Resource Summary Report

Generated by T1D on Sep 5, 2026

Polygenic Score Catalog

RRID:SCR_023558
Type: Tool

Proper Citation

Polygenic Score Catalog (RRID:SCR_023558)

Resource Information

URL: https://www.pgscatalog.org/

Proper Citation: Polygenic Score Catalog (RRID:SCR_023558)

Description: Open database of polygenic scores and relevant metadata required for accurate application and evaluation. Used for reproducibility and systematic evaluation.

Synonyms: The Polygenic Score (PGS) Catalog

Resource Type: data or information resource, database

Defining Citation: PMID:33692568

Keywords: polygenic scores and relevant metadata, reproducibility and systematic evaluation,

Funding: British Heart Foundation ;
Canadian Institutes of Health Research postdoctoral fellowship ;
European Molecular Biology Laboratory ;
Health Data Research UK ;
Munz Chair of Cardiovascular Prediction and Prevention ;
National Institute for Health Research ;
NHGRI U41HG007823;
UK Medical Research Council

Availability: Free, Freely available,

Resource Name: Polygenic Score Catalog

Resource ID: SCR_023558

Record Creation Time: 20230510T050220+0000

Record Last Update: 20260904T000324+0000

Ratings and Alerts

No rating or validation information has been found for Polygenic Score Catalog.

No alerts have been found for Polygenic Score Catalog.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 139 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Kirchler M, et al. (2026) Large language models improve transferability of electronic health record-based predictions across countries and coding systems. NPJ digital medicine, 9(1), 177.

Lai D, et al. (2026) Genome-wide meta-analyses of cross substance use disorders in diverse populations. Molecular psychiatry, 31(3), 1619.

Chen H, et al. (2026) Optimizing colorectal cancer screening through polygenic risk score-based risk stratification: evidence from a population-based cohort and screening trial. Genome medicine, 18(1).

Strickler C, et al. (2026) Association of a polygenic risk score with low trauma fractures in people with HIV - The swiss HIV cohort study. PloS one, 21(2), e0342748.

Li WF, et al. (2026) Dissecting Alzheimer's disease heterogeneity by cross-trait polygenic prediction. bioRxiv : the preprint server for biology.

Boumtje V, et al. (2026) Clinical usefulness of polygenic risk scores in risk prediction models for lung cancer screening and lung nodule management. Translational oncology, 68, 102771.

White SL, et al. (2026) Global multi-ancestry genome-wide analyses identify genes and biological pathways associated with thyroid cancer and benign thyroid diseases. Nature genetics, 58(2), 307.

Huerta-Chagoya A, et al. (2026) Multi-ancestry polygenic risk scores for the prediction of type 2 diabetes and complications in diverse ancestries. The lancet. Diabetes & endocrinology, 14(7), 558.

Eriksen BO, et al. (2026) Polygenic Risk Scores Predicting Estimated GFR Validated With Iohexol Clearance. Kidney international reports, 11(1), 196.

Takahashi N, et al. (2026) Causal effects of serum testosterone on septic shock mortality: a Mendelian randomization study. Critical care (London, England), 30(1), 84.

Li YJ, et al. (2026) Leveraging genetic propensity to identify modifiable factors for the age at onset of Alzheimer's disease. Alzheimer's & dementia : the journal of the Alzheimer's Association, 22(2), e71111.

Xu H, et al. (2026) Polygenic predisposition modifies the associations of fish oil supplementation with circulating omega-3 fatty acids: a cross-sectional gene-diet interaction study in UK Biobank. medRxiv : the preprint server for health sciences.

He J, et al. (2026) A Comprehensive Assessment of the Causal Relationship between Atopic Conditions and Pancreatic Cancer Risk: A Two-Sample Mendelian Randomization Study. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 35(6), 1009.

He X, et al. (2026) Improving the accuracy of fetal growth restriction diagnosis by integrating fetal genetic growth potential: a proof of concept study. BMC pregnancy and childbirth, 26(1).

Tanha HM, et al. (2026) Performance of different polygenic risk scores for breast cancer risk prediction: in-depth evaluations across large UK and Australian cohorts. European journal of human genetics : EJHG, 34(2), 278.

Ullah E, et al. (2026) Comprehensive genomic analysis of non-BRCA familial breast cancer in an Arab population. NPJ breast cancer, 12(1).

Kany S, et al. (2026) Multitrait analyses identify genetic variants associated with aortic valve function and aortic stenosis risk. Nature genetics, 58(1), 47.

Small AM, et al. (2026) Genomic and transcriptomic analyses of aortic stenosis enhance therapeutic target discovery and disease prediction. Nature genetics, 58(1), 57.

Schneider N, et al. (2026) Improvements in blood and fitness tracker biomarkers in a longitudinal real-world cohort of digital health platform users. PLOS digital health, 5(3), e0001271.

Armstrong RA, et al. (2026) The genetic architecture of postoperative delirium after major surgery and its relationship with nonpostoperative neurocognitive conditions: A genome-wide association study. PLoS medicine, 23(3), e1004963.