Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 23, 2025

UCSC Xena

RRID:SCR_018938
Type: Tool

Proper Citation

UCSC Xena (RRID:SCR_018938)

Resource Information

URL: http://xena.ucsc.edu/

Proper Citation: UCSC Xena (RRID:SCR_018938)

Description: Web tool where one component is front end Xena Browser and another component is back end Xena Hubs. Web based Xena Browser empowers biologists to explore data across multiple Xena Hubs with variety of visualizations and analyses. Xena Hubs host genomics data from laptops, public servers, behind firewall, or in cloud, and can be public or private. Xena Browser receives data simultaneously from multiple Xena Hubs and integrates them into single coherent visualization within browser. Allows users to explore functional genomic data sets for correlations between genomic and/or phenotypic variables.

Synonyms: UCSC Xena Browser, Xena Browser

Resource Type: analysis service resource, data access protocol, portal, software resource, production service resource, web service, service resource, data or information resource

Keywords: Data visualization, data analysis, genomics data, explore functional genomic data, functional genomic, data sets, genomic variable correlation, phenotypic variables correlation

Funding:

Availability: Free, Freely available

Resource Name: UCSC Xena

Resource ID: SCR_018938

Alternate URLs: https://xenabrowser.net/

Record Creation Time: 20220129T080342+0000

Record Last Update: 20250423T061053+0000

Ratings and Alerts

No rating or validation information has been found for UCSC Xena.

No alerts have been found for UCSC Xena.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2097 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Kim JH, et al. (2025) Differential expression of ORAI channels and STIM proteins in renal cell carcinoma subtypes: implications for metastasis and therapeutic targeting. The Korean journal of physiology & pharmacology : official journal of the Korean Physiological Society and the Korean Society of Pharmacology, 29(1), 33.

Lengyel M, et al. (2025) Zymogen granule protein 16B (ZG16B) is a druggable epigenetic target to modulate the mammary extracellular matrix. Cancer science, 116(1), 81.

Taya M, et al. (2025) Beyond endocrine resistance: estrogen receptor (ESR1) activating mutations mediate chemotherapy resistance through the JNK/c-Jun MDR1 pathway in breast cancer. Breast cancer research and treatment, 209(2), 431.

Yang J, et al. (2025) Identification of a mitophagy-related gene signature for predicting overall survival and response to immunotherapy in rectal cancer. BMC cancer, 25(1), 15.

Pang J, et al. (2025) Multiomics analysis reveals the involvement of NET1 in tumour immune regulation and malignant progression. Scientific reports, 15(1), 56.

Verma RK, et al. (2025) Comprehensive analysis of inhibin-? A as a potential biomarker for gastrointestinal tract cancers through bioinformatics approaches. Scientific reports, 15(1), 1090.

Yu X, et al. (2025) Integrative bioinformatics and immunohistochemical analysis unravel the prognostic significance and immunological implication of LIMCH1 in breast cancer: a

retrospective study. Scientific reports, 15(1), 1446.

Tal O, et al. (2025) Unlocking prognostic potential: A genomic signature of caloric restriction in patients with epithelial ovarian cancer. PloS one, 20(1), e0317502.

Song W, et al. (2025) Role of immune cell homeostasis in research and treatment response in hepatocellular carcinoma. Clinical and experimental medicine, 25(1), 42.

Hua M, et al. (2025) Multiomic machine learning on lactylation for molecular typing and prognosis of lung adenocarcinoma. Scientific reports, 15(1), 3075.

Liu L, et al. (2025) Revealing the role of cancer-associated fibroblast senescence in prognosis and immune landscape in pancreatic cancer. iScience, 28(1), 111612.

Liu M, et al. (2025) Mechanistic insights into pachymic acid's action on triple-negative breast Cancer through TOP2A targeting. Scientific reports, 15(1), 2856.

Zhang H, et al. (2025) Endothelial STING-JAK1 interaction promotes tumor vasculature normalization and antitumor immunity. The Journal of clinical investigation, 135(2).

Yang X, et al. (2025) Characterization of stem cell landscape and identification of stemness-relevant prognostic gene signature to aid immunotherapy in breast cancer. Discover oncology, 16(1), 9.

Shi K, et al. (2025) The high-risk model associated with SYTL4 predicts poor prognosis and correlates with immune infiltration in AML. Biochemistry and biophysics reports, 41, 101859.

Zhao D, et al. (2025) Identification of TUBB3 as an immunotherapy target in lung cancer by genome wide in vivo CRISPR screening. Neoplasia (New York, N.Y.), 60, 101100.

Smith NJ, et al. (2025) Differentiation signals induce APOBEC3A expression via GRHL3 in squamous epithelia and squamous cell carcinoma. The EMBO journal, 44(1), 1.

Wang H, et al. (2025) ER?-regulated circATP2B1/miR-204-3p/TWIST1 positive feedback loop facilitates epithelial to mesenchymal transition in clear cell renal cell carcinoma. Translational oncology, 51, 102213.

Zou C, et al. (2025) Identification of CENPM as a key gene driving adrenocortical carcinoma metastasis via physical interaction with immune checkpoint ligand FGL1. Clinical and translational medicine, 15(1), e70182.

Wang X, et al. (2025) A novel basement membrane-related gene signature for predicting prognosis of HNSCC. Medicine, 104(3), e41316.