

Resource Summary Report

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Agilent: BioAnalyzer 2100

RRID:SCR_019715

Type: Tool

Proper Citation

Agilent: BioAnalyzer 2100 (RRID:SCR_019715)

Resource Information

URL: <https://www.agilent.com/cs/library/posters/Public/BioAnalyzer.PDF>

Proper Citation: Agilent: BioAnalyzer 2100 (RRID:SCR_019715)

Description: 2100 Bioanalyzer system is an established automated electrophoresis tool for the sample quality control of biomolecules. The 2100 Bioanalyzer instrument, together with the 2100 Expert Software and Bioanalyzer assays, provide highly precise 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 a timely manner and delivers objective assessment of sizing, quantitation, integrity and purity from DNA, RNA, and proteins. Minimal sample volumes are required for an accurate result, and the data may be exported in a many different formats for ease-of-use.

Resource Type: instrument resource

Keywords: Bioanalyzer system, Instrument, Equipment, USEdit

Specification URL: https://raw.githubusercontent.com/SciCrunch/RRID-Instruments/refs/heads/main/PDF/SCR_019715.pdf

Resource Name: Agilent: BioAnalyzer 2100

Resource ID: SCR_019715

Alternate IDs: Model_Number_Agilent_2100

Record Creation Time: 20220129T080346+0000

Record Last Update: 20260725T190919+0000

Ratings and Alerts

No rating or validation information has been found for Agilent: BioAnalyzer 2100.

No alerts have been found for Agilent: BioAnalyzer 2100.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 943 mentions in open access literature.

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

Ramponi V, et al. (2025) H4K20me3-Mediated Repression of Inflammatory Genes Is a Characteristic and Targetable Vulnerability of Persister Cancer Cells. *Cancer research*, 85(1), 32.

Hoffmann J, et al. (2025) Steatohepatitis-induced vascular niche alterations promote melanoma metastasis. *Cancer & metabolism*, 13(1), 5.

Arenillas C, et al. (2025) Convergent Genetic Adaptation in Human Tumors Developed Under Systemic Hypoxia and in Populations Living at High Altitudes. *Cancer discovery*, 15(5), 1037.

Wang X, et al. (2025) Spatial and Single-Cell Analyses Reveal Heterogeneity of DNAM-1 Receptor-Ligand Interactions That Instructs Intratumoral ??T-cell Activity. *Cancer research*, 85(2), 277.

Engel K, et al. (2025) Segment specific loss of NFAT5 function in the kidneys is sufficient to induce a global kidney injury like phenotype. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 39(2), e70352.

Li J, et al. (2025) Chronic degenerative failure of salivary glands can be reversed through restoring mitochondrial function. *bioRxiv : the preprint server for biology*.

Chen XX, et al. (2025) Microbial dysbiosis with tryptophan metabolites alteration in lower respiratory tract is associated with clinical responses to anti-PD-1 immunotherapy in advanced non-small cell lung cancer. *Cancer immunology, immunotherapy : CII*, 74(4), 140.

Castro-Arnau J, et al. (2025) Post-testicular spermatozoa of a marine teleost can conduct de novo cytoplasmic and mitochondrial translation. *iScience*, 28(1), 111537.

Villano DJ, et al. (2025) Widespread 3D genome reorganization precedes programmed DNA rearrangement in *Oxytricha trifallax*. *bioRxiv : the preprint server for biology*.

Silver LW, et al. (2025) Temporal Loss of Genome-Wide and Immunogenetic Diversity in a Near-Extinct Parrot. *Molecular ecology*, 34(9), e17746.

Muratoğlu B, et al. (2025) Circadian rhythm and aryl hydrocarbon receptor crosstalk in bone marrow adipose tissue and implications in leukemia. *Scientific reports*, 15(1), 16387.

Kosek DM, et al. (2025) Mapping effective microRNA pairing beyond the seed using abasic modifications. *Nucleic acids research*, 53(8).

Zhang Q, et al. (2025) Secretome enriched with small extracellular vesicles derived from human gingiva-derived mesenchymal stem cells enhances rat tongue muscle regeneration. *Journal of nanobiotechnology*, 23(1), 434.

Walter DM, et al. (2025) U2AF1 mutations rescue deleterious exon skipping induced by KRAS mutations. *bioRxiv : the preprint server for biology*.

Park JG, et al. (2025) Revealing the role of increased SK3 expression in sulfonylurea resistance triggered by prolonged exposure. *Nutrition & diabetes*, 15(1), 29.

Huang J, et al. (2025) Transcriptomic analysis of human cartilage identified potential therapeutic targets for hip osteoarthritis. *Human molecular genetics*, 34(5), 444.

Sabikunnahar B, et al. (2025) Natural genetic variation in wild-derived mice controls host survival and transcriptional responses during endotoxic shock. *ImmunoHorizons*, 9(5).

Séguéla A, et al. (2025) Integrated Co-extraction Protocol for Transcriptomic and H NMR Metabolomic Analysis of Multi-species Biofilms. *Bio-protocol*, 15(5), e5237.

Cooke WR, et al. (2025) A method to isolate syncytiotrophoblast-derived medium-large extracellular vesicle small RNA from maternal plasma. *Placenta*, 166, 91.

Milewski TM, et al. (2025) Rapid changes in plasma corticosterone and medial amygdala transcriptome profiles during social status change reveal molecular pathways associated with a major life history transition in mouse dominance hierarchies. *PLoS genetics*, 21(1), e1011548.