Resource Summary Report

Generated by T1D on Aug 1, 2026

LUMPY

RRID:SCR_003253
Type: Tool

Proper Citation

LUMPY (RRID:SCR_003253)

Resource Information

URL: https://github.com/arq5x/lumpy-sv/

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Description: Software package as probabilistic framework for structural variant discovery. Capable of integrating any number of SV detection signals including those generated from read alignments or prior evidence. Simplified wrapper for standard analyses, LUMPY Express, can also be executed.

Synonyms: lumpy-sv, LUMPY Express

Resource Type: data analysis software, software application, data processing software, software resource, standalone software, simulation software

Defining Citation: PMID:24970577

Keywords: probabilistic, framework, structural, variant, discovery

Funding: NHGRI R01 HG006693;
NIH Office of the Director DP2 OD006493;
Burroughs Wellcome Fund Career Award

Availability: Free, Available for download, Freely available

Resource Name: LUMPY

Resource ID: SCR_003253

Alternate IDs: OMICS_04674

Alternate URLs: https://sources.debian.org/src/lumpy-sv/

License: MIT License

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260801T042530+0000

Ratings and Alerts

No rating or validation information has been found for LUMPY.

No alerts have been found for LUMPY.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 447 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Garcia GL, et al. (2025) Aged and BRCA-Mutated Stromal Cells Drive Epithelial Cell Transformation. Cancer discovery, 15(6), 1203.

Ricciardi V, et al. (2025) The genome of Vitis vinifera cv. Mgaloblishvili reveals resistance and susceptibility factors to downy mildew in the Rpv29 and Rpv31 loci. Horticulture research, 12(6), uhaf055.

Marín-Garzón NA, et al. (2025) Detection and functional assessment of structural variants using whole-genome re-sequencing data in Nellore cattle. Scientific reports, 15(1), 30364.

Jeong M, et al. (2025) NF2 is Essential for Human Endoderm Development. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(17), e2410909.

Sircoulomb F, et al. (2025) Genotype B of deformed wing virus and related recombinant viruses become dominant in European honey bee colonies. Scientific reports, 15(1), 4804.

Estévez-Gómez N, et al. (2025) Differential performance of strategies for single-cell whole-genome amplification. Cell reports methods, 5(4), 101025.

Li N, et al. (2025) Multi-omics analyses unveil dual genetic loci governing four distinct watermelon flesh color phenotypes. Molecular horticulture, 5(1), 46.

Velásquez-Escobar AM, et al. (2025) Snrnp25 is a candidate for the peri-implantation lethal phenotype of the Hba deletions. Mammalian genome : official journal of the International Mammalian Genome Society, 36(3), 727.

Xu J, et al. (2025) Clinical use of whole-genome sequencing in children with developmental delay or intellectual disability. BMC medical genomics, 18(1), 188.

Ye H, et al. (2025) Integrated chloroplast genomics and whole-genome resequencing reveals demographic history and selection signatures of black walnuts. The plant genome, 18(4), e70172.

Liu Y, et al. (2025) Copy number variations contribute to malignant tumor development in children with serious birth defects. Molecular oncology, 19(3), 899.

Wei K, et al. (2025) Copy Number Variation Shapes Structural Genomic Diversity Associated With Ecological Adaptation in the Wild Tomato Solanum chilense. Molecular biology and evolution, 42(8).

Nørgaard M, et al. (2025) Deep targeted sequencing of circulating tumor DNA to inform treatment in patients with metastatic castration-resistant prostate cancer. Journal of experimental & clinical cancer research : CR, 44(1), 120.

Liu S, et al. (2025) Direct long-read visualization reveals hidden variation in GCH1 gene copy number and precise expansion steps. BMC genomics, 26(1), 671.

Li Y, et al. (2025) A zebrafish model of chronic heart failure caused by protein aggregation in heart valves. Communications biology, 8(1), 1520.

Mondino A, et al. (2025) Familial Narcolepsy in Dogo Argentino Dogs Is Caused by a Tandem Duplication Mutation in HCRTR2. Journal of veterinary internal medicine, 39(2), e70056.

Jensen TD, et al. (2025) Integration of transcriptomics and long-read genomics prioritizes structural variants in rare disease. Genome research, 35(4), 914.

Vialle RA, et al. (2025) Structural variants linked to Alzheimer's disease and other common age-related clinical and neuropathologic traits. Genome medicine, 17(1), 20.

Zeng Y, et al. (2025) Mapping the chromothripsis landscape in urothelial carcinoma unravels great intratumoral and intertumoral heterogeneity. iScience, 28(1), 111510.

Kim JW, et al. (2025) Clinical implementation of next-generation sequencing testing and genomically-matched therapy: a real-world data in a tertiary hospital. Scientific reports, 15(1), 2171.