

# Jan Baumbach

## List of Publications by Citations

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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.

203  
papers

4,125  
citations

35  
h-index

58  
g-index

225  
ext. papers

5,850  
ext. citations

7.5  
avg, IF

5.74  
L-index

#	Paper	IF	Citations
203	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 436	3.6	337
202	AltAnalyze and DomainGraph: analyzing and visualizing exon expression data. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W755-62	20.1	217
201	Comprehensive evaluation of transcriptome-based cell-type quantification methods for immuno-oncology. <i>Bioinformatics</i> , <b>2019</b> , 35, i436-i445	7.2	209
200	Graph-based analysis and visualization of experimental results with ONDEX. <i>Bioinformatics</i> , <b>2006</b> , 22, 1383-90	7.2	159
199	Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , <b>2020</b> , 579, 409-414	50.4	144
198	Comparing the performance of biomedical clustering methods. <i>Nature Methods</i> , <b>2015</b> , 12, 1033-8	21.6	140
197	Exploring the SARS-CoV-2 virus-host-drug interactome for drug repurposing. <i>Nature Communications</i> , <b>2020</b> , 11, 3518	17.4	104
196	Osteogenesis depends on commissioning of a network of stem cell transcription factors that act as repressors of adipogenesis. <i>Nature Genetics</i> , <b>2019</b> , 51, 716-727	36.3	89
195	The GlxR regulon of the amino acid producer <i>Corynebacterium glutamicum</i> : in silico and in vitro detection of DNA binding sites of a global transcription regulator. <i>Journal of Biotechnology</i> , <b>2008</b> , 135, 340-50	3.7	84
194	GPSy: Genomic island prediction software. <i>Journal of Biotechnology</i> , <b>2016</b> , 232, 2-11	3.7	76
193	Partitioning biological data with transitivity clustering. <i>Nature Methods</i> , <b>2010</b> , 7, 419-20	21.6	73
192	Analysis of the airway microbiota of healthy individuals and patients with chronic obstructive pulmonary disease by T-RFLP and clone sequencing. <i>PLoS ONE</i> , <b>2013</b> , 8, e68302	3.7	72
191	From single drug targets to synergistic network pharmacology in ischemic stroke. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 7129-7136	11.5	67
190	Evidence for reductive genome evolution and lateral acquisition of virulence functions in two <i>Corynebacterium pseudotuberculosis</i> strains. <i>PLoS ONE</i> , <b>2011</b> , 6, e18551	3.7	67
189	Molecular networks in Network Medicine: Development and applications. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , <b>2020</b> , 12, e1489	6.6	63
188	PIPS: pathogenicity island prediction software. <i>PLoS ONE</i> , <b>2012</b> , 7, e30848	3.7	56
187	CoryneRegNet 4.0 - A reference database for corynebacterial gene regulatory networks. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 429	3.6	56

186	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22, 642-663	13.4	56
185	CoryneRegNet 6.0--Updated database content, new analysis methods and novel features focusing on community demands. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D610-4	20.1	54
184	KeyPathwayMiner 4.0: condition-specific pathway analysis by combining multiple omics studies and networks with Cytoscape. <i>BMC Systems Biology</i> , <b>2014</b> , 8, 99	3.5	48
183	Large scale clustering of protein sequences with FORCE -A layout based heuristic for weighted cluster editing. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 396	3.6	48
182	Metagenomic evidence for the presence of phototrophic Gemmatimonadetes bacteria in diverse environments. <i>Environmental Microbiology Reports</i> , <b>2016</b> , 8, 139-49	3.7	46
181	Comprehensive cluster analysis with Transitivity Clustering. <i>Nature Protocols</i> , <b>2011</b> , 6, 285-95	18.8	44
180	CoryneRegNet: an ontology-based data warehouse of corynebacterial transcription factors and regulatory networks. <i>BMC Genomics</i> , <b>2006</b> , 7, 24	4.5	43
179	PanRV: Pangenome-reverse vaccinology approach for identifications of potential vaccine candidates in microbial pangenome. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 123	3.6	41
178	The Economic Impact of Artificial Intelligence in Health Care: Systematic Review. <i>Journal of Medical Internet Research</i> , <b>2020</b> , 22, e16866	7.6	41
177	SARS-CoV-2 infection is associated with a pro-thrombotic platelet phenotype. <i>Cell Death and Disease</i> , <b>2021</b> , 12, 50	9.8	41
176	On the performance of de novo pathway enrichment. <i>Npj Systems Biology and Applications</i> , <b>2017</b> , 3, 6	5	38
175	Efficient key pathway mining: combining networks and OMICS data. <i>Integrative Biology (United Kingdom)</i> , <b>2012</b> , 4, 756-64	3.7	38
174	KeyPathwayMiner: Detecting Case-Specific Biological Pathways Using Expression Data. <i>Internet Mathematics</i> , <b>2011</b> , 7, 299-313	0	38
173	From Corynebacterium glutamicum to Mycobacterium tuberculosis--towards transfers of gene regulatory networks and integrated data analyses with MycoRegNet. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, e97	20.1	37
172	De novo pathway-based biomarker identification. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e151	20.1	36
171	Rapid hybrid de novo assembly of a microbial genome using only short reads: Corynebacterium pseudotuberculosis I19 as a case study. <i>Journal of Microbiological Methods</i> , <b>2011</b> , 86, 218-23	2.8	36
170	Integrated analysis and reconstruction of microbial transcriptional gene regulatory networks using CoryneRegNet. <i>Nature Protocols</i> , <b>2009</b> , 4, 992-1005	18.8	36
169	Lessons from the COVID-19 pandemic for advancing computational drug repurposing strategies. <i>Nature Computational Science</i> , <b>2021</b> , 1, 33-41		36

