

# Jan Baumbach

## List of Publications by Year in descending order

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Version: 2024-02-01

203  
papers

7,127  
citations

76196

40  
h-index

82410

72  
g-index

225  
all docs

225  
docs citations

225  
times ranked

10759  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Comprehensive evaluation of transcriptome-based cell-type quantification methods for immuno-oncology. <i>Bioinformatics</i> , 2019, 35, i436-i445.   | 1.8  | 576       |
| 2  | clusterMaker: a multi-algorithm clustering plugin for Cytoscape. <i>BMC Bioinformatics</i> , 2011, 12, 436.  | 1.2  | 541       |
| 3  | Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , 2020, 579, 409-414.   | 13.7 | 328       |
| 4  | AltAnalyze and DomainGraph: analyzing and visualizing exon expression data. <i>Nucleic Acids Research</i> , 2010, 38, W755-W762.   | 6.5  | 310       |
| 5  | Comparing the performance of biomedical clustering methods. <i>Nature Methods</i> , 2015, 12, 1033-1038.   | 9.0  | 195       |
| 6  | Graph-based analysis and visualization of experimental results with ONDEX. <i>Bioinformatics</i> , 2006, 22, 1383-1390.  | 1.8  | 193       |
| 7  | Osteogenesis depends on commissioning of a network of stem cell transcription factors that act as repressors of adipogenesis. <i>Nature Genetics</i> , 2019, 51, 716-727.  | 9.4  | 156       |
| 8  | Exploring the SARS-CoV-2 virus-host-drug interactome for drug repurposing. <i>Nature Communications</i> , 2020, 11, 3518.  | 5.8  | 144       |
| 9  | Primer, Pipelines, Parameters: Issues in 16S rRNA Gene Sequencing. <i>MSphere</i> , 2021, 6, .   | 1.3  | 140       |
| 10 | 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> , 2019, 116, 7129-7136.                                  | 3.3  | 132       |
| 11 | Network analysis methods for studying microbial communities: A mini review. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2687-2698.   | 1.9  | 130       |
| 12 | GPSy: Genomic island prediction software. <i>Journal of Biotechnology</i> , 2016, 232, 2-11.   | 1.9  | 128       |
| 13 | Molecular networks in Network Medicine: Development and applications. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1489.  | 6.6  | 128       |
| 14 | Systematic Review of Economic Impact Studies of Artificial Intelligence in Health Care. <i>Journal of Medical Internet Research</i> , 2020, 22, e16866.  | 2.1  | 121       |
| 15 | Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021, 22, 642-663.   | 3.2  | 110       |
| 16 | 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> , 2021, 70, 522-530.            | 6.1  | 96        |
| 17 | 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> , 2013, 8, e68302.  | 1.1  | 90        |
| 18 | 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> , 2008, 135, 340-350. | 1.9  | 89        |

