Veit SchwÃ¤mmle

List of Publications by Year
in descending order

85 papers	3,143 citations	147801 31 h-index	175258 52 g-index
102 all docs	102 docs citations	102 times ranked	4575 citing authors

#	Article	IF	Citations
1	Quantitative Assessment of In-solution Digestion Efficiency Identifies Optimal Protocols for Unbiased Protein Analysis. Molecular and Cellular Proteomics, 2013, 12, 2992-3005.	3.8	229
2	A simple and fast method to determine the parameters for fuzzy c‑means cluster analysis. Bioinformatics, 2010, 26, 2841-2848.	4.1	174
3	Solitary wave behaviour of sand dunes. Nature, 2003, 426, 619-620.	27.8	134
4	A Novel Method for the Simultaneous Enrichment, Identification, and Quantification of Phosphopeptides and Sialylated Glycopeptides Applied to a Temporal Profile of Mouse Brain Development. Molecular and Cellular Proteomics, 2012, 11, 1191-1202.	3.8	121
5	Assessment and Improvement of Statistical Tools for Comparative Proteomics Analysis of Sparse Data Sets with Few Experimental Replicates. Journal of Proteome Research, 2013, 12, 3874-3883.	3.7	116
6	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	14.5	113
7	Consequences of the H theorem from nonlinear Fokker-Planck equations. Physical Review E, 2007, 76, 041123.	2.1	103
8	Dune formation under bimodal winds. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 22085-22089.	7.1	98
9	Accumulation of histone variant H3.3 with age is associated with profound changes in the histone methylation landscape. Nucleic Acids Research, 2017, 45, 9272-9289.	14.5	98
10	A general nonlinear Fokker-Planck equation and its associated entropy. European Physical Journal B, 2007, 58, 159-165.	1.5	76
11	Middle‑down hybrid chromatography/tandem mass spectrometry workflow for characterization of combinatorial post‑translational modifications in histones. Proteomics, 2014, 14, 2200-2211.	2.2	76
12	Systems Level Analysis of Histone H3 Post-translational Modifications (PTMs) Reveals Features of PTM Crosstalk in Chromatin Regulation. Molecular and Cellular Proteomics, 2016, 15, 2715-2729.	3.8	76
13	Precision Mapping of Coexisting Modifications in Histone H3 Tails from Embryonic Stem Cells by ETD-MS/MS. Analytical Chemistry, 2013, 85, 8232-8239.	6.5	70
14	Time-Resolved Quantitative Phosphoproteomics: New Insights into Angiotensin-(1‑7) Signaling Networks in Human Endothelial Cells. Journal of Proteome Research, 2012, 11, 3370-3381.	3.7	67
15	Large Scale Analysis of Co-existing Post-translational Modifications in Histone Tails Reveals Global Fine Structure of Cross-talk. Molecular and Cellular Proteomics, 2014, 13, 1855-1865.	3.8	65
16	High‑performance hybrid Orbitrap mass spectrometers for quantitative proteome analysis: Observations and implications. Proteomics, 2016, 16, 907-914.	2.2	64
17	Quantifying Online News Media Coverage of the COVID-19 Pandemic: Text Mining Study and Resource. Journal of Medical Internet Research, 2021, 23, e28253.	4.3	60
18	Strictly and asymptotically scale invariant probabilistic models of N correlated binary random variables having q-Gaussians as $N \to \infty$ limiting distributions. Journal of Statistical Mechanics: Theory and Experiment, 2008, 2008, P09006.	2.3	54

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19	Performance of Isobaric and Isotopic Labeling in Quantitative Plant Proteomics. Journal of Proteome Research, 2012, 11, 3046-3052.	3.7	52
20	The Cultural Divide: Exponential Growth in Classical 2D and Metabolic Equilibrium in 3D Environments. PLoS ONE, 2014, 9, e106973.	2.5	52
21	Quantitative Proteomics Analysis of Streptomyces coelicolor Development Demonstrates That Onset of Secondary Metabolism Coincides with Hypha Differentiation. Molecular and Cellular Proteomics, 2010, 9, 1423-1436.	3.8	50
22	Modelling transverse dunes. Earth Surface Processes and Landforms, 2004, 29, 769-784.	2.5	47
23	Dynamics of normal and anomalous diffusion in nonlinear Fokker-Planck equations. European Physical Journal B, 2009, 70, 107-116.	1.5	47
24	A proteomics sample metadata representation for multiomics integration and big data analysis. Nature Communications, 2021, 12, 5854.	12.8	45
25	Profile measurement and simulation of a transverse dune field in the Lençóis Maranhenses. Geomorphology, 2006, 81, 29-42.	2.6	44
26	The dune size distribution and scaling relations of barchan dune fields. Granular Matter, 2009, 11, 7-11.	2.2	39
27	Quantitative Proteome Analysis ofStreptomyces coelicolorNonsporulating Liquid Cultures Demonstrates a Complex Differentiation Process Comparable to That Occurring in Sporulating Solid Cultures. Journal of Proteome Research, 2010, 9, 4801-4811.	3.7	39
28	Quantitative Proteomic and Phosphoproteomic Analysis of Trypanosoma cruzi Amastigogenesis. Molecular and Cellular Proteomics, 2014, 13, 3457-3472.	3.8	39
29	Automated workflow composition in mass spectrometry-based proteomics. Bioinformatics, 2019, 35, 656-664.	4.1	39
30	The bio.tools registry of software tools and data resources for the life sciences. Genome Biology, 2019, 20, 164.	8.8	39
31	The AIMe registry for artificial intelligence in biomedical research. Nature Methods, 2021, 18, 1128-1131.	19.0	38
32	Two-parameter generalization of the logarithm and exponential functions and Boltzmann-Gibbs-Shannon entropy. Journal of Mathematical Physics, 2007, 48, 113301.	1.1	36
33	ProForma: A Standard Proteoform Notation. Journal of Proteome Research, 2018, 17, 1321-1325.	3.7	35
34	Distinct urinary glycoprotein signatures in prostate cancer patients. Oncotarget, 2018, 9, 33077-33097.	1.8	33
35	q-Gaussians in the porous-medium equation: stability and time evolution. European Physical Journal B, 2008, 66, 537-546.	1.5	30
36	Size distribution and structure of Barchan dune fields. Nonlinear Processes in Geophysics, 2011, 18, 455-467.	1.3	30