168	High-resolution detection of DNA binding sites of the global transcriptional regulator GlxR in <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , <b>2013</b> , 159, 12-22	2.9	35
167	On the performance of pre-microRNA detection algorithms. <i>Nature Communications</i> , <b>2017</b> , 8, 330	17.4	34
166	KeyPathwayMinerWeb: online multi-omics network enrichment. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, W98-W104	10.4	33
165	Drug repurposing by integrated literature mining and drug-gene-disease triangulation. <i>Drug Discovery Today</i> , <b>2017</b> , 22, 615-619	8.8	33
164	EXACT AND HEURISTIC ALGORITHMS FOR WEIGHTED CLUSTER EDITING <b>2007</b> ,		33
163	Classification of Breast Cancer Subtypes by combining Gene Expression and DNA Methylation Data. <i>Journal of Integrative Bioinformatics</i> , <b>2014</b> , 11, 1-14	3.8	30
162	Molecular signature of different lesion types in the brain white matter of patients with progressive multiple sclerosis. <i>Acta Neuropathologica Communications</i> , <b>2019</b> , 7, 205	7.3	29
161	Linking Cytoscape and the corynebacterial reference database CoryneRegNet. <i>BMC Genomics</i> , <b>2008</b> , 9, 184	4.5	28
160	CoryneRegNet 3.0--an interactive systems biology platform for the analysis of gene regulatory networks in corynebacteria and <i>Escherichia coli</i> . <i>Journal of Biotechnology</i> , <b>2007</b> , 129, 279-89	3.7	28
159	Long-term instability of the intestinal microbiome is associated with metabolic liver disease, low microbiota diversity, diabetes mellitus and impaired exocrine pancreatic function. <i>Gut</i> , <b>2021</b> , 70, 522-530	19.2	26
158	An integrative in-silico approach for therapeutic target identification in the human pathogen <i>Corynebacterium diphtheriae</i> . <i>PLoS ONE</i> , <b>2017</b> , 12, e0186401	3.7	25
157	Computational methods for metabolomic data analysis of ion mobility spectrometry data--reviewing the state of the art. <i>Metabolites</i> , <b>2012</b> , 2, 733-55	5.6	24
156	<i>E. coli</i> gene regulatory networks are inconsistent with gene expression data. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 85-92	20.1	24
155	On the power and limits of evolutionary conservation--unraveling bacterial gene regulatory networks. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 7877-84	20.1	23
154	Robust de novo pathway enrichment with KeyPathwayMiner 5. <i>F1000Research</i> , <b>2016</b> , 5, 1531	3.6	23
153	DeepCLIP: predicting the effect of mutations on protein-RNA binding with deep learning. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 7099-7118	20.1	22
152	Reliable transfer of transcriptional gene regulatory networks between taxonomically related organisms. <i>BMC Systems Biology</i> , <b>2009</b> , 3, 8	3.5	22
151	How little do we actually know? On the size of gene regulatory networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2012</b> , 9, 1293-300	3	21

