Resource Summary Report

Generated by dkNET on Apr 30, 2025

CNVPartition

RRID:SCR_010925
Type: Tool

Proper Citation

CNVPartition (RRID:SCR_010925)

Resource Information

URL: http://www.illumina.com/software/illumina_connect.ilmn

Proper Citation: CNVPartition (RRID:SCR_010925)

Description: Software that estimates copy number and annotates regions with copy number variants(CNV).

Abbreviations: CNVPartition

Resource Type: software resource

Funding:

Resource Name: CNVPartition

Resource ID: SCR_010925

Alternate IDs: OMICS_00716

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250420T014515+0000

Ratings and Alerts

No rating or validation information has been found for CNVPartition.

No alerts have been found for CNVPartition.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 125 mentions in open access literature.

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

Zhang S, et al. (2025) Preimplantation genetic testing for structural rearrangements by genome-wide SNP genotyping and haplotype analysis: a prospective multicenter clinical study. EBioMedicine, 111, 105514.

Khan H, et al. (2024) Biallelic variants identified in 36 Pakistani families and trios with autism spectrum disorder. Scientific reports, 14(1), 9230.

Viggiano M, et al. (2024) Genomic analysis of 116 autism families strengthens known risk genes and highlights promising candidates. NPJ genomic medicine, 9(1), 21.

Dahawi M, et al. (2024) Genetic heterogeneity in familial forms of genetic generalized epilepsy: from mono- to oligogenism. Human genomics, 18(1), 130.

Chen Y, et al. (2024) Novel evidence of CNV deletion in KCTD13 related to the severity of isolated hypospadias in Chinese population. Frontiers in pediatrics, 12, 1409264.

Yu K, et al. (2024) Genomic landscape of patients with germline RUNX1 variants and familial platelet disorder with myeloid malignancy. Blood advances, 8(2), 497.

Wagstaff LJ, et al. (2024) CRISPR-edited human ES-derived oligodendrocyte progenitor cells improve remyelination in rodents. Nature communications, 15(1), 8570.

Chan ER, et al. (2024) Importance of copy number variants in childhood apraxia of speech and other speech sound disorders. Communications biology, 7(1), 1273.

De Angeli P, et al. (2024) Splicing defects and CRISPR-Cas9 correction in isogenic homozygous photoreceptor precursors harboring clustered deep-intronic ABCA4 variants. Molecular therapy. Nucleic acids, 35(1), 102113.

Wesely J, et al. (2024) A repository of Ogden syndrome patient derived iPSC lines and isogenic pairs by X-chromosome screening and genome-editing. bioRxiv : the preprint server for biology.

Jin Y, et al. (2024) Modeling Lewy body disease with SNCA triplication iPSC-derived cortical organoids and identifying therapeutic drugs. Science advances, 10(37), eadk3700.

Pommerenke C, et al. (2024) Molecular Characterization and Subtyping of Breast Cancer Cell Lines Provide Novel Insights into Cancer Relevant Genes. Cells, 13(4).

Carlisle SG, et al. (2023) Rare Genomic Copy Number Variants Implicate New Candidate Genes for Bicuspid Aortic Valve. medRxiv : the preprint server for health sciences.

Xu P, et al. (2023) OGM and WES identifies translocation breakpoints in PKD1 gene in an polycystic kidney patient and healthy baby delivered using PGT. BMC medical genomics, 16(1), 285.

Bacchelli E, et al. (2023) Whole genome analysis of rare deleterious variants adds further evidence to BRSK2 and other risk genes in Autism Spectrum Disorder. Research square.

Winden KD, et al. (2023) Increased degradation of FMRP contributes to neuronal hyperexcitability in tuberous sclerosis complex. Cell reports, 42(8), 112838.

Tobin MP, et al. (2023) Differences in cell shape, motility, and growth reflect chromosomal number variations that can be visualized with live-cell ChReporters. Molecular biology of the cell, 34(13), br19.

Bray D, et al. (2022) CASCADE: high-throughput characterization of regulatory complex binding altered by non-coding variants. Cell genomics, 2(2).

Bianco AM, et al. (2022) What Is the Exact Contribution of PITX1 and TBX4 Genes in Clubfoot Development? An Italian Study. Genes, 13(11).

Seah C, et al. (2022) Modeling gene × environment interactions in PTSD using human neurons reveals diagnosis-specific glucocorticoid-induced gene expression. Nature neuroscience, 25(11), 1434.