

# Jan Baumbach

## List of Publications by Year in Descending Order

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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	SPLINK: a hybrid federated tool as a robust alternative to meta-analysis in genome-wide association studies.. <i>Genome Biology</i> , <b>2022</b> , 23, 32	18.3	1
202	CTCF regulates the PI3K-Akt pathway and it is a target for personalized ovarian cancer therapy.. <i>Npj Systems Biology and Applications</i> , <b>2022</b> , 8, 5	5	0
201	Enabling technologies towards personalization of scaffolds for large bone defect regeneration.. <i>Current Opinion in Biotechnology</i> , <b>2022</b> , 74, 263-270	11.4	0
200	A Systematic Review of Tissue and Single Cell Transcriptome/Proteome Studies of the Brain in Multiple Sclerosis.. <i>Frontiers in Immunology</i> , <b>2022</b> , 13, 761225	8.4	0
199	MoSBI: Automated signature mining for molecular stratification and subtyping.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2022</b> , 119, e2118210119	11.5	1
198	Tumour cell budding and spread through air spaces in squamous cell carcinoma of the lung - Determination and validation of optimal prognostic cut-offs.. <i>Lung Cancer</i> , <b>2022</b> , 169, 1-12	5.9	0
197	Flimma: a federated and privacy-aware tool for differential gene expression analysis.. <i>Genome Biology</i> , <b>2021</b> , 22, 338	18.3	2
196	KeyPathwayMineR: Pathway Enrichment in the R Ecosystem.. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 812853	4.5	1
195	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
194	A systematic comparison of novel and existing differential analysis methods for CyTOF data. <i>Briefings in Bioinformatics</i> , <b>2021</b> ,	13.4	2
193	A framework for modeling epistatic interaction. <i>Bioinformatics</i> , <b>2021</b> , 37, 1708-1716	7.2	1
192	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
191	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
190	On the Consistency between Gene Expression and the Gene Regulatory Network of. <i>Network and Systems Medicine</i> , <b>2021</b> , 4, 51-59	4	1
189	On the limits of active module identification. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	4
188	Machine learning for deciphering cell heterogeneity and gene regulation. <i>Nature Computational Science</i> , <b>2021</b> , 1, 183-191		3
187	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

186	Global Gene Expression Profiling and Transcription Factor Network Analysis of Cognitive Aging in Monozygotic Twins. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 675587	4.5	2
185	An Integrated Database of Small RNAs and Their Interplay With Transcriptional Gene Regulatory Networks in Corynebacteria. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 656435	5.7	1
184	Success Factors of Artificial Intelligence Implementation in Healthcare. <i>Frontiers in Digital Health</i> , <b>2021</b> , 3, 594971	2.3	3
183	Multi-Omics Analysis in a Network Context <b>2021</b> , 224-233		1
182	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
181	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
180	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
179	SPONGEdb: a pan-cancer resource for competing endogenous RNA interactions. <i>NAR Cancer</i> , <b>2021</b> , 3, zcaa042	5.2	5
178	Lessons from the COVID-19 pandemic for advancing computational drug repurposing strategies. <i>Nature Computational Science</i> , <b>2021</b> , 1, 33-41		36
177	Joining European Scientific Forces to Face Pandemics. <i>Trends in Microbiology</i> , <b>2021</b> , 29, 92-97	12.4	3
176	An Early Stage Researcher's Primer on Systems Medicine Terminology. <i>Network and Systems Medicine</i> , <b>2021</b> , 4, 2-50	4	4
175	Primer, Pipelines, Parameters: Issues in 16S rRNA Gene Sequencing. <i>MSphere</i> , <b>2021</b> , 6,	5	16
174	Novel DNA methylation marker discovery by assumption-free genome-wide association analysis of cognitive function in twins. <i>Aging Cell</i> , <b>2021</b> , 20, e13293	9.9	2
173	CSF proteome in multiple sclerosis subtypes related to brain lesion transcriptomes. <i>Scientific Reports</i> , <b>2021</b> , 11, 4132	4.9	2
172	Enabling single-cell trajectory network enrichment. <i>Nature Computational Science</i> , <b>2021</b> , 1, 153-163		2
171	splice-aware RNA-Seq data simulation. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	1
170	The AIME registry for artificial intelligence in biomedical research. <i>Nature Methods</i> , <b>2021</b> , 18, 1128-1131	21.6	11
169	Differential lncRNA expression profiling of cognitive function in middle and old aged monozygotic twins using generalized association analysis. <i>Journal of Psychiatric Research</i> , <b>2021</b> , 140, 197-204	5.2	0

