

Resource Summary Report

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IndelGenotyper

RRID:SCR_016663

Type: Tool

Proper Citation

IndelGenotyper (RRID:SCR_016663)

Resource Information

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

Proper Citation: IndelGenotyper (RRID:SCR_016663)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on July 18th,2023. Software package for genome analysis. Used for analysis of next generation genomic data in cancer.

Abbreviations: GATK

Synonyms: GATK Indel Genotyper, Genome Analysis Toolkit (GATK) Indel Genotyper, Indel Genotyper, GATK IndelGenotyper

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

Keywords: next, generation, analysis, genomic, data, cancer, genome

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: IndelGenotyper

Resource ID: SCR_016663

Alternate URLs: <https://github.com/broadinstitute/gatk/>,
<https://sources.debian.org/src/gatk/>

License: BSD 3-clause licence

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260731T043003+0000

Ratings and Alerts

No rating or validation information has been found for IndelGenotyper.

No alerts have been found for IndelGenotyper.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 63 mentions in open access literature.

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

Al-Yazeedi T, et al. (2026) Genetic Mapping of Resistance: ddRADseq-Based QTL and Associated Polymorphism Conferring Resistance to Alpha-Cypermethrin in *Anopheles funestus*. *Molecular ecology*, 35(1), e70207.

Sacchi S, et al. (2025) A phosphoserine phosphatase variant present in the brain of Alzheimer's disease patients favors nuclear mistargeting. *The FEBS journal*, 292(18), 4955.

Rebello RJ, et al. (2025) Whole genome sequencing improves tissue-of-origin diagnosis and treatment options for cancer of unknown primary. *Nature communications*, 16(1), 4422.

Batlle-Masó L, et al. (2025) Somatic reversion in CD137 deficiency correlating with Epstein-Barr virus control and clinical improvement. *NPJ genomic medicine*, 10(1), 78.

Lu Y, et al. (2025) Cystic fibrosis-causing variants in Chinese patients with congenital absence of the vas deferens: a cohort and meta-analysis. *Asian journal of andrology*, 27(5), 611.

Huang H, et al. (2025) De novo transcriptomes of floral bracts for 22 *Bougainvillea* accessions. *Scientific data*, 12(1), 645.

Vogel GF, et al. (2025) Congenital enteropathy caused by ezrin deficiency. *Human genetics*, 144(5), 505.

Shadrina M, et al. (2025) Efficient identification of de novo mutations in family trios: a consensus-based informatic approach. *Life science alliance*, 8(6).

Jun S, et al. (2025) Mapping QTLs for PHS resistance and development of a deep learning model to measure PHS rate in japonica rice. *The plant genome*, 18(3), e70109.

Martins Rodrigues F, et al. (2025) Germline predisposition in multiple myeloma. *iScience*, 28(1), 111620.

Messingschlager M, et al. (2025) DNA methylation changes during acute COVID-19 are associated with long-term transcriptional dysregulation in patients' airway epithelial cells.

EMBO molecular medicine, 17(5), 923.

Perez-Riverol Y, et al. (2025) Open-Source and FAIR Research Software for Proteomics. *Journal of proteome research*, 24(5), 2222.

Van Renne N, et al. (2025) Detection of hepatitis B virus mRNA from single cell RNA sequencing data without prior knowledge. *PloS one*, 20(2), e0314060.

Bose A, et al. (2025) APOBEC3A-Induced DNA Damage Drives Polymerase ? Dependency and Synthetic Lethality in Cancer. *bioRxiv : the preprint server for biology*.

Liu CL, et al. (2025) Genome-Wide Association Integrating a Transcriptomic Meta-Analysis Suggests That Genes Related to Fat Deposition and Muscle Development Are Closely Associated with Growth in Huaxi Cattle. *Veterinary sciences*, 12(2).

Batlle-Masó L, et al. (2025) De Novo or inherited: gonosomal mosaicism in hereditary angioedema due to C1 inhibitor deficiency. *Frontiers in immunology*, 16, 1550380.

Kong W, et al. (2025) Genomic analysis of 1,325 *Camellia* accessions sheds light on agronomic and metabolic traits for tea plant improvement. *Nature genetics*, 57(4), 997.

Chen L, et al. (2025) Genomic and Cis-Regulatory Basis of a Plastic C3-C4 Photosynthesis in *Eleocharis Baldwinii*. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(32), e15681.

Ishikawa R, et al. (2025) Immunohistochemical and molecular evolutionary features of jejunoileal adenocarcinoma unveiled through comparative analysis with colorectal adenocarcinoma. *Neoplasia (New York, N.Y.)*, 66, 101180.

Mikhaylenko DS, et al. (2025) Patients with Papillary Renal Cancer and Germline Duplication of MET Exons 5-21. *Biomedicines*, 13(6).