# Resource Summary Report

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## 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 RRID .

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.