

Resource Summary Report

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GATK

RRID:SCR_001876

Type: Tool

Proper Citation

GATK (RRID:SCR_001876)

Resource Information

URL: <https://software.broadinstitute.org/gatk/>

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Description: A software package to analyze next-generation resequencing data. The toolkit offers a wide variety of tools, with a primary focus on variant discovery and genotyping as well as strong emphasis on data quality assurance. Its robust architecture, powerful processing engine and high-performance computing features make it capable of taking on projects of any size. This software library makes writing efficient analysis tools using next-generation sequencing data very easy, and second it's a suite of tools for working with human medical resequencing projects such as 1000 Genomes and The Cancer Genome Atlas. These tools include things like a depth of coverage analyzers, a quality score recalibrator, a SNP/indel caller and a local realigner. (entry from Genetic Analysis Software)

Abbreviations: GATK

Synonyms: Genome Analysis ToolKit

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

Defining Citation: [PMID:21478889](#)

Keywords: gene, genetic, genomic, next-generation resequencing, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: GATK

Resource ID: SCR_001876

Alternate IDs: nlx_154324, OMICS_00286, biotools:gatk

Alternate URLs:

http://www.broadinstitute.org/gsa/wiki/index.php/The_Genome_Analysis_Toolkit,
<https://bio.tools/gatk>

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260912T195533+0000

Ratings and Alerts

No rating or validation information has been found for GATK.

No alerts have been found for GATK.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18211 mentions in open access literature.

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

Sakrepatna Nagaraj A, et al. (2026) Ex Vivo Immuno-Oncology Platform Reveals Spatial T-cell Infiltration Patterns Linked to ATR Inhibition Responses in High-Grade Serous Ovarian Cancer. *Cancer immunology research*, 14(4), 625.

Yuan DJ, et al. (2026) Genotype-to-Phenotype Mapping of Somatic Clonal Mosaicism via Single-Cell Co-Capture of DNA Mutations and mRNA Transcripts. *Cancer discovery*, 16(4), 721.

Kamimae-Lanning AN, et al. (2026) Metabolite-induced DNA damage drives stochastic stem cell loss and clonal hematopoiesis. *Cell stem cell*, 33(4), 642.

Hayward MK, et al. (2026) Tissue tension fosters macrophage-driven lipid peroxidation-induced DNA damage. *Cancer cell*, 44(6), 1255.

Monti M, et al. (2026) Integrating interferon gamma receptor pathways, antigenicity, and immune contexture as predictors of immunotherapeutic strategies for mucosal melanomas. *Journal for immunotherapy of cancer*, 14(3).

Chen S, et al. (2026) Endogenous retrovirus-derived RNA-DNA hybrids induce microglial synaptic pruning in autism models. *Neuron*, 114(10), 1765.

Sun W, et al. (2026) Reconstruction of T cell infiltration in an osteosarcoma PDX-organoid interactive biobank for personalized immunotherapy. *Cell reports. Medicine*, 7(3), 102644.

Zhang Y, et al. (2026) Co-occurrence of transcriptionally distinct persister cell states underpins neoadjuvant therapy resistance in triple-negative breast cancer. *Genome*

medicine, 18(1).

Denis H, et al. (2026) Contrasting population structures of reef-building corals and their algal symbionts inform adaptive potential across the western Pacific. *Current biology : CB*, 36(11), 2808.

Kryeziu K, et al. (2026) Patient-derived organoids from metastatic colorectal cancer mirror tumor heterogeneity and predict patient survival and drug sensitivity. *Cell reports. Medicine*, 7(6), 102840.

Kawazu M, et al. (2026) Genomic and Transcriptomic Analysis of High-Grade Endometrial Carcinoma Reveals Biological Heterogeneity and Molecular Classification Challenges. *Cancer research communications*, 6(4), 961.

Dong YP, et al. (2026) Early replication fragile sites are associated with cancer-related CNVs and SNVs in human embryonic stem cells. *Stem cell reports*, 21(7), 102968.

Sun L, et al. (2026) Genomic Profile and Clinicopathologic Analyses of Wild-Type Gastrointestinal Stromal Tumors. *Molecular cancer research : MCR*, 24(4), 232.

Cappadona C, et al. (2026) Multi-omics identifies oxidative stress, prothrombotic pathways, and lactoperoxidase variants as key factors in COVID-19 severity. *EBioMedicine*, 123, 106111.

Ma Y, et al. (2026) Gene-culture coevolution shapes olfactory receptor gene diversity in Orang Asli populations. *Cell reports*, 117181.

Buckley KH, et al. (2026) Gastric Epithelium from BRCA1 and BRCA2 Carriers Harbors Increased Double-Stranded DNA Damage and Enhanced Growth Potential. *Molecular cancer research : MCR*, 24(7), 589.

Radulovich N, et al. (2026) Preclinical Combination Targeting VEGF and PI3K in a Rare, Aggressive Mixed Endometrial Carcinoma: An Applied Case Report. *Cancer research communications*, 6(4), 832.

Tirtei E, et al. (2026) Mapping Genomic Heterogeneity in Pediatric and Adolescent-Young Adult Sarcomas: Insights from the Italian SAR-GEN2016 and SAR-GEN_ITA Prospective Multicenter Trials. *Cancer research communications*, 6(4), 857.

Andersen L, et al. (2026) Cell-Free DNA-Derived Immune Cell Ratios Uncover Cancer-Associated Systemic Changes. *Cancer research communications*, 6(4), 811.

Liu H, et al. (2026) Long-term outcomes by clinical and molecular risk stratification in patients with medulloblastoma receiving risk-adapted therapy. *Med (New York, N.Y.)*, 7(5), 101076.