Resource Summary Report

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Penn State College of Medicine Genome Sciences Core Facility

RRID:SCR_021123
Type: Tool

Proper Citation

Penn State College of Medicine Genome Sciences Core Facility (RRID:SCR_021123)

Resource Information

URL: https://research.med.psu.edu/core-facilities/genome-sciences/

Proper Citation: Penn State College of Medicine Genome Sciences Core Facility (RRID:SCR_021123)

Description: Provides consultation, instrumentation and services in genomic, epigenomic and transcriptomic studies, analysis of candidate SNPs and mRNAs to whole genome, exome, epigenome and transcriptome sequencing. Services are also available for variety of study designs extending from few laboratory samples to large clinical projects involving hundreds or thousands of samples.Bioinformatics service is available for data analysis.Facility receives either tissue, DNA/RNA or customer generated NGS libraries. Samples are processed based on agreement reached during consultations on design of experiment.

Synonyms: Genome Sciences and Bioinformatics Facility, Pennsylvania State University Genome Sciences and Bioinformatics Facility

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

Keywords: genomic, epigenomic, transcriptomic, consultation, instrumentation, services, iLab, ABRF, ABRF

Availability: open

Resource Name: Penn State College of Medicine Genome Sciences Core Facility

Resource ID: SCR_021123

Alternate IDs: ABRF_1162

Alternate URLs: https://coremarketplace.org/?FacilityID=1162

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260729T044502+0000

Ratings and Alerts

No rating or validation information has been found for Penn State College of Medicine Genome Sciences Core Facility.

No alerts have been found for Penn State College of Medicine Genome Sciences Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 47 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Popova EY, et al. (2025) Epigenetic Modifiers to Treat Retinal Degenerative Diseases. Cells, 14(13).

Lawrence SS, et al. (2025) Interferon-?/Janus Kinase 1/STAT1 Signaling Represses Forkhead Box A1 and Drives a Basal Transcriptional State in Muscle-Invasive Bladder Cancer. The American journal of pathology, 195(5), 1013.

Chan K, et al. (2025) Genome Instability Precedes Viral Integration in Human Papillomavirus-Transformed Tonsillar Keratinocytes. Molecular cancer research : MCR, 23(2), 119.

Kim SY, et al. (2025) Involvement of p38 MAPK and MAPKAPK2 in promoting cell death and the inflammatory response to ischemic stress associated with necrotic glioblastoma. Cell death & disease, 16(1), 12.

Morais LH, et al. (2025) The gut microbiome promotes mitochondrial respiration in the brain of a Parkinson's disease mouse model. NPJ Parkinson's disease, 11(1), 301.

Manjila SB, et al. (2025) Brain-wide connectivity and novelty response of the dorsal endopiriform nucleus in mice. Cell reports, 44(7), 115827.

Apsley AT, et al. (2025) Cross-tissue comparison of epigenetic aging clocks in humans. Aging cell, 24(4), e14451.

Strömbäck C, et al. (2025) Positive anticipated affective reactions increase pro-environmental behavior. iScience, 28(5), 112389.

Kumar R, et al. (2025) The HCMV tegument protein UL88 degrades MyD88 and reduces innate immune activation. Journal of virology, 99(8), e0041425.

Butic AB, et al. (2025) PD-1 regulates CD4+ T cell-mediated CD8+ T cell responses in the brain to balance viral control and neuroinflammation. bioRxiv : the preprint server for biology.

Dhamdhere MR, et al. (2025) IGF2BP1 fosters an immunosuppressive tumor microenvironment in high-risk neuroblastoma, contributing to their resistance to immunotherapy. Oncoimmunology, 14(1), 2584408.

Montemarano A, et al. (2025) Projection-defined ventral tegmental area neurons exhibit fentanyl-induced molecular and functional adaptations that differentially support drug-context associations. bioRxiv : the preprint server for biology.

VanCleave AM, et al. (2025) Rapid proteasomal degradation of the stress response protein REDD2 is mediated by the E3 ligase HUWE1. Biochemical and biophysical research communications, 777, 152270.

Hanafiah A, et al. (2024) PRC1 and CTCF-Mediated Transition from Poised to Active Chromatin Loops Drives Bivalent Gene Activation. bioRxiv : the preprint server for biology.

Geng Z, et al. (2024) AUTS2 disruption causes neuronal differentiation defects in human cerebral organoids through hyperactivation of the WNT/?-catenin pathway. Scientific reports, 14(1), 19522.

Torres MC, et al. (2024) Activity of DNA polymerase ? across the genome in human fibroblasts. Proceedings of the National Academy of Sciences of the United States of America, 121(28), e2403130121.

Kapur MM, et al. (2024) Heterologous expression of the human wild-type and variant NaV 1.8 (A1073V) in rat sensory neurons. Neurogastroenterology and motility, 36(3), e14748.

Straka J, et al. (2024) CAF-1 promotes efficient PrimPol recruitment to nascent DNA for single-stranded DNA gap formation. Nucleic acids research, 52(22), 13865.

Hattori T, et al. (2024) ER stress elicits non-canonical CASP8 (caspase 8) activation on autophagosomal membranes to induce apoptosis. Autophagy, 20(2), 349.

Popova EY, et al. (2024) Temporal changes in mouse hippocampus transcriptome after pilocarpine-induced seizures. Frontiers in neuroscience, 18, 1384805.