Resource Summary Report

Generated by NIF on Aug 12, 2026

BioBankEngine

RRID:SCR_015678
Type: Tool

Proper Citation

BioBankEngine (RRID:SCR_015678)

Resource Information

URL: https://biobankengine.stanford.edu/

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Description: This engine presents case-control association results from the UK Biobank hospital in-patient health-related outcomes summary information data (Data-Field 41202); computational grouping of phenotypes with cancer (Category 100092) registry, death registry data (Category 100093), algorithmically-defined outcomes (Category 42), and verbal questionnaire data (Category 100071); and manually curated grouping of phenotypes.

Resource Type: software tool

Resource Name: BioBankEngine

Resource ID: SCR_015678

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260808T190039+0000

Ratings and Alerts

No rating or validation information has been found for BioBankEngine.

No alerts have been found for BioBankEngine.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Justesen JM, et al. (2026) A loss-of-function variant in GFRAL associates with increased alcohol consumption in humans. bioRxiv : the preprint server for biology.

Zucker R, et al. (2025) Integrative Gene-Centric Analysis Reveals Cellular Pathways Associated with Heritable Breast Cancer Predisposition. Cancers, 17(24).

Li X, et al. (2024) Antibody immune responses and causal relationships in four immune skin diseases: Evidence from Mendelian randomization and Bayesian Weighting (Antibody Responses in Skin Diseases: MR & Bayesian). Skin research and technology : official journal of International Society for Bioengineering and the Skin (ISBS) [and] International Society for Digital Imaging of Skin (ISDIS) [and] International Society for Skin Imaging (ISSI), 30(8), e13875.

Pinto EM, et al. (2024) Multiple TP53 p.R337H haplotypes and implications for tumor susceptibility. HGG advances, 5(1), 100244.

Pinto EM, et al. (2023) Clinical and functional analysis of the germline TP53 p.K164E acetylation site variant. Cold Spring Harbor molecular case studies, 9(4).

Park S, et al. (2022) Serum bilirubin and kidney function: a Mendelian randomization study. Clinical kidney journal, 15(9), 1755.

Bomba L, et al. (2022) Whole-exome sequencing identifies rare genetic variants associated with human plasma metabolites. American journal of human genetics, 109(6), 1038.

Amar D, et al. (2021) Graphical analysis for phenome-wide causal discovery in genotyped population-scale biobanks. Nature communications, 12(1), 350.

Lee KS, et al. (2021) A genome wide association study for lung function in the Korean population using an exome array. The Korean journal of internal medicine, 36(Suppl 1), S142.

Sinnott-Armstrong N, et al. (2021) Genetics of 35 blood and urine biomarkers in the UK Biobank. Nature genetics, 53(2), 185.

Ilardo M, et al. (2021) An Erythropoietin-Independent Mechanism of Erythrocytic Precursor Proliferation Underlies Hypoxia Tolerance in Sea Nomads. Frontiers in physiology, 12, 760851.

DeBoever C, et al. (2020) Assessing Digital Phenotyping to Enhance Genetic Studies of Human Diseases. American journal of human genetics, 106(5), 611.

Li Z, et al. (2020) Integrating Mouse and Human Genetic Data to Move beyond GWAS and Identify Causal Genes in Cholesterol Metabolism. Cell metabolism, 31(4), 741.

Qian J, et al. (2020) A fast and scalable framework for large-scale and ultrahigh-dimensional sparse regression with application to the UK Biobank. PLoS genetics, 16(10),

e1009141.

Hellwege JN, et al. (2019) Heritability and genome-wide association study of benign prostatic hyperplasia (BPH) in the eMERGE network. Scientific reports, 9(1), 6077.

McInnes G, et al. (2019) Global Biobank Engine: enabling genotype-phenotype browsing for biobank summary statistics. Bioinformatics (Oxford, England), 35(14), 2495.

Br?i? L, et al. (2019) Genome-wide association analysis suggests novel loci underlying thyroid antibodies in Hashimoto's thyroiditis. Scientific reports, 9(1), 5360.

Abul-Husn NS, et al. (2019) Personalized Medicine and the Power of Electronic Health Records. Cell, 177(1), 58.

Ilardo MA, et al. (2018) Physiological and Genetic Adaptations to Diving in Sea Nomads. Cell, 173(3), 569.

Sadler JBA, et al. (2018) A cancer-associated polymorphism in ESCRT-III disrupts the abscission checkpoint and promotes genome instability. Proceedings of the National Academy of Sciences of the United States of America, 115(38), E8900.