150	Classification of breast cancer subtypes by combining gene expression and DNA methylation data. <i>Journal of Integrative Bioinformatics</i> , <b>2014</b> , 11, 236	3.8	20
149	On the power of epigenome-wide association studies using a disease-discordant twin design. <i>Bioinformatics</i> , <b>2018</b> , 34, 4073-4078	7.2	19
148	Mature Epitope Density--a strategy for target selection based on immunoinformatics and exported prokaryotic proteins. <i>BMC Genomics</i> , <b>2013</b> , 14 Suppl 6, S4	4.5	19
147	Cluster Editing. <i>Lecture Notes in Computer Science</i> , <b>2013</b> , 33-44	0.9	19
146	Conserved host-pathogen PPIs. Globally conserved inter-species bacterial PPIs based conserved host-pathogen interactome derived novel target in <i>C. pseudotuberculosis</i> , <i>C. diphtheriae</i> , <i>M. tuberculosis</i> , <i>C. ulcerans</i> , <i>Y. pestis</i> , and <i>E. coli</i> targeted by Piper betel compounds. <i>Integrative Biology (United Kingdom)</i> , <b>2013</b> , 5, 495-509	3.7	18
145	Multiple graph edit distance <b>2014</b> ,		18
144	Peak detection method evaluation for ion mobility spectrometry by using machine learning approaches. <i>Metabolites</i> , <b>2013</b> , 3, 277-93	5.6	18
143	Towards the integrated analysis, visualization and reconstruction of microbial gene regulatory networks. <i>Briefings in Bioinformatics</i> , <b>2009</b> , 10, 75-83	13.4	18
142	IMS2 [An integrated medical software system for early lung cancer detection using ion mobility spectrometry data of human breath. <i>Journal of Integrative Bioinformatics</i> , <b>2007</b> , 4, 186-197	3.8	18
141	Orthologous proteins of experimental de- and remyelination are differentially regulated in the CSF proteome of multiple sclerosis subtypes. <i>PLoS ONE</i> , <b>2018</b> , 13, e0202530	3.7	16
140	Carotta: Revealing Hidden Confounder Markers in Metabolic Breath Profiles. <i>Metabolites</i> , <b>2015</b> , 5, 344-636	3.6	16
139	Primer, Pipelines, Parameters: Issues in 16S rRNA Gene Sequencing. <i>MSphere</i> , <b>2021</b> , 6,	5	16
138	CytoGEDEVO-global alignment of biological networks with Cytoscape. <i>Bioinformatics</i> , <b>2016</b> , 32, 1259-61	7.2	15
137	Elucidation of epithelial-mesenchymal transition-related pathways in a triple-negative breast cancer cell line model by multi-omics interactome analysis. <i>Integrative Biology (United Kingdom)</i> , <b>2014</b> , 6, 1058-68	3.7	15
136	Density parameter estimation for finding clusters of homologous proteins--tracing actinobacterial pathogenicity lifestyles. <i>Bioinformatics</i> , <b>2013</b> , 29, 215-22	7.2	15
135	CoNVaQ: a web tool for copy number variation-based association studies. <i>BMC Genomics</i> , <b>2018</b> , 19, 369	4.5	14
134	Differentially Methylated Genomic Regions in Birth-Weight Discordant Twin Pairs. <i>Annals of Human Genetics</i> , <b>2016</b> , 80, 81-7	2.2	14
133	Exploratory analysis of age and sex dependent DNA methylation patterns on the X-chromosome in whole blood samples. <i>Genome Medicine</i> , <b>2020</b> , 12, 39	14.4	13

