

Markus Müller

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.

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	Sensitive Immunopeptidomics by Leveraging Available Large-Scale Multi-HLA Spectral Libraries, Data-Independent Acquisition, and MS/MS Prediction. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100080	7.6	10
58	Integrated proteogenomic deep sequencing and analytics accurately identify non-canonical peptides in tumor immunopeptidomes. <i>Nature Communications</i> , 2020 , 11, 1293	17.4	78
57	Wnt-controlled sphingolipids modulate Anthrax Toxin Receptor palmitoylation to regulate oriented mitosis in zebrafish. <i>Nature Communications</i> , 2020 , 11, 3317	17.4	4
56	Mass Spectrometry Based Immunopeptidomics Leads to Robust Predictions of Phosphorylated HLA Class I Ligands. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 390-404	7.6	19
55	Chemical Genetics of AGC-kinases Reveals Shared Targets of Ypk1, Protein Kinase A and Sch9. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 655-671	7.6	7
54	Automatic Annotation and Dereplication of Tandem Mass Spectra of Peptidic Natural Products. <i>Analytical Chemistry</i> , 2020 , 92, 15862-15871	7.8	7
53	Biogenesis of HLA Ligand Presentation in Immune Cells Upon Activation Reveals Changes in Peptide Length Preference. <i>Frontiers in Immunology</i> , 2020 , 11, 1981	8.4	4
52	Feasibility and safety of ultra-low tidal volume ventilation without extracorporeal circulation in moderately severe and severe ARDS patients. <i>Intensive Care Medicine</i> , 2019 , 45, 1590-1598	14.5	16
51	Detection of Unknown Chemical Adduct Modifications on Proteins: From Wet to Dry Laboratory. <i>Methods in Molecular Biology</i> , 2019 , 1977, 99-113	1.4	
50	Comment on "A subset of HLA-I peptides are not genomically templated: Evidence for cis- and trans-spliced peptide ligands". <i>Science Immunology</i> , 2019 , 4,	28	24
49	High-throughput and Sensitive Immunopeptidomics Platform Reveals Profound Interferon- γ Mediated Remodeling of the Human Leukocyte Antigen (HLA) Ligandome. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 533-548	7.6	92
48	Estimating the Contribution of Proteasomal Spliced Peptides to the HLA-I Ligandome. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2347-2357	7.6	62
47	Large-Scale Reanalysis of Publicly Available HeLa Cell Proteomics Data in the Context of the Human Proteome Project. <i>Journal of Proteome Research</i> , 2018 , 17, 4160-4170	5.6	10
46	Minimal Information About an Immuno-Peptidomics Experiment (MIAIPE). <i>Proteomics</i> , 2018 , 18, e18001108	10.8	14
45	Optimization by infusion of multiple reaction monitoring transitions for sensitive quantification of peptides by liquid chromatography/mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2017 , 31, 753-761	2.2	6
44	Glycoforest 1.0. <i>Analytical Chemistry</i> , 2017 , 89, 10932-10940	7.8	16
43	Hotspots of Antigen Presentation Revealed by Human Leukocyte Antigen Ligandomics for Neoantigen Prioritization. <i>Frontiers in Immunology</i> , 2017 , 8, 1367	8.4	50

42	Mining Large Scale Tandem Mass Spectrometry Data for Protein Modifications Using Spectral Libraries. <i>Journal of Proteome Research</i> , 2016 , 15, 721-31	5.6	19
41	Detection of busulfan adducts on proteins. <i>Rapid Communications in Mass Spectrometry</i> , 2016 , 30, 2517-2528		3
40	MzJava: An open source library for mass spectrometry data processing. <i>Journal of Proteomics</i> , 2015 , 129, 63-70	3.9	23
39	Unrestricted modification search reveals lysine methylation as major modification induced by tissue formalin fixation and paraffin embedding. <i>Proteomics</i> , 2015 , 15, 2568-79	4.8	35
38	Processing strategies and software solutions for data-independent acquisition in mass spectrometry. <i>Proteomics</i> , 2015 , 15, 964-80	4.8	105
37	Comparative Proteomic Profiling of Ehrlichia ruminantium Pathogenic Strain and Its High-Passaged Attenuated Strain Reveals Virulence and Attenuation-Associated Proteins. <i>PLoS ONE</i> , 2015 , 10, e0145328	3.7	13
36	Open source libraries and frameworks for mass spectrometry based proteomics: a developer's perspective. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 63-76	4	59
35	PanelomiX: A threshold-based algorithm to create panels of biomarkers. <i>Translational Proteomics</i> , 2013 , 1, 57-64		22
34	EasyProt--an easy-to-use graphical platform for proteomics data analysis. <i>Journal of Proteomics</i> , 2013 , 79, 146-60	3.9	52
33	Clustering and filtering tandem mass spectra acquired in data-independent mode. <i>Journal of the American Society for Mass Spectrometry</i> , 2013 , 24, 1862-71	3.5	14
32	Isoelectric point optimization using peptide descriptors and support vector machines. <i>Journal of Proteomics</i> , 2012 , 75, 2269-74	3.9	30
31	Bioinformatics Tools for Detecting Post-Translational Modifications in Mass Spectrometry Data		2011 , 463-475
30	In silico analysis of accurate proteomics, complemented by selective isolation of peptides. <i>Journal of Proteomics</i> , 2011 , 74, 2071-82	3.9	27
29	Matrix metalloproteinase-9 and intercellular adhesion molecule 1 are powerful staging markers for human African trypanosomiasis. <i>Tropical Medicine and International Health</i> , 2011 , 16, 119-26	2.3	32
28	pROC: an open-source package for R and S+ to analyze and compare ROC curves. <i>BMC Bioinformatics</i> , 2011 , 12, 77	3.6	5242
27	An improved method for the construction of decoy peptide MS/MS spectra suitable for the accurate estimation of false discovery rates. <i>Proteomics</i> , 2011 , 11, 4085-95	4.8	21
26	QuickMod: A tool for open modification spectrum library searches. <i>Journal of Proteome Research</i> , 2011 , 10, 2913-21	5.6	50
25	LC/MS data processing for label-free quantitative analysis. <i>Methods in Molecular Biology</i> , 2011 , 696, 369-77		1