168	Platelet Surface Protein Expression and Reactivity upon TRAP Stimulation after BNT162b2 Vaccination. <i>Thrombosis and Haemostasis</i> , <b>2021</b> ,	7	5
167	Unbiased examination of genome-wide human endogenous retrovirus transcripts in MS brain lesions. <i>Multiple Sclerosis Journal</i> , <b>2021</b> , 27, 1829-1837	5	2
166	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
165	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
164	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
163	Mass cytometry of platelet-rich plasma: a new approach to analyze platelet surface expression and reactivity.. <i>Platelets</i> , <b>2021</b> , 1-8	3.6	1
162	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
161	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
160	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
159	Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , <b>2020</b> , 579, 409-414	50.4	144
158	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
157	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
156	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype. <i>PLoS Biology</i> , <b>2020</b> , 18, e3000885	9.7	8
155	Generalized correlation coefficient for genome-wide association analysis of cognitive ability in twins. <i>Aging</i> , <b>2020</b> , 12, 22457-22494	5.6	1
154	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
153	BiCoN: Network-constrained biclustering of patients and omics data. <i>Bioinformatics</i> , <b>2020</b> ,	7.2	5
152	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
151	Inflammatory Breast Cancer: Clinical Implications of Genomic Alterations and Mutational Profiling. <i>Cancers</i> , <b>2020</b> , 12,	6.6	6

150	BALSAM-An Interactive Online Platform for Breath Analysis, Visualization and Classification. <i>Metabolites</i> , <b>2020</b> , 10,	5.6	4
149	Exploring the SARS-CoV-2 virus-host-drug interactome for drug repurposing. <i>Nature Communications</i> , <b>2020</b> , 11, 3518	17.4	104
148	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
147	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
146	PTPN2 Deficiency Enhances Programmed T Cell Expansion and Survival Capacity of Activated T Cells. <i>Cell Reports</i> , <b>2020</b> , 32, 107957	10.6	2
145	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 <sup>4</sup>		10
144	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
143	A global network for network medicine. <i>Npj Systems Biology and Applications</i> , <b>2020</b> , 6, 29	5	6
142	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
141	Differential long noncoding RNA profiling of BMI in twins. <i>Epigenomics</i> , <b>2020</b> , 12, 1531-1541	4.4	0
140	Age-dependent DNA methylation patterns on the Y chromosome in elderly males. <i>Aging Cell</i> , <b>2020</b> , 19, e12907	9.9	13
139	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
138	EpiGEN: an epistasis simulation pipeline. <i>Bioinformatics</i> , <b>2020</b> , 36, 4957-4959	7.2	2
137	netDx: Software for building interpretable patient classifiers by multi-omic data integration using patient similarity networks. <i>F1000Research</i> , <b>2020</b> , 9, 1239	3.6	1
136	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype <b>2020</b> , 18, e3000885		
135	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype <b>2020</b> , 18, e3000885		
134	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype <b>2020</b> , 18, e3000885		
133	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype <b>2020</b> , 18, e3000885		

132	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype <b>2020</b> , 18, e3000885		
131	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype <b>2020</b> , 18, e3000885		
130	NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype <b>2020</b> , 18, e3000885		
129	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
128	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
127	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
126	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
125	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
124	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
123	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
122	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
121	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
120	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
119	Retraction Note: 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, 136	7.3	2
118	Comprehensive evaluation of transcriptome-based cell-type quantification methods for immuno-oncology. <i>Bioinformatics</i> , <b>2019</b> , 35, i436-i445	7.2	209
117	Enriched power of disease-concordant twin-case-only design in detecting interactions in genome-wide association studies. <i>European Journal of Human Genetics</i> , <b>2019</b> , 27, 631-636	5.3	2
116	BioAtlas verbindet Mikrobiomsequenzdaten und GEO-Informationen. <i>BioSpektrum</i> , <b>2019</b> , 25, 795-795	0.1	
115	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

114	E. coli gene regulatory networks are inconsistent with gene expression data. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 85-92	20.1	24
113	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
112	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
111	DiMmer: Discovery of Differentially Methylated Regions in Epigenome-Wide Association Study (EWAS) Data. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1807, 51-62	1.4	0
110	CoNVaQ: a web tool for copy number variation-based association studies. <i>BMC Genomics</i> , <b>2018</b> , 19, 369	4.5	14
109	The Druggable Pocketome of : A New Approach for Putative Druggable Targets. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 44	4.5	5
108	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
107	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
106	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
105	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
104	Weighted gene co-expression network analysis of microarray mRNA expression profiling in response to electroacupuncture <b>2018</b> ,		1
103	Parameter estimation of qualitative biological regulatory networks on high performance computing hardware. <i>BMC Systems Biology</i> , <b>2018</b> , 12, 146	3.5	2
102	Guiding biomedical clustering with ClustEval. <i>Nature Protocols</i> , <b>2018</b> , 13, 1429-1444	18.8	3
101	Interactive microbial distribution analysis using BioAtlas. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, W509-W513	20.1	8
100	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
99	De novo pathway-based biomarker identification. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e151	20.1	36
98	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
97	Efficient detection of differentially methylated regions using DiMmeR. <i>Bioinformatics</i> , <b>2017</b> , 33, 549-551	7.2	5



