Resource Summary Report

Generated by NIF on Apr 16, 2025

Stanford TMA Software

RRID:SCR_005598
Type: Tool

Proper Citation

Stanford TMA Software (RRID:SCR_005598)

Resource Information

URL: http://genome-www.stanford.edu/TMA/

Proper Citation: Stanford TMA Software (RRID:SCR_005598)

Description: Software Tools for High-Throughput Analysis and Archiving of Immunohistochemistry Staining Data Obtained with Tissue Microarrays.

Abbreviations: Stanford TMA

Synonyms: Stanford TMA Software website, Stanford Tissue Microarray Software

Resource Type: software resource

Defining Citation: PMID:12414504

Keywords: tissue microarray

Funding:

Resource Name: Stanford TMA Software

Resource ID: SCR_005598

Alternate IDs: OMICS_00819

Record Creation Time: 20220129T080231+0000

Record Last Update: 20250410T065311+0000

Ratings and Alerts

No rating or validation information has been found for Stanford TMA Software.

No alerts have been found for Stanford TMA Software.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Koketsu K, et al. (2015) Gremlin, a bone morphogenetic protein antagonist, is a crucial angiogenic factor in pituitary adenoma. International journal of endocrinology, 2015, 834137.