Resource Summary Report

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Illumina: HiSeq 2500 System

RRID:SCR_016383
Type: Tool

Proper Citation

Illumina: HiSeq 2500 System (RRID:SCR_016383)

Resource Information

URL: https://support.illumina.com/sequencing/sequencing_instruments/hiseq_2500.html

Proper Citation: Illumina: HiSeq 2500 System (RRID:SCR_016383)

Description: High-throughput sequencing system. High-quality data using proven Illumina SBS chemistry has made it the instrument of choice for major genome centers and research institutions throughout the world.HiSeq 2500 System has been discontinued. Illumina will support the instrument and intends to supply the reagents through February 28, 2023.

Synonyms: HiSeq 2500

Resource Type: instrument resource

Keywords: Illumina, Sequencing System, Instrument Equipment, USEDit,

Specification URL: https://raw.githubusercontent.com/SciCrunch/RRID-Instruments/refs/heads/main/PDF/SCR_016383.pdf

Resource Name: Illumina: HiSeq 2500 System

Resource ID: SCR_016383

Alternate IDs: SCR_020123, Model_Number_HiSeq 2500

Alternate URLs: https://support.illumina.com/content/dam/illumina-support/documents/documentation/system_documentation/hiseq2500/hiseq-2500-system-guide-15035786-03.pdf, https://support.illumina.com/content/dam/illumina-support/documents/documentation/system_documentation/hiseq2500/hiseq-2500-system-guide-15035786-03.pdf

Old URLs: https://www.illumina.com/systems/sequencing-platforms/hiseq-2500.html

Record Creation Time: 20220129T080330+0000

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Ratings and Alerts

No rating or validation information has been found for Illumina: HiSeq 2500 System.

No alerts have been found for Illumina: HiSeq 2500 System.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 85 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Dalley R, et al. (2026) Human Neocortical Glutamatergic Neurons Revealed Through Multimodal Profiling. bioRxiv : the preprint server for biology.

Yang W, et al. (2026) Multi-omics reveals co-regulation of hepatic bile acid metabolism in laying hens by host genetics and the cecal Anaerostipes. Poultry science, 105(3), 106388.

Márquez R, et al. (2025) A draft genome assembly for the dart-poison frog Phyllobates terribilis. GigaByte (Hong Kong, China), 2025, gigabyte157.

Goshayeshi L, et al. (2025) Germline variants in patients from the Iranian hereditary colorectal cancer registry. Cancer cell international, 25(1), 140.

Umeda M, et al. (2025) Fusion oncoproteins and cooperating mutations define disease phenotypes in NUP98-rearranged leukemia. medRxiv : the preprint server for health sciences.

Savage N, et al. (2025) CRISPR screen reveals SOX2 as a critical regulator of CD133 and cellular stress response in glioblastoma. Scientific reports, 15(1), 36228.

Micoli G, et al. (2025) Decoding the Genomic and Functional Landscape of Emerging Subtypes in Ovarian Cancer. Cancer discovery, 15(11), 2262.

Yim KM, et al. (2025) Cell-type-specific dysregulation of gene expression due to Chd8 haploinsufficiency during mouse cortical development. Cell genomics, 100986.

Figuerola-Bou E, et al. (2025) KDM6 Demethylases Contribute to EWSR1::FLI1-Driven Oncogenic Reprogramming in Ewing Sarcoma. Cancer research, 85(22), 4485.

Maurya SK, et al. (2025) Mucin 5AC Promotes Breast Cancer Brain Metastasis through cMET/CD44v6. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(5), 921.

Zhang Y, et al. (2025) Immune Dysregulation and Endometrial Receptivity Impairment in Women with Repeated Implantation Failure and Dyslipidemia. The Journal of clinical endocrinology and metabolism.

Kim AR, et al. (2025) Co-blockade of TGF? and PD-1 Reinvigorates Glioblastoma-Infiltrating CD8+ T Cells That Characteristically Upregulate TGF?RI Expression. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(15), 3306.

Pan S, et al. (2025) A holistic genome dataset of bacteria and archaea of mangrove sediments. GigaScience, 14.

Stockem CF, et al. (2025) Biomarker Analysis and Treatment Dynamics Following Preoperative Ipilimumab plus Nivolumab in Locally Advanced Urothelial Cancer from the Phase IB NABUCCO Study. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(18), 3897.

Jain N, et al. (2024) Absence of BTK, BCL2, and PLCG2 Mutations in Chronic Lymphocytic Leukemia Relapsing after First-Line Treatment with Fixed-Duration Ibrutinib plus Venetoclax. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(3), 498.

Umeda M, et al. (2024) A new genomic framework to categorize pediatric acute myeloid leukemia. Nature genetics, 56(2), 281.

Baroncelli R, et al. (2024) Genome evolution and transcriptome plasticity is associated with adaptation to monocot and dicot plants in Colletotrichum fungi. GigaScience, 13.

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.

Wang H, et al. (2024) The genomes of Dahlia pinnata, Cosmos bipinnatus, and Bidens alba in tribe Coreopsideae provide insights into polyploid evolution and inulin biosynthesis. GigaScience, 13.

Oh J, et al. (2024) Swd2/Cps35 determines H3K4 tri-methylation via interactions with Set1 and Rad6. BMC biology, 22(1), 105.