

Resource Summary Report

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CASAVA

RRID:SCR_001802

Type: Tool

Proper Citation

CASAVA (RRID:SCR_001802)

Resource Information

URL: http://support.illumina.com/sequencing/sequencing_software/casava.html

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Description: Software package that creates genomic builds, calls SNPs, detects indels, and counts reads from data generated from one or more sequencing runs. In addition, CASAVA automatically generates a range of statistics, such as mean depth and percentage chromosome coverage, to enable comparison with previous builds or other samples. CASAVA analyzes sequencing reads in three stages: * FASTQ file generation and demultiplexing * Alignment to a reference genome * Variant detection and counting

Abbreviations: CASAVA

Synonyms: Consensus Assessment of Sequence And VAriation

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, linux

Availability: Free, Available for download, Freely available

Resource Name: CASAVA

Resource ID: SCR_001802

Alternate IDs: nlx_154257, OMICS_01123

Old URLs: http://www.illumina.com/software/genome_analyzer_software.ilmn

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260829T183040+0000

Ratings and Alerts

No rating or validation information has been found for CASAVA.

No alerts have been found for CASAVA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1960 mentions in open access literature.

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

Vilarrubi A, et al. (2026) SMARCB1 Deficiency in Tumors Confers a Vulnerability to H3K27 Demethylase Inhibitors via Autophagy Disruption. Cancer research.

Brodsky AL, et al. (2026) Combination Therapy with Copanlisib and Niraparib in Patients with Recurrent Endometrial and Ovarian Cancer (COPANIRA): Efficacy, Toxicity, and Translational Insights. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(7), 1234.

Torigata K, et al. (2026) Human iPSC cardiomyocyte patch transplantation modifies extracellular matrix and fibroblast behavior after myocardial infarction. iScience, 29(4), 115341.

Cerezo-Wallis D, et al. (2026) Architecture of the neutrophil compartment. Nature, 649(8098), 1003.

Hung CL, et al. (2026) Oral bioavailable ITRI-148 degrades androgen receptor variants and overcomes antiandrogen resistance in advanced prostate cancer. Neoplasia (New York, N.Y.), 71, 101253.

Kumar A, et al. (2026) Development and validation of high-density SNP array for genomic studies in Indian yak populations. BMC genomic data, 27(1), 16.

Devabhakthini N, et al. (2026) Exploring the genetic diversity of the IPK Medicago germplasm collection using GBS. Plant biology (Stuttgart, Germany), 28(2), 345.

Ye D, et al. (2026) Multi-omics reveals heterogeneity and functional populations of oligodendrocyte progenitor cells induced by human neural stem cells. Cell death discovery, 12(1).

Jan S, et al. (2026) Deciphering Cold Stress Resilience: Multiomics Insights in Contrasting Wheat Genotypes From the Western Himalayas. Plant biotechnology journal, 24(7), 4577.

Naing A, et al. (2026) Biomarker study of pembrolizumab in patients with advanced rare cancers. Cell reports. Medicine, 7(6), 102827.

Xian S, et al. (2026) Prenatal Diagnosis of Short Rib-Polydactyly Syndrome (SRPS), DYNC2I1-Related: Identification of a Novel Homozygous Missense Variant by Clinical Exome Sequencing. *Clinical case reports*, 14(6), e72795.

Shao C, et al. (2026) Phenotypic and molecular characterization of K64 putative hypervirulent carbapenem-resistant *Klebsiella pneumoniae*. *PloS one*, 21(6), e0351561.

Macleod R, et al. (2026) Lethal plague outbreaks in Lake Baikal hunter-gatherers 5,500 years ago. *Nature*, 654(8119), 697.

Cai Y, et al. (2026) Meningeal lymphatic dysfunction drives cognitive impairment after experimental subarachnoid hemorrhage. *Neurotherapeutics : the journal of the American Society for Experimental NeuroTherapeutics*, 23(1), e00819.

Dong M, et al. (2026) Targeting aberrant DNA methylation across subtypes of pediatric high-grade glioma inhibits tumor growth and RUNX3 represents a targetable methylated tumor suppressor. *Cell communication and signaling : CCS*, 24(1).

Liu L, et al. (2026) Phenotypic and genomic characterization of tigecycline-insensitive *Klebsiella pneumoniae* strains and validation of highly virulent MDR strains. *Microbiology spectrum*, 14(5), e0322825.

Sun L, et al. (2026) Prenatal phenotypic delineation of a de novo EYA1 likely pathogenic variant in branchio-oto-renal syndrome. *BMC medical genomics*, 19(1).

Bohner F, et al. (2026) Micafungin microevolution in *Candida auris* reveals resistance development without in vivo fitness compromise. *Virulence*, 17(1), 2664993.

Blokzijl R, et al. (2026) Using Nuclear Genomic Data to Address Intractable Relationships and Gene Tree Discordance in an Ancient Group of Gymnosperms (*Ephedra*, Gnetales). *Ecology and evolution*, 16(7), e73863.

Li X, et al. (2026) Dynamic transcriptomic landscape of myogenesis in Muscovy ducks (*Cairina moschata*): integrative analysis of hub genes post-hatching. *Animal bioscience*, 39(1), 250159.