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|----|--|-----|-----------|
| 19 | Lessons from the COVID-19 pandemic for advancing computational drug repurposing strategies. <i>Nature Computational Science</i> , 2021, 1, 33-41.                                    | 3.8 | 88        |
| 20 | Partitioning biological data with transitivity clustering. <i>Nature Methods</i> , 2010, 7, 419-420.   | 9.0 | 84        |
| 21 | PanRV: Pangenome-reverse vaccinology approach for identifications of potential vaccine candidates in microbial pangenome. <i>BMC Bioinformatics</i> , 2019, 20, 123.                 | 1.2 | 80        |
| 22 | SARS-CoV-2 infection is associated with a pro-thrombotic platelet phenotype. <i>Cell Death and Disease</i> , 2021, 12, 50.   | 2.7 | 77        |
| 23 | Evidence for Reductive Genome Evolution and Lateral Acquisition of Virulence Functions in Two <i>Corynebacterium pseudotuberculosis</i> Strains. <i>PLoS ONE</i> , 2011, 6, e18551.  | 1.1 | 75        |
| 24 | PIPS: Pathogenicity Island Prediction Software. <i>PLoS ONE</i> , 2012, 7, e30848.   | 1.1 | 70        |
| 25 | Metagenomic evidence for the presence of phototrophic <i>Chloroflexus</i> bacteria in diverse environments. <i>Environmental Microbiology Reports</i> , 2016, 8, 139-149.            | 1.0 | 66        |
| 26 | CoryneRegNet 6.0—Updated database content, new analysis methods and novel features focusing on community demands. <i>Nucleic Acids Research</i> , 2012, 40, D610-D614.               | 6.5 | 62        |
| 27 | CoryneRegNet 4.0 “A reference database for corynebacterial gene regulatory networks. <i>BMC Bioinformatics</i> , 2007, 8, 429.   | 1.2 | 61        |
| 28 | Molecular signature of different lesion types in the brain white matter of patients with progressive multiple sclerosis. <i>Acta Neuropathologica Communications</i> , 2019, 7, 205. | 2.4 | 61        |
| 29 | <i>E. coli</i> gene regulatory networks are inconsistent with gene expression data. <i>Nucleic Acids Research</i> , 2019, 47, 85-92.   | 6.5 | 60        |
| 30 | KeyPathwayMiner 4.0: condition-specific pathway analysis by combining multiple omics studies and networks with Cytoscape. <i>BMC Systems Biology</i> , 2014, 8, 99.                  | 3.0 | 59        |
| 31 | Large scale clustering of protein sequences with FORCE -A layout based heuristic for weighted cluster editing. <i>BMC Bioinformatics</i> , 2007, 8, 396.                             | 1.2 | 56        |
| 32 | Efficient key pathway mining: combining networks and OMICS data. <i>Integrative Biology (United Kingdom)</i> , 2019, 11, 1-14.   | 0.6 | 54        |
| 33 | DeepCLIP: predicting the effect of mutations on protein-RNA binding with deep learning. <i>Nucleic Acids Research</i> , 2020, 48, 7099-7118.   | 6.5 | 54        |
| 34 | CoryneRegNet: An ontology-based data warehouse of corynebacterial transcription factors and regulatory networks. <i>BMC Genomics</i> , 2006, 7, 24.                                  | 1.2 | 52        |
| 35 | Classification of Breast Cancer Subtypes by combining Gene Expression and DNA Methylation Data. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 1-14.                       | 1.0 | 52        |
| 36 | On the performance of de novo pathway enrichment. <i>Npj Systems Biology and Applications</i> , 2017, 3, 6.  | 1.4 | 51        |

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|----|---|-----|-----------|
| 37 | De novo pathway-based biomarker identification. <i>Nucleic Acids Research</i> , 2017, 45, e151-e151.  | 6.5 | 48        |
| 38 | Comprehensive cluster analysis with Transitivity Clustering. <i>Nature Protocols</i> , 2011, 6, 285-295.  | 5.5 | 47        |
| 39 | KeyPathwayMiner: Detecting Case-Specific Biological Pathways Using Expression Data. <i>Internet Mathematics</i> , 2011, 7, 299-313.   | 0.7 | 47        |
| 40 | On the performance of pre-microRNA detection algorithms. <i>Nature Communications</i> , 2017, 8, 330.   | 5.8 | 47        |
| 41 | KeyPathwayMinerWeb: online multi-omics network enrichment. <i>Nucleic Acids Research</i> , 2016, 44, W98-W104.  | 6.5 | 45        |
| 42 | Drug repurposing by integrated literature mining and drug-gene-disease triangulation. <i>Drug Discovery Today</i> , 2017, 22, 615-619.  | 3.2 | 45        |
| 43 | High-resolution detection of DNA binding sites of the global transcriptional regulator GlxR in <i>Corynebacterium glutamicum</i> . <i>Microbiology (United Kingdom)</i> , 2013, 159, 12-22.                                 | 0.7 | 44        |
| 44 | EXACT AND HEURISTIC ALGORITHMS FOR WEIGHTED CLUSTER EDITING. , 2007, , .  |     | 43        |
| 45 | 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> , 2011, 86, 218-223.                   | 0.7 | 40        |
| 46 | 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> , 2009, 37, e97-e97. | 6.5 | 39        |
| 47 | Integrated analysis and reconstruction of microbial transcriptional gene regulatory networks using CoryneRegNet. <i>Nature Protocols</i> , 2009, 4, 992-1005.   | 5.5 | 39        |
| 48 | Network medicine for disease module identification and drug repurposing with the NeDRex platform. <i>Nature Communications</i> , 2021, 12, 6848.  | 5.8 | 39        |
| 49 | The AIME registry for artificial intelligence in biomedical research. <i>Nature Methods</i> , 2021, 18, 1128-1131.  | 9.0 | 38        |
| 50 | Clinical epigenetics settings for cancer and cardiovascular diseases: real-life applications of network medicine at the bedside. <i>Clinical Epigenetics</i> , 2021, 13, 66.  | 1.8 | 36        |
| 51 | An integrative in-silico approach for therapeutic target identification in the human pathogen <i>Corynebacterium diphtheriae</i> . <i>PLoS ONE</i> , 2017, 12, e0186401.  | 1.1 | 35        |
| 52 | 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> , 2007, 129, 279-289.                 | 1.9 | 32        |
| 53 | Linking Cytoscape and the corynebacterial reference database CoryneRegNet. <i>BMC Genomics</i> , 2008, 9, 184.  | 1.2 | 32        |
| 54 | Comparative transcriptome analysis reveals key epigenetic targets in SARS-CoV-2 infection. <i>Npj Systems Biology and Applications</i> , 2021, 7, 21.   | 1.4 | 32        |

