

Resource Summary Report

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Illumina: NovaSeq 6000 Sequencing System

RRID:SCR_016387

Type: Tool

Proper Citation

Illumina: NovaSeq 6000 Sequencing System (RRID:SCR_016387)

Resource Information

URL: <https://www.illumina.com/systems/sequencing-platforms/novaseq.html>

Proper Citation: Illumina: NovaSeq 6000 Sequencing System (RRID:SCR_016387)

Description: High-throughput platform used for next-generation sequencing (NGS) applications, including whole-genome, whole-exome, and whole-transcriptome sequencing. It is designed to provide a scalable, high-volume, and reliable way to sequence DNA and RNA for a wide range of genomic studies, from research to clinical applications.

Synonyms: Illumina NovaSeq 6000 Sequencing, Illumina NovaSeq 6000

Resource Type: instrument resource

Keywords: Instrument, equipment, sequencer, sequencing, dna, rna, platform, novaseq, sequencing system, USEdit

Specification URL: https://raw.githubusercontent.com/SciCrunch/RRID-Instruments/refs/heads/main/PDF/SCR_016387.pdf

Resource Name: Illumina: NovaSeq 6000 Sequencing System

Resource ID: SCR_016387

Alternate IDs: SCR_020150, Model_Number_NovaSeq_6000

Alternate URLs: <https://www.illumina.com/systems/sequencing-platforms/novaseq/specifications.html>

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260801T190538+0000

Ratings and Alerts

No rating or validation information has been found for Illumina: NovaSeq 6000 Sequencing System.

No alerts have been found for Illumina: NovaSeq 6000 Sequencing System.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 277 mentions in open access literature.

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

Lasse Opsahl EL, et al. (2026) Fibroblast STAT3 Activation Drives Organ-Specific Premetastatic Niche Formation. *Cancer research*, 86(1), 22.

Goala P, et al. (2026) IFN- γ -driven skewing towards Th1 over Th17 differentiation underlies CRS and neutropenia in CAR-T therapy. *The Journal of clinical investigation*, 136(1).

Barajas JM, et al. (2026) Tandem Duplications in UBTF Create XPO1-Dependent Nuclear Export Signals that Reveal a Leukemic Therapeutic Dependency. *Blood cancer discovery*, 7(1), 51.

Scourzic L, et al. (2026) T follicular helper cells transiently unlock a plasticity state in germinal centre B cells during the humoral immune response. *Nature cell biology*, 28(1), 35.

Cappadona C, et al. (2026) Multi-omics identifies oxidative stress, prothrombotic pathways, and lactoperoxidase variants as key factors in COVID-19 severity. *EBioMedicine*, 123, 106111.

Maerz MD, et al. (2026) BCG vaccination induces antibacterial effector functions among V α 1/3 T cells that are associated with protection against tuberculosis. *Cell reports. Medicine*, 102536.

Eme-Solan E, et al. (2026) Remodeling of skull bone channels regulates immune infiltration into the meninges during neuroinflammation. *Immunity*, 59(1), 116.

Furuya RL, et al. (2026) Comparison of breast and gastric HER2 immunohistochemistry (IHC) scoring criteria in the assessment of endometrial carcinoma. *Gynecologic oncology*, 204, 17.

Magee D, et al. (2025) Characterization of Plasma Cell-Free DNA Variants as of Tumor or Clonal Hematopoiesis Origin in 16,812 Advanced Cancer Patients. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(13), 2710.

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

Jinnou H, et al. (2025) Outer radial glia promotes white matter regeneration after neonatal brain injury. Cell reports. Medicine, 6(3), 101986.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. GigaScience, 14.

Ali MM, et al. (2025) Mechanisms of mitochondrial reactive oxygen species action in bone mesenchymal cells. bioRxiv : the preprint server for biology.

Kono T, et al. (2025) Protocol for characterizing craniopharyngioma subtypes and their microenvironments using single-cell RNA sequencing and immunohistochemistry. STAR protocols, 6(2), 103760.

Itkin B, et al. (2025) Next-generation sequencing failure rates in rare tumors: A real-world single-institution analysis. Medicine international, 5(3), 27.

Yoshimura T, et al. (2025) High-Throughput Drug Screening of Clear Cell Ovarian Cancer Organoids Reveals Vulnerability to Proteasome Inhibitors and Dinaciclib and Identifies AGR2 as a Therapeutic Target. Cancer research communications, 5(6), 1018.

Ning G, et al. (2025) BCAS2 promotes primitive hematopoiesis by sequestering β -catenin within the nucleus. eLife, 13.

Mehrabani-Tabari AA, et al. (2025) Inhibition of autophagy-lysosomal function exacerbates microglial and monocyte lipid metabolism reprogramming and dysfunction after brain injury. bioRxiv : the preprint server for biology.

Zhao W, et al. (2025) A prognostic signature for lung adenocarcinoma in people who have never smoked. bioRxiv : the preprint server for biology.

Luo H, et al. (2025) Large-Scale T-cell Receptor Repertoire Profiling Unveils Tumor-Specific Signals for Diagnosing Indeterminate Pulmonary Nodules. Cancer research, 85(24), 5141.