Markus Mller

List of Publications by Citations

59 papers	7,681 citations	27 h-index	60 g-index
60 ext. papers	10,032 ext. citations	7 avg, IF	5.66 L-index

#	Paper	IF	Citations
59	pROC: an open-source package for R and S+ to analyze and compare ROC curves. *BMC Bioinformatics*, **2011**, 12, 77	3.6	5242
58	SuperHirn - a novel tool for high resolution LC-MS-based peptide/protein profiling. *Proteomics*, **2007**, 7, 3470-80	4.8	269
57	An integrated mass spectrometric and computational framework for the analysis of protein interaction networks. *Nature Biotechnology*, **2007**, 25, 345-52	44.5	147
56	Processing and classification of protein mass spectra. *Mass Spectrometry Reviews*, **2006**, 25, 409-49	11	136
55	The Fab-8 boundary defines the distal limit of the bithorax complex iab-7 domain and insulates iab-7 from initiation elements and a PRE in the adjacent iab-8 domain. *Development (Cambridge)*, **2000**, 127, 779-790	6.6	132
54	Automated protein identification by tandem mass spectrometry: issues and strategies. *Mass Spectrometry Reviews*, **2006**, 25, 235-54	11	125
53	A molecular scanner to automate proteomic research and to display proteome images. *Analytical Chemistry*, **1999**, 71, 4981-8	7.8	118
52	Improving protein identification from peptide mass fingerprinting through a parameterized multi-level scoring algorithm and an optimized peak detection. *Electrophoresis*, **1999**, 20, 3535-50	3.6	117
51	Processing strategies and software solutions for data-independent acquisition in mass spectrometry. *Proteomics*, **2015**, 15, 964-80	4.8	105
50	Quantitative proteomic analysis of protein complexes: concurrent identification of interactors and their state of phosphorylation. *Molecular and Cellular Proteomics*, **2008**, 7, 326-46	7.6	95
49	High-throughput and Sensitive Immunopeptidomics Platform Reveals Profound Interferon-Mediated Remodeling of the Human Leukocyte Antigen (HLA) Ligandome. *Molecular and Cellular Proteomics*, **2018**, 17, 533-548	7.6	92
48	Integrated proteogenomic deep sequencing and analytics accurately identify non-canonical peptides in tumor immunopeptidomes. *Nature Communications*, **2020**, 11, 1293	17.4	78
47	Unrestricted identification of modified proteins using MS/MS. *Proteomics*, **2010**, 10, 671-86	4.8	77
46	Glycation isotopic labeling with 13C-reducing sugars for quantitative analysis of glycated proteins in human plasma. *Molecular and Cellular Proteomics*, **2010**, 9, 579-92	7.6	64
45	Estimating the Contribution of Proteasomal Spliced Peptides to the HLA-I Ligandome. *Molecular and Cellular Proteomics*, **2018**, 17, 2347-2357	7.6	62
44	Open source libraries and frameworks for mass spectrometry based proteomics: a developer's perspective. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2014**, 1844, 63-76	4	59
43	A combined CXCL10, CXCL8 and H-FABP panel for the staging of human African trypanosomiasis patients. *PLoS Neglected Tropical Diseases*, **2009**, 3, e459	4.8	55

42	EasyProt--an easy-to-use graphical platform for proteomics data analysis. *Journal of Proteomics*, **2013**, 79, 146-60	3.9	52
41	Hotspots of Antigen Presentation Revealed by Human Leukocyte Antigen Ligandomics for Neoantigen Prioritization. *Frontiers in Immunology*, **2017**, 8, 1367	8.4	50
40	QuickMod: A tool for open modification spectrum library searches. *Journal of Proteome Research*, **2011**, 10, 2913-21	5.6	50
39	Bioinformatics for protein biomarker panel classification: what is needed to bring biomarker panels into in vitro diagnostics?. *Expert Review of Proteomics*, **2009**, 6, 675-89	4.2	43
38	Machine learning approaches to lung cancer prediction from mass spectra. *Proteomics*, **2003**, 3, 1716-9	4.8	41
37	Unrestricted modification search reveals lysine methylation as major modification induced by tissue formalin fixation and paraffin embedding. *Proteomics*, **2015**, 15, 2568-79	4.8	35
36	Matrix metalloproteinase-9 and intercellular adhesion molecule 1 are powerful staging markers for human African trypanosomiasis. *Tropical Medicine and International Health*, **2011**, 16, 119-26	2.3	32
35	Isoelectric point optimization using peptide descriptors and support vector machines. *Journal of Proteomics*, **2012**, 75, 2269-74	3.9	30
34	In silico analysis of accurate proteomics, complemented by selective isolation of peptides. *Journal of Proteomics*, **2011**, 74, 2071-82	3.9	27
33	A simple workflow to increase MS2 identification rate by subsequent spectral library search. *Proteomics*, **2009**, 9, 1731-6	4.8	27
32	The molecular scanner: concept and developments. *Current Opinion in Biotechnology*, **2004**, 15, 17-23	11.4	26
31	Visualization and analysis of molecular scanner peptide mass spectra. *Journal of the American Society for Mass Spectrometry*, **2002**, 13, 221-31	3.5	26
30	Comment on "A subset of HLA-I peptides are not genomically templated: Evidence for cis- and trans-spliced peptide ligands". *Science Immunology*, **2019**, 4,	28	24
29	MzJava: An open source library for mass spectrometry data processing. *Journal of Proteomics*, **2015**, 129, 63-70	3.9	23
28	PanelomiX: A threshold-based algorithm to create panels of biomarkers. *Translational Proteomics*, **2013**, 1, 57-64		22
27	An improved method for the construction of decoy peptide MS/MS spectra suitable for the accurate estimation of false discovery rates. *Proteomics*, **2011**, 11, 4085-95	4.8	21
26	Mass Spectrometry Based Immunopeptidomics Leads to Robust Predictions of Phosphorylated HLA Class I Ligands. *Molecular and Cellular Proteomics*, **2020**, 19, 390-404	7.6	19
25	Mining Large Scale Tandem Mass Spectrometry Data for Protein Modifications Using Spectral Libraries. *Journal of Proteome Research*, **2016**, 15, 721-31	5.6	19

