Resource Summary Report

Generated by <u>dkNET</u> on May 18, 2025

TMAJ

RRID:SCR_005601 Type: Tool

Proper Citation

TMAJ (RRID:SCR_005601)

Resource Information

URL: http://tmaj.pathology.jhmi.edu/

Proper Citation: TMAJ (RRID:SCR_005601)

Description: Open-source software to support information and images related to tissue micro-arrays. It contains support for multiple organ systems, multiple users, image analysis, and is designed to be compliant with HIPPA regulations. Patients, specimens, blocks, slides, cores, images, and scores can all be stored and viewed. Features include advanced security, custom dynamic fields, and an image analysis program.

Abbreviations: TMAJ

Synonyms: TMAJ Software Project

Resource Type: software resource

Keywords: tissue microarray, java, java swing, bio.tools

Funding:

Availability: GNU General Public License, v3

Resource Name: TMAJ

Resource ID: SCR_005601

Alternate IDs: biotools:tmaj, OMICS_00823

Alternate URLs: https://bio.tools/tmaj

Record Creation Time: 20220129T080231+0000

Record Last Update: 20250420T014256+0000

Ratings and Alerts

No rating or validation information has been found for TMAJ.

No alerts have been found for TMAJ.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Ouellet V, et al. (2022) The Movember Global Action Plan 1 (GAP1): Unique Prostate Cancer Tissue Microarray Resource. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 31(4), 715.

Vidal I, et al. (2021) GSTP1 positive prostatic adenocarcinomas are more common in Black than White men in the United States. PloS one, 16(6), e0241934.

Zhong X, et al. (2019) CBX3/HP1? promotes tumor proliferation and predicts poor survival in hepatocellular carcinoma. Aging, 11(15), 5483.

Haffner MC, et al. (2018) Comprehensive Evaluation of Programmed Death-Ligand 1 Expression in Primary and Metastatic Prostate Cancer. The American journal of pathology, 188(6), 1478.

Lotan TL, et al. (2017) PTEN loss detection in prostate cancer: comparison of PTEN immunohistochemistry and PTEN FISH in a large retrospective prostatectomy cohort. Oncotarget, 8(39), 65566.

Su S, et al. (2017) Blocking the recruitment of naive CD4+ T cells reverses immunosuppression in breast cancer. Cell research, 27(4), 461.

Trock BJ, et al. (2016) PTEN loss and chromosome 8 alterations in Gleason grade 3 prostate cancer cores predicts the presence of un-sampled grade 4 tumor: implications for active surveillance. Modern pathology : an official journal of the United States and Canadian Academy of Pathology, Inc, 29(7), 764.

Lotan TL, et al. (2016) Analytic validation of a clinical-grade PTEN immunohistochemistry assay in prostate cancer by comparison with PTEN FISH. Modern pathology : an official journal of the United States and Canadian Academy of Pathology, Inc, 29(8), 904.

Carvalho FL, et al. (2015) HES6 promotes prostate cancer aggressiveness independently of Notch signalling. Journal of cellular and molecular medicine, 19(7), 1624.

Koh CM, et al. (2011) Alterations in nucleolar structure and gene expression programs in prostatic neoplasia are driven by the MYC oncogene. The American journal of pathology, 178(4), 1824.