

Resource Summary Report

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Agilent Genomic Workbench

RRID:SCR_010918

Type: Tool

Proper Citation

Agilent Genomic Workbench (RRID:SCR_010918)

Resource Information

URL: <https://earray.chem.agilent.com/cghanalytics/index.html>

Proper Citation: Agilent Genomic Workbench (RRID:SCR_010918)

Description: A comprehensive design and analysis tool for setting up and interpreting your microarray experiments.

Abbreviations: Agilent Genomic Workbench

Resource Type: software resource

Resource Name: Agilent Genomic Workbench

Resource ID: SCR_010918

Alternate IDs: OMICS_00702

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260801T190418+0000

Ratings and Alerts

No rating or validation information has been found for Agilent Genomic Workbench.

No alerts have been found for Agilent Genomic Workbench.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 248 mentions in open access literature.

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

Vujaklija I, et al. (2025) Detecting a wide range of epitranscriptomic modifications using a nanopore-sequencing-based computational approach with 1D score-clustering. *Nucleic acids research*, 53(1).

Zhao M, et al. (2025) Genetic variation in IL-4 activated tissue resident macrophages determines strain-specific synergistic responses to LPS epigenetically. *Nature communications*, 16(1), 1030.

Zhao M, et al. (2024) Genetic variation in IL-4 activated tissue resident macrophages alters the epigenetic state to determine strain specific synergistic responses to LPS. *Research square*.

Hoogenboom A, et al. (2024) Novel PUF60 variant suggesting an interaction between Verheij and Cornelia de Lange syndrome: phenotype description and review of the literature. *European journal of human genetics : EJHG*, 32(4), 435.

Zhu M, et al. (2024) Genomic and transcriptomic profiling of hepatocellular carcinoma reveals a rare molecular subtype. *Discover. Oncology*, 15(1), 10.

Li Z, et al. (2024) Clinical sequencing reveals diagnostic, therapeutic, and prognostic biomarkers for adult-type diffuse gliomas. *Heliyon*, 10(18), e37712.

Scimeca M, et al. (2024) Genetically driven predisposition leads to an unusually genomic unstable renal cell carcinoma. *Discover oncology*, 15(1), 80.

Mendonca D, et al. (2024) Generation of five induced pluripotent stem cell lines from patients with MECP2 Duplication Syndrome. *Stem cell research*, 74, 103292.

Nieto-Romero V, et al. (2024) Restored glyoxylate metabolism after AGXT gene correction and direct reprogramming of primary hyperoxaluria type 1 fibroblasts. *iScience*, 27(4), 109530.

Pehlivan D, et al. (2024) Structural variant allelic heterogeneity in MECP2 duplication syndrome provides insight into clinical severity and variability of disease expression. *Genome medicine*, 16(1), 146.

Amoako E, et al. (2024) Targeted gene panel sequencing of liquid and tissue biopsies reveals actionable genomic alterations in Ghanaian metastatic breast cancer cases. *Translational oncology*, 49, 102100.

Kim Y, et al. (2023) Comparison of Homologous Recombination Repair Gene Next-Generation Sequencing Analysis in Patients With Metastatic Castration-Resistant Prostate Cancer Between Local and Central Laboratories in Korea. *Annals of laboratory medicine*, 43(1), 64.

Tang W, et al. (2023) Population-specific Mutation Patterns in Breast Tumors from African American, European American, and Kenyan Patients. *Cancer research communications*, 3(11), 2244.

Han Y, et al. (2023) A BRCA2 germline mutation and high expression of immune checkpoints in a TNBC patient. *Cell death discovery*, 9(1), 370.

Rodrigues L, et al. (2023) Shared hotspot mutations in oncogenes position dogs as an unparalleled comparative model for precision therapeutics. *Scientific reports*, 13(1), 10935.

Pan X, et al. (2023) CRISPR-Cas9 Engineered Extracellular Vesicles for the Treatment of Dominant Progressive Hearing Loss. *bioRxiv : the preprint server for biology*.

van der Laan L, et al. (2023) Prenatal identification of an inverted duplicated 13q marker chromosome with a neocentromere. *Molecular cytogenetics*, 16(1), 34.

Lourenço RA, et al. (2023) BRCA1 VUS: A functional analysis to differentiate pathogenic from benign variants identified in clinical diagnostic panels for breast cancer. *Molecular medicine reports*, 28(1).

Yang X, et al. (2023) A primary luminal/HER2 negative breast cancer patient with mismatch repair deficiency. *Cell death discovery*, 9(1), 365.

Soltysova A, et al. (2023) Genome-wide DNA methylome and transcriptome changes induced by inorganic nanoparticles in human kidney cells after chronic exposure. *Cell biology and toxicology*, 39(5), 1939.