

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 resource, software application

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: 20260731T042620+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 1899 mentions in open access literature.

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

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.

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.

Welti J, et al. (2025) NXP800 Activates the Unfolded Protein Response, Altering AR and E2F Function to Impact Castration-Resistant Prostate Cancer Growth. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(6), 1109.

Varadarajan K, et al. (2025) Efficacy of ATR Kinase Inhibitor Elimusertib Monotherapy or Combination in Tumors with DNA Damage Response Pathway and Other Genomic Alterations. *Molecular cancer therapeutics*, 24(9), 1402.

Köhne M, et al. (2025) Satb1 directs the differentiation of TH17 cells through suppression of IL-2 expression. *Cell reports*, 44(7), 115866.

Hilliam Y, et al. (2025) Induction of lipid A modification genes in *Pseudomonas aeruginosa* cells tolerant to a commercially available contact lens disinfection solution. *Journal of medical microbiology*, 74(9).

Huang X, et al. (2025) CDK4/6 Inhibition Reverses MEIS2 Suppression of CRL4 CRBN to Enhance Immunomodulatory Drug Therapy in Multiple Myeloma. *bioRxiv : the preprint server for biology*.

Kaldhusdal V, et al. (2025) Spatial transcriptomics unveils estrogen-modulated immune responses and structural alterations in the ectocervical mucosa of depot medroxyprogesterone acetate users. *Scientific reports*, 15(1), 1014.

Li P, et al. (2025) A new pipeline SPICE identifies novel JUN-IKZF1 composite elements. *eLife*, 12.

Di Rienzi SC, et al. (2025) *Limosilactobacillus reuteri* promotes the expression and secretion of enteroendocrine- and enterocyte-derived hormones. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 39(6), e70408.

Huang Y, et al. (2025) FBN2 pathogenic mutation in congenital contractural arachnodactyly with severe skeletal manifestations. *Molecular genetics and metabolism reports*, 42, 101193.

Wang T, et al. (2025) Transcriptomics reveals preterm birth risk: identification and validation of key genes in monocytes. *BMC pregnancy and childbirth*, 25(1), 174.

Cyréus P, et al. (2025) Atherosclerotic plaque instability in symptomatic non-significant carotid stenoses. *JVS-vascular science*, 6, 100280.

Zhang Z, et al. (2025) Whole genome sequencing identifies pathogenic genetic variants in Han Chinese patients with familial venous thromboembolism. *Communications biology*, 8(1), 604.

Liu F, et al. (2025) Single-cell profiling of bone metastasis ecosystems from multiple cancer types reveals convergent and divergent mechanisms of bone colonization. *Cell genomics*, 5(7), 100888.

Chabronova A, et al. (2025) Exploring the roles of snoRNA-induced ribosome heterogeneity in equine osteoarthritis. *Frontiers in veterinary science*, 12, 1562508.

Roy S, et al. (2025) BLIMP1 negatively regulates IL-2 signaling in T cells. *Science advances*, 11(29), eadx8105.

Chen AXY, et al. (2025) Rewiring endogenous genes in CAR T cells for tumour-restricted payload delivery. *Nature*, 644(8075), 241.

Barrington J, et al. (2025) Interleukin-1 regulates myeloid cell trafficking and cerebral blood flow following intracerebral haemorrhage. *Disease models & mechanisms*, 18(10).

Taliadoros D, et al. (2025) Genome Variation in Three Anthophora Bee Species Reflects Divergent Demographic Histories. *Molecular ecology*, 34(24), e70204.