96	On the performance of pre-microRNA detection algorithms. <i>Nature Communications</i> , <b>2017</b> , 8, 330	17.4	34
95	CytoMCS: A Multiple Maximum Common Subgraph Detection Tool for Cytoscape. <i>Journal of Integrative Bioinformatics</i> , <b>2017</b> , 14,	3.8	3
94	LifeStyle-Specific-Islands (LiSSI): Integrated Bioinformatics Platform for Genomic Island Analysis. <i>Journal of Integrative Bioinformatics</i> , <b>2017</b> , 14,	3.8	1
93	On the performance of de novo pathway enrichment. <i>Npj Systems Biology and Applications</i> , <b>2017</b> , 3, 6	5	38
92	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
91	Efficient Management of High-Throughput Screening Libraries with SAVANAH. <i>SLAS Discovery</i> , <b>2017</b> , 22, 196-202	3.4	4
90	GIPSy: Genomic island prediction software. <i>Journal of Biotechnology</i> , <b>2016</b> , 232, 2-11	3.7	76
89	A Simulated Annealing Algorithm for Maximum Common Edge Subgraph Detection in Biological Networks <b>2016</b> ,		3
88	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
87	Comprehensive analysis of high-throughput screens with HiTSeekR. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 6639-48	20.1	13
86	KeyPathwayMinerWeb: online multi-omics network enrichment. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, W98-W104	10.4	33
85	CytoGEDEVO-global alignment of biological networks with Cytoscape. <i>Bioinformatics</i> , <b>2016</b> , 32, 1259-61	7.2	15
84	Robust de novo pathway enrichment with KeyPathwayMiner 5. <i>F1000Research</i> , <b>2016</b> , 5, 1531	3.6	23
83	PetriScape - A plugin for discrete Petri net simulations in Cytoscape. <i>Journal of Integrative Bioinformatics</i> , <b>2016</b> , 13, 1-6	3.8	2
82	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
81	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
80	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
79	Comparing the performance of biomedical clustering methods. <i>Nature Methods</i> , <b>2015</b> , 12, 1033-8	21.6	140



78	CMRegNet-An interspecies reference database for corynebacterial and mycobacterial regulatory networks. <i>BMC Genomics</i> , <b>2015</b> , 16, 452	4.5	4
77	Covering tree with stars. <i>Journal of Combinatorial Optimization</i> , <b>2015</b> , 29, 141-152	0.9	
76	OpenLabNotes [An Electronic Laboratory Notebook Extension for OpenLabFramework. <i>Journal of Integrative Bioinformatics</i> , <b>2015</b> , 12, 16-25	3.8	1
75	Carotta: Revealing Hidden Confounder Markers in Metabolic Breath Profiles. <i>Metabolites</i> , <b>2015</b> , 5, 344-63.6	3.6	16
74	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
73	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
72	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
71	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
70	Massive fungal biodiversity data re-annotation with multi-level clustering. <i>Scientific Reports</i> , <b>2014</b> , 4, 6837	4.9	8
69	Efficient sample tracking with OpenLabFramework. <i>Scientific Reports</i> , <b>2014</b> , 4, 4278	4.9	12
68	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
67	Multiple graph edit distance <b>2014</b> ,		18
66	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
65	Microarray R-based analysis of complex lysate experiments with MIRACLE. <i>Bioinformatics</i> , <b>2014</b> , 30, i631-82	3.8	8
64	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
63	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
62	Value of a newly sequenced bacterial genome. <i>World Journal of Biological Chemistry</i> , <b>2014</b> , 5, 161-8	3.8	9
61	Complexity of Dense Bicluster Editing Problems. <i>Lecture Notes in Computer Science</i> , <b>2014</b> , 154-165	0.9	2

