

Resource Summary Report

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

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: 20260729T044430+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 [nidm-terms](#) .

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 β 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.