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37	A proteomics approach to the identification of biomarkers for psoriasis utilising keratome biopsy. Journal of Proteomics, 2013, 94, 176-185.	2.4	30
38	Selective renal vasoconstriction, exaggerated natriuresis and excretion rates of exosomic proteins in essential hypertension. Acta Physiologica, 2014, 212, 106-118.	3.8	29
39	Computational and statistical methods for high-throughput analysis of post-translational modifications of proteins. Journal of Proteomics, 2015, 129, 3-15.	2.4	28
40	A <i>Lotus japonicus</i> cytoplasmic kinase connects Nod factor perception by the NFR5 LysM receptor to nodulation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14339-14348.	7.1	28
41	Isotope Labeling-Based Quantitative Proteomics of Developing Seeds of Castor Oil Seed (<i>Ricinus) Tj ETQq1 1 0.784314 rgBT /Overlo	3.7	27
42	Extensive Characterization of Heavily Modified Histone Tails by 193 nm Ultraviolet Photodissociation Mass Spectrometry via a Middle–Down Strategy. Analytical Chemistry, 2018, 90, 10425-10433.	6.5	26
43	SIMULATION FOR COMPETITION OF LANGUAGES WITH AN AGING SEXUAL POPULATION. International Journal of Modern Physics C, 2005, 16, 1519-1526.	1.7	25
44	Maximizing Sequence Coverage in Top-Down Proteomics By Automated Multimodal Gas-Phase Protein Fragmentation. Analytical Chemistry, 2018, 90, 12519-12526.	6.5	25
45	PolySTest: Robust Statistical Testing of Proteomics Data with Missing Values Improves Detection of Biologically Relevant Features. Molecular and Cellular Proteomics, 2020, 19, 1396-1408.	3.8	23
46	VSClust: feature-based variance-sensitive clustering of omics data. Bioinformatics, 2018, 34, 2965-2972.	4.1	22
47	Spatial and Temporal Effects in Protein Post-translational Modification Distributions in the Developing Mouse Brain. Journal of Proteome Research, 2014, 13, 260-267.	3.7	21
48	Analysis of the Effect of Intestinal Ischemia and Reperfusion on the Rat Neutrophils Proteome. Frontiers in Molecular Biosciences, 2018, 5, 89.	3.5	18
49	One Thousand and One Software for Proteomics: Tales of the Toolmakers of Science. Journal of Proteome Research, 2019, 18, 3580-3585.	3.7	18
50	Depolarization-dependent Induction of Site-specific Changes in Sialylation on N-linked Glycoproteins in Rat Nerve Terminals. Molecular and Cellular Proteomics, 2020, 19, 1418-1435.	3.8	18
51	Middle-Down Proteomic Analyses with Ion Mobility Separations of Endogenous Isomeric Proteoforms. Analytical Chemistry, 2020, 92, 2364-2368.	6.5	18
52	The morphology of dunes. Physica A: Statistical Mechanics and Its Applications, 2005, 358, 30-38.	2.6	14
53	ComplexBrowser: A Tool for Identification and Quantification of Protein Complexes in Large-scale Proteomics Datasets. Molecular and Cellular Proteomics, 2019, 18, 2324-2334.	3.8	14
54	PHASE TRANSITION IN A SEXUAL AGE-STRUCTURED MODEL OF LEARNING FOREIGN LANGUAGES. International Journal of Modern Physics C, 2006, 17, 103-111.	1.7	13

