

Resource Summary Report

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UCSC Xena

RRID:SCR_018938

Type: Tool

Proper Citation

UCSC Xena (RRID:SCR_018938)

Resource Information

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

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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: portal, analysis service resource, web service, software resource, data access protocol, production service resource, 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

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: 20260805T044426+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 2828 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Mogi M, et al. (2026) Pan-cancer analysis of RNA expression signatures associated with cancer tissue architecture. *British journal of cancer*, 134(1), 141.

Kim M, et al. (2026) Prognostic Implications of Exosomal miRNA Networks Regulating TGF β 1-induced Epithelial-Mesenchymal Transition Signature in Oral Squamous Cell Carcinoma. *Cancer genomics & proteomics*, 23(1), 50.

Xiong Z, et al. (2026) C/EBP β -induced alternative splicing of RCAN1 generates a potent TCR-T target in mesenchymal glioblastoma. *Cellular & molecular immunology*, 23(1), 94.

Fu C, et al. (2026) The Clinical Prognostic Value of Lactylation-Regulated Proteins in Gastric Cancer. *Journal of proteome research*, 25(1), 446.

Arcos-Montoya D, et al. (2026) Assessing progesterone receptor modulation in glioblastoma: from in vitro and animal model to a human pilot protocol. *Cancer biology & therapy*, 27(1), 2603095.

Luan R, et al. (2026) Pan-cancer multi-omics reveals DCAF7 as an immune-modulating prognostic driver and Wnt/ β -catenin activator in hepatocellular carcinoma. *Clinical and translational medicine*, 16(1), e70572.

Yang YF, et al. (2026) Integrative analysis identifies PIGK as an oncogenic glycosylphosphatidylinositol transamidase subunit with prognostic, immunological, and therapeutic relevance in head and neck cancer. *International journal of medical sciences*, 23(1), 161.

Pan R, et al. (2026) Basement membrane-associated gene P3H2 regulates osteosarcoma progression and epithelial-mesenchymal transition through AKT/mTOR signaling axis. *Translational oncology*, 63, 102569.

Hou CH, et al. (2026) FGF-23 facilitates osteosarcoma metastasis by modulating the miR-4463/LOXL2 axis expression via the ERK, p38, and JNK signaling pathway. *International journal of medical sciences*, 23(1), 12.

Chiang YC, et al. (2026) Multi-Omics and Single-Cell Dissection of Exostosin Glycosyltransferases (EXT1/EXT2) Reveals Divergent Oncogenic Roles and Therapeutic Vulnerabilities in Gliomas. *Journal of Cancer*, 17(1), 177.

Wang P, et al. (2026) Development and validation of a prognostic model based on T cell signature genes in colon cancer using single-cell RNA sequencing. *Clinical and experimental medicine*, 26(1), 69.

Xiaoxia F, et al. (2025) CD147 regulates the Rap1 signaling pathway to promote proliferation, migration, and invasion, and inhibit apoptosis in colorectal cancer cells. *Scientific reports*, 15(1), 13647.

Jin K, et al. (2025) Harnessing CD39 inhibition to boost antitumor immunity with extracellular ATP. *Journal of immunology (Baltimore, Md. : 1950)*.

Coscia F, et al. (2025) A Proteogenomic View of Synchronous Endometrioid Endometrial and Ovarian Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(11), 2230.

Mu H, et al. (2025) Methionine intervention induces PD-L1 expression to enhance the immune checkpoint therapy response in MTAP-deleted osteosarcoma. *Cell reports. Medicine*, 6(3), 101977.

Kuo P, et al. (2025) Trop-2 expression in non-small cell lung cancer. *PloS one*, 20(4), e0321555.

Baker MJ, et al. (2025) VAV2 Drives EGFR-Mediated Rac1 Responses in Prostate Cancer. *Molecular cancer research : MCR*, 23(8), 684.

Cao D, et al. (2025) MAF1 inhibits hepatocarcinogenesis by fostering an immunostimulatory tumor microenvironment. *Journal for immunotherapy of cancer*, 13(1).

Liu X, et al. (2025) Increasing Stemness Drives Prostate Cancer Progression, Plasticity, Therapy Resistance and Poor Patient Survival. *bioRxiv : the preprint server for biology*.

Briceno NJ, et al. (2025) Beyond the Promoter: Total MGMT Gene Methylation Modulates Response to DNA Alkylating Agents in Glioma. *Molecular cancer therapeutics*.