60	Compactness-Preserving Mapping on Trees. <i>Lecture Notes in Computer Science</i> , <b>2014</b> , 162-171	0.9	
59	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
58	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
57	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
56	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
55	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
54	NABEECO <b>2013</b> ,		5
53	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
52	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
51	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
50	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
49	Covering Tree with Stars. <i>Lecture Notes in Computer Science</i> , <b>2013</b> , 373-384	0.9	3
48	Cluster Editing. <i>Lecture Notes in Computer Science</i> , <b>2013</b> , 33-44	0.9	19
47	Neighborhood-Preserving Mapping between Trees. <i>Lecture Notes in Computer Science</i> , <b>2013</b> , 427-438	0.9	1
46	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
45	On the trail of EHEC/EAEC--unraveling the gene regulatory networks of human pathogenic <i>Escherichia coli</i> bacteria. <i>Integrative Biology (United Kingdom)</i> , <b>2012</b> , 4, 728-33	3.7	6
44	Efficient key pathway mining: combining networks and OMICS data. <i>Integrative Biology (United Kingdom)</i> , <b>2012</b> , 4, 756-64	3.7	38
43	Efficient algorithms for extracting biological key pathways with global constraints <b>2012</b> ,		4

42	PIPS: pathogenicity island prediction software. <i>PLoS ONE</i> , <b>2012</b> , 7, e30848	3.7	56
41	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
40	Integrated simultaneous analysis of different biomedical data types with exact weighted bi-cluster editing. <i>Journal of Integrative Bioinformatics</i> , <b>2012</b> , 9, 53-67	3.8	2
39	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
38	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
37	Rapid hybrid de novo assembly of a microbial genome using only short reads: <i>Corynebacterium pseudotuberculosis</i> I19 as a case study. <i>Journal of Microbiological Methods</i> , <b>2011</b> , 86, 218-23	2.8	36
36	Extension and Robustness of Transitivity Clustering for Protein-Protein Interaction Network Analysis. <i>Internet Mathematics</i> , <b>2011</b> , 7, 255-273	0	8
35	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
34	Comprehensive cluster analysis with Transitivity Clustering. <i>Nature Protocols</i> , <b>2011</b> , 6, 285-95	18.8	44
33	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 436	3.6	337
32	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
31	RhizoRegNet--a database of rhizobial transcription factors and regulatory networks. <i>Journal of Biotechnology</i> , <b>2011</b> , 155, 127-34	3.7	11
30	KeyPathwayMiner: Detecting Case-Specific Biological Pathways Using Expression Data. <i>Internet Mathematics</i> , <b>2011</b> , 7, 299-313	0	38
29	Partitioning biological data with transitivity clustering. <i>Nature Methods</i> , <b>2010</b> , 7, 419-20	21.6	73
28	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
27	AltAnalyze and DomainGraph: analyzing and visualizing exon expression data. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W755-62	20.1	217
26	Efficient Online Transcription Factor Binding Site Adjustment by Integrating Transitive Graph Projection with MoRAine 2.0. <i>Journal of Integrative Bioinformatics</i> , <b>2010</b> , 7,	3.8	1
25	From <i>Corynebacterium glutamicum</i> to <i>Mycobacterium tuberculosis</i> --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

24	Reliable transfer of transcriptional gene regulatory networks between taxonomically related organisms. <i>BMC Systems Biology</i> , <b>2009</b> , 3, 8	3.5	22
23	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
22	MotifAdjuster: a tool for computational reassessment of transcription factor binding site annotations. <i>Genome Biology</i> , <b>2009</b> , 10, R46	18.3	2
21	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
20	Linking Cytoscape and the corynebacterial reference database CoryneRegNet. <i>BMC Genomics</i> , <b>2008</b> , 9, 184	4.5	28
19	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
18	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
17	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
16	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
15	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
14	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
13	CoryneRegNet 4.0 - A reference database for corynebacterial gene regulatory networks. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 429	3.6	56
12	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
11	EXACT AND HEURISTIC ALGORITHMS FOR WEIGHTED CLUSTER EDITING <b>2007</b> ,		33
10	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
9	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
8	Graph-based analysis and visualization of experimental results with ONDEX. <i>Bioinformatics</i> , <b>2006</b> , 22, 1383-90	7.2	159
7	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

6	BiCoN: Network-constrained biclustering of patients and omics data	1
5	sPLINK: A Federated, Privacy-Preserving Tool as a Robust Alternative to Meta-Analysis in Genome-Wide Association Studies	6
4	Comprehensive evaluation of computational cell-type quantification methods for immuno-oncology	3
3	MS Atlas - A molecular map of brain lesion stages in progressive multiple sclerosis	1
2	Platelet expression and reactivity after BNT162b2 vaccine administration	2
1	Namco: A microbiome explorer	1