Resource Summary Report

Generated by RRID on Apr 18, 2025

Trans-Omics for Precision Medicine (TOPMed) Program

RRID:SCR_015677
Type: Tool

Proper Citation

Trans-Omics for Precision Medicine (TOPMed) Program (RRID:SCR_015677)

Resource Information

URL: https://www.nhlbi.nih.gov/research/resources/nhlbi-precision-medicine-initiative/topmed

Proper Citation: Trans-Omics for Precision Medicine (TOPMed) Program (RRID:SCR_015677)

Description: Funding program for Precision Medicine genome sequencing from the National Institutes of Health, NHBLI.

Abbreviations: TOPMED

Resource Type: tissue bank, material resource, biomaterial supply resource

Funding:

Resource Name: Trans-Omics for Precision Medicine (TOPMed) Program

Resource ID: SCR_015677

Record Creation Time: 20220129T080327+0000

Record Last Update: 20250418T055430+0000

Ratings and Alerts

No rating or validation information has been found for Trans-Omics for Precision Medicine (TOPMed) Program.

No alerts have been found for Trans-Omics for Precision Medicine (TOPMed) Program.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Huang X, et al. (2024) Evaluation of multiple breast cancer polygenic risk score panels in women of Latin American heritage. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology.

Sheehan PW, et al. (2023) An astrocyte BMAL1-BAG3 axis protects against alpha-synuclein and tau pathology. Neuron, 111(15), 2383.

Nassar AH, et al. (2022) Ancestry-driven recalibration of tumor mutational burden and disparate clinical outcomes in response to immune checkpoint inhibitors. Cancer cell, 40(10), 1161.

Lewis MA, et al. (2022) Investigating the characteristics of genes and variants associated with self-reported hearing difficulty in older adults in the UK Biobank. BMC biology, 20(1), 150.

Sarnowski C, et al. (2018) Whole genome sequence analyses of brain imaging measures in the Framingham Study. Neurology, 90(3), e188.

Girolami F, et al. (2018) Contemporary genetic testing in inherited cardiac disease: tools, ethical issues, and clinical applications. Journal of cardiovascular medicine (Hagerstown, Md.), 19(1), 1.

Zerbino DR, et al. (2018) Ensembl 2018. Nucleic acids research, 46(D1), D754.

Novak AM, et al. (2017) A graph extension of the positional Burrows-Wheeler transform and its applications. Algorithms for molecular biology : AMB, 12, 18.

He KY, et al. (2017) Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS genetics, 13(3), e1006678.

Zhang D, et al. (2017) SEQSpark: A Complete Analysis Tool for Large-Scale Rare Variant Association Studies Using Whole-Genome and Exome Sequence Data. American journal of human genetics, 101(1), 115.

Smith JG, et al. (2017) Molecular Epidemiology of Heart Failure: Translational Challenges and Opportunities. JACC. Basic to translational science, 2(6), 757.

Auer PL, et al. (2016) Guidelines for Large-Scale Sequence-Based Complex Trait

Association Studies: Lessons Learned from the NHLBI Exome Sequencing Project. American journal of human genetics, 99(4), 791.