

John T Prince

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,244
citations

430874

18
h-index

434195

31
g-index

36
all docs

36
docs citations

36
times ranked

2668
citing authors

#	ARTICLE	IF	CITATIONS
1	Imbalanced sphingolipid signaling is maintained as a core proponent of a cancerous phenotype in spite of metabolic pressure and epigenetic drift. <i>Oncotarget</i> , 2019, 10, 449-479.	1.8	6
2	<i>Yersinia pseudotuberculosis</i> BarA-UvrY Two-Component Regulatory System Represses Biofilms via CsrB. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 323.	3.9	9
3	Probabilistic Generation of Mass Spectrometry Molecular Abundance Variance for Case and Control Replicates. <i>Journal of Proteome Research</i> , 2017, 16, 2429-2434.	3.7	2
4	Whole blood and urine bioactive Hepcidin-25 determination using liquid chromatography mass spectrometry. <i>Analytical Biochemistry</i> , 2017, 517, 23-30.	2.4	6
5	Current controlled vocabularies are insufficient to uniquely map molecular entities to mass spectrometry signal. <i>BMC Bioinformatics</i> , 2015, 16, S2.	2.6	8
6	Structures of the G β -CCT and PhLP1-G β -CCT complexes reveal a mechanism for G-protein β -subunit folding and G $\beta\gamma$ dimer assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2413-2418.	7.1	49
7	Automated structural classification of lipids by machine learning. <i>Bioinformatics</i> , 2015, 31, 621-625.	4.1	3
8	JAMSS: proteomics mass spectrometry simulation in Java. <i>Bioinformatics</i> , 2015, 31, 791-793.	4.1	10
9	LC-MS alignment in theory and practice: a comprehensive algorithmic review. <i>Briefings in Bioinformatics</i> , 2015, 16, 104-117.	6.5	96
10	A comprehensive protein-protein interactome for yeast PAS kinase 1 reveals direct inhibition of respiration through the phosphorylation of Cbf1. <i>Molecular Biology of the Cell</i> , 2014, 25, 2199-2215.	2.1	13
11	Programmed Cell Death Protein 5 Interacts with the Cytosolic Chaperonin Containing Tailless Complex Polypeptide 1 (CCT) to Regulate β -Tubulin Folding. <i>Journal of Biological Chemistry</i> , 2014, 289, 4490-4502.	3.4	31
12	The Genomes, Proteomes, and Structures of Three Novel Phages That Infect the <i>Bacillus cereus</i> Group and Carry Putative Virulence Factors. <i>Journal of Virology</i> , 2014, 88, 11846-11860.	3.4	37
13	Metabolic-Stress-Induced Rearrangement of the 14-3-3 η Interactome Promotes Autophagy via a ULK1- and AMPK-Regulated 14-3-3 η Interaction with Phosphorylated Atg9. <i>Molecular and Cellular Biology</i> , 2014, 34, 4379-4388.	2.3	93
14	Proteomics, lipidomics, metabolomics: a mass spectrometry tutorial from a computer scientist's point of view. <i>BMC Bioinformatics</i> , 2014, 15, S9.	2.6	56
15	Controlling for confounding variables in MS-omics protocol: why modularity matters. <i>Briefings in Bioinformatics</i> , 2014, 15, 768-770.	6.5	14
16	Massifquant: open-source Kalman filter-based XC-MS isotope trace feature detection. <i>Bioinformatics</i> , 2014, 30, 2636-2643.	4.1	39
17	Metriculator: quality assessment for mass spectrometry-based proteomics. <i>Bioinformatics</i> , 2013, 29, 2948-2949.	4.1	20
18	Rubabel: wrapping open Babel with Ruby. <i>Journal of Cheminformatics</i> , 2013, 5, 35.	6.1	8

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19	In Vitro Oxidation of Snap-25 Leads to Double Disulfide Bond Formation and Protein Destabilization. <i>Biophysical Journal</i> , 2013, 104, 622a.	0.5	0
20	Mspire-Simulator: LC-MS Shotgun Proteomic Simulator for Creating Realistic Gold Standard Data. <i>Journal of Proteome Research</i> , 2013, 12, 5742-5749.	3.7	20
21	Resolving double disulfide bond patterns in SNAP25B using liquid chromatography-ion trap mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2013, 48, 660-668.	1.6	0
22	Mitochondrial fission mediates ceramide-induced metabolic disruption in skeletal muscle. <i>Biochemical Journal</i> , 2013, 456, 427-439.	3.7	66
23	Statistical agglomeration: peak summarization for direct infusion lipidomics. <i>Bioinformatics</i> , 2013, 29, 2445-2451.	4.1	7
24	Novel algorithms and the benefits of comparative validation. <i>Bioinformatics</i> , 2013, 29, 1583-1585.	4.1	32
25	Programmed cell death protein 5 may exert its apoptotic function through CCT. <i>FASEB Journal</i> , 2013, 27, 784.8.	0.5	0
26	Structures of the β -CCT and PhLP1- β -CCT complexes reveal a molecular mechanism for G protein beta subunit folding and β -gamma dimer assembly. <i>FASEB Journal</i> , 2013, 27, 1040.4.	0.5	0
27	Sequence and Structural Characterization of Great Salt Lake Bacteriophage CW02, a Member of the T7-Like Supergroup. <i>Journal of Virology</i> , 2012, 86, 7907-7917.	3.4	31
28	AICAR inhibits ceramide biosynthesis in skeletal muscle. <i>Diabetology and Metabolic Syndrome</i> , 2012, 4, 45.	2.7	25
29	Oxidation of SNAP25-syntaxin complex reduce its stability and prevents refolding. <i>FASEB Journal</i> , 2012, 26, 692.6.	0.5	0
30	The Case of the Disappearing Drug Target. <i>Molecular Cell</i> , 2010, 37, 455-456.	9.7	5
31	Integrating shotgun proteomics and mRNA expression data to improve protein identification. <i>Bioinformatics</i> , 2009, 25, 1397-1403.	4.1	59
32	mspire: mass spectrometry proteomics in Ruby. <i>Bioinformatics</i> , 2008, 24, 2796-2797.	4.1	23
33	Chromatographic Alignment of ESI-LC-MS Proteomics Data Sets by Ordered Bijective Interpolated Warping. <i>Analytical Chemistry</i> , 2006, 78, 6140-6152.	6.5	219
34	A fast coarse filtering method for peptide identification by mass spectrometry. <i>Bioinformatics</i> , 2006, 22, 1524-1531.	4.1	36
35	Mass spectrometry of the <i>M. smegmatis</i> proteome: Protein expression levels correlate with function, operons, and codon bias. <i>Genome Research</i> , 2005, 15, 1118-1126.	5.5	64
36	The need for a public proteomics repository. <i>Nature Biotechnology</i> , 2004, 22, 471-472.	17.5	157