

# Marc Kirchner

## List of Publications by Year in descending order

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22  
papers

1,253  
citations

516710

16  
h-index

677142

22  
g-index

22  
all docs

22  
docs citations

22  
times ranked

2188  
citing authors

#	ARTICLE	IF	CITATIONS
1	An in-depth comparison of the male pediatric and adult urinary proteomes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1044-1050.	2.3	25
2	Co-regulation proteomics reveals substrates and mechanisms of APC/C-dependent degradation. <i>EMBO Journal</i> , 2014, 33, 385-399.	7.8	72
3	mz5: Space- and Time-efficient Storage of Mass Spectrometry Data Sets. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.011379.	3.8	56
4	Overcoming Species Boundaries in Peptide Identification with Bayesian Information Criterion-driven Error-tolerant Peptide Search (BICEPS). <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014167-1-M111.014167-12.	3.8	24
5	Measuring Phosphorylation-Specific Changes in Response to Kinase Inhibitors in Mammalian Cells Using Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2012, 795, 217-231.	0.9	2
6	A Practical Guide to the FLEXIQuant Method. <i>Methods in Molecular Biology</i> , 2012, 893, 295-319.	0.9	19
7	Automated detection and analysis of bimodal isotope peak distributions in H/D exchange mass spectrometry using HeXicon. <i>International Journal of Mass Spectrometry</i> , 2011, 302, 125-131.	1.5	22
8	Life Cycle Stage-resolved Proteomic Analysis of the Excretome/Secretome from <i>Strongyloides ratti</i> —Identification of Stage-specific Proteases. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010157.	3.8	78
9	libfbi: a C++ implementation for fast box intersection and application to sparse mass spectrometry data. <i>Bioinformatics</i> , 2011, 27, 1166-1167.	4.1	4
10	Computational protein profile similarity screening for quantitative mass spectrometry experiments. <i>Bioinformatics</i> , 2010, 26, 77-83.	4.1	16
11	Deuteration distribution estimation with improved sequence coverage for HX/MS experiments. <i>Bioinformatics</i> , 2010, 26, 1535-1541.	4.1	44
12	Non-linear classification for on-the-fly fractional mass filtering and targeted precursor fragmentation in mass spectrometry experiments. <i>Bioinformatics</i> , 2010, 26, 791-797.	4.1	14
13	Proteome Scale Characterization of Human S-Acylated Proteins in Lipid Raft-enriched and Non-raft Membranes. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 54-70.	3.8	252
14	Estimating the Confidence of Peptide Identifications without Decoy Databases. <i>Analytical Chemistry</i> , 2010, 82, 4314-4318.	6.5	23
15	MGFp: An Open Mascot Generic Format Parser Library Implementation. <i>Journal of Proteome Research</i> , 2010, 9, 2762-2763.	3.7	8
16	When less can yield more — Computational preprocessing of MS/MS spectra for peptide identification. <i>Proteomics</i> , 2009, 9, 4978-4984.	2.2	73
17	Toward Digital Staining using Imaging Mass Spectrometry and Random Forests. <i>Journal of Proteome Research</i> , 2009, 8, 3558-3567.	3.7	87
18	Multivariate Watershed Segmentation of Compositional Data. <i>Lecture Notes in Computer Science</i> , 2009, , 180-192.	1.3	1

#	ARTICLE	IF	CITATIONS
19	NITPICK: peak identification for mass spectrometry data. BMC Bioinformatics, 2008, 9, 355.	2.6	66
20	Robust Prediction of the MASCOT Score for an Improved Quality Assessment in Mass Spectrometric Proteomics. Journal of Proteome Research, 2008, 7, 3708-3717.	3.7	182
21	Different phosphorylation states of the anaphase promoting complex in response to antimetabolic drugs: A quantitative proteomic analysis. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6069-6074.	7.1	77
22	Concise Representation of Mass Spectrometry Images by Probabilistic Latent Semantic Analysis. Analytical Chemistry, 2008, 80, 9649-9658.	6.5	108