Resource Summary Report

Generated by RRID on Aug 6, 2026

Data Browser

RRID:SCR_017561
Type: Tool

Proper Citation

Data Browser (RRID:SCR_017561)

Resource Information

URL: https://databrowser.researchallofus.org/

Proper Citation: Data Browser (RRID:SCR_017561)

Description: National research resource to provide interactive views of publicly available All of Us Research Program participant data including electronic health record data, biospecimens, surveys, and other measures taken at time of participant enrollment. Data platform will be open to researchers all over world and show data for groups of de-identified participants. Data is updated periodically.

Resource Type: portal, data or information resource, organization portal

Keywords: All of Us Research, program, participant, data, surey, physical, measurement, electronic, health, record

Resource Name: Data Browser

Resource ID: SCR_017561

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260807T042906+0000

Ratings and Alerts

No rating or validation information has been found for Data Browser.

No alerts have been found for Data Browser.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 30 mentions in open access literature.

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

Han S, et al. (2026) Sex differences in pain in 2 large and diverse US databases. Pain reports, 11(1), e1371.

Ng BG, et al. (2026) A homozygous nonsense variant in the oligosaccharyltransferase complex gene, RPN1, causes a congenital disorder of glycosylation. HGG advances, 7(3), 100604.

Jurgens SJ, et al. (2026) Rare coding variant architecture and gene discovery from 130,000 sequenced cases of atrial fibrillation. Research square.

Hoffmann M, et al. (2026) How Genomic and Structural Context Could Shape JAK-STAT Variant Pathogenicity. Twin research and human genetics : the official journal of the International Society for Twin Studies, 1.

Jackson A, et al. (2026) Biallelic variants in RNU2-2 cause a remarkably frequent developmental and epileptic encephalopathy. Nature genetics, 58(4), 798.

Hoffmann M, et al. (2025) Spotlight on amino acid changing mutations in the JAK-STAT pathway: from disease-specific mutation to general mutation databases. Scientific reports, 15(1), 6202.

Jain N, et al. (2025) Determinants of chromosome-specific telomere lengths among 2,573 All of Us participants. Research square.

Sardell JM, et al. (2025) Identification and Validation of Novel Combinatorial Genetic Risk Factors for Endometriosis across Multiple UK and US Patient Cohorts. medRxiv : the preprint server for health sciences.

Mogire RM, et al. (2025) OSBPL11 is an African-specific locus associated with 25-hydroxyvitamin D concentrations and cardiometabolic health. medRxiv : the preprint server for health sciences.

Nguyen MN, et al. (2025) Dhdds T206A and Dhdds K42E knock-in mouse models of retinitis pigmentosa 59 are phenotypically similar. Disease models & mechanisms, 18(7).

Bradfield M, et al. (2025) Characterizing rurality using the All of Us Research Program data. PloS one, 20(12), e0328958.

Lee JA, et al. (2025) Comorbidity prevalence and incidence in cancer survivors: a longitudinal All of Us study. JNCI cancer spectrum, 9(6).

Kamizela AE, et al. (2025) Timing and trajectory of BCR::ABL1-driven chronic myeloid leukaemia. Nature, 640(8060), 982.

Thomas L, et al. (2025) Pharmacogenomic heterogeneity of N-acetyltransferase 2: a comprehensive analysis of real world data in Indian tuberculosis patients and from

literature and database review. Annals of medicine, 57(1), 2478316.

Sardell J, et al. (2025) Reproducibility of genetic risk factors identified for long COVID using combinatorial analysis across US and UK patient cohorts with diverse ancestries. Journal of translational medicine, 23(1), 516.

Zheng H, et al. (2025) Case report: Whole exome sequencing identifies a novel variant in the HPRT1 gene in a male with developmental delay. Frontiers in genetics, 16, 1512070.

Butensky SD, et al. (2025) Patient-Reported Barriers to Healthcare Access Among Patients with Gastrointestinal Cancer: Insights from 45,000 Participants in the All of Us Research Program. Research square.

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.

Garimella KV, et al. (2025) Population-scale Long-read Sequencing in the All of Us Research Program. medRxiv : the preprint server for health sciences.

Chen Y, et al. (2024) De novo variants in the RNU4-2 snRNA cause a frequent neurodevelopmental syndrome. Nature, 632(8026), 832.