Resource Summary Report

Generated by RRID on Aug 5, 2026

PsychENCODE Knowledge Portal

RRID:SCR_017500
Type: Tool

Proper Citation

PsychENCODE Knowledge Portal (RRID:SCR_017500)

Resource Information

URL: https://www.synapse.org/#!Synapse:syn4921369/wiki/235539

Proper Citation: PsychENCODE Knowledge Portal (RRID:SCR_017500)

Description: Portal of PsychENCODE Consortium to study role of rare genetic variants involved in several psychiatric disorders. Database of regulatory elements, epigenetic modifications, RNA and protein in brain.

Resource Type: database, portal, project portal, data or information resource

Keywords: Rare, genetic, variant, psychiatric, disorder, regulatory, element, epigenetic, modification, RNA, protein, brain

Availability: Restricted

Resource Name: PsychENCODE Knowledge Portal

Resource ID: SCR_017500

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260805T044409+0000

Ratings and Alerts

No rating or validation information has been found for PsychENCODE Knowledge Portal.

No alerts have been found for PsychENCODE Knowledge Portal.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Fehr K, et al. (2025) Protocol: the International Milk Composition (IMiC) Consortium - a harmonized secondary analysis of human milk from four studies. Frontiers in nutrition, 12, 1548739.

Hou X, et al. (2025) Machine-learning based strategy identifies a robust protein biomarker panel for Alzheimer's disease in cerebrospinal fluid. Alzheimer's research & therapy, 17(1), 147.

Lüleci HB, et al. (2024) A benchmark of RNA-seq data normalization methods for transcriptome mapping on human genome-scale metabolic networks. NPJ systems biology and applications, 10(1), 124.

Zhang H, et al. (2024) mosGraphGen: a novel tool to generate multi-omics signaling graphs to facilitate integrative and interpretable graph AI model development. Bioinformatics advances, 4(1), vbae151.

Sanz-Garcia E, et al. (2024) Genomic Characterization and Clinical Outcomes of Patients with Peritoneal Metastases from the AACR GENIE Biopharma Collaborative Colorectal Cancer Registry. Cancer research communications, 4(2), 475.

Wang D, et al. (2023) cLD: Rare-variant linkage disequilibrium between genomic regions identifies novel genomic interactions. PLoS genetics, 19(12), e1011074.

Bernaola N, et al. (2023) Learning massive interpretable gene regulatory networks of the human brain by merging Bayesian networks. PLoS computational biology, 19(12), e1011443.

Ahsan F, et al. (2022) PhyloPGM: boosting regulatory function prediction accuracy using evolutionary information. Bioinformatics (Oxford, England), 38(Suppl 1), i299.

Wang Y, et al. (2022) Non-linear archetypal analysis of single-cell RNA-seq data by deep autoencoders. PLoS computational biology, 18(4), e1010025.

Rodríguez A, et al. (2022) TGF? pathway is required for viable gestation of Fanconi anemia embryos. PLoS genetics, 18(11), e1010459.

Benecke J, et al. (2021) Retrospective analysis and time series forecasting with automated machine learning of ascariasis, enterobiasis and cystic echinococcosis in Romania. PLoS neglected tropical diseases, 15(11), e0009831.

Tognetti M, et al. (2021) Deciphering the signaling network of breast cancer improves drug sensitivity prediction. Cell systems, 12(5), 401.