Resource Summary Report

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Agilent CytoGenomics software

RRID:SCR_010917
Type: Tool

Proper Citation

Agilent CytoGenomics software (RRID:SCR_010917)

Resource Information

URL: http://www.genomics.agilent.com/en/product.jsp?cid=AG-PT-111&tabId=AG-PR-1017&_requestid=587725

Proper Citation: Agilent CytoGenomics software (RRID:SCR_010917)

Description: Software for a complete CGH and CGH+SNP microarray data analysis and data reporting solution to streamline the day-to-day cytogenetic sample analysis research workflow.

Abbreviations: Agilent CytoGenomics software

Resource Type: software resource

Resource Name: Agilent CytoGenomics software

Resource ID: SCR_010917

Alternate IDs: OMICS_00701

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260725T190707+0000

Ratings and Alerts

No rating or validation information has been found for Agilent CytoGenomics software.

No alerts have been found for Agilent CytoGenomics software.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 117 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Ormieres C, et al. (2025) Deciphering the genetic basis of developmental language disorder in children without intellectual disability, autism or apraxia of speech. Molecular autism, 16(1), 10.

DA Costa LM, et al. (2025) High-Resolution aCGH Analysis of the Jurkat Cell Line: Copy Number Alterations and Their Association With Cancer Hallmarks. Cancer genomics & proteomics, 22(5), 824.

Baggiani M, et al. (2024) Generation of a human induced pluripotent stem cell line (FSMi001-A) from fibroblasts of a patient carrying heterozygous mutation in the REEP1 gene. Stem cell research, 79, 103472.

Pfeifer M, et al. (2024) Tracheal agenesis versus tracheal atresia: anatomical conditions, pathomechanisms and causes with a possible link to a novel MAPK11 variant in one case. Orphanet journal of rare diseases, 19(1), 114.

Lucia-Campos C, et al. (2024) An intragenic duplication in the AFF2 gene associated with Cornelia de Lange syndrome phenotype. Frontiers in genetics, 15, 1472543.

Calcagni G, et al. (2024) Congenital Heart Defects in Patients with Molecularly Confirmed Sotos Syndrome. Diagnostics (Basel, Switzerland), 14(6).

Alhazmi S, et al. (2024) Copy number variations in autistic children. Biomedical reports, 21(1), 107.

Alesi V, et al. (2024) Structural rearrangements as a recurrent pathogenic mechanism for SETBP1 haploinsufficiency. Human genomics, 18(1), 29.

Bauleo A, et al. (2023) 3q29 microduplication syndrome: New evidence for the refinement of the critical region. Molecular genetics & genomic medicine, 11(4), e2130.

Qin S, et al. (2023) Delineation of an inverted tandem Xq23-26.3 duplication in a female featuring extremely short stature and mild mental deficiency. Molecular cytogenetics, 16(1), 33.

Gajjar K, et al. (2023) Array Comparative Genomic Hybridization Analysis of Products of Conception in Recurrent Pregnancy Loss for specific anomalies detected by USG. Reproduction & fertility, 4(2).

Socha M, et al. (2023) A pure de novo 16p13.3 duplication and amplification in a patient with femoral hypoplasia, psychomotor retardation, heart defect, and facial dysmorphism-a case report and literature review of the partial 16p13.3 trisomy syndrome. Journal of applied genetics, 64(1), 125.

Montanaro FAM, et al. (2023) PTCHD1 gene mutation/deletion: the cognitive-behavioral phenotyping of four case reports. Frontiers in psychiatry, 14, 1327802.

Cullot G, et al. (2023) Cell cycle arrest and p53 prevent ON-target megabase-scale rearrangements induced by CRISPR-Cas9. Nature communications, 14(1), 4072.

Gopal RK, et al. (2023) Effectors Enabling Adaptation to Mitochondrial Complex I Loss in Hürthle Cell Carcinoma. Cancer discovery, 13(8), 1904.

Smits WK, et al. (2023) Elevated enhancer-oncogene contacts and higher oncogene expression levels by recurrent CTCF inactivating mutations in acute T cell leukemia. Cell reports, 42(4), 112373.

Qiu S, et al. (2023) Nexus between genome-wide copy number variations and autism spectrum disorder in Northeast Han Chinese population. BMC psychiatry, 23(1), 96.

Qin S, et al. (2023) Prenatal diagnosis of mosaic chromosomal aneuploidy and uniparental disomy and clinical outcomes evaluation of four fetuses. Molecular cytogenetics, 16(1), 35.

Orlando V, et al. (2022) A Complex Genomic Rearrangement Resulting in Loss of Function of SCN1A and SCN2A in a Patient with Severe Developmental and Epileptic Encephalopathy. International journal of molecular sciences, 23(21).

Samara N, et al. (2022) New insights regarding origin of monosomy occurrence in early developing embryos as demonstrated in preimplantation genetic testing. Molecular cytogenetics, 15(1), 11.