Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

University of Pennsylvania Penn Genomics and Sequencing Core Facility

RRID:SCR_024999
Type: Tool

Proper Citation

University of Pennsylvania Penn Genomics and Sequencing Core Facility (RRID:SCR_024999)

Resource Information

URL: https://genetics.med.upenn.edu/cores/pgsc/

Proper Citation: University of Pennsylvania Penn Genomics and Sequencing Core Facility (RRID:SCR_024999)

Description: Provided services include molecular profiling of DNA and RNA on different platforms, Sanger sequencing, full service Next Generation Sequencing with different applications and bioinformatics, fragment analysis including human cell line authentication., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: , Penn Genomics and Sequencing Core, University of Pennsylvania Penn Genomics and Sequencing Core

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

Keywords: ABRF, molecular profiling of DNA and RNA, Sanger sequencing, Next Generation Sequencing, fragment analysis, human cell line authentication,

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: University of Pennsylvania Penn Genomics and Sequencing Core Facility

Resource ID: SCR_024999

Alternate IDs: ABRF_2627

Alternate URLs: https://coremarketplace.org/?FacilityID=2627&citation=1

Record Creation Time: 20240209T050239+0000

Record Last Update: 20260912T200435+0000

Ratings and Alerts

No rating or validation information has been found for University of Pennsylvania Penn Genomics and Sequencing Core Facility.

No alerts have been found for University of Pennsylvania Penn Genomics and Sequencing Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Riley JF, et al. (2026) PINK1/Parkin-dependent mitophagy mediates astrocytic inflammatory responses to mitochondrial damage. bioRxiv : the preprint server for biology.

Rood JE, et al. (2026) Optimal murine CD4+ T cell priming by mRNA-lipid nanoparticle vaccines requires endogenous antigen processing. Nature communications, 17(1), 1327.

Moses R, et al. (2026) Variation at the R181 residue of p53 confers loss of p53 DNA binding cooperativity with the retention of mitochondrial-associated apoptosis. Molecular cancer research : MCR.

Moses R, et al. (2025) Variation at the R181 residue of p53 confers loss of p53 DNA binding cooperativity with the retention of mitochondrial-associated apoptosis. bioRxiv : the preprint server for biology.

Tondi Resta I, et al. (2025) Mucinous Cystadenocarcinomas of the Breast Exhibit Heterogeneous Genomic Profile as Triple Negative Breast Cancer, Harbor Alterations in PIK3CA, PTEN, AKT1, and GNAS Genes, and May Not Be Indolent. International journal of surgical pathology, 33(7), 1583.

Onecha VV, et al. (2025) Space- and Time-Defined Monte Carlo Dosimetry Explains Ovarian Cancer Cell Viability in Targeted ??-Particle Therapy With Astatine 211-ParaThanatrace. International journal of radiation oncology, biology, physics.

Litichevskiy L, et al. (2025) Gut metagenomes reveal interactions between dietary restriction, ageing and the microbiome in genetically diverse mice. Nature microbiology, 10(5), 1240.

Sehgal P, et al. (2025) NRCAM variant defined by microexon skipping is a targetable cell surface proteoform in high-grade gliomas. Cell reports, 44(8), 116099.