Resource Summary Report

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Agilent 2100 Bioanalyzer Instrument

RRID:SCR_018043
Type: Tool

Proper Citation

Agilent 2100 Bioanalyzer Instrument (RRID:SCR_018043)

Resource Information

URL: https://www.agilent.com/en/product/automated-electrophoresis/bioanalyzer-systems/bioanalyzer-instrument/2100-bioanalyzer-instrument-228250

Proper Citation: Agilent 2100 Bioanalyzer Instrument (RRID:SCR_018043)

Description: Bioanalyzer system is automated electrophoresis tool that providesa analytical evaluation of various samples types in many workflows, including next generation sequencing NGS, gene expression, biopharmaceutical, and gene editing research. Digital data is provided in timely manner and delivers assessment of sizing, quantitation, integrity and purity from DNA, RNA, and proteins. Minimal sample volumes are required for accurate result, and data may be exported in many different formats.

Synonyms: Agilent 2100 Bioanalyzer, , 2100 Bioanalyzer (Agilent Technologies)

Resource Type: instrument resource

Keywords: ABRF, bioanalyzer, electrophoresis, DNA, RNA, protein, data analysis, instrument, equipment

Funding:

Resource Name: Agilent 2100 Bioanalyzer Instrument

Resource ID: SCR_018043

Alternate IDs: SCR_019389, Model_Number_2100 Bioanalyzer

Alternate URLs:
https://www.agilent.com/cs/library/usermanuals/public/2100_Bioanalyzer_Expert_USR.pdf

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Ratings and Alerts

No rating or validation information has been found for Agilent 2100 Bioanalyzer Instrument.

No alerts have been found for Agilent 2100 Bioanalyzer Instrument.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 144 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Torozan DA, et al. (2025) Metagenomic Profiling of Oral Microbiome Dynamics During Chemoradiotherapy in Head and Neck Squamous Cell Carcinoma Patients. Cancer medicine, 14(1), e70589.

Ruiz-Gabarre D, et al. (2024) Intron retention as a productive mechanism in human MAPT: RNA species generated by retention of intron 3. EBioMedicine, 100, 104953.

Poch T, et al. (2024) Intergenic risk variant rs56258221 skews the fate of naive CD4+ T cells via miR4464-BACH2 interplay in primary sclerosing cholangitis. Cell reports. Medicine, 5(7), 101620.

Pussila M, et al. (2024) Mitotic abnormalities precede microsatellite instability in lynch syndrome-associated colorectal tumourigenesis. EBioMedicine, 103, 105111.

Zhao L, et al. (2024) Diminished representation of vitamin-B12-producing bacteria in constipated elders with frailty. iScience, 27(8), 110403.

Li L, et al. (2024) Comprehensive Proteogenomic Profiling Reveals the Molecular Characteristics of Colorectal Cancer at Distinct Stages of Progression. Cancer research, 84(17), 2888.

Sekyi MT, et al. (2024) Demyelination and neurodegeneration early in experimental autoimmune encephalomyelitis contribute to functional deficits in the anterior visual pathway. Scientific reports, 14(1), 24048.

Bennett NK, et al. (2024) Systems-level analyses dissociate genetic regulators of reactive

oxygen species and energy production. Proceedings of the National Academy of Sciences of the United States of America, 121(3), e2307904121.

Shouse AN, et al. (2024) Interleukin-2 receptor signaling acts as a checkpoint that influences the distribution of regulatory T cell subsets. iScience, 27(12), 111248.

Gill AS, et al. (2024) Transcriptomic analysis of Asparagus officinalis cultivars with varying levels of freezing tolerance over fall acclimation and spring deacclimation periods. Frontiers in plant science, 15, 1442784.

Ramirez MD, et al. (2024) Cellular-resolution gene expression mapping reveals organization in the head ganglia of the gastropod, Berghia stephanieae. The Journal of comparative neurology, 532(6), e25628.

Heller DT, et al. (2024) Astrocyte ensheathment of calyx-forming axons of the auditory brainstem precedes accelerated expression of myelin genes and myelination by oligodendrocytes. The Journal of comparative neurology, 532(2), e25552.

Grandi C, et al. (2024) Decoupled degradation and translation enables noise modulation by poly(A) tails. Cell systems, 15(6), 526.

Kellett DO, et al. (2024) Transcriptional response of the heart to vagus nerve stimulation. Physiological genomics, 56(2), 167.

Abusdal M, et al. (2024) PCSK1N as a tumor size marker and an ER stress response protein in corticotroph pituitary adenomas. The Journal of clinical endocrinology and metabolism.

Marshall Moscon S, et al. (2024) A common variant in the iron regulatory gene (Hfe) alters the metabolic and transcriptional landscape in brain regions vulnerable to neurodegeneration. Journal of neurochemistry, 168(9), 3132.

Regunath K, et al. (2024) Systematic Characterization of p53-Regulated Long Noncoding RNAs across Human Cancers Reveals Remarkable Heterogeneity among Different Tumor Types. Molecular cancer research : MCR, 22(6), 555.

De Cauwer A, et al. (2023) Measuring the transcriptome-wide effects of aging on murine adipocytes using RNAseq. STAR protocols, 4(3), 102397.

Salari K, et al. (2023) Development and Multicenter Case-Control Validation of Urinary Comprehensive Genomic Profiling for Urothelial Carcinoma Diagnosis, Surveillance, and Risk-Prediction. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(18), 3668.

Booher WC, et al. (2023) Hippocampal RNA sequencing in mice selectively bred for high and low activity. Genes, brain, and behavior, 22(2), e12832.