

Veit Schwämmle

List of Publications by Year in descending order

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Version: 2024-02-01

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	MS2AI: automated repurposing of public peptide LC-MS data for machine learning applications. <i>Bioinformatics</i> , 2022, 38, 875-877.	4.1	6
2	VIQoR: a web service for visually supervised protein inference and protein quantification. <i>Bioinformatics</i> , 2022, 38, 2757-2764.	4.1	0
3	Distinct and diverse chromatin proteomes of ageing mouse organs reveal protein signatures that correlate with physiological functions. <i>ELife</i> , 2022, 11, .	6.0	10
4	Analysis of Label-Based Quantitative Proteomics Data Using. <i>Methods in Molecular Biology</i> , 2021, 2361, 61-73.	0.9	1
5	A Tutorial for Variance-Sensitive Clustering and the Quantitative Analysis of Protein Complexes. <i>Methods in Molecular Biology</i> , 2021, 2228, 433-451.	0.9	0
6	biotoolsSchema: a formalized schema for bioinformatics software description. <i>GigaScience</i> , 2021, 10, .	6.4	7
7	APE in the Wild: Automated Exploration of Proteomics Workflows in the bio.tools Registry. <i>Journal of Proteome Research</i> , 2021, 20, 2157-2165.	3.7	8
8	Proteomics Software in bio.tools: Coverage and Annotations. <i>Journal of Proteome Research</i> , 2021, 20, 1821-1825.	3.7	2
9	The European Bioinformatics Community for Mass Spectrometry (EuBICâ€MS): an open community for bioinformatics training and research. <i>Rapid Communications in Mass Spectrometry</i> , 2021, , e9087.	1.5	3
10	Quantifying Online News Media Coverage of the COVID-19 Pandemic: Text Mining Study and Resource. <i>Journal of Medical Internet Research</i> , 2021, 23, e28253.	4.3	60
11	The AIme registry for artificial intelligence in biomedical research. <i>Nature Methods</i> , 2021, 18, 1128-1131.	19.0	38
12	Perspectives on automated composition of workflows in the life sciences. <i>F1000Research</i> , 2021, 10, 897.	1.6	7
13	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021, 12, 5854.	12.8	45
14	Community curation of bioinformatics software and data resources. <i>Briefings in Bioinformatics</i> , 2020, 21, 1697-1705.	6.5	12
15	Phosphoproteomic Analysis of Rat Neutrophils Shows the Effect of Intestinal Ischemia/Reperfusion and Preconditioning on Kinases and Phosphatases. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5799.	4.1	6
16	PolySTest: Robust Statistical Testing of Proteomics Data with Missing Values Improves Detection of Biologically Relevant Features. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1396-1408.	3.8	23
17	JIB.tools 2.0 â€“ A Bioinformatics Registry for Journal Published Tools with Interoperability to bio.tools. <i>Journal of Integrative Bioinformatics</i> , 2020, 16, .	1.5	2
18	Depolarization-dependent Induction of Site-specific Changes in Sialylation on N-linked Glycoproteins in Rat Nerve Terminals. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1418-1435.	3.8	18

