

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.

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.

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

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.

Shafer AM, et al. (2025) Immunocompetent Murine Models Recapitulate the Heterogeneous Tumor-Immune Microenvironment of Human Liposarcoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(23), 5078.

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

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.

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

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

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

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.

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.

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*.