Marc Kirchner

List of Publications by Year
in descending order

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	Proteome Scale Characterization of Human S-Acylated Proteins in Lipid Raft-enriched and Non-raft Membranes. Molecular and Cellular Proteomics, 2010, 9, 54-70.	3.8	252
2	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
3	Concise Representation of Mass Spectrometry Images by Probabilistic Latent Semantic Analysis. Analytical Chemistry, 2008, 80, 9649-9658.	6.5	108
4	Toward Digital Staining using Imaging Mass Spectrometry and Random Forests. Journal of Proteome Research, 2009, 8, 3558-3567.	3.7	87
5	Life Cycle Stage-resolved Proteomic Analysis of the Excretome/Secretome from Strongyloides ratti—Identification of Stage-specific Proteases. Molecular and Cellular Proteomics, 2011, 10, M111.010157.	3.8	78
6	Different phosphorylation states of the anaphase promoting complex in response to antimitotic 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
7	When less can yield more – Computational preprocessing of MS/MS spectra for peptide identification. Proteomics, 2009, 9, 4978-4984.	2.2	73
8	Co-regulation proteomics reveals substrates and mechanisms of APC/C-dependent degradation. EMBO Journal, 2014, 33, 385-399.	7.8	72
9	NITPICK: peak identification for mass spectrometry data. BMC Bioinformatics, 2008, 9, 355.	2.6	66
10	mz5: Space- and Time-efficient Storage of Mass Spectrometry Data Sets. Molecular and Cellular Proteomics, 2012, 11, O111.011379.	3.8	56
11	Deuteration distribution estimation with improved sequence coverage for HX/MS experiments. Bioinformatics, 2010, 26, 1535-1541.	4.1	44
12	An in-depth comparison of the male pediatric and adult urinary proteomes. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1044-1050.	2.3	25
13	Overcoming Species Boundaries in Peptide Identification with Bayesian Information Criterion-driven Error-tolerant Peptide Search (BICEPS). Molecular and Cellular Proteomics, 2012, 11, M111.014167-1-M111.014167-12.	3.8	24
14	Estimating the Confidence of Peptide Identifications without Decoy Databases. Analytical Chemistry, 2010, 82, 4314-4318.	6.5	23
15	Automated detection and analysis of bimodal isotope peak distributions in H/D exchange mass spectrometry using HeXicon. International Journal of Mass Spectrometry, 2011, 302, 125-131.	1.5	22
16	A Practical Guide to the FLEXIQuant Method. Methods in Molecular Biology, 2012, 893, 295-319.	0.9	19
17	Computational protein profile similarity screening for quantitative mass spectrometry experiments. Bioinformatics, 2010, 26, 77-83.	4.1	16
18	Non-linear classification for on-the-fly fractional mass filtering and targeted precursor fragmentation in mass spectrometry experiments. Bioinformatics, 2010, 26, 791-797.	4.1	14

#	Article	IF	Citations
19	MGFp: An Open Mascot Generic Format Parser Library Implementation. Journal of Proteome Research, 2010, 9, 2762-2763.	3.7	8
20	libfbi: a C++ implementation for fast box intersection and application to sparse mass spectrometry data. Bioinformatics, 2011, 27, 1166-1167.	4.1	4
21	Measuring Phosphorylation-Specific Changes in Response to Kinase Inhibitors in Mammalian Cells Using Quantitative Proteomics. Methods in Molecular Biology, 2012, 795, 217-231.	0.9	2
22	Multivariate Watershed Segmentation of Compositional Data. Lecture Notes in Computer Science, 2009, , 180-192.	1.3	1