

James T Webber

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1722518/publications.pdf>

Version: 2024-02-01

18
papers

19,016
citations

567281

15
h-index

839539

18
g-index

21
all docs

21
docs citations

21
times ranked

30191
citing authors

#	ARTICLE	IF	CITATIONS
1	SciPy 1.0: fundamental algorithms for scientific computing in Python. <i>Nature Methods</i> , 2020, 17, 261-272.	19.0	17,539
2	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012, 487, 491-495.	27.8	349
3	Ageing hallmarks exhibit organ-specific temporal signatures. <i>Nature</i> , 2020, 583, 596-602.	27.8	317
4	Isocitrate Dehydrogenase Mutations Confer Dasatinib Hypersensitivity and SRC Dependence in Intrahepatic Cholangiocarcinoma. <i>Cancer Discovery</i> , 2016, 6, 727-739.	9.4	126
5	Online Nanoflow Multidimensional Fractionation for High Efficiency Phosphopeptide Analysis. <i>Molecular and Cellular Proteomics</i> , 2011, 10, O111.011064.	3.8	93
6	Synthetic Lethal Targeting of <i>ARID1A</i> -Mutant Ovarian Clear Cell Tumors with Dasatinib. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 1472-1484.	4.1	73
7	Oncogene Mimicry as a Mechanism of Primary Resistance to BRAF Inhibitors. <i>Cell Reports</i> , 2014, 8, 1037-1048.	6.4	69
8	multiplierz: an extensible API based desktop environment for proteomics data analysis. <i>BMC Bioinformatics</i> , 2009, 10, 364.	2.6	64
9	Kinome rewiring reveals ALRKA limits PI3K-pathway inhibitor efficacy in breast cancer. <i>Nature Chemical Biology</i> , 2018, 14, 768-777.	8.0	64
10	Online Nanoflow Reversed Phase-Strong Anion Exchange-Reversed Phase Liquid Chromatography-Tandem Mass Spectrometry Platform for Efficient and In-Depth Proteome Sequence Analysis of Complex Organisms. <i>Analytical Chemistry</i> , 2011, 83, 6996-7005.	6.5	62
11	Unbiased Proteomic Profiling Uncovers a Targetable GNAS/PKA/PP2A Axis in Small Cell Lung Cancer Stem Cells. <i>Cancer Cell</i> , 2020, 38, 129-143.e7.	16.8	57
12	Nanoflow Low Pressure High Peak Capacity Single Dimension LC-MS/MS Platform for High-Throughput, In-Depth Analysis of Mammalian Proteomes. <i>Analytical Chemistry</i> , 2012, 84, 5133-5139.	6.5	56
13	<i>C/EBPβ</i> and DEK coordinately regulate myeloid differentiation. <i>Blood</i> , 2012, 119, 4878-4888.	1.4	45
14	An Optimized Chromatographic Strategy for Multiplexing In Parallel Reaction Monitoring Mass Spectrometry: Insights from Quantitation of Activated Kinases. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 265-277.	3.8	42
15	Integration of Tumor Genomic Data with Cell Lines Using Multi-dimensional Network Modules Improves Cancer Pharmacogenomics. <i>Cell Systems</i> , 2018, 7, 526-536.e6.	6.2	23
16	mzServer: Web-based Programmatic Access for Mass Spectrometry Data Analysis. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003988.	3.8	8
17	mzResults: An Interactive Viewer for Interrogation and Distribution of Proteomics Results. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003970.	3.8	8
18	Library dependent <i>LC-MS/MS</i> acquisition via <i>mzAPI</i> . <i>Proteomics</i> , 2013, 13, 1412-1416.	2.2	4