Resource Summary Report

Generated by dkNET on May 20, 2025

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

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, 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

Record Creation Time: 20220129T080235+0000

Record Last Update: 20250519T204320+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 818 mentions in open access literature.

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

Chen L, et al. (2025) Molecular characterization of gliosarcoma reveals prognostic biomarkers and clinical parallels with glioblastoma. Journal of neuro-oncology, 171(2), 403.

Silverman D, et al. (2025) Activation of locus coeruleus noradrenergic neurons rapidly drives homeostatic sleep pressure. Science advances, 11(3), eadq0651.

Wang Y, et al. (2025) Integrating single-cell RNA and T?cell/B?cell receptor sequencing with mass cytometry reveals dynamic trajectories of human peripheral immune cells from birth to

old age. Nature immunology, 26(2), 308.

Kimmey BA, et al. (2025) Convergent state-control of endogenous opioid analgesia. bioRxiv : the preprint server for biology.

Olney KC, et al. (2025) Distinct transcriptional alterations distinguish Lewy body disease from Alzheimer's disease. Brain : a journal of neurology, 148(1), 69.

Fink R, et al. (2025) PinkyCaMP a mScarlet-based calcium sensor with exceptional brightness, photostability, and multiplexing capabilities. bioRxiv : the preprint server for biology.

Huang X, et al. (2025) Predicting Alzheimer's disease subtypes and understanding their molecular characteristics in living patients with transcriptomic trajectory profiling. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(1), e14241.

Torang A, et al. (2025) Enterocyte-like differentiation defines metabolic gene signatures of CMS3 colorectal cancers and provides therapeutic vulnerability. Nature communications, 16(1), 264.

Jia Y, et al. (2025) xQTLatlas: a comprehensive resource for human cellular-resolution multi-omics genetic regulatory landscape. Nucleic acids research, 53(D1), D1270.

Abbad Andaloussi M, et al. (2025) Exploring adult glioma through MRI: A review of publicly available datasets to guide efficient image analysis. Neuro-oncology advances, 7(1), vdae197.

Taube JM, et al. (2025) Society for Immunotherapy of Cancer: updates and best practices for multiplex immunohistochemistry (IHC) and immunofluorescence (IF) image analysis and data sharing. Journal for immunotherapy of cancer, 13(1).

Huang F, et al. (2025) Cholecystokinin facilitates the formation of long-term heterosynaptic plasticity in the distal subiculum. Communications biology, 8(1), 153.

de Bruijn I, et al. (2024) Sharing Data from the Human Tumor Atlas Network through Standards, Infrastructure, and Community Engagement. bioRxiv : the preprint server for biology.

Rademacher K, et al. (2024) Chronic hyperactivation of midbrain dopamine neurons causes preferential dopamine neuron degeneration. bioRxiv : the preprint server for biology.

Sudalagunta PR, et al. (2024) The Functional Transcriptomic Landscape Informs Therapeutic Strategies in Multiple Myeloma. Cancer research.

Bertelsen N, et al. (2024) Patient Engagement and Patient Experience Data in Regulatory Review and Health Technology Assessment: A Global Landscape Review. Therapeutic innovation & regulatory science, 58(1), 63.

Cornean J, et al. (2024) Heterogeneity of synaptic connectivity in the fly visual system.

Nature communications, 15(1), 1570.

Austin GI, et al. (2024) Processing-bias correction with DEBIAS-M improves cross-study generalization of microbiome-based prediction models. bioRxiv : the preprint server for biology.

De Bastiani MA, et al. (2024) Cross-species comparative hippocampal transcriptomics in Alzheimer's disease. iScience, 27(1), 108671.

Copperman J, et al. (2024) Single-cell morphodynamical trajectories enable prediction of gene expression accompanying cell state change. bioRxiv : the preprint server for biology.