals a memory B cell-like subtype of follicular lymphoma with increased transformation risk. Nature communications, 13(1), 6772.

D Antonio M, et al. (2017) Identifying DNase I hypersensitive sites as driver distal regulatory elements in breast cancer. Nature communications, 8(1), 436.

Alakus H, et al. (2015) BAP1 mutation is a frequent somatic event in peritoneal malignant mesothelioma. Journal of translational medicine, 13, 122.

Lee JY, et al. (2015) Tumor evolution and intratumor heterogeneity of an epithelial ovarian cancer investigated using next-generation sequencing. BMC cancer, 15, 85.