24	Glycation isotopic labeling with ¹³ C-reducing sugars for quantitative analysis of glycated proteins in human plasma. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 579-92	7.6	64
23	Unrestricted identification of modified proteins using MS/MS. <i>Proteomics</i> , 2010 , 10, 671-86	4.8	77
22	A simple workflow to increase MS2 identification rate by subsequent spectral library search. <i>Proteomics</i> , 2009 , 9, 1731-6	4.8	27
21	Bioinformatics for protein biomarker panel classification: what is needed to bring biomarker panels into in vitro diagnostics?. <i>Expert Review of Proteomics</i> , 2009 , 6, 675-89	4.2	43
20	A combined CXCL10, CXCL8 and H-FABP panel for the staging of human African trypanosomiasis patients. <i>PLoS Neglected Tropical Diseases</i> , 2009 , 3, e459	4.8	55
19	Quantitative proteomic analysis of protein complexes: concurrent identification of interactors and their state of phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 326-46	7.6	95
18	SuperHirn - a novel tool for high resolution LC-MS-based peptide/protein profiling. <i>Proteomics</i> , 2007 , 7, 3470-80	4.8	269
17	An integrated mass spectrometric and computational framework for the analysis of protein interaction networks. <i>Nature Biotechnology</i> , 2007 , 25, 345-52	44.5	147
16	Automated protein identification by tandem mass spectrometry: issues and strategies. <i>Mass Spectrometry Reviews</i> , 2006 , 25, 235-54	11	125
15	Processing and classification of protein mass spectra. <i>Mass Spectrometry Reviews</i> , 2006 , 25, 409-49	11	136
14	Proteomics and Mass Spectrometry 2005 , 225-281		
13	Signal Traitment and Virtual Images Production (1/2) 2005 , 151-168		
12	Signal Traitment and Virtual Images Production (2/2) 2005 , 169-188		
11	The molecular scanner: concept and developments. <i>Current Opinion in Biotechnology</i> , 2004 , 15, 17-23	11.4	26
10	Machine learning approaches to lung cancer prediction from mass spectra. <i>Proteomics</i> , 2003 , 3, 1716-9	4.8	41
9	Scoring Functions for Mass Spectrometric Protein Identification 2003 , 477-485		
8	Molecular scanner experiment with human plasma: improving protein identification by using intensity distributions of matching peptide masses. <i>Proteomics</i> , 2002 , 2, 1413-25	4.8	14
7	Visualization and analysis of molecular scanner peptide mass spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 2002 , 13, 221-31	3.5	26

6	Proteomics and Mass Spectrometry 2001 , 93-145		0
5	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. <i>Development (Cambridge)</i> , 2000 , 127, 779-790	6.6	132
4	Improving protein identification from peptide mass fingerprinting through a parameterized multi-level scoring algorithm and an optimized peak detection. <i>Electrophoresis</i> , 1999 , 20, 3535-50	3.6	117
3	A molecular scanner to automate proteomic research and to display proteome images. <i>Analytical Chemistry</i> , 1999 , 71, 4981-8	7.8	118
2	Estimating the Contribution of Proteasomal Spliced Peptides to the HLA-I Ligandome		1
1	Integrated Proteogenomic Deep Sequencing and Analytics Accurately Identify Non-Canonical Peptides in Tumor Immunopeptidomes		1