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|----|---|-----|-----------|
| 55 | CytoGEDEVOâ€”global alignment of biological networks with Cytoscape. <i>Bioinformatics</i> , 2016, 32, 1259-1261.   | 1.8 | 31        |
| 56 | On the power of epigenome-wide association studies using a disease-discordant twin design. <i>Bioinformatics</i> , 2018, 34, 4073-4078.   | 1.8 | 31        |
| 57 | On the power and limits of evolutionary conservationâ€”unraveling bacterial gene regulatory networks. <i>Nucleic Acids Research</i> , 2010, 38, 7877-7884.  | 6.5 | 30        |
| 58 | DIGGER: exploring the functional role of alternative splicing in protein interactions. <i>Nucleic Acids Research</i> , 2021, 49, D309-D318.   | 6.5 | 30        |
| 59 | On the limits of active module identification. <i>Briefings in Bioinformatics</i> , 2021, 22, .   | 3.2 | 30        |
| 60 | Robust de novo pathway enrichment with KeyPathwayMiner 5. <i>F1000Research</i> , 2016, 5, 1531.   | 0.8 | 30        |
| 61 | Computational Methods for Metabolomic Data Analysis of Ion Mobility Spectrometry Data&mdash;Reviewing the State of the Art. <i>Metabolites</i> , 2012, 2, 733-755.  | 1.3 | 29        |
| 62 | CoNVaQ: a web tool for copy number variation-based association studies. <i>BMC Genomics</i> , 2018, 19, 369.  | 1.2 | 29        |
| 63 | Success Factors of Artificial Intelligence Implementation in Healthcare. <i>Frontiers in Digital Health</i> , 2021, 3, 594971.  | 1.5 | 29        |
| 64 | Reliable transfer of transcriptional gene regulatory networks between taxonomically related organisms. <i>BMC Systems Biology</i> , 2009, 3, 8.   | 3.0 | 28        |
| 65 | Orthologous proteins of experimental de- and remyelination are differentially regulated in the CSF proteome of multiple sclerosis subtypes. <i>PLoS ONE</i> , 2018, 13, e0202530.   | 1.1 | 28        |
| 66 | PTPN2 Deficiency Enhances Programmed T Cell Expansion and Survival Capacity of Activated T Cells. <i>Cell Reports</i> , 2020, 32, 107957.   | 2.9 | 28        |
| 67 | RhizoRegNetâ€”A database of rhizobial transcription factors and regulatory networks. <i>Journal of Biotechnology</i> , 2011, 155, 127-134.  | 1.9 | 27        |
| 68 | Ageâ€”dependent DNA methylation patterns on the Y chromosome in elderly males. <i>Aging Cell</i> , 2020, 19, e12907.  | 3.0 | 27        |
| 69 | Multiple graph edit distance. , 2014, , .   |     | 26        |
| 70 | Exploratory analysis of age and sex dependent DNA methylation patterns on the X-chromosome in whole blood samples. <i>Genome Medicine</i> , 2020, 12, 39.   | 3.6 | 26        |
| 71 | How Little Do We Actually Know? On the Size of Gene Regulatory Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1293-1300.   | 1.9 | 25        |
| 72 | Conserved hostâ€”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 <i>Piper betel</i> compounds. <i>Integrative Biology (United Kingdom)</i> , 2013, 5, 495-509. | 0.6 | 24        |

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|----|---|-----|-----------|
| 73 | Peak Detection Method Evaluation for Ion Mobility Spectrometry by Using Machine Learning Approaches. <i>Metabolites</i> , 2013, 3, 277-293.   | 1.3 | 24        |
| 74 | NOX5-induced uncoupling of endothelial NO synthase is a causal mechanism