Resource Summary Report

Generated by NIF on Sep 22, 2026

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: 20260919T195322+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 384 mentions in open access literature.

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

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

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.

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. GigaScience, 15.

Kelley RK, et al. (2026) T-Cell Receptor and Immune Gene Expression Pharmacodynamics for Durvalumab Alone and with Tremelimumab or Bevacizumab in Unresectable Hepatocellular Carcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(4), 694.

Huerga Encabo H, et al. (2026) Human TET2-Mutant Clonal Hematopoiesis Expansion Is Driven by Distinct Inflammatory Signaling Responses in Stem Cells Versus Myeloid Progeny. Blood cancer discovery, 7(2), 287.

Maeda M, et al. (2026) CRISPR screen of human pancreatic cancer xenografts identifies a KLF5 proliferation vulnerability through epigenetic modifiers NCAPD2 and MTHFD1. Molecular cancer, 25(1).

Jiang S, et al. (2026) Transcription factor EGR1 orchestrates ferroptosis to mitigate sepsis-induced myocardial injury by enhancing ferroportin expression. CytoJournal, 23, 3.

Ponz-Sarvisé M, et al. (2026) Lenvatinib plus Pembrolizumab for Patients with Previously Treated Advanced Gastric, Biliary Tract, or Pancreatic Cancer: Results from the Phase II LEAP-005 Study. Cancer research communications, 6(3), 673.

Spalato Ceruso M, et al. (2026) Adenosine A2B Receptor Promotes Tumor Progression and Metastases in Undifferentiated Pleomorphic Sarcoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1887.

Gholami S, et al. (2026) CXCR4 mRNA overexpression: an indicator of poor survival and predictor of response to immune checkpoint inhibitors in patients with metastatic colorectal cancer. BMJ oncology, 5(1), e001003.

DePuyt AE, et al. (2026) Type 1-polarized DC immunotherapeutic contains heterogeneous populations with IL-12p70 production restricted to a rare subset. bioRxiv : the preprint server for biology.

Kim S, et al. (2026) Gut microbiota transfer from autoimmune dry eye mice imprints stereotypic B cell receptor repertoires in the lacrimal gland and induces disease. Frontiers in immunology, 17, 1827057.

Bischoff AC, et al. (2026) Wilms Tumor 1-Expressing Stromal Cells Promote Pancreatic Cancer Progression. Cancer research, 86(2), 331.

Brodsky AL, et al. (2026) Combination Therapy with Copanlisib and Niraparib in Patients with Recurrent Endometrial and Ovarian Cancer (COPANIRA): Efficacy, Toxicity, and Translational Insights. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(7), 1234.

Sanz-Garcia E, et al. (2026) Investigating Early Kinetics in Plasma ctDNA and Peripheral T-cell Receptor Repertoire to Predict Treatment Outcomes to PD-1 Inhibitors in Head and Neck Squamous Cell Carcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(4), 735.

Valentín López JC, et al. (2026) Evolution of AR and Non-AR Alterations in ctDNA of Patients with Metastatic Prostate Cancer Treated in the Phase III Alliance A031201 Trial. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(12), 2413.

Zeng L, et al. (2026) Functional genomics reveals key gene families and molecular pathways for extreme cold survival in the khapra beetle. BMC biology, 24(1).

Kawazu M, et al. (2026) Genomic and Transcriptomic Analysis of High-Grade Endometrial Carcinoma Reveals Biological Heterogeneity and Molecular Classification Challenges. Cancer research communications, 6(4), 961.

Wang J, et al. (2026) Tumor-Resident Streptococcus pneumoniae Promotes Malignant Progression and Pazopanib Resistance in Clear Cell Renal Cell Carcinoma. Cancer research, 86(9), 2237.

Sahin IH, et al. (2026) Clinical and molecular characteristics of Class II and III BRAF mutations in colorectal cancer. NPJ precision oncology, 10(1).