Benno Schwikowski

List of Publications by Year
in descending order

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Version: 2024-02-01

63 papers	45,999 citations	182225 30 h-index	156644 58 g-index
67 all docs	67 docs citations	67 times ranked	79782 citing authors

#	Article	IF	Citations
1	An overview of machine learning methods for monotherapy drug response prediction. Briefings in Bioinformatics, 2022, 23, .	3.2	19
2	A shared disease-associated oligodendrocyte signature among multiple CNS pathologies. Nature Neuroscience, 2022, 25, 876-886.	7.1	84
3	Immune Profiling Enables Stratification of Patients With Active Tuberculosis Disease or <i>Mycobacteriu</i> <i>m tuberculosis</i> Infection. Clinical Infectious Diseases, 2021, 73, e3398-e3408.	2.9	18
4	Deciphering the state of immune silence in fatal COVID-19 patients. Nature Communications, 2021, 12, 1428.	5.8	107
5	Differential levels of IFNÎ± subtypes in autoimmunity and viral infection. Cytokine, 2021, 144, 155533.	1.4	12
6	Host-Viral Infection Maps Reveal Signatures of Severe COVID-19 Patients. Cell, 2020, 181, 1475-1488.e12.	13.5	405
7	Associations between consumption of dietary fibers and the risk of cardiovascular diseases, cancers, type 2 diabetes, and mortality in the prospective NutriNet-SantÃ© cohort. American Journal of Clinical Nutrition, 2020, 112, 195-207.	2.2	60
8	Bystander IFN-Î³ activity promotes widespread and sustained cytokine signaling altering the tumor microenvironment. Nature Cancer, 2020, 1, 302-314.	5.7	93
9	LGP2 binds to PACT to regulate RIG-Iâ€“ and MDA5-mediated antiviral responses. Science Signaling, 2019, 12, .	1.6	51
10	Single-Cell Analysis of Diverse Pathogen Responses Defines a Molecular Roadmap for Generating Antigen-Specific Immunity. Cell Systems, 2019, 8, 109-121.e6.	2.9	39
11	A Blood RNA Signature Detecting Severe Disease in Young Dengue Patients at Hospital Arrival. Journal of Infectious Diseases, 2018, 217, 1690-1698.	1.9	27
12	Distinctive roles of age, sex, and genetics in shaping transcriptional variation of human immune responses to microbial challenges. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E488-E497.	3.3	181
13	Network module identificationâ€"A widespread theoretical bias and best practices. Methods, 2018, 132, 19-25.	1.9	28
14	The Cytoscape Automation app article collection. F1000Research, 2018, 7, 800.	0.8	17
15	Network-based analysis of omics data: the LEAN method. Bioinformatics, 2017, 33, 701-709.	1.8	29
16	From the exposome to mechanistic understanding of chemical-induced adverse effects. Environment International, 2017, 99, 97-106.	4.8	146
17	Common and phylogenetically widespread coding for peptides by bacterial small RNAs. BMC Genomics, 2017, 18, 553.	1.2	32
18	Detecting multi-way epistasis in family-based association studies. Briefings in Bioinformatics, 2016, 18, bbw039.	3.2	4

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19	The Milieu IntÃ©rieur study â€” An integrative approach for study of human immunological variance. Clinical Immunology, 2015, 157, 277-293.	1.4	71
20	Automated flow cytometric analysis across large numbers of samples and cell types. Clinical Immunology, 2015, 157, 249-260.	1.4	26
21	Bacterial Internalization, Localization, and Effectors Shape the Epithelial Immune Response during Shigella flexneri Infection. Infection and Immunity, 2015, 83, 3624-3637.	1.0	12
22	Filter-free exhaustive odds ratio-based genome-wide interaction approach pinpoints evidence for interaction in the HLA region in psoriasis. BMC Genetics, 2015, 16, 11.	2.7	2
23	The Cyni framework for network inference in Cytoscape. Bioinformatics, 2015, 31, 1499-1501.	1.8	9
24	Functional Analysis via Standardized Whole-Blood Stimulation Systems Defines the Boundaries of a Healthy Immune Response to Complex Stimuli. Immunity, 2014, 40, 436-450.	6.6	192
25	The Cytoscape app article collection. F1000Research, 2014, 3, 138.	0.8	10
26	Identification of additional proteins in differential proteomics using protein interaction networks. Proteomics, 2013, 13, 1065-1076.	1.3	19
27	TLM-Quant: An Open-Source Pipeline for Visualization and Quantification of Gene Expression Heterogeneity in Growing Microbial Cells. PLoS ONE, 2013, 8, e68696.	1.1	6
28	Analysis of Time-Resolved Gene Expression Measurements across Individuals. PLoS ONE, 2013, 8, e82340.	1.1	7
29	Feature Detection with Controlled Error Rates in LC/MS Images. Journal of Computational Biology, 2012, 19, 349-364.	0.8	0
30	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> Metabolism. Science, 2012, 335, 1099-1103.	6.0	255
31	Automated Phosphopeptide Identification Using Multiple MS/MS Fragmentation Modes. Journal of Proteome Research, 2012, 11, 5695-5703.	1.8	16
32	Condition-Dependent Transcriptome Reveals High-Level Regulatory Architecture in <i>Bacillus subtilis</i>. Science, 2012, 335, 1103-1106.	6.0	809
33	Mining proteomic data for biomedical research. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2012, 2, 1-13.	4.6	11
34	Fragmentationâ€free LCâ€MS can identify hundreds of proteins. Proteomics, 2011, 11, 22-32.	1.3	8
35	Evolution of metabolic network organization. BMC Systems Biology, 2010, 4, 59.	3.0	42
36	MUDE: A New Approach for Optimizing Sensitivity in the Target-Decoy Search Strategy for Large-Scale Peptide/Protein Identification. Journal of Proteome Research, 2010, 9, 2265-2277.	1.8	20

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37	Indexing and Searching a Mass Spectrometry Database. Lecture Notes in Computer Science, 2010, , 62-76.	1.0	1
38	Alignment of LCâ€MS images, with applications to biomarker discovery and protein identification. Proteomics, 2008, 8, 650-672.	1.3	92
39	Phylogenetic distances are encoded in networks of interacting pathways. Bioinformatics, 2008, 24, 2579-2585.	1.8	44
40	Assessing Bias in Experiment Design for Large Scale Mass Spectrometry-based Quantitative Proteomics. Molecular and Cellular Proteomics, 2007, 6, 1741-1748.	2.5	52
41	GOlorize: a Cytoscape plug-in for network visualization with Gene Ontology-based layout and coloring. Bioinformatics, 2007, 23, 394-396.	1.8	105
42	Integration of biological networks and gene expression data using Cytoscape. Nature Protocols, 2007, 2, 2366-2382.	5.5	2,275
43	Graph-based methods for analysing networks in cell biology. Briefings in Bioinformatics, 2006, 7, 243-255.	3.2	368
44	Signal Maps for Mass Spectrometry-based Comparative Proteomics. Molecular and Cellular Proteomics, 2006, 5, 423-432.	2.5	110
45	Tools enabling the elucidation of molecular pathways active in human disease: application to Hepatitis C virus infection. BMC Bioinformatics, 2005, 6, 154.	1.2	14
46	ProbIDtree: An automated software program capable of identifying multiple peptides from a single collision-induced dissociation spectrum collected by a tandem mass spectrometer. Proteomics, 2005, 5, 4096-4106.	1.3	70
47	Predicting protein-peptide interactions via a network-based motif sampler. Bioinformatics, 2004, 20, i274-i282.	1.8	40
48	Towards Optimally Multiplexed Applications of Universal Arrays. Journal of Computational Biology, 2004, 11, 476-492.	0.8	4
49	Weighted sequence graphs: boosting iterated dynamic programming using locally suboptimal solutions. Discrete Applied Mathematics, 2003, 127, 95-117.	0.5	9
50	Cytoscape: A Software Environment for Integrated Models of Biomolecular Interaction Networks. Genome Research, 2003, 13, 2498-2504.	2.4	37,062
51	The Restriction Scaffold Problem. Journal of Computational Biology, 2003, 10, 385-398.	0.8	16
52	Towards optimally multiplexed applications of universal DNA tag systems. , 2003, , .		7
53	Algorithms for Phylogenetic Footprinting. Journal of Computational Biology, 2002, 9, 211-223.	0.8	138
54	Discovering regulatory and signalling circuits in molecular interaction networks. Bioinformatics, 2002, 18, S233-S240.	1.8	1,098

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55	ProbID: A probabilistic algorithm to identify peptides through sequence database searching using tandem mass spectral data. Proteomics, 2002, 2, 1406-1412.	1.3	201
56	On enumerating all minimal solutions of feedback problems. Discrete Applied Mathematics, 2002, 117, 253-265.	0.5	57
57	A network of proteinâ€"protein interactions in yeast. Nature Biotechnology, 2000, 18, 1257-1261.	9.4	1,281
58	Universal DNA tag systems. , 2000, , .		13
59	Universal DNA Tag Systems: A Combinatorial Design Scheme. Journal of Computational Biology, 2000, 7, 503-519.	0.8	52
60	The deferred path heuristic for the generalized tree alignment problem. , 1997, , .		7
61	The Deferred Path Heuristic for the Generalized Tree Alignment Problem. Journal of Computational Biology, 1997, 4, 415-431.	0.8	15
62	A clustering approach to Generalized Tree Alignment with application to Alu repeats. Lecture Notes in Computer Science, 1996, , 115-124.	1.0	1
63	Discovery of pathways using multiple genome-scale data sets. , 0, 2005, .		0