

Resource Summary Report

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[mgatk](#)

RRID:SCR_021159

Type: Tool

Proper Citation

mgatk (RRID:SCR_021159)

Resource Information

URL: <https://github.com/caleblareau/mgatk>

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Description: Software python-based command line interface for processing .bam files with mitochondrial reads and generating high-quality heteroplasmy estimation from sequencing data. This package places a special emphasis on mitochondrial genotypes generated from single-cell genomics data, primarily mtscATAC-seq, but is generally applicable across other assays.

Synonyms: mitochondrial genome analysis toolkit

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

Defining Citation: [DOI:10.1038/s41587-020-0645-6](https://doi.org/10.1038/s41587-020-0645-6)

Keywords: processing .bam files, mitochondrial reads, heteroplasmy estimation, sequencing data, mitochondrial genotypes, mtscATAC-seq

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NCI R01 CA208756;
NCI P01 CA206978;
NCI U10 CA180861;
NIDDK R01 DK103794;
NHLBI R33 HL120791

Availability: Free, Available for download, Freely available

Resource Name: mgatk

Resource ID: SCR_021159

License: MIT License

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260801T042832+0000

Ratings and Alerts

No rating or validation information has been found for mgatk.

No alerts have been found for mgatk.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Liu V, et al. (2025) Clonal lineage tracing of innate immune cells in human cancer. bioRxiv : the preprint server for biology.

Penter L, et al. (2021) Longitudinal Single-Cell Dynamics of Chromatin Accessibility and Mitochondrial Mutations in Chronic Lymphocytic Leukemia Mirror Disease History. Cancer discovery, 11(12), 3048.