24	Feasibility and safety of ultra-low tidal volume ventilation without extracorporeal circulation in moderately severe and severe ARDS patients. *Intensive Care Medicine*, **2019**, 45, 1590-1598	14.5	16
23	Glycoforest 1.0. *Analytical Chemistry*, **2017**, 89, 10932-10940	7.8	16
22	Clustering and filtering tandem mass spectra acquired in data-independent mode. *Journal of the American Society for Mass Spectrometry*, **2013**, 24, 1862-71	3.5	14
21	Molecular scanner experiment with human plasma: improving protein identification by using intensity distributions of matching peptide masses. *Proteomics*, **2002**, 2, 1413-25	4.8	14
20	Minimal Information About an Immuno-Peptidomics Experiment (MIAIPE). *Proteomics*, **2018**, 18, e1800110	4.8	14
19	Comparative Proteomic Profiling of Ehrlichia ruminantium Pathogenic Strain and Its High-Passaged Attenuated Strain Reveals Virulence and Attenuation-Associated Proteins. *PLoS ONE*, **2015**, 10, e0145328	3.7	13
18	Sensitive Immunopeptidomics by Leveraging Available Large-Scale Multi-HLA Spectral Libraries, Data-Independent Acquisition, and MS/MS Prediction. *Molecular and Cellular Proteomics*, **2021**, 20, 100080	7.6	10
17	Large-Scale Reanalysis of Publicly Available HeLa Cell Proteomics Data in the Context of the Human Proteome Project. *Journal of Proteome Research*, **2018**, 17, 4160-4170	5.6	10
16	Chemical Genetics of AGC-kinases Reveals Shared Targets of Ypk1, Protein Kinase A and Sch9. *Molecular and Cellular Proteomics*, **2020**, 19, 655-671	7.6	7
15	Automatic Annotation and Dereplication of Tandem Mass Spectra of Peptidic Natural Products. *Analytical Chemistry*, **2020**, 92, 15862-15871	7.8	7
14	Optimization by infusion of multiple reaction monitoring transitions for sensitive quantification of peptides by liquid chromatography/mass spectrometry. *Rapid Communications in Mass Spectrometry*, **2017**, 31, 753-761	2.2	6
13	Wnt-controlled sphingolipids modulate Anthrax Toxin Receptor palmitoylation to regulate oriented mitosis in zebrafish. *Nature Communications*, **2020**, 11, 3317	17.4	4
12	Biogenesis of HLA Ligand Presentation in Immune Cells Upon Activation Reveals Changes in Peptide Length Preference. *Frontiers in Immunology*, **2020**, 11, 1981	8.4	4
11	Detection of busulfan adducts on proteins. *Rapid Communications in Mass Spectrometry*, **2016**, 30, 2517-2528	2.2	3
10	LC/MS data processing for label-free quantitative analysis. *Methods in Molecular Biology*, **2011**, 696, 369-77	1.4	1
9	Estimating the Contribution of Proteasomal Spliced Peptides to the HLA-I Ligandome		1
8	Integrated Proteogenomic Deep Sequencing and Analytics Accurately Identify Non-Canonical Peptides in Tumor Immunopeptidomes		1
7	Proteomics and Mass Spectrometry **2001**, 93-145		0

List of Publications

6 Detection of Unknown Chemical Adduct Modifications on Proteins: From Wet to Dry Laboratory. *Methods in Molecular Biology*, **2019**, 1977, 99-113 1.4

5 Bioinformatics Tools for Detecting Post-Translational Modifications in Mass Spectrometry Data **2011**, 463-475

4 Proteomics and Mass Spectrometry **2005**, 225-281

3 Signal Traitment and Virtual Images Production (1/2) **2005**, 151-168

2 Signal Traitment and Virtual Images Production (2/2) **2005**, 169-188

1 Scoring Functions for Mass Spectrometric Protein Identification **2003**, 477-485