

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

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: 20260903T235359+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 88 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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.

Dominguez-Alonso S, et al. (2026) Non-coding Regulatory Variants in ASD (Autism Spectrum Disorders) Disrupt CTCF Domains and Shape Cell-Type-Specific Neurodevelopmental Landscapes Revealed by Single-Cell Analyses and Cortical Organoids. *Research square*.

Dea A, et al. (2026) Physiological architecture and evolutionary origins of cellular adaptability. *bioRxiv : the preprint server for biology*.

Yang SH, et al. (2026) ML-ExonCNV: a robust XGBoost multi-expert ensemble framework for rare exon CNV detection in whole-exome sequencing data. *Briefings in bioinformatics*, 27(2).

Litman A, et al. (2026) Variant-resolved prediction of context-specific isoform variation with a graph-based attention model. *Cell genomics*, 6(4), 101126.

Thambiraja M, et al. (2026) Genetic basis of immunity in Indian cattle as revealed by comparative analysis of *Bos* genome. *Scientific reports*, 16(1).

Becquart P, et al. (2026) Wnt-presenting materials sustain H3K14-acetylation in human skeletal stem cells for tissue engineering and bone repair. *NPJ Regenerative medicine*, 11(1).

Andersen S, et al. (2026) Oncostatin M receptor deficiency as a novel candidate genetic cause of autosomal recessive hyper-IgE syndrome. *Journal of human immunity*, 2(3), e20250119.

Blazyte A, et al. (2026) Fifteen Years of the Genome Analysis Toolkit as the De Facto Standard in Short-Read Variant Calling. *International journal of molecular sciences*, 27(9).

Zhao H, et al. (2026) Integrated analyses of host genetics and gut microbiota provide mechanistic insights into feed efficiency in ducks. *Journal of animal science and biotechnology*, 17(1).

Bi D, et al. (2026) Integrating ANI and phylogenies for re-evaluation of *Fusobacterium* taxonomy and disease associations. *Nature communications*, 17(1).

Wang M, et al. (2026) Revision of *Amana yunjuensis* (Liliaceae) based on morphological and molecular evidence: synonym of *Amana anhuiensis*. *PhytoKeys*, 269, 275.

Hackl L, et al. (2025) Homozygous DHCR7 p.Val330Met Variant Associated with Mild Non-Syndromic Intellectual Disability and Elevated Serum 7-Dehydrocholesterol Levels in Two Siblings. *Genes*, 16(7).

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

Cheng T, et al. (2025) Genome-wide identification, expression profile and selection analysis of the CPK gene family in *Nelumbo nucifera*. *BMC genomics*, 26(1), 461.

Yang T, et al. (2025) Chromosome-level genome assembly provides insights into flavonoid biosynthesis in stems and leaves and fatty acid biosynthesis in kernels of *Erythralum scandens*. *BMC plant biology*, 25(1), 1000.

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.

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

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.