Resource Summary Report

Generated by NIF on Apr 16, 2025

Vanderbilt BioVU

RRID:SCR_004632
Type: Tool

Proper Citation

Vanderbilt BioVU (RRID:SCR_004632)

Resource Information

URL: http://dbmi.mc.vanderbilt.edu/research/dnadatabank.html

Proper Citation: Vanderbilt BioVU (RRID:SCR_004632)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 11, 2023. BioVU is a research resource providing a View into biology at the level of DNA and other important macromolecules. BioVU has two major components. The first is a repository of DNA samples (extracted from discarded blood samples) that are coded solely by a Research Unique Identifier (RUI) derived from the Medical Record Number (MRN) using a one-way hash function. This is a computer algorithm that creates a transformation of each MRN such that the resulting RUI (which is in this instance is a 512 byte identifier) is unique, and has the property that it is not possible to infer or compute the MRN that generated it. As of early 2009, over 50,000 DNA samples were in the biobank, with new samples being added at the rate of approximately 700 per week. The second component of the resource is the creation of a database known as the Synthetic Derivative which is a collection of de-identified information extracted from VUMC''s electronic clinical information systems, indexed by the same one-way RUI used to track samples, and with content changed by deletion or permutation of all identifiers contained within each record. The Synthetic Derivative search interface is available to Vanderbilt researchers via the StarBRITE research portal created and maintained by the Vanderbilt Institute for Clinical and Translational Research. This user interface enables investigators meeting protocol approval criteria and other user agreement requirements to receive protocol-specific sets of data derived from DNA samples and from the Synthetic Derivative.

Abbreviations: BioVU

Synonyms: BioVU: Vanderbilts DNA Databank, BioVU: Vanderbilt''s DNA Databank, BioVU DNA Databank

Resource Type: biomaterial supply resource, material resource

Keywords: dna, blood, clinical, FASEB list

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Vanderbilt BioVU

Resource ID: SCR_004632

Alternate IDs: nlx_63125

Record Creation Time: 20220129T080225+0000

Record Last Update: 20250410T065202+0000

Ratings and Alerts

No rating or validation information has been found for Vanderbilt BioVU.

No alerts have been found for Vanderbilt BioVU.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 110 mentions in open access literature.

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

Douville NJ, et al. (2025) Polygenic Score for the Prediction of Postoperative Nausea and Vomiting: A Retrospective Derivation and Validation Cohort Study. Anesthesiology, 142(1), 52.

Wang C, et al. (2025) Integrating electronic health records and GWAS summary statistics to predict the progression of autoimmune diseases from preclinical stages. Nature communications, 16(1), 180.

Middha P, et al. (2024) Polygenic risk score for ulcerative colitis predicts immune checkpoint inhibitor-mediated colitis. Nature communications, 15(1), 2568.

Sealock JM, et al. (2024) Cross-EHR validation of antidepressant response algorithm and

links with genetics of psychiatric traits. medRxiv : the preprint server for health sciences.

Guare LA, et al. (2024) Enhancing genetic association power in endometriosis through unsupervised clustering of clinical subtypes identified from electronic health records. Research square.

Kerchberger VE, et al. (2024) Electronic health record biobank cohort recapitulates an association between the MUC5B promoter polymorphism and ARDS in critically ill adults. medRxiv : the preprint server for health sciences.

Keaton JM, et al. (2024) Genome-wide analysis in over 1 million individuals of European ancestry yields improved polygenic risk scores for blood pressure traits. Nature genetics, 56(5), 778.

Vlasschaert C, et al. (2024) Clonal hematopoiesis of indeterminate potential is associated with acute kidney injury. Nature medicine, 30(3), 810.

Niarchou M, et al. (2024) Medical and genetic correlates of long-term buprenorphine treatment in the electronic health records. Translational psychiatry, 14(1), 20.

Ueland TE, et al. (2024) Multiancestry transferability of a polygenic risk score for diverticulitis. BMJ open gastroenterology, 11(1).

Carmona-Berrio D, et al. (2024) SOX6 expression and aneurysms of the thoracic and abdominal aorta. iScience, 27(9), 110436.

Johnson EC, et al. (2024) Cross-ancestry genetic investigation of schizophrenia, cannabis use disorder, and tobacco smoking. Neuropsychopharmacology : official publication of the American College of Neuropsychopharmacology, 49(11), 1655.

Jasper EA, et al. (2024) Genetic predictors of blood pressure traits are associated with preeclampsia. Scientific reports, 14(1), 17613.

Aggarwal SK, et al. (2024) Individualized Dose-Response to Statins Associated with Cardiovascular Disease Outcomes. JACC. Advances, 3(4).

Kresge HA, et al. (2024) Phenomewide Association Study of Health Outcomes Associated With the Genetic Correlates of 25 Hydroxyvitamin D Concentration and Vitamin D Binding Protein Concentration. Twin research and human genetics : the official journal of the International Society for Twin Studies, 27(2), 69.

Miller-Fleming TW, et al. (2024) Developing a phenotype risk score for tic disorders in a large, clinical biobank. Translational psychiatry, 14(1), 311.

Davis CN, et al. (2024) Multivariate, Multi-omic Analysis in 799,429 Individuals Identifies 134 Loci Associated with Somatoform Traits. medRxiv : the preprint server for health sciences.

Poisner H, et al. (2024) Genetic determinants and phenotypic consequences of blood T-cell proportions in 207,000 diverse individuals. Nature communications, 15(1), 6732.

Rich AL, et al. (2024) The broad impact of cell death genes on the human disease phenome. Cell death & disease, 15(4), 251.

Meng X, et al. (2024) Multi-ancestry genome-wide association study of major depression aids locus discovery, fine mapping, gene prioritization and causal inference. Nature genetics, 56(2), 222.