Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

Synapse

RRID:SCR_006307
Type: Tool

Proper Citation

Synapse (RRID:SCR_006307)

Resource Information

URL: https://www.synapse.org/

Proper Citation: Synapse (RRID:SCR_006307)

Description: A cloud-based collaborative platform which co-locates data, code, and computing resources for analyzing genome-scale data and seamlessly integrates these services allowing scientists to share and analyze data together. Synapse consists of a web portal integrated with the R/Bioconductor statistical package and will be integrated with additional tools. The web portal is organized around the concept of a Project which is an environment where you can interact, share data, and analysis methods with a specific group of users or broadly across open collaborations. Projects provide an organizational structure to interact with data, code and analyses, and to track data provenance. A project can be created by anyone with a Synapse account and can be shared among all Synapse users or restricted to a specific team. Public data projects include the Synapse Commons Repository (SCR) (syn150935) and the metaGenomics project (syn275039). The SCR provides access to raw data and phenotypic information for publicly available genomic data sets, such as GEO and TCGA. The metaGenomics project provides standardized preprocessed data and precomputed analysis of the public SCR data.

Abbreviations: Synapse

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Keywords: data sharing, collaboration, data management, analysis, genome, phenotype, crowd sourcing, open data, provenance, resource management, annotation, authoring, markup, r, python, java, command-line, cloud, FASEB list

Related Condition: Cancer, Normal, Cardiovascular disease, Floppy hat syndrome

Funding: Life Sciences Discovery Fund ;
NCI ;
NHLBI ;

Alfred P. Sloan Foundation

Availability: The community can contribute to this resource

Resource Name: Synapse

Resource ID: SCR_006307

Alternate IDs: nlx_151983, DOI:10.17616/R3B934, r3d100011894, DOI:10.7303

Alternate URLs: https://doi.org/10.17616/R3B934, https://doi.org/10.48550/arxiv.1506.00272, https://doi.org/10.7303/, https://dx.doi.org/10.7303, https://doi.org/10.17616/R3B934

Record Creation Time: 20220129T080235+0000

Record Last Update: 20260905T133000+0000

Ratings and Alerts

No rating or validation information has been found for Synapse.

No alerts have been found for Synapse.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1104 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Rub J, et al. (2026) Deep-Learning Tool ScVital Enables Species-Agnostic Integration of Cancer Cell States. Cancer research, 86(4), 858.

Liu S, et al. (2026) RET signaling as a mediator of estrogen receptor positive breast cancer brain metastasis. Communications biology.

Kobayashi H, et al. (2026) A self-amplifying nerve-fibroblast circuit drives colorectal cancer progression. Cancer cell.

Iqbal J, et al. (2026) A prelimbic molecular clock of protein synthesis for memory persistence. bioRxiv : the preprint server for biology.

Liu Y, et al. (2026) Functional variants at 1p36.23 confer risk of schizophrenia through modulating RERE. Nature communications, 17(1), 1742.

Huc M, et al. (2026) Sex differences in placebo and antidepressant response to intranasal esketamine for treatment-resistant depression. Molecular psychiatry, 31(7), 3674.

Wang Y, et al. (2026) Agent-based modeling of cellular dynamics in adoptive cell therapy. Communications biology, 9(1).

Castelo A, et al. (2026) Quality versus quantity of training datasets for artificial intelligence-based whole liver segmentation. medRxiv : the preprint server for health sciences.

Klinger HM, et al. (2026) Whole blood gene expression moderates associations between AD biomarkers and cognitive decline in cognitively unimpaired older adults. Alzheimer's & dementia : the journal of the Alzheimer's Association, 22(2), e71225.

Yun HJ, et al. (2026) CEBPB Expression in Tumor Cells Drives Immune Evasion in Colorectal Cancer via CTLA4 Up-regulation in T Cells. Cancer communications (London, England), 46, 0013.

Zambrano-Astorga MF, et al. (2026) Reproducibility-driven discovery and systematic benchmarking reveal a robust cerebrospinal fluid proteomic signature in Alzheimer's disease. medRxiv : the preprint server for health sciences.

Gutierrez JC, et al. (2026) Resolving human neuronal herpesvirus reactivation via petabase-scale association studies. bioRxiv : the preprint server for biology.

Sheng J, et al. (2026) iS2C2: a cointelligent platform for mechanistic discovery of disease cellular crosstalk. Signal transduction and targeted therapy, 11(1).

Xu N, et al. (2026) Local global feature enhanced transformer with attention pruning for precise medical image segmentation. iScience, 29(7), 116382.

Zhao D, et al. (2026) MetaScreener: a robust dual-mode framework for directional prioritization of actionable signatures through multi-dataset and multi-approach integration. Journal of translational medicine, 24(1).

Peroz M, et al. (2026) Deep learning-based assessment of PD-L1 expression in NSCLC predicts outcome for patients treated with anti-PD-1 immunotherapy. Frontiers in immunology, 17, 1750816.

Tsai WY, et al. (2026) Multi-platform integration of brain and CSF proteomes reveals biomarker panels for Alzheimer's disease. Briefings in bioinformatics, 27(1).

Chen L, et al. (2026) Genetic control of non-coding RNAs in the human brain and their implications for complex traits. American journal of human genetics, 113(1), 149.

Du T, et al. (2026) A prognostic gene model with psychological stress-related genes captures immune activation in breast cancer. Breast (Edinburgh, Scotland), 85, 104678.

Laroche VT, et al. (2026) Epigenomic subtypes of late-onset Alzheimer's disease reveal distinct microglial signatures. Acta neuropathologica, 151(1).