

James T Webber

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

19
papers

7,227
citations

14
h-index

21
g-index

21
ext. papers

12,991
ext. citations

14.1
avg, IF

4.54
L-index

#	Paper	IF	Citations
19	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	24.3	22
18	SciPy 1.0: fundamental algorithms for scientific computing in Python. <i>Nature Methods</i> , 2020 , 17, 261-272	21.6	6244
17	Ageing hallmarks exhibit organ-specific temporal signatures. <i>Nature</i> , 2020 , 583, 596-602	50.4	82
16	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	10.6	10
15	Kinome rewiring reveals AURKA limits PI3K-pathway inhibitor efficacy in breast cancer. <i>Nature Chemical Biology</i> , 2018 , 14, 768-777	11.7	39
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	7.6	28
13	Synthetic Lethal Targeting of ARID1A-Mutant Ovarian Clear Cell Tumors with Dasatinib. <i>Molecular Cancer Therapeutics</i> , 2016 , 15, 1472-84	6.1	54
12	Isocitrate Dehydrogenase Mutations Confer Dasatinib Hypersensitivity and SRC Dependence in Intrahepatic Cholangiocarcinoma. <i>Cancer Discovery</i> , 2016 , 6, 727-39	24.4	94
11	Oncogene mimicry as a mechanism of primary resistance to BRAF inhibitors. <i>Cell Reports</i> , 2014 , 8, 1037-48	48.6	57
10	Library dependent LC-MS/MS acquisition via mzAPI/Live. <i>Proteomics</i> , 2013 , 13, 1412-6	4.8	3
9	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, 5133-9	7.8	47
8	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012 , 487, 491-5	50.4	294
7	C/EBP β and DEK coordinately regulate myeloid differentiation. <i>Blood</i> , 2012 , 119, 4878-88	2.2	36
6	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	7.8	51
5	Online nanoflow multidimensional fractionation for high efficiency phosphopeptide analysis. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, O111.011064	7.6	83
4	mzServer: web-based programmatic access for mass spectrometry data analysis. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.003988	7.6	7
3	mzResults: an interactive viewer for interrogation and distribution of proteomics results. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.003970	7.6	8

2	multiplierz: an extensible API based desktop environment for proteomics data analysis. <i>BMC Bioinformatics</i> , 2009 , 10, 364	3.6	59
1	Molecular Cross-Validation for Single-Cell RNA-seq		9