

Markus MÃ¼ller

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

11,792
citations

159525

30
h-index

189801

50
g-index

60
all docs

60
docs citations

60
times ranked

24358
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	2.5	49
2	Automatic Annotation and Dereplication of Tandem Mass Spectra of Peptidic Natural Products. <i>Analytical Chemistry</i> , 2020, 92, 15862-15871.	3.2	18
3	Biogenesis of HLA Ligand Presentation in Immune Cells Upon Activation Reveals Changes in Peptide Length Preference. <i>Frontiers in Immunology</i> , 2020, 11, 1981.	2.2	9
4	Integrated proteogenomic deep sequencing and analytics accurately identify non-canonical peptides in tumor immunopeptidomes. <i>Nature Communications</i> , 2020, 11, 1293.	5.8	196
5	Wnt-controlled sphingolipids modulate Anthrax Toxin Receptor palmitoylation to regulate oriented mitosis in zebrafish. <i>Nature Communications</i> , 2020, 11, 3317.	5.8	8
6	Mass Spectrometry Based Immunopeptidomics Leads to Robust Predictions of Phosphorylated HLA Class I Ligands. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 390-404.	2.5	47
7	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.	2.5	16
8	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, .	5.6	39
9	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.	3.9	27
10	Detection of Unknown Chemical Adduct Modifications on Proteins: From Wet to Dry Laboratory. <i>Methods in Molecular Biology</i> , 2019, 1977, 99-113.	0.4	0
11	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.	2.5	224
12	Estimating the Contribution of Proteasomal Spliced Peptides to the HLA-I Ligandome*. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2347-2357.	2.5	105
13	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.	1.8	21
14	Minimal Information About an Immunopeptidomics Experiment (MIAIPE). <i>Proteomics</i> , 2018, 18, e1800110.	1.3	23
15	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.	0.7	8
16	Glycoforest 1.0. <i>Analytical Chemistry</i> , 2017, 89, 10932-10940.	3.2	24
17	"Hotspots"™ of Antigen Presentation Revealed by Human Leukocyte Antigen Ligandomics for Neoantigen Prioritization. <i>Frontiers in Immunology</i> , 2017, 8, 1367.	2.2	133
18	Detection of busulfan adducts on proteins. <i>Rapid Communications in Mass Spectrometry</i> , 2016, 30, 2517-2528.	0.7	3

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19	Mining Large Scale Tandem Mass Spectrometry Data for Protein Modifications Using Spectral Libraries. <i>Journal of Proteome Research</i> , 2016, 15, 721-731.	1.8	26
20	Unrestricted modification search reveals lysine methylation as major modification induced by tissue formalin fixation and paraffin embedding. <i>Proteomics</i> , 2015, 15, 2568-2579.	1.3	40
21	Processing strategies and software solutions for data-independent acquisition in mass spectrometry. <i>Proteomics</i> , 2015, 15, 964-980.	1.3	143
22	MzJava: An open source library for mass spectrometry data processing. <i>Journal of Proteomics</i> , 2015, 129, 63-70.	1.2	25
23	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.	1.1	28
24	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.	1.1	67
25	PanelomiX: A threshold-based algorithm to create panels of biomarkers. <i>Translational Proteomics</i> , 2013, 1, 57-64.	1.2	29
26	EasyProt – An easy-to-use graphical platform for proteomics data analysis. <i>Journal of Proteomics</i> , 2013, 79, 146-160.	1.2	57
27	Clustering and Filtering Tandem Mass Spectra Acquired in Data-Independent Mode. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1862-1871.	1.2	15
28	Isoelectric point optimization using peptide descriptors and support vector machines. <i>Journal of Proteomics</i> , 2012, 75, 2269-2274.	1.2	36
29	QuickMod: A Tool for Open Modification Spectrum Library Searches. <i>Journal of Proteome Research</i> , 2011, 10, 2913-2921.	1.8	58
30	In silico analysis of accurate proteomics, complemented by selective isolation of peptides. <i>Journal of Proteomics</i> , 2011, 74, 2071-2082.	1.2	30
31	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, 119-126.	1.0	33
32	pROC: an open-source package for R and S+ to analyze and compare ROC curves. <i>BMC Bioinformatics</i> , 2011, 12, 77.	1.2	8,498
33	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, 4085-4095.	1.3	25
34	LC/MS Data Processing for Label-Free Quantitative Analysis. <i>Methods in Molecular Biology</i> , 2011, 696, 369-377.	0.4	1
35	Unrestricted identification of modified proteins using MS/MS. <i>Proteomics</i> , 2010, 10, 671-686.	1.3	86
36	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, 579-592.	2.5	70

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37	A simple workflow to increase MS2 identification rate by subsequent spectral library search. <i>Proteomics</i> , 2009, 9, 1731-1736.	1.3	32
38	Bioinformatics for protein biomarker panel classification: what is needed to bring biomarker panels into <i>in vitro</i> diagnostics?. <i>Expert Review of Proteomics</i> , 2009, 6, 675-689.	1.3	51
39	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.	1.3	62
40	Quantitative Proteomic Analysis of Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 326-346.	2.5	99
41	SuperHirn – a novel tool for high resolution LC-MS based peptide/protein profiling. <i>Proteomics</i> , 2007, 7, 3470-3480.	1.3	295
42	An integrated mass spectrometric and computational framework for the analysis of protein interaction networks. <i>Nature Biotechnology</i> , 2007, 25, 345-352.	9.4	156
43	Analysis of Proteomes Using the Molecular Scanner. <i>Cold Spring Harbor Protocols</i> , 2007, 2007, pdb.prot4592-pdb.prot4592.	0.2	0
44	Automated protein identification by tandem mass spectrometry: Issues and strategies. <i>Mass Spectrometry Reviews</i> , 2006, 25, 235-254.	2.8	143
45	Processing and classification of protein mass spectra. <i>Mass Spectrometry Reviews</i> , 2006, 25, 409-449.	2.8	163
46	<i>Proteomics and Mass Spectrometry</i> . , 2005, , 225-281.		0
47	Signal Treatment and Virtual Images Production (1/2). , 2005, , 151-168.		0
48	Signal Treatment and Virtual Images Production (2/2). , 2005, , 169-188.		0
49	The molecular scanner: concept and developments. <i>Current Opinion in Biotechnology</i> , 2004, 15, 17-23.	3.3	28
50	Machine learning approaches to lung cancer prediction from mass spectra. <i>Proteomics</i> , 2003, 3, 1716-1719.	1.3	52
51	Scoring Functions for Mass Spectrometric Protein Identification. , 2003, , 477-485.		1
52	Molecular scanner experiment with human plasma: Improving protein identification by using intensity distributions of matching peptide masses. <i>Proteomics</i> , 2002, 2, 1413-1425.	1.3	16
53	Visualization and analysis of molecular scanner peptide mass spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 221-231.	1.2	31
54	<i>Proteomics and Mass Spectrometry</i> . , 2001, , 93-145.		3

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55	The <i>Fab-8</i> boundary defines the distal limit of the bithorax complex <i>iab-7</i> domain and insulates <i>iab-7</i> from initiation elements and a PRE in the adjacent <i>iab-8</i> domain. <i>Development</i> (Cambridge), 2000, 127, 779-790.	1.2	171
56	Improving protein identification from peptide mass fingerprinting through a parameterized multi-level scoring algorithm and an optimized peak detection. <i>Electrophoresis</i> , 1999, 20, 3535-3550.	1.3	140
57	A Molecular Scanner To Automate Proteomic Research and To Display Proteome Images. <i>Analytical Chemistry</i> , 1999, 71, 4981-4988.	3.2	127