

Resource Summary Report

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Penn Next-Generation Sequencing Core

RRID:SCR_010026

Type: Tool

Proper Citation

Penn Next-Generation Sequencing Core (RRID:SCR_010026)

Resource Information

URL: <http://eagle-i.itmat.upenn.edu/i/00000138-babb-5786-9cd7-d7e280000000>

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Description: Core facility that provides the following services: Sequencing sample preparation service, Illumina sequencing service, Initial analysis of sequencing data, Next-generation sequencing data delivery. The NGSC offers ultra high throughput sequencing services for the Perelman School of Medicine research community. We offer library quality assessments, sequencing, and optional preliminary data analysis for a wide variety of experimental protocols including ChIP-seq, RNA-Seq, HITS-CLIP, miR-Seq, exome capture, and BIS-seq. We offer limited library preparation services, but can advise on library preparation techniques. We have two Illumina hiSeq2000s for large-scale sequencing and a MiSeq for sample evaluation or library testing. To get started, visit our website, create an account for yourself, then create a new experiment and we will contact you.

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

Keywords: library preparation, protein interaction detection, exome sequencing, dna sequencing, rna sequencing, mirna expression analysis, chip-seq assay, data analysis, sequencing assay, data transfer

Resource Name: Penn Next-Generation Sequencing Core

Resource ID: SCR_010026

Alternate IDs: nlx_156496

Record Creation Time: 20220129T080256+0000

Record Last Update: 20260904T000653+0000

Ratings and Alerts

No rating or validation information has been found for Penn Next-Generation Sequencing Core.

No alerts have been found for Penn Next-Generation Sequencing Core.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Xiao E, et al. (2017) Diabetes Enhances IL-17 Expression and Alters the Oral Microbiome to Increase Its Pathogenicity. Cell host & microbe, 22(1), 120.