

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 analysis software, software application, software resource, sequence analysis software, data processing software

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: 20260801T190550+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 [ASWG](#).

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).