Resource Summary Report

Generated by RRID on Sep 10, 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, data processing software, simulation software, software application, software resource, standalone software

Defining Citation: PMID:24970577

Keywords: probabilistic, framework, structural, variant, discovery

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

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: 20260905T132500+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 499 mentions in open access literature.

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

Mortazavi M, et al. (2026) Long-read genome sequencing improves detection and functional interpretation of structural and repeat variants in autism. Cell genomics, 6(5), 101186.

Valentín López JC, et al. (2026) Evolution of AR and Non-AR Alterations in ctDNA of Patients with Metastatic Prostate Cancer Treated in the Phase III Alliance A031201 Trial. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(12), 2413.

Brown N, et al. (2026) Replication stress increases de novo CNVs across the malaria parasite genome. Nucleic acids research, 54(1).

Brown N, et al. (2026) SVCROWS: a user-defined tool for interpreting significant structural variants in heterogeneous datasets. Nucleic acids research, 54(1).

Lam Shang Leen J, et al. (2026) Transient neonatal hyperparathyroidism caused by a monoallelic TRPV6 dominant negative variant. JBMR plus, 10(2), ziaf159.

Dong Y, et al. (2026) Structural variation drives enhancer hijacking via 3D genome disruption in ccRCC. NPJ digital medicine, 9(1), 85.

Hu H, et al. (2026) Structural variation drives rhizome innovation and adaptive divergence in sister Medicago species. Journal of integrative plant biology, 68(2), 406.

Wei L, et al. (2026) The landscape and regulatory potential of eccDNAs in mammalian preimplantation embryos. Nature communications, 17(1).

Zhang J, et al. (2026) Cancer genome standards for long-read sequencing using cancer cell line mixtures. GigaScience, 15.

Kubo S, et al. (2026) Characterization of fucoxanthin-deficient strains in the haptophyte Tisochrysis lutea induced by heavy-ion beam irradiation. Plant & cell physiology, 67(3), 265.

Hong J, et al. (2026) Convergence for Inactivation of TGF? Signaling Is a Common Feature of Advanced Pancreatic Cancer. Cancer discovery, 16(6), 1087.

Yang L, et al. (2026) Phased-assembly-driven pangenome graphs for structural variant genotyping and complex trait mapping in dairy cattle. Nature communications, 17(1).

Watson DJ, et al. (2026) Single vs dual genetic disease in children with congenital anomalies and solid tumors. Genetics in medicine open, 4, 104357.

Fauqueux J, et al. (2026) Compound heterozygous structural variants resulting in CNTNAP2 biallelic loss-of-function: rare mechanisms unveiled by genome sequencing. Human genomics, 20(1).

Chetabi FA, et al. (2026) Structural Genomic Variation and Its Potential Role in Deer Speciation. Molecular ecology, 35(9), e70365.

Zhao C, et al. (2026) Genome-wide variation landscape reveals temperature adaptation in Chinese indigenous cattle. Journal of animal science and biotechnology, 17(1).

Lee H, et al. (2026) Multimodal antigenic escape to GPRC5D-targeted T cell engagers in multiple myeloma. Nature medicine, 32(3), 964.

Wang W, et al. (2026) Whole-genome resequencing and genetic diversity of five indigenous cattle breeds from China. Scientific data, 13(1), 282.

Das A, et al. (2026) Assembling unmapped reads reveals hidden variation in South Asian genomes. Nature communications, 17(1).

Steensma MJ, et al. (2026) Deficiency in homozygous haplotypes reveals recessive lethal variants affecting fertility and viability in the Friesian horse. BMC genomics, 27(1).