132	Comprehensive analysis of high-throughput screens with HiTSeekR. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 6639-48	20.1	13
131	Community effort endorsing multiscale modelling, multiscale data science and multiscale computing for systems medicine. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 1057-1062	13.4	13
130	Age-dependent DNA methylation patterns on the Y chromosome in elderly males. <i>Aging Cell</i> , <b>2020</b> , 19, e12907	9.9	13
129	Efficient sample tracking with OpenLabFramework. <i>Scientific Reports</i> , <b>2014</b> , 4, 4278	4.9	12
128	Network analysis methods for studying microbial communities: A mini review. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 2687-2698	6.8	12
127	DNA methylome profiling of all-cause mortality in comparison with age-associated methylation patterns. <i>Clinical Epigenetics</i> , <b>2019</b> , 11, 23	7.7	11
126	The epigenetic factor BORIS (CTCF) controls the androgen receptor regulatory network in ovarian cancer. <i>Oncogenesis</i> , <b>2019</b> , 8, 41	6.6	11
125	Bi-Force: large-scale bicluster editing and its application to gene expression data biclustering. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, e78	20.1	11
124	RhizoRegNet—a database of rhizobial transcription factors and regulatory networks. <i>Journal of Biotechnology</i> , <b>2011</b> , 155, 127-34	3.7	11
123	The AIMe registry for artificial intelligence in biomedical research. <i>Nature Methods</i> , <b>2021</b> , 18, 1128-1131	21.6	11
122	Exact and heuristic algorithms for weighted cluster editing. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , <b>2007</b> , 6, 391-401		11
121	Elucidation of Altered Pathways in Tumor-Initiating Cells of Triple-Negative Breast Cancer: A Useful Cell Model System for Drug Screening. <i>Stem Cells</i> , <b>2017</b> , 35, 1898-1912	5.8	10
120	On the limits of computational functional genomics for bacterial lifestyle prediction. <i>Briefings in Functional Genomics</i> , <b>2014</b> , 13, 398-408	4.9	10
119	An Integrative Clinical Database and Diagnostics Platform for Biomarker Identification and Analysis in Ion Mobility Spectra of Human Exhaled Air. <i>Journal of Integrative Bioinformatics</i> , <b>2013</b> , 10, 35-47	3.8	10
118	CoryneCenter - an online resource for the integrated analysis of corynebacterial genome and transcriptome data. <i>BMC Systems Biology</i> , <b>2007</b> , 1, 55	3.5	10
117	Network and Systems Medicine: Position Paper of the European Collaboration on Science and Technology Action on Open Multiscale Systems Medicine. <i>Network and Systems Medicine</i> , <b>2020</b> , 3, 67-90	4	10
116	Increased Levels of Genomic Instability and Mutations in Homologous Recombination Genes in Locally Advanced Rectal Carcinomas. <i>Frontiers in Oncology</i> , <b>2019</b> , 9, 395	5.3	9
115	Value of a newly sequenced bacterial genome. <i>World Journal of Biological Chemistry</i> , <b>2014</b> , 5, 161-8	3.8	9

114	CoryneRegNet 7, the reference database and analysis platform for corynebacterial gene regulatory networks. <i>Scientific Data</i> , <b>2020</b> , 7, 142	8.2	9
113	Clinical epigenetics settings for cancer and cardiovascular diseases: real-life applications of network medicine at the bedside. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 66	7.7	9
112	Comparative transcriptome analysis reveals key epigenetic targets in SARS-CoV-2 infection. <i>Npj Systems Biology and Applications</i> , <b>2021</b> , 7, 21	5	9
111	Interactive microbial distribution analysis using BioAtlas. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, W509-W513	20.1	8
110	DNA methylome profiling in identical twin pairs discordant for body mass index. <i>International Journal of Obesity</i> , <b>2019</b> , 43, 2491-2499	5.5	8
109	Mechanistic Modeling and Multiscale Applications for Precision Medicine: Theory and Practice. <i>Network and Systems Medicine</i> , <b>2020</b> , 3, 36-56	4	8
108	Massive fungal biodiversity data re-annotation with multi-level clustering. <i>Scientific Reports</i> , <b>2014</b> , 4, 6837	4.9	8
107	Microarray R-based analysis of complex lysate experiments with MIRACLE. <i>Bioinformatics</i> , <b>2014</b> , 30, i631-82	7.8	8
106	Extension and Robustness of Transitivity Clustering for Protein-Protein Interaction Network Analysis. <i>Internet Mathematics</i> , <b>2011</b> , 7, 255-273	0	8
105	CoryneRegNet 2: An Integrative Bioinformatics Approach for Reconstruction and Comparison of Transcriptional Regulatory Networks in Prokaryotes. <i>Journal of Integrative Bioinformatics</i> , <b>2006</b> , 3, 1-13	3.8	8
104	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and therapeutic target of an age-related hypertension endotype. <i>PLoS Biology</i> , <b>2020</b> , 18, e3000885	9.7	8
103	DIGGER: exploring the functional role of alternative splicing in protein interactions. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D309-D318	20.1	8
102	The End of Medicine as We Know It: Introduction to the New Journal, Systems Medicine. <i>Systems Medicine (New Rochelle, N Y)</i> , <b>2018</b> , 1, 1-2	1.6	7
101	Comprehensive Analysis of DNA Methylation and Prediction of Response to Neoadjuvant Therapy in Locally Advanced Rectal Cancer. <i>Cancers</i> , <b>2020</b> , 12,	6.6	7
100	On the trail of EHEC/EAEC--unraveling the gene regulatory networks of human pathogenic Escherichia coli bacteria. <i>Integrative Biology (United Kingdom)</i> , <b>2012</b> , 4, 728-33	3.7	6
99	sPLINK: A Federated, Privacy-Preserving Tool as a Robust Alternative to Meta-Analysis in Genome-Wide Association Studies		6
98	Inflammatory Breast Cancer: Clinical Implications of Genomic Alterations and Mutational Profiling. <i>Cancers</i> , <b>2020</b> , 12,	6.6	6
97	Network Medicine-Based Unbiased Disease Modules for Drug and Diagnostic Target Identification in ROSopathies. <i>Handbook of Experimental Pharmacology</i> , <b>2021</b> , 264, 49-68	3.2	6



