Resource Summary Report

Generated by T1D on Aug 3, 2026

Codex

RRID:SCR_027783
Type: Tool

Proper Citation

Codex (RRID:SCR_027783)

Resource Information

URL: https://codex.flywire.ai

Proper Citation: Codex (RRID:SCR_027783)

Description: Web based platform for exploring full brain connectomic datasets. Used for exploring and analyzing large connectomics datasets.

Synonyms: Codex - Connectome Data Explorer

Resource Type: web application, data or information resource, software resource

Keywords: exploring and analyzing large connectomics datasets, full brain, connectomic datasets,

Availability: Restricted

Resource Name: Codex

Resource ID: SCR_027783

Record Creation Time: 20251213T054634+0000

Record Last Update: 20260803T040943+0000

Ratings and Alerts

No rating or validation information has been found for Codex.

No alerts have been found for Codex.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Trigila AP, et al. (2025) Comparative genomics sheds light on mammalian and avian gene regulation and phenotypic evolution. Nature communications, 16(1), 9111.

Barlow GL, et al. (2025) The extra-islet pancreas supports autoimmunity in human type 1 diabetes. eLife, 13.

Wang T, et al. (2025) scProAtlas: an atlas of multiplexed single-cell spatial proteomics imaging in human tissues. Nucleic acids research, 53(D1), D582.

Trehan R, et al. (2025) SPP1 + macrophages cause exhaustion of tumor-specific T cells in liver metastases. Nature communications, 16(1), 4242.

Giakoumas DS, et al. (2025) Connectomic mapping of pharyngeal and gut sensory circuits in adult Drosophila. bioRxiv : the preprint server for biology.

Roider T, et al. (2024) Multimodal and spatially resolved profiling identifies distinct patterns of T cell infiltration in nodal B cell lymphoma entities. Nature cell biology, 26(3), 478.

Zahraeifard S, et al. (2024) Loss of tumor suppressors promotes inflammatory tumor microenvironment and enhances LAG3+T cell mediated immune suppression. Nature communications, 15(1), 5873.

Meschi E, et al. (2024) Compensatory enhancement of input maintains aversive dopaminergic reinforcement in hungry Drosophila. Neuron, 112(14), 2315.

Wu R, et al. (2024) Gasdermin C promotes Stemness and Immune Evasion in Pancreatic Cancer via Pyroptosis-Independent Mechanism. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(42), e2308990.

Hickey JW, et al. (2023) Organization of the human intestine at single-cell resolution. Nature, 619(7970), 572.

Sexton T, et al. (2023) Competition between transcription and loop extrusion modulates promoter and enhancer dynamics. Research square.

Antaki D, et al. (2022) A phenotypic spectrum of autism is attributable to the combined effects of rare variants, polygenic risk and sex. Nature genetics, 54(9), 1284.

Mantsoki A, et al. (2021) Identification and Characterisation of Putative Enhancer Elements in Mouse Embryonic Stem Cells. Bioinformatics and biology insights, 15, 1177932220974623.

Zhang L, et al. (2021) Sex-specific DNA methylation differences in Alzheimer's disease pathology. Acta neuropathologica communications, 9(1), 77.

Rendeiro AF, et al. (2020) Chromatin mapping and single-cell immune profiling define the temporal dynamics of ibrutinib response in CLL. Nature communications, 11(1), 577.

Moreno-Cabrera JM, et al. (2020) Evaluation of CNV detection tools for NGS panel data in genetic diagnostics. European journal of human genetics : EJHG, 28(12), 1645.

Schürch CM, et al. (2020) Coordinated Cellular Neighborhoods Orchestrate Antitumoral Immunity at the Colorectal Cancer Invasive Front. Cell, 182(5), 1341.

Schick S, et al. (2019) Systematic characterization of BAF mutations provides insights into intracomplex synthetic lethalities in human cancers. Nature genetics, 51(9), 1399.