Resource Summary Report

Generated by kravitz2 on Aug 1, 2026

All of Us

RRID:SCR_027032
Type: Tool

Proper Citation

All of Us (RRID:SCR_027032)

Resource Information

URL: https://www.researchallofus.org

Proper Citation: All of Us (RRID:SCR_027032)

Description: Portal stores health data from participants from across the United States. Provides interactive Data Browser where anyone can learn about the type and quantity of data that All of Us collects. Users can explore aggregate data including genomic variants, survey responses, physical measurements, electronic health record information, and wearables data.

Resource Type: portal, data or information resource, database

Keywords: health data, United States data, genomic variants, survey responses, physical measurements, electronic health record information,

Availability: Free, Freely available,

Resource Name: All of Us

Resource ID: SCR_027032

Record Creation Time: 20250605T060221+0000

Record Last Update: 20260801T191404+0000

Ratings and Alerts

No rating or validation information has been found for All of Us.

No alerts have been found for All of Us.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 24 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Chan IN, et al. (2025) Associations of sleep-associated variants with wearable-derived sleep stages in the All of Us research program. Sleep, 48(11).

Kim D, et al. (2025) Genetic underpinnings of the heterogeneous impact of obesity on lipid levels and cardiovascular disease. Genome medicine, 17(1), 113.

Chen HH, et al. (2025) Population-specific polygenic risk scores for people of Han Chinese ancestry. Nature, 648(8092), 128.

Berry ASF, et al. (2025) X and Y gene dosage effects are primary contributors to human sexual dimorphism: The case of height. Proceedings of the National Academy of Sciences of the United States of America, 122(22), e2503039122.

Lin MR, et al. (2025) Whole exome sequencing and polygenic risk assessment for kidney functions and clinical management in both hospital-based cohort and population-based Asian cohorts. Journal of biomedical science, 32(1), 72.

Sanders K, et al. (2025) GWAS for Periodontitis Phenotypes Using Multi-Ancestry All of Us Research Platform. medRxiv : the preprint server for health sciences.

Jin Q, et al. (2025) Opportunistic screening of type 2 diabetes with deep metric learning using electronic health records. Scientific reports, 15(1), 41892.

Eun Y, et al. (2025) Comorbidities and systemic steroids drive pneumonia risk in inflammatory bowel disease: Propensity score-matched cohort study. World journal of gastrointestinal pharmacology and therapeutics, 16(2), 105335.

Banerjee D, et al. (2025) Discovery of obesity genes through cross-ancestry analysis. Nature communications, 16(1), 9319.

Gupta AK, et al. (2025) Understanding the evolving treatment landscape of hidradenitis suppurativa: An analysis of All of Us. PloS one, 20(8), e0331032.

Jones AB, et al. (2025) A feasibility study of whole genome germline testing as an adjunct screening tool in a UK general private practice. Scientific reports, 15(1), 38526.

Morley F, et al. (2025) Perceived stress and allostatic load: Results from the All of Us Research Program. PloS one, 20(8), e0330106.

Li AR, et al. (2025) Sleep and circadian disorders as risk factors for autoimmune disease: A population-based study. Neurobiology of sleep and circadian rhythms, 18, 100129.

Doku R, et al. (2025) Medication-Stratified Analysis of LDL-C Equation Miscalibration in Diabetes: Evidence from the All of Us Research Program and a Medication-Agnostic Machine-Learning Correction. medRxiv : the preprint server for health sciences.

Doku R, et al. (2025) Nonfasting, Telehealth-Ready LDL-C Testing With Machine Learning to Improve Cardiovascular Access and Equity. medRxiv : the preprint server for health sciences.

Yang X, et al. (2025) Disruptions of healthcare visits and viral suppression for people living with HIV during the COVID-19 pandemic in the US. BMC infectious diseases, 25(1), 1295.

Fu B, et al. (2025) A biobank-scale test of marginal epistasis reveals genome-wide signals of polygenic interaction effects. Nature genetics, 57(12), 3175.

Green RF, et al. (2025) A comparison of family health history of breast cancer, colorectal cancer, and diabetes in self-reported survey and electronic health records data, All of Us Research Program. Genetics in medicine open, 3, 103439.

Shah J, et al. (2025) Association of Ptosis with Mental Health Conditions in Adults from a Large United States Research Database. Complex psychiatry, 11(1), 94.

Cudic M, et al. (2025) Putting Polygenic Scores in Context: How Intersectional Factors Affect Relative and Absolute Genetic Risk. medRxiv : the preprint server for health sciences.