

Resource Summary Report

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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: access service resource, core facility, service resource

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

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: 20260905T133430+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 42 mentions in open access literature.

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

Zameer S, et al. (2026) Genome-wide DNA methylation profiling in COVID-19 positive patients reveals alterations in pathways linked to neurological dysfunction. *Clinical epigenetics*, 18(1).

Panzeri I, et al. (2026) Chronic High-Fat Diet Does Not Alter Overall Cancer Incidence in Trp53R270H/+ Mice. *Cancer research communications*, 6(6), 1336.

Zeng TB, et al. (2026) SETDB1 enables development beyond cleavage stages by extinguishing the MERVL-driven two-cell totipotency transcriptional program in the mouse embryo. *eLife*, 15.

Roth MO, et al. (2026) Molecular basis for methylation-sensitive editing by Cas9. *Nature*, 653(8116), 1229.

Gruber T, et al. (2026) Midbrain Tet1 dosage defines inter-individual binge-eating susceptibility. *bioRxiv : the preprint server for biology*.

Jang HJ, et al. (2026) Bone marrow immunosuppressive states associate with survival after guadecitabine and atezolizumab therapy in HMA-R/R MDS. *Blood neoplasia*, 3(3), 100243.

Booms A, et al. (2026) Characterization of selection on immune regulatory elements and MHC gene diversity in Holstein cattle. *Journal of dairy science*.

Perez-Mojica JE, et al. (2025) Resolving early embryonic metabolism in *Drosophila* through single-embryo metabolomics and transcriptomics. *Nature metabolism*.

Dahabieh MS, et al. (2025) The prostacyclin receptor PTGIR is a NRF2-dependent regulator of CD8+ T cell exhaustion. *Nature immunology*, 26(7), 1139.

Panzeri I, et al. (2025) TRIM28-dependent developmental heterogeneity determines cancer susceptibility through distinct epigenetic states. *Nature cancer*, 6(2), 385.

Diegel CR, et al. (2025) The class A repeats of LRP5 are required for normal development of bone, retinal vasculature and mammary gland in vivo. *Disease models & mechanisms*, 18(11).

Spix NJ, et al. (2025) High-coverage allele-resolved single-cell DNA methylation profiling reveals cell lineage, X-inactivation state, and replication dynamics. *Nature communications*, 16(1), 6273.

Chomiak AA, et al. (2025) Dual EZH1/2 inhibition enhances DNMT inhibitor efficacy in colon cancer through targeting H3K27me1. *bioRxiv : the preprint server for biology*.

Liu Y, et al. (2025) EHMT2 Controls Neural Crest-Derived Craniofacial Development but is Dispensable in Limb Development. *bioRxiv : the preprint server for biology*.

Finneran DJ, et al. (2025) Mature tau pathology is not improved by interfering with interleukin-1 receptor signaling in two mouse models of tauopathy. *PLoS one*, 20(11), e0335409.

Beddows I, et al. (2025) Impact of BRCA mutations, age, surgical indication, and hormone status on the molecular phenotype of the human Fallopian tube. *Nature communications*, 16(1), 2981.

Zhong ZA, et al. (2025) Local Misalignment Scoring Reveals Spatially Uniform Chondrocyte Disorganization in a Wnt5a-C83S Knock-in Model of Robinow Syndrome. *Research square*.

Xue Z, et al. (2025) Expression of ENL YEATS domain tumor mutations in nephrogenic or stromal lineage impairs kidney development. *Nature communications*, 16(1), 2531.

Liu M, et al. (2025) Dnmt3a2 expression during embryonic development is required for phenotypic stability. *Communications biology*, 9(1), 44.

Oswald BM, et al. (2025) Dietary restriction reprograms CD8+ T cell fate to enhance anti-tumour immunity and immunotherapy responses. *Nature metabolism*, 7(12), 2489.