Resource Summary Report

Generated by ASWG on Aug 5, 2026

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 ASWG .

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.

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

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.

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.

Louren??o 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).

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

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.