

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

UNC School of Medicine Integrated Genomics Cores High Throughput Sequencing Core Facility

RRID:SCR_022620

Type: Tool

Proper Citation

UNC School of Medicine Integrated Genomics Cores High Throughput Sequencing Core Facility (RRID:SCR_022620)

Resource Information

URL: <https://www.med.unc.edu/genomics/about/>

Proper Citation: UNC School of Medicine Integrated Genomics Cores High Throughput Sequencing Core Facility (RRID:SCR_022620)

Description: Full service sequencing facility to assist with genetic and genomic research. Part of Integrated Genomics Cores. Offers comprehensive library services, NextGen sequencing and alternative technologies including long reads. Offers library preparations and multiple sequencing platforms including MiSeq, HiSeq, NovaSeq, NextSeq, BioNano, Oxford Nanopore. Services also include using techniques and data analyses via sister core BARC.

Abbreviations: HTSF

Synonyms: UNC School of Medicine Integrated Genomics Cores HighThroughput Sequencing Facility, University of North Carolina at Chapel Hill School of Medicine Integrated Genomics Cores High-Throughput Sequencing Facility, UNC School of Medicine HighThroughput Sequencing Facility

Resource Type: access service resource, core facility, service resource

Keywords: NextGen sequencing, library preparations, Illumina kits, non Illumina kits, novel R&D, Oxford Nanopore, BioNano, MiSeq, HiSeq, NovaSeq, NextSeq, BioNano, Oxford Nanopore, sequencing platforms, ABRF, USEdit

Availability: open

Resource Name: UNC School of Medicine Integrated Genomics Cores High Throughput Sequencing Core Facility

Resource ID: SCR_022620

Record Creation Time: 20220803T050137+0000

Record Last Update: 20260728T043640+0000

Ratings and Alerts

No rating or validation information has been found for UNC School of Medicine Integrated Genomics Cores High Throughput Sequencing Core Facility.

No alerts have been found for UNC School of Medicine Integrated Genomics Cores High Throughput Sequencing Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Hu K, et al. (2025) Development and Application of MiMouse, a Comprehensive Genomic Profiling Panel for Credentialing Mouse Tumor Models. Cancer research communications, 5(10), 1910.

Pantazis JC, et al. (2025) Integrating functional genomics and proteomics identifies Folate Carrier SLC19A1 as a predictor of pralatrexate sensitivity in T-cell lymphoma. bioRxiv : the preprint server for biology.