

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Virginia Tech Biocomplexity Institute Genomics Sequencing Center Core Facility

RRID:SCR_017958

Type: Tool

Proper Citation

Virginia Tech Biocomplexity Institute Genomics Sequencing Center Core Facility
(RRID:SCR_017958)

Resource Information

URL: <https://www.bi.vt.edu/services/genomics-sequencing-center>

Proper Citation: Virginia Tech Biocomplexity Institute Genomics Sequencing Center Core Facility (RRID:SCR_017958)

Description: Core for development and application of Next-Generation Sequencing technologies. Provides experimental design consultation, and genomic, transcriptomic, and functional-genomics services. Specializes in development and application of Next-Generation Sequencing technologies and bioinformatics analyses. Instruments include Illumina NovaSeq 6000, Illumina NextSeq 500, Illumina MiSeq, Thermo Ion S5. Services include mRNA-Seq: Stranded and non-stranded, high levels of multiplexing up to 96 or more samples on NovaSeq; Standard amounts, Stranded-Seq: 500 ng total RNA, RIN 8; Low Input amounts, Stranded-Seq: 5 ng to 100 ng total RNA; Ultra Low Input amounts, Non-Stranded-Seq: 1-1000 cells or 10 pg - 10 ng; Total RNA-Seq - Stranded: 5-250 ng; Small RNA-Seq: 1 ug, multiplexing up to 48 samples/NextSeq run; Partially degraded samples - Stranded and Non-Stranded: LCM, FFPE samples, both stranded and non-stranded, 50 -100 ng; Microbial rRNA depletion and RNA-Seq with amounts as low as 1-5 ug of total RNA; Whole Genome Sequencing; Human / Animal / Plant; Microbial; As low as 1 ng De novo Sequencing; Exome/Targeted capture re-sequencing: Enables high sequencing depths; Agilent and Illumina platforms; Human, Mouse, Canine and other species; Targeted re-sequencing: High levels of multiplexing up to 200 samples / MiSeq run; PCR Amplicon sequencing; Illumina and Agilent platforms; ChIP-Seq; Transcription factor analysis; Histone modifications; DNA Methylation; MeDIP- and MBD-Seq; MethylC-Seq; Agilent SureSelect MethylC-Seq; Nucleosome Mapping; FAIRE-Seq and DNase I-Seq; 16S / 18S / ITS amplicon sequencing; Whole Genome Metagenomic sequencing; Metatranscriptomic analysis; DNA/chromatin fragmentation by Covaris DNA / RNA quality analysis: BioAnalyzer / TapeStation assay, Qubit (Picogreen) assays; qPCR services.

Abbreviations: GSC

Synonyms: Genomics Sequencing Center

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

Keywords: Genomic, sequencing, next, generation, design, consultation, transcriptomic, functional, service, analysis, DNA, RNA, PCR, qPCR, core, ABRF

Availability: Open

Resource Name: Virginia Tech Biocomplexity Institute Genomics Sequencing Center Core Facility

Resource ID: SCR_017958

Alternate IDs: ABRF_991

Record Creation Time: 20220129T080337+0000

Record Last Update: 20260905T133416+0000

Ratings and Alerts

No rating or validation information has been found for Virginia Tech Biocomplexity Institute Genomics Sequencing Center Core Facility.

No alerts have been found for Virginia Tech Biocomplexity Institute Genomics Sequencing Center 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 [Kravitz](#) .

Mancarella C, et al. (2023) Extracellular vesicle-associated IGF2BP3 tunes Ewing sarcoma cell migration and affects PI3K/Akt pathway in neighboring cells. Cancer gene therapy, 30(9), 1285.

Wang J, et al. (2022) Vaccination with Designed Neopeptides Induces Intratumoral, Cross-reactive CD4+ T-cell Responses in Glioblastoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 28(24), 5368.