Resource Summary Report

Generated by RRID on Aug 4, 2026

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: 20260801T190633+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 RRID .

Egawa M, et al. (2025) Generation of Monosomy 21q Human iPS 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.

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.

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.

Felicio PS, et al. (2018) Genetic alterations detected by comparative genomic hybridization in BRCAX 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.