

Ted Liefeld

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11643078/publications.pdf>

Version: 2024-02-01

19
papers

15,209
citations

516561

16
h-index

794469

19
g-index

20
all docs

20
docs citations

20
times ranked

30056
citing authors

#	ARTICLE	IF	CITATIONS
1	The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. <i>Nature</i> , 2012, 483, 603-607.	13.7	6,473
2	The landscape of somatic copy-number alteration across human cancers. <i>Nature</i> , 2010, 463, 899-905.	13.7	3,331
3	GenePattern 2.0. <i>Nature Genetics</i> , 2006, 38, 500-501.	9.4	1,848
4	Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis. <i>Cell</i> , 2011, 144, 296-309.	13.5	843
5	Correlating chemical sensitivity and basal gene expression reveals mechanism of action. <i>Nature Chemical Biology</i> , 2016, 12, 109-116.	3.9	636
6	An Interactive Resource to Identify Cancer Genetic and Lineage Dependencies Targeted by Small Molecules. <i>Cell</i> , 2013, 154, 1151-1161.	13.5	615
7	Harnessing Connectivity in a Large-Scale Small-Molecule Sensitivity Dataset. <i>Cancer Discovery</i> , 2015, 5, 1210-1223.	7.7	575
8	Parallel genome-scale loss of function screens in 216 cancer cell lines for the identification of context-specific genetic dependencies. <i>Scientific Data</i> , 2014, 1, 140035.	2.4	328
9	Cytoscape: the network visualization tool for GenomeSpace workflows. <i>F1000Research</i> , 2014, 3, 151.	0.8	157
10	Globally distributed object identification for biological knowledgebases. <i>Briefings in Bioinformatics</i> , 2004, 5, 59-70.	3.2	124
11	GeNets: a unified web platform for network-based genomic analyses. <i>Nature Methods</i> , 2018, 15, 543-546.	9.0	62
12	Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. <i>Nature Methods</i> , 2016, 13, 245-247.	9.0	44
13	The GenePattern Notebook Environment. <i>Cell Systems</i> , 2017, 5, 149-151.e1.	2.9	34
14	The impact of Life Science Identifier on informatics data. <i>Drug Discovery Today</i> , 2005, 10, 1566-1572.	3.2	25
15	GeneCruiser: a web service for the annotation of microarray data. <i>Bioinformatics</i> , 2005, 21, 3681-3682.	1.8	23
16	NASA GeneLab RNA-seq consensus pipeline: Standardized processing of short-read RNA-seq data. <i>IScience</i> , 2021, 24, 102361.	1.9	20
17	GenePattern flow cytometry suite. <i>Source Code for Biology and Medicine</i> , 2013, 8, 14.	1.7	16
18	Imaging-AMARETTO: An Imaging Genomics Software Tool to Interrogate Multiomics Networks for Relevance to Radiography and Histopathology Imaging Biomarkers of Clinical Outcomes. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 421-435.	1.0	10

#	ARTICLE	IF	CITATIONS
19	A phenotypically supervised single-cell analysis protocol to study within-cell-type heterogeneity of cultured mammalian cells. STAR Protocols, 2021, 2, 100561.	0.5	1