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19	Visualization of the dynamics of histone modifications and their crosstalk using PTM-CrossTalkMapper. <i>Methods</i> , 2020, 184, 78-85.	3.8	11
20	Middle-Down Proteomic Analyses with Ion Mobility Separations of Endogenous Isomeric Proteoforms. <i>Analytical Chemistry</i> , 2020, 92, 2364-2368.	6.5	18
21	A Genome-Wide Integrative Association Study of DNA Methylation and Gene Expression Data and Later Life Cognitive Functioning in Monozygotic Twins. <i>Frontiers in Neuroscience</i> , 2020, 14, 233.	2.8	5
22	Gene Co-expression Network Analysis Associated with Acupuncture Treatment of Rheumatoid Arthritis: An Animal Model. <i>Journal of Acupuncture Research</i> , 2020, 37, 128-135.	0.3	0
23	Automated workflow composition in mass spectrometry-based proteomics. <i>Bioinformatics</i> , 2019, 35, 656-664.	4.1	39
24	One Thousand and One Software for Proteomics: Tales of the Toolmakers of Science. <i>Journal of Proteome Research</i> , 2019, 18, 3580-3585.	3.7	18
25	The bio.tools registry of software tools and data resources for the life sciences. <i>Genome Biology</i> , 2019, 20, 164.	8.8	39
26	ComplexBrowser: A Tool for Identification and Quantification of Protein Complexes in Large-scale Proteomics Datasets. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2324-2334.	3.8	14
27	CoExpresso: assess the quantitative behavior of protein complexes in human cells. <i>BMC Bioinformatics</i> , 2019, 20, 17.	2.6	9
28	A <i>Lotus japonicus</i> cytoplasmic kinase connects Nod factor perception by the NFR5 LysM receptor to nodulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14339-14348.	7.1	28
29	IsoProt: A Complete and Reproducible Workflow To Analyze iTRAQ/TMT Experiments. <i>Journal of Proteome Research</i> , 2019, 18, 1751-1759.	3.7	11
30	Quantitative Proteomic Map of the Trypanosomatid <i>Strigomonas culicis</i> : The Biological Contribution of its Endosymbiotic Bacterium. <i>Protist</i> , 2019, 170, 125698.	1.5	5
31	VSClust: feature-based variance-sensitive clustering of omics data. <i>Bioinformatics</i> , 2018, 34, 2965-2972.	4.1	22
32	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018, 17, 1321-1325.	3.7	35
33	Automated Composition of Scientific Workflows in Mass Spectrometry-Based Proteomics. , 2018, , .		0
34	Maximizing Sequence Coverage in Top-Down Proteomics By Automated Multimodal Gas-Phase Protein Fragmentation. <i>Analytical Chemistry</i> , 2018, 90, 12519-12526.	6.5	25
35	Analysis of the Effect of Intestinal Ischemia and Reperfusion on the Rat Neutrophils Proteome. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 89.	3.5	18
36	Extensive Characterization of Heavily Modified Histone Tails by 193 nm Ultraviolet Photodissociation Mass Spectrometry via a Middle-Down Strategy. <i>Analytical Chemistry</i> , 2018, 90, 10425-10433.	6.5	26

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37	Distinct urinary glycoprotein signatures in prostate cancer patients. <i>Oncotarget</i> , 2018, 9, 33077-33097.	1.8	33
38	Accumulation of histone variant H3.3 with age is associated with profound changes in the histone methylation landscape. <i>Nucleic Acids Research</i> , 2017, 45, 9272-9289.	14.5	98
39	Nuclear phosphoproteome analysis of 3T3 preadipocyte differentiation reveals system-wide phosphorylation of transcriptional regulators. <i>Proteomics</i> , 2017, 17, 1600248.	2.2	10
40	Computational and Statistical Methods for High-Throughput Mass Spectrometry-Based PTM Analysis. <i>Methods in Molecular Biology</i> , 2017, 1558, 437-458.	0.9	5
41	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017, 6, 875.	1.6	13
42	High-performance hybrid Orbitrap mass spectrometers for quantitative proteome analysis: Observations and implications. <i>Proteomics</i> , 2016, 16, 907-914.	2.2	64
43	Systems Level Analysis of Histone H3 Post-translational Modifications (PTMs) Reveals Features of PTM Crosstalk in Chromatin Regulation. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2715-2729.	3.8	76
44	Tools and data services registry: a community effort to document bioinformatics resources. <i>Nucleic Acids Research</i> , 2016, 44, D38-D47.	14.5	113
45	Computational and statistical methods for high-throughput analysis of post-translational modifications of proteins. <i>Journal of Proteomics</i> , 2015, 129, 3-15.	2.4	28
46	The Cultural Divide: Exponential Growth in Classical 2D and Metabolic Equilibrium in 3D Environments. <i>PLoS ONE</i> , 2014, 9, e106973.	2.5	52
47	Large Scale Analysis of Co-existing Post-translational Modifications in Histone Tails Reveals Global Fine Structure of Cross-talk. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1855-1865.	3.8	65
48	Selective renal vasoconstriction, exaggerated natriuresis and excretion rates of exosomal proteins in essential hypertension. <i>Acta Physiologica</i> , 2014, 212, 106-118.	3.8	29
49	Spatial and Temporal Effects in Protein Post-translational Modification Distributions in the Developing Mouse Brain. <i>Journal of Proteome Research</i> , 2014, 13, 260-267.	3.7	21
50	Quantitative Proteomic and Phosphoproteomic Analysis of <i>Trypanosoma cruzi</i> Amastigogenesis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3457-3472.	3.8	39
51	Middle-down hybrid chromatography/tandem mass spectrometry workflow for characterization of combinatorial post-translational modifications in histones. <i>Proteomics</i> , 2014, 14, 2200-2211.	2.2	76
52	Neuronal process structure and growth proteins are targets of heavy PTM regulation during brain development. <i>Journal of Proteomics</i> , 2014, 101, 77-87.	2.4	12
53	Assessment and Improvement of Statistical Tools for Comparative Proteomics Analysis of Sparse Data Sets with Few Experimental Replicates. <i>Journal of Proteome Research</i> , 2013, 12, 3874-3883.	3.7	116
54	Precision Mapping of Coexisting Modifications in Histone H3 Tails from Embryonic Stem Cells by ETD-MS/MS. <i>Analytical Chemistry</i> , 2013, 85, 8232-8239.	6.5	70