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55	A community proposal to integrate proteomics activities in ELIXIR. F1000Research, 2017, 6, 875.	1.6	13
56	Neuronal process structure and growth proteins are targets of heavy PTM regulation during brain development. Journal of Proteomics, 2014, 101, 77-87.	2.4	12
57	Community curation of bioinformatics software and data resources. Briefings in Bioinformatics, 2020, 21, 1697-1705.	6.5	12
58	Thermodynamic behavior of a phase transition in a model for sympatric speciation. Physical Review E, 2006, 74, 021910.	2.1	11
59	IsoProt: A Complete and Reproducible Workflow To Analyze iTRAQ/TMT Experiments. Journal of Proteome Research, 2019, 18, 1751-1759.	3.7	11
60	Visualization of the dynamics of histone modifications and their crosstalk using PTM-CrossTalkMapper. Methods, 2020, 184, 78-85.	3.8	11
61	Nuclear phosphoproteome analysis of 3T3â€Ł1 preadipocyte differentiation reveals systemâ€wide phosphorylation of transcriptional regulators. Proteomics, 2017, 17, 1600248.	2.2	10
62	Distinct and diverse chromatin proteomes of ageing mouse organs reveal protein signatures that correlate with physiological functions. ELife, 2022, 11, .	6.0	10
63	CoExpresso: assess the quantitative behavior of protein complexes in human cells. BMC Bioinformatics, 2019, 20, 17.	2.6	9
64	APE in the Wild: Automated Exploration of Proteomics Workflows in the bio.tools Registry. Journal of Proteome Research, 2021, 20, 2157-2165.	3.7	8
65	Reply to the discussion on â€˜Barchan Dunes: why they cannot be treated as â€œsolitonsâ€•or â€œsolitary wavesâ€â€™. Earth Surface Processes and Landforms, 2005, 30, 517-517.	2.5	7
66	A simple branching model that reproduces language family and language population distributions. Physica A: Statistical Mechanics and Its Applications, 2009, 388, 2874-2879.	2.6	7
67	biotoolsSchema: a formalized schema for bioinformatics software description. GigaScience, 2021, 10, .	6.4	7
68	Perspectives on automated composition of workflows in the life sciences. F1000Research, 2021, 10, 897.	1.6	7
69	A Computational Model for Histone Mark Propagation Reproduces the Distribution of Heterochromatin in Different Human Cell Types. PLoS ONE, 2013, 8, e73818.	2.5	7
70	Phosphoproteomic Analysis of Rat Neutrophils Shows the Effect of Intestinal Ischemia/Reperfusion and Preconditioning on Kinases and Phosphatases. International Journal of Molecular Sciences, 2020, 21, 5799.	4.1	6
71	MS2AI: automated repurposing of public peptide LC-MS data for machine learning applications. Bioinformatics, 2022, 38, 875-877.	4.1	6
72	Speciational view of macroevolution: Are micro and macroevolution decoupled?. Europhysics Letters, 2006, 75, 342-348.	2.0	5

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73	Quantitative Proteomic Map of the Trypanosomatid Strigomonas culicis: The Biological Contribution of its Endosymbiotic Bacterium. Protist, 2019, 170, 125698.	1.5	5
74	A Genome-Wide Integrative Association Study of DNA Methylation and Gene Expression Data and Later Life Cognitive Functioning in Monozygotic Twins. Frontiers in Neuroscience, 2020, 14, 233.	2.8	5
75	Computational and Statistical Methods for High-Throughput Mass Spectrometry-Based PTM Analysis. Methods in Molecular Biology, 2017, 1558, 437-458.	0.9	5
76	The European Bioinformatics Community for Mass Spectrometry (EuBICâ€MS): an open community for bioinformatics training and research. Rapid Communications in Mass Spectrometry, 2021, , e9087.	1.5	3
77	JIB.tools 2.0 â€" A Bioinformatics Registry for Journal Published Tools with Interoperability to bio.tools. Journal of Integrative Bioinformatics, 2020, 16, .	1.5	2
78	Proteomics Software in bio.tools: Coverage and Annotations. Journal of Proteome Research, 2021, 20, 1821-1825.	3.7	2
79	Phase transition in a mean-field model for sympatric speciation. Physica A: Statistical Mechanics and Its Applications, 2006, 369, 612-618.	2.6	1
80	Evolving cellular automata for diversity generation and pattern recognition: deterministic versus random strategy. Journal of Statistical Mechanics: Theory and Experiment, 2013, 2013, P08006.	2.3	1
81	Analysis of Label-Based Quantitative Proteomics Data Using. Methods in Molecular Biology, 2021, 2361, 61-73.	0.9	1
82	Automated Composition of Scientific Workflows in Mass Spectrometry-Based Proteomics. , 2018, , .		0
83	A Tutorial for Variance-Sensitive Clustering and the Quantitative Analysis of Protein Complexes. Methods in Molecular Biology, 2021, 2228, 433-451.	0.9	0
84	Gene Co-expression Network Analysis Associated with Acupuncture Treatment of Rheumatoid Arthritis: An Animal Model. Journal of Acupuncture Research, 2020, 37, 128-135.	0.3	0
85	VIQoR: a web service for visually supervised protein inference and protein quantification. Bioinformatics, 2022, 38, 2757-2764.	4.1	0