Jeremy L Muhlich

List of Publications by Year
in descending order

20 papers	1,741 citations	567281 15 h-index	752698 20 g-index
29 all docs	29 docs citations	29 times ranked	3391 citing authors

#	Article	IF	Citations
1	Scope2Screen: Focus+Context Techniques for Pathology Tumor Assessment in Multivariate Image Data. IEEE Transactions on Visualization and Computer Graphics, 2022, 28, 259-269.	4.4	9
2	Narrative online guides for the interpretation of digital-pathology images and tissue-atlas data. Nature Biomedical Engineering, 2022, 6, 515-526.	22.5	17
3	MCMICRO: a scalable, modular image-processing pipeline for multiplexed tissue imaging. Nature Methods, 2022, 19, 311-315.	19.0	102
4	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	19.0	37
5	shinyDepMap, a tool to identify targetable cancer genes and their functional connections from Cancer Dependency Map data. ELife, 2021, 10, .	6.0	45
6	A Simple Method for Creating a High‐Content Microscope for Imaging Multiplexed Tissue Microarrays. Current Protocols, 2021, 1, e68.	2.9	5
7	SYLARAS: A Platform for the Statistical Analysis and Visual Display of Systemic Immunoprofiling Data and Its Application to Glioblastoma. Cell Systems, 2020, 11, 272-285.e9.	6.2	8
8	Receptor-Driven ERK Pulses Reconfigure MAPK Signaling and Enable Persistence of Drug-Adapted BRAF-Mutant Melanoma Cells. Cell Systems, 2020, 11, 478-494.e9.	6.2	71
9	piNET: a versatile web platform for downstream analysis and visualization of proteomics data. Nucleic Acids Research, 2020, 48, W85-W93.	14.5	18
10	Minerva: a light-weight, narrative image browser for multiplexed tissue images. Journal of Open Source Software, 2020, 5, 2579.	4.6	22
11	Highly multiplexed immunofluorescence images and single-cell data of immune markers in tonsil and lung cancer. Scientific Data, 2019, 6, 323.	5.3	39
12	A Systems Toxicology Approach for the Prediction of Kidney Toxicity and Its Mechanisms In Vitro. Toxicological Sciences, 2019, 169, 54-69.	3.1	16
13	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. Cell Systems, 2018, 6, 13-24.	6.2	327
14	From word models to executable models of signaling networks using automated assembly. Molecular Systems Biology, 2017, 13, 954.	7.2	137
15	GRcalculator: an online tool for calculating and mining dose‐response data. BMC Cancer, 2017, 17, 698.	2.6	64
16	A Quantitative Approach to Screen for Nephrotoxic Compounds In Vitro. Journal of the American Society of Nephrology: JASN, 2016, 27, 1015-1028.	6.1	94
17	LINCS Canvas Browser: interactive web app to query, browse and interrogate LINCS L1000 gene expression signatures. Nucleic Acids Research, 2014, 42, W449-W460.	14.5	280
18	Metadata Standard and Data Exchange Specifications to Describe, Model, and Integrate Complex and Diverse High-Throughput Screening Data from the Library of Integrated Network-based Cellular Signatures (LINCS). Journal of Biomolecular Screening, 2014, 19, 803-816.	2.6	80

#	ARTICLE	IF	CITATIONS
19	Programming biological models in Python using PySB. Molecular Systems Biology, 2013, 9, 646.	7.2	216
20	Properties of cell death models calibrated and compared using Bayesian approaches. Molecular Systems Biology, 2013, 9, 644.	7.2	89