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55	Isotope Labeling-Based Quantitative Proteomics of Developing Seeds of Castor Oil Seed (<i>Ricinus</i>) Tj ETQq1 1 0.784314 rgBT /Overbo	3.7	27
56	A proteomics approach to the identification of biomarkers for psoriasis utilising keratome biopsy. Journal of Proteomics, 2013, 94, 176-185.	2.4	30
57	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
58	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
59	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
60	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
61	Performance of Isobaric and Isotopic Labeling in Quantitative Plant Proteomics. Journal of Proteome Research, 2012, 11, 3046-3052.	3.7	52
62	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
63	Size distribution and structure of Barchan dune fields. Nonlinear Processes in Geophysics, 2011, 18, 455-467.	1.3	30
64	Quantitative Proteomics Analysis of <i>Streptomyces coelicolor</i> Development Demonstrates That Onset of Secondary Metabolism Coincides with Hypha Differentiation. Molecular and Cellular Proteomics, 2010, 9, 1423-1436.	3.8	50
65	A simple and fast method to determine the parameters for fuzzy c-means cluster analysis. Bioinformatics, 2010, 26, 2841-2848.	4.1	174
66	Quantitative Proteome Analysis of <i>Streptomyces coelicolor</i> Nonsporulating 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
67	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
68	The dune size distribution and scaling relations of barchan dune fields. Granular Matter, 2009, 11, 7-11.	2.2	39
69	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
70	Dynamics of normal and anomalous diffusion in nonlinear Fokker-Planck equations. European Physical Journal B, 2009, 70, 107-116.	1.5	47
71	q-Gaussians in the porous-medium equation: stability and time evolution. European Physical Journal B, 2008, 66, 537-546.	1.5	30
72	Strictly and asymptotically scale invariant probabilistic models of correlated binary random variables having q-Gaussians as limiting distributions. Journal of Statistical Mechanics: Theory and Experiment, 2008, 2008, P09006.	2.3	54

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73	Consequences of the $<\text{mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" display="inline"><\text{mml:mi mathvariant="italic">H</mml:mi></mml:math>}$ theorem from nonlinear Fokker-Planck equations. Physical Review E, 2007, 76, 041123.	2.1	103
74	Two-parameter generalization of the logarithm and exponential functions and Boltzmann-Gibbs-Shannon entropy. Journal of Mathematical Physics, 2007, 48, 113301.	1.1	36
75	A general nonlinear Fokker-Planck equation and its associated entropy. European Physical Journal B, 2007, 58, 159-165.	1.5	76
76	Profile measurement and simulation of a transverse dune field in the Lençóis Maranhenses. Geomorphology, 2006, 81, 29-42.	2.6	44
77	Phase transition in a mean-field model for sympatric speciation. Physica A: Statistical Mechanics and Its Applications, 2006, 369, 612-618.	2.6	1
78	Speciational view of macroevolution: Are micro and macroevolution decoupled?. Europhysics Letters, 2006, 75, 342-348.	2.0	5
79	Thermodynamic behavior of a phase transition in a model for sympatric speciation. Physical Review E, 2006, 74, 021910.	2.1	11
80	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
81	The morphology of dunes. Physica A: Statistical Mechanics and Its Applications, 2005, 358, 30-38.	2.6	14
82	Reply to the discussion on "Barchan Dunes: why they cannot be treated as "solitons" or "solitary waves". Earth Surface Processes and Landforms, 2005, 30, 517-517.	2.5	7
83	SIMULATION FOR COMPETITION OF LANGUAGES WITH AN AGING SEXUAL POPULATION. International Journal of Modern Physics C, 2005, 16, 1519-1526.	1.7	25
84	Modelling transverse dunes. Earth Surface Processes and Landforms, 2004, 29, 769-784.	2.5	47
85	Solitary wave behaviour of sand dunes. Nature, 2003, 426, 619-620.	27.8	134