Resource Summary Report

Generated by NIF on May 19, 2025

Van Andel Institute Genomics Core Facility

RRID:SCR_022913
Type: Tool

Proper Citation

Van Andel Institute Genomics Core Facility (RRID:SCR_022913)

Resource Information

URL: https://genomicscore.vai.org

Proper Citation: Van Andel Institute Genomics Core Facility (RRID:SCR_022913)

Description: Provides services including Next Generation Sequencing, single cell Genomics, and Spatial Transcriptomics facility. Provides experimental design support, library generation, and Illumina and Nanopore Sequencing.

Synonyms: Van Andel Institute VAI - Genomics Core, VAI - Genomics Core

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

Keywords: USEDit, ABRF, Next Generation Sequencing, single cell Genomics, Spatial Transcriptomics facility

Funding:

Resource Name: Van Andel Institute Genomics Core Facility

Resource ID: SCR_022913

Alternate IDs: ABRF_1600

Alternate URLs: https://coremarketplace.org/?FacilityID=1600&citation=1

Record Creation Time: 20221022T050155+0000

Record Last Update: 20250517T060522+0000

Ratings and Alerts

No rating or validation information has been found for Van Andel Institute Genomics Core Facility.

No alerts have been found for Van Andel Institute Genomics Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Goralski TM, et al. (2024) Spatial transcriptomics reveals molecular dysfunction associated with cortical Lewy pathology. Nature communications, 15(1), 2642.

Kochmanski J, et al. (2024) Developmental origins of Parkinson's disease risk: perinatal exposure to the organochlorine pesticide dieldrin leads to sex-specific DNA modifications in critical neurodevelopmental pathways in the mouse midbrain. bioRxiv : the preprint server for biology.

Booms A, et al. (2024) Parkinson's disease risk enhancers in microglia. iScience, 27(2), 108921.

Chomiak AA, et al. (2024) Select EZH2 inhibitors enhance viral mimicry effects of DNMT inhibition through a mechanism involving NFAT:AP-1 signaling. Science advances, 10(13), eadk4423.

Vatsa N, et al. (2024) Network analysis of ?-synuclein pathology progression reveals p21-activated kinases as regulators of vulnerability. bioRxiv : the preprint server for biology.

Guak H, et al. (2024) Transcriptional programming mediated by the histone demethylase KDM5C regulates dendritic cell population heterogeneity and function. Cell reports, 43(8), 114506.

Tiedemann RL, et al. (2024) UHRF1 ubiquitin ligase activity supports the maintenance of low-density CpG methylation. Nucleic acids research, 52(22), 13733.

Tiedemann RL, et al. (2024) UHRF1 ubiquitin ligase activity supports the maintenance of low-density CpG methylation. bioRxiv : the preprint server for biology.

Xue Z, et al. (2024) A potent and selective ENL degrader suppresses oncogenic gene expression and leukemia progression. Science advances, 10(35), eado1432.

Paul EN, et al. (2023) Cysteine-rich intestinal protein 1 is a novel surface marker for human

myometrial stem/progenitor cells. Communications biology, 6(1), 686.

Pérez-Mojica JE, et al. (2023) Single-embryo RNA sequencing for continuous and sex-specific gene expression analysis on Drosophila. STAR protocols, 4(3), 102535.

Panzeri I, et al. (2023) Developmental priming of cancer susceptibility. bioRxiv : the preprint server for biology.

Goralski T, et al. (2023) Spatial transcriptomics reveals molecular dysfunction associated with Lewy pathology. bioRxiv : the preprint server for biology.

Paul EN, et al. (2023) Cysteine-Rich Intestinal Protein 1 is a Novel Surface Marker for Myometrial Stem/Progenitor Cells. bioRxiv : the preprint server for biology.