

Jeremy L Muhlich

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2783363/publications.pdf>

Version: 2024-02-01

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	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. <i>Cell Systems</i> , 2018, 6, 13-24.	6.2	327
2	LINCS Canvas Browser: interactive web app to query, browse and interrogate LINCS L1000 gene expression signatures. <i>Nucleic Acids Research</i> , 2014, 42, W449-W460.	14.5	280
3	Programming biological models in Python using PySB. <i>Molecular Systems Biology</i> , 2013, 9, 646.	7.2	216
4	From word models to executable models of signaling networks using automated assembly. <i>Molecular Systems Biology</i> , 2017, 13, 954.	7.2	137
5	MCMICRO: a scalable, modular image-processing pipeline for multiplexed tissue imaging. <i>Nature Methods</i> , 2022, 19, 311-315.	19.0	102
6	A Quantitative Approach to Screen for Nephrotoxic Compounds In Vitro. <i>Journal of the American Society of Nephrology: JASN</i> , 2016, 27, 1015-1028.	6.1	94
7	Properties of cell death models calibrated and compared using Bayesian approaches. <i>Molecular Systems Biology</i> , 2013, 9, 644.	7.2	89
8	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). <i>Journal of Biomolecular Screening</i> , 2014, 19, 803-816.	2.6	80
9	Receptor-Driven ERK Pulses Reconfigure MAPK Signaling and Enable Persistence of Drug-Adapted BRAF-Mutant Melanoma Cells. <i>Cell Systems</i> , 2020, 11, 478-494.e9.	6.2	71
10	GRcalculator: an online tool for calculating and mining dose-response data. <i>BMC Cancer</i> , 2017, 17, 698.	2.6	64
11	shinyDepMap, a tool to identify targetable cancer genes and their functional connections from Cancer Dependency Map data. <i>ELife</i> , 2021, 10, .	6.0	45
12	Highly multiplexed immunofluorescence images and single-cell data of immune markers in tonsil and lung cancer. <i>Scientific Data</i> , 2019, 6, 323.	5.3	39
13	MITI minimum information guidelines for highly multiplexed tissue images. <i>Nature Methods</i> , 2022, 19, 262-267.	19.0	37
14	Minerva: a light-weight, narrative image browser for multiplexed tissue images. <i>Journal of Open Source Software</i> , 2020, 5, 2579.	4.6	22
15	piNET: a versatile web platform for downstream analysis and visualization of proteomics data. <i>Nucleic Acids Research</i> , 2020, 48, W85-W93.	14.5	18
16	Narrative online guides for the interpretation of digital-pathology images and tissue-atlas data. <i>Nature Biomedical Engineering</i> , 2022, 6, 515-526.	22.5	17
17	A Systems Toxicology Approach for the Prediction of Kidney Toxicity and Its Mechanisms In Vitro. <i>Toxicological Sciences</i> , 2019, 169, 54-69.	3.1	16
18	Scope2Screen: Focus+Context Techniques for Pathology Tumor Assessment in Multivariate Image Data. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2022, 28, 259-269.	4.4	9

#	ARTICLE	IF	CITATIONS
19	SYLARAS: A Platform for the Statistical Analysis and Visual Display of Systemic Immunoprofiling Data and Its Application to Glioblastoma. <i>Cell Systems</i> , 2020, 11, 272-285.e9.	6.2	8
20	A Simple Method for Creating a High-Content Microscope for Imaging Multiplexed Tissue Microarrays. <i>Current Protocols</i> , 2021, 1, e68.	2.9	5