

Resource Summary Report

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Agilent: SureScan Dx Microarray Scanner

RRID:SCR_019544

Type: Tool

Proper Citation

Agilent: SureScan Dx Microarray Scanner (RRID:SCR_019544)

Resource Information

URL: <https://www.agilent.com/en/product/gene-expression-microarray-platform/gene-expression-microarray-scanners-equipment/surescan-dx-microarray-scanner-228492>

Proper Citation: Agilent: SureScan Dx Microarray Scanner (RRID:SCR_019544)

Description: SureScan Dx microarray scanner system analyzes many genomics and cytogenetics microarrays.

Resource Type: instrument resource

Keywords: Agilent, Microarray Scanner, Instrument, Equipment,

Availability: Commercially available

Specification URL: https://raw.githubusercontent.com/SciCrunch/RRID-Instruments/refs/heads/main/PDF/SCR_019544.pdf

Resource Name: Agilent: SureScan Dx Microarray Scanner

Resource ID: SCR_019544

Alternate IDs: Model_Number_Dx

Record Creation Time: 20220129T080345+0000

Record Last Update: 20260905T132854+0000

Ratings and Alerts

No rating or validation information has been found for Agilent: SureScan Dx Microarray Scanner.

No alerts have been found for Agilent: SureScan Dx Microarray Scanner.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Egawa M, et al. (2025) Generation of Monosomy 21q Human iPSC Cells by CRISPR/Cas9-Mediated Interstitial Megabase Deletion. *Genes to cells : devoted to molecular & cellular mechanisms*, 30(1), e13184.

Gandhi G, et al. (2024) Revealing the potential role of hsa-miR-663a in modulating the PI3K-Akt signaling pathway via miRNA microarray in spinal muscular atrophy patient fibroblast-derived iPSCs. *Journal of neuropathology and experimental neurology*, 83(10), 822.

Imai A, et al. (2023) Loss of Dead end1 induces testicular teratomas from primordial germ cells that failed to undergo sexual differentiation in embryonic testes. *Scientific reports*, 13(1), 6398.

Alsagaby SA, et al. (2022) Investigating the impact of RNA integrity variation on the transcriptome of human leukemic cells. *3 Biotech*, 12(8), 160.

Wijesiriwardhana P, et al. (2021) Copy Number Variants Captured by the Array Comparative Genomic Hybridization in a Cohort of Patients Affected with Hereditary Colorectal Cancer in Sri Lanka: The First CNV Analysis Study of the Hereditary Colorectal Cancer in the Sri Lankan Population. *Asian Pacific journal of cancer prevention : APJCP*, 22(6), 1957.

Rovas A, et al. (2021) Analysis of periodontitis-associated miRNAs in gingival tissue, gingival crevicular fluid, saliva and blood plasma. *Archives of oral biology*, 126, 105125.

Aziz MNM, et al. (2021) Anti-Metastatic and Anti-Angiogenic Effects of Curcumin Analog DK1 on Human Osteosarcoma Cells In Vitro. *Pharmaceuticals (Basel, Switzerland)*, 14(6).

Shen L, et al. (2021) Genome-wide analysis of DNA methylation in 106 schizophrenia family trios in Han Chinese. *EBioMedicine*, 72, 103609.

Gong K, et al. (2020) Importance of glycosylation in the interaction of Tamm-Horsfall protein with collectin-11 and acute kidney injury. *Journal of cellular and molecular medicine*, 24(6), 3572.

Diaz M, et al. (2020) Differential DNA methylation profile in infants born small-for-gestational-age: association with markers of adiposity and insulin resistance from birth to age 24 months. *BMJ open diabetes research & care*, 8(1).

Rosenthal SH, et al. (2020) Development and Validation of a 34-Gene Inherited Cancer Predisposition Panel Using Next-Generation Sequencing. *BioMed research international*,

2020, 3289023.

Alsagaby SA, et al. (2020) Transcriptomics-Based Characterization of the Toxicity of ZnO Nanoparticles Against Chronic Myeloid Leukemia Cells. *International journal of nanomedicine*, 15, 7901.

Fushimi A, et al. (2020) Osteogenic cocktail induces calcifications in human breast cancer cell line via placental alkaline phosphatase expression. *Scientific reports*, 10(1), 12669.

Felicio PS, et al. (2018) Genetic alterations detected by comparative genomic hybridization in BRCA1 breast and ovarian cancers of Brazilian population. *Oncotarget*, 9(44), 27525.

Vallacchi V, et al. (2016) microRNA Expression in Sentinel Nodes from Progressing Melanoma Patients Identifies Networks Associated with Dysfunctional Immune Response. *Genes*, 7(12).

Ghevaria H, et al. (2016) The origin and significance of additional aneuploidy events in couples undergoing preimplantation genetic diagnosis for translocations by array comparative genomic hybridization. *Reproductive biomedicine online*, 32(2), 178.

Stankevicius V, et al. (2016) Gene and miRNA expression signature of Lewis lung carcinoma LLC1 cells in extracellular matrix enriched microenvironment. *BMC cancer*, 16(1), 789.

Zheng H, et al. (2015) Application of next-generation sequencing for 24-chromosome aneuploidy screening of human preimplantation embryos. *Molecular cytogenetics*, 8, 38.

Idogawa M, et al. (2014) Array-based genome-wide RNAi screening to identify shRNAs that enhance p53-related apoptosis in human cancer cells. *Oncotarget*, 5(17), 7540.

Ghosh S, et al. (2014) Copy number variation in the horse genome. *PLoS genetics*, 10(10), e1004712.