Resource Summary Report

Generated by T1D on Jul 29, 2026

PrediXcan

RRID:SCR_016739
Type: Tool

Proper Citation

PrediXcan (RRID:SCR_016739)

Resource Information

URL: https://github.com/hakyimlab/PrediXcan

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Description: Software tool to detect known and novel genes associated with disease traits and provide insights into the mechanism of these associations. Used to test the molecular mechanisms through which genetic variation affects phenotype.

Resource Type: software application, software resource, data analysis software, data processing software

Defining Citation: PMID:26258848

Keywords: detect, gene, disease, associate, trait, mechanism, molecular, variation, phenotype

Funding: NCI K12 CA139160;
NCI F32CA165823;
NIMH T32 MH020065;
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NIGMS U01 GM61393;
NIMH P50 MH094267;
NIGMS U01 GM092691;
NHLBI U19 HL065962;
NIDA P50 DA037844;
NIDDK P30 DK20595;
NIDDK P60 DK20595

Availability: Free, Available for download, Freely available

Resource Name: PrediXcan

Resource ID: SCR_016739

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260729T044422+0000

Ratings and Alerts

No rating or validation information has been found for PrediXcan.

No alerts have been found for PrediXcan.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Jen Y, et al. (2025) Identification of Hub Genes Involved in Early-onset Schizophrenia: From Genetic Susceptibility to Predicted Regulated Gene Expression. Research square.

Xu X, et al. (2025) Transcriptome-wide association study of alternative polyadenylation identifies susceptibility genes in non-small cell lung cancer. Oncogene, 44(26), 2127.

Shao M, et al. (2024) Multiome-wide Association Studies: Novel Approaches for Understanding Diseases. Genomics, proteomics & bioinformatics, 22(5).

Lo Faro V, et al. (2024) Novel ancestry-specific primary open-angle glaucoma loci and shared biology with vascular mechanisms and cell proliferation. Cell reports. Medicine, 5(2), 101430.

Trastulla L, et al. (2024) Distinct genetic liability profiles define clinically relevant patient strata across common diseases. Nature communications, 15(1), 5534.

Diz-de Almeida S, et al. (2024) Novel risk loci for COVID-19 hospitalization among admixed American populations. eLife, 13.

Cho C, et al. (2024) Large-scale cross-ancestry genome-wide meta-analysis of serum urate. Nature communications, 15(1), 3441.

Zhu Q, et al. (2022) UACA locus is associated with breast cancer chemoresistance and survival. NPJ breast cancer, 8(1), 39.

Hu X, et al. (2022) Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. American journal of human genetics, 109(5), 857.

Martínez-Pinteño A, et al. (2021) Identification of EP300 as a Key Gene Involved in Antipsychotic-Induced Metabolic Dysregulation Based on Integrative Bioinformatics Analysis of Multi-Tissue Gene Expression Data. Frontiers in pharmacology, 12, 729474.

Bhat A, et al. (2021) Transcriptome-wide association study reveals two genes that influence mismatch negativity. Cell reports, 34(11), 108868.

Ruggiero D, et al. (2021) Genetics of PlGF plasma levels highlights a role of its receptors and supports the link between angiogenesis and immunity. Scientific reports, 11(1), 16821.

Hale AT, et al. (2021) Multi-omic analysis elucidates the genetic basis of hydrocephalus. Cell reports, 35(5), 109085.

Fryett JJ, et al. (2020) Investigation of prediction accuracy and the impact of sample size, ancestry, and tissue in transcriptome-wide association studies. Genetic epidemiology, 44(5), 425.

Zhou X, et al. (2020) CORE GREML for estimating covariance between random effects in linear mixed models for complex trait analyses. Nature communications, 11(1), 4208.

Huckins LM, et al. (2020) Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. Cell reports, 31(9), 107716.

Deutelmoser H, et al. (2020) Genotype-Based Gene Expression in Colon Tissue-Prediction Accuracy and Relationship with the Prognosis of Colorectal Cancer Patients. International journal of molecular sciences, 21(21).

Rodriguez-López J, et al. (2020) Identification of relevant hub genes for early intervention at gene coexpression modules with altered predicted expression in schizophrenia. Progress in neuro-psychopharmacology & biological psychiatry, 98, 109815.

Bien SA, et al. (2019) Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. Human genetics, 138(4), 307.

Miller JE, et al. (2019) Innovative strategies for annotating the "relationSNP" between variants and molecular phenotypes. BioData mining, 12, 10.