96	A global network for network medicine. <i>Npj Systems Biology and Applications</i> , <b>2020</b> , 6, 29	5	6
95	Multiple Sclerosis Atlas: A Molecular Map of Brain Lesion Stages in Progressive Multiple Sclerosis. <i>Network and Systems Medicine</i> , <b>2020</b> , 3, 122-129	4	6
94	The Selection of a Hepatocyte Cell Line Susceptible to Sporozoite Invasion That Is Associated With Expression of Glypican-3. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 127	5.7	5
93	Unique RNA signature of different lesion types in the brain white matter in progressive multiple sclerosis. <i>Acta Neuropathologica Communications</i> , <b>2019</b> , 7, 58	7.3	5
92	Time-Resolved Systems Medicine Reveals Viral Infection-Modulating Host Targets. <i>Systems Medicine (New Rochelle, N Y)</i> , <b>2019</b> , 2, 1-9	1.6	5
91	Efficient detection of differentially methylated regions using DiMmeR. <i>Bioinformatics</i> , <b>2017</b> , 33, 549-551	7.2	5
90	The Druggable Pocketome of : A New Approach for Putative Druggable Targets. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 44	4.5	5
89	BiCluE - Exact and heuristic algorithms for weighted bi-cluster editing of biomedical data. <i>BMC Proceedings</i> , <b>2013</b> , 7, S9	2.3	5
88	NABEECO <b>2013</b> ,		5
87	MoRAine - A web server for fast computational transcription factor binding motif re-annotation. <i>Journal of Integrative Bioinformatics</i> , <b>2008</b> , 5,	3.8	5
86	Global Regulator of Rubber Degradation in <i>Gordonia polyisoprenivorans</i> VH2: Identification and Involvement in the Regulation Network. <i>Applied and Environmental Microbiology</i> , <b>2020</b> , 86,	4.8	5
85	Network medicine for disease module identification and drug repurposing with the NeDRex platform. <i>Nature Communications</i> , <b>2021</b> , 12, 6848	17.4	5
84	BiCoN: Network-constrained biclustering of patients and omics data. <i>Bioinformatics</i> , <b>2020</b> ,	7.2	5
83	SPONGEdb: a pan-cancer resource for competing endogenous RNA interactions. <i>NAR Cancer</i> , <b>2021</b> , 3, zcaa042	5.2	5
82	Platelet Surface Protein Expression and Reactivity upon TRAP Stimulation after BNT162b2 Vaccination. <i>Thrombosis and Haemostasis</i> , <b>2021</b> ,	7	5
81	MoRAine--a web server for fast computational transcription factor binding motif re-annotation. <i>Journal of Integrative Bioinformatics</i> , <b>2008</b> , 5,	3.8	5
80	CMRegNet-An interspecies reference database for corynebacterial and mycobacterial regulatory networks. <i>BMC Genomics</i> , <b>2015</b> , 16, 452	4.5	4
79	Efficient Management of High-Throughput Screening Libraries with SAVANAH. <i>SLAS Discovery</i> , <b>2017</b> , 22, 196-202	3.4	4



