Resource Summary Report

Generated by NIF on Sep 13, 2026

AstraZeneca PheWAS Portal

RRID:SCR_021643
Type: Tool

Proper Citation

AstraZeneca PheWAS Portal (RRID:SCR_021643)

Resource Information

URL: https://azphewas.com/

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Description: Repository of gene phenotype associations for phenotypes derived from electronic health records, questionnaire data, and continuous traits computed on exomes released by UK Biobank. Repository was made available by AstraZeneca for public research.

Resource Type: data or information resource, portal

Defining Citation: DOI:10.1038/s41586-021-03855-y

Keywords: Phenotypic data linked to medical records, rare protein coding variants, exome sequencing data, rare variants, common disease, gene-phenotype associations, AstraZeneca

Availability: Free, Freely available

Resource Name: AstraZeneca PheWAS Portal

Resource ID: SCR_021643

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260912T200110+0000

Ratings and Alerts

No rating or validation information has been found for AstraZeneca PheWAS Portal.

No alerts have been found for AstraZeneca PheWAS Portal.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2225 mentions in open access literature.

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

Fang K, et al. (2026) Elucidating the causal effects of plasma metabolites on breast cancer from multiple perspectives. International journal of surgery (London, England), 112(1), 537.

Hernandez-Beeftink T, et al. (2026) Contribution of dominant and recessive model effects to the genetic architecture of Idiopathic Pulmonary Fibrosis. medRxiv : the preprint server for health sciences.

Hu X, et al. (2026) Causal cross-trait mapping at single-cell resolution identifies shared immunogenetic drivers of migraine and Meniere's disease. The journal of headache and pain, 27(1).

Chua NK, et al. (2026) The E3-ome gene-centric compendium reveals the human E3 ligase landscape. Cell, 189(7), 2167.

Lin M, et al. (2026) Identification and validation of druggable targets for cataract using mendelian randomization: functional insights from multi-omics and an oxidative stress model. Frontiers in medicine, 13, 1741371.

Brock DC, et al. (2026) Rare heterozygous missense variants in VSX2 are associated with retinal detachment. PLoS genetics, 22(2), e1012027.

Fu L, et al. (2026) Genetic insights and mechanistic parallels in gestational diabetes mellitus and type 2 diabetes. Nature communications, 17(1), 660.

Giri R, et al. (2026) Pathogenic OTUD3 Mutations Predispose to Ulcerative Colitis Due to Barrier Dysfunction. Cellular and molecular gastroenterology and hepatology, 20(2), 101659.

Wang Y, et al. (2026) Mitochondrial dysfunction in the pathogenesis of intervertebral disc herniation: a mitochondrial related genome-wide Mendelian randomization analysis. Journal of translational medicine, 24(1).

Pan Y, et al. (2026) PPP1R14A in male erectile dysfunction: key role in smooth muscle cells. Sexual medicine, 14(3), qfag021.

Bi J, et al. (2026) Genetic Identification of Potential Drug Targets for Dental Caries: A Mendelian Randomization Study. Health science reports, 9(5), e72546.

Mei H, et al. (2026) IL3RA identified as novel biomarker and therapeutic target for ER+ breast cancer through plasma proteome-wide mendelian randomization and TCGA database analysis. Clinical proteomics, 23(1).

Ji T, et al. (2026) The Role of Programmed Cell Death-Related Genes in Asthma, Chronic Obstructive Pulmonary Disease, and Lung Function: A Multi-Omics Mendelian Randomization Study. International journal of chronic obstructive pulmonary disease, 21, 561510.

Yuan Y, et al. (2026) Rare coding and noncoding variants map 1,342 diseases and biomarkers in 490,549 whole genomes. medRxiv : the preprint server for health sciences.

Anker-Hansen C, et al. (2026) Contribution of rare variation to degenerative orthopedic diseases. Osteoarthritis and cartilage open, 8(2), 100767.

Jiang B, et al. (2026) Integrative multi-omics Mendelian randomization and functional validation identifies RNASET2 as a novel therapeutic target for autoimmune thyroiditis. Frontiers in endocrinology, 17, 1715937.

Lou S, et al. (2026) Integrated Genome-wide Association and Single-cell Transcriptomic Analysis Identifies OAT as Therapeutic Targets for Periodontitis. Inflammation, 49(1).

Wang T, et al. (2026) Multi-Omics Dissection of the Shared Genetic Architecture Between Sleep Traits and Epilepsy. Biology, 15(11).

Zou XZ, et al. (2026) Phenome-wide analysis of copy number variants in 470,727 UK Biobank genomes. Nature, 652(8110), 675.

Hu Y, et al. (2026) Integrative multi-omics analyses identify key genes and elucidate bidirectional regulatory mechanisms in thyroid dysfunction. PloS one, 21(1), e0338805.