Resource Summary Report

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BIRDSUITE

RRID:SCR_001794
Type: Tool

Proper Citation

BIRDSUITE (RRID:SCR_001794)

Resource Information

URL: https://www.broadinstitute.org/birdsuite/birdsuite

Proper Citation: BIRDSUITE (RRID:SCR_001794)

Description: Open-source set of tools to detect and report SNP genotypes, common Copy-Number Polymorphisms (CNPs), and novel, rare, or de novo CNVs in samples processed with the Affymetrix platform. While most of the components of the suite can be run individually (for instance, to only do SNP genotyping), the Birdsuite is especially intended for integrated analysis of SNPs and CNVs.

Abbreviations: Birdsuite

Resource Type: software application, software resource

Defining Citation: PMID:18776909

Keywords: gene, genetic, genomic, snp, genotype, copy number polymorphism, copy number variant, affymetrix

Availability: Free, Available for download, Freely available

Resource Name: BIRDSUITE

Resource ID: SCR_001794

Alternate IDs: OMICS_00705, nlx_154245

License: Open unspecified license

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260727T040310+0000

Ratings and Alerts

No rating or validation information has been found for BIRDSUITE.

No alerts have been found for BIRDSUITE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 43 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Linstra R, et al. (2025) MYC controls STING levels to downregulate inflammatory signaling in breast cancer cells upon DNA damage. The Journal of biological chemistry, 301(6), 108560.

Engchuan W, et al. (2025) Psychiatric disorders converge on common pathways but diverge in cellular context, spatial distribution, and directionality of genetic effects. medRxiv : the preprint server for health sciences.

Sokolowski DJ, et al. (2025) iModEst: disentangling -omic impacts on gene expression variation across genes and tissues. NAR genomics and bioinformatics, 7(1), lqaf011.

Romdhane L, et al. (2024) Ethnic and functional differentiation of copy number polymorphisms in Tunisian and HapMap population unveils insights on genome organizational plasticity. Scientific reports, 14(1), 4654.

Pagadala M, et al. (2023) Germline modifiers of the tumor immune microenvironment implicate drivers of cancer risk and immunotherapy response. Nature communications, 14(1), 2744.

Ozcan Z, et al. (2022) Chromosomal imbalances detected via RNA-sequencing in 28 cancers. Bioinformatics (Oxford, England), 38(6), 1483.

Balagué-Dobón L, et al. (2022) Fully exploiting SNP arrays: a systematic review on the tools to extract underlying genomic structure. Briefings in bioinformatics, 23(2).

Shi M, et al. (2022) Genetic Architecture of Plasma Alpha-Aminoadipic Acid Reveals a Relationship With High-Density Lipoprotein Cholesterol. Journal of the American Heart Association, 11(11), e024388.

Romdhane L, et al. (2021) A map of copy number variations in the Tunisian population: a valuable tool for medical genomics in North Africa. NPJ genomic medicine, 6(1), 3.

Rong Y, et al. (2021) DDRS: Detection of drug response SNPs specifically in patients receiving drug treatment. Computational and structural biotechnology journal, 19, 3650.

Toh C, et al. (2021) Genetic risk score for ovarian cancer based on chromosomal-scale length variation. BioData mining, 14(1), 18.

Hubbard L, et al. (2021) Rare Copy Number Variants Are Associated With Poorer Cognition in Schizophrenia. Biological psychiatry, 90(1), 28.

Fan X, et al. (2021) Accucopy: accurate and fast inference of allele-specific copy number alterations from low-coverage low-purity tumor sequencing data. BMC bioinformatics, 22(1), 23.

Schmitz-Abe K, et al. (2020) Homozygous deletions implicate non-coding epigenetic marks in Autism spectrum disorder. Scientific reports, 10(1), 14045.

Dai JY, et al. (2020) DNA methylation and cis-regulation of gene expression by prostate cancer risk SNPs. PLoS genetics, 16(3), e1008667.

Merino J, et al. (2020) Interaction Between Type 2 Diabetes Prevention Strategies and Genetic Determinants of Coronary Artery Disease on Cardiometabolic Risk Factors. Diabetes, 69(1), 112.

Fortin JP, et al. (2019) Multiple-gene targeting and mismatch tolerance can confound analysis of genome-wide pooled CRISPR screens. Genome biology, 20(1), 21.

Cheng L, et al. (2019) Integration of genomic copy number variations and chemotherapy-response biomarkers in pediatric sarcoma. BMC medical genomics, 12(Suppl 1), 23.

Lee AS, et al. (2019) Rare mutations in the complement regulatory gene CSMD1 are associated with male and female infertility. Nature communications, 10(1), 4626.

Zhang X, et al. (2019) Genome-wide Burden of Rare Short Deletions Is Enriched in Major Depressive Disorder in Four Cohorts. Biological psychiatry, 85(12), 1065.