78	Efficient algorithms for extracting biological key pathways with global constraints <b>2012</b> ,		4
77	BALSAM-An Interactive Online Platform for Breath Analysis, Visualization and Classification. <i>Metabolites</i> , <b>2020</b> , 10,	5.6	4
76	Individuating Possibly Repurposable Drugs and Drug Targets for COVID-19 Treatment Through Hypothesis-Driven Systems Medicine Using CoVex. <i>Assay and Drug Development Technologies</i> , <b>2020</b> , 18, 348-355	2.1	4
75	On the limits of active module identification. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	4
74	An Early Stage Researcher's Primer on Systems Medicine Terminology. <i>Network and Systems Medicine</i> , <b>2021</b> , 4, 2-50	4	4
73	Jllumina - A comprehensive Java-based API for statistical Illumina Infinium HumanMethylation450 and MethylationEPIC data processing. <i>Journal of Integrative Bioinformatics</i> , <b>2016</b> , 13, 294	3.8	4
72	A Simulated Annealing Algorithm for Maximum Common Edge Subgraph Detection in Biological Networks <b>2016</b> ,		3
71	CytoMCS: A Multiple Maximum Common Subgraph Detection Tool for Cytoscape. <i>Journal of Integrative Bioinformatics</i> , <b>2017</b> , 14,	3.8	3
70	BacillusRegNet: A transcriptional regulation database and analysis platform for Bacillus species. <i>Journal of Integrative Bioinformatics</i> , <b>2014</b> , 11, 106-119	3.8	3
69	A singular value decomposition approach for improved taxonomic classification of biological sequences. <i>BMC Genomics</i> , <b>2011</b> , 12 Suppl 4, S11	4.5	3
68	An integrative clinical database and diagnostics platform for biomarker identification and analysis in ion mobility spectra of human exhaled air. <i>Journal of Integrative Bioinformatics</i> , <b>2013</b> , 10, 218	3.8	3
67	BacillusRegNet: a transcriptional regulation database and analysis platform for Bacillus species. <i>Journal of Integrative Bioinformatics</i> , <b>2014</b> , 11, 244	3.8	3
66	Covering Tree with Stars. <i>Lecture Notes in Computer Science</i> , <b>2013</b> , 373-384	0.9	3
65	De Novo and Supervised Endophenotyping Using Network-Guided Ensemble Learning. <i>Systems Medicine (New Rochelle, N Y)</i> , <b>2020</b> , 3, 8-21	1.6	3
64	Comprehensive evaluation of computational cell-type quantification methods for immuno-oncology		3
63	Machine learning for deciphering cell heterogeneity and gene regulation. <i>Nature Computational Science</i> , <b>2021</b> , 1, 183-191		3
62	Success Factors of Artificial Intelligence Implementation in Healthcare. <i>Frontiers in Digital Health</i> , <b>2021</b> , 3, 594971	2.3	3
61	Joining European Scientific Forces to Face Pandemics. <i>Trends in Microbiology</i> , <b>2021</b> , 29, 92-97	12.4	3

60	Guiding biomedical clustering with ClustEval. <i>Nature Protocols</i> , <b>2018</b> , 13, 1429-1444	18.8	3
59	Functional enrichment of alternative splicing events with NEASE reveals insights into tissue identity and diseases. <i>Genome Biology</i> , <b>2021</b> , 22, 327	18.3	3
58	Integrated simultaneous analysis of different biomedical data types with exact weighted bi-cluster editing. <i>Journal of Integrative Bioinformatics</i> , <b>2012</b> , 9, 197	3.8	3
57	Weighted Gene Coregulation Network Analysis of Promoter DNA Methylation on All-Cause Mortality in Old-Aged Birth Cohorts Finds Modules of High-Risk Associated Biomarkers. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , <b>2020</b> , 75, 2249-2257	6.4	2
56	Jllumina - A comprehensive Java-based API for statistical Illumina Infinium HumanMethylation450 and Infinium MethylationEPIC BeadChip data processing. <i>Journal of Integrative Bioinformatics</i> , <b>2016</b> , 13, 24-32	3.8	2
55	A case-only genome-wide association study on gene-sex interaction in allergic rhinitis. <i>Annals of Allergy, Asthma and Immunology</i> , <b>2018</b> , 121, 366-367.e2	3.2	2
54	Online Interactive Microbial Classification and Geospatial Distributional Analysis Using BioAtlas. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1807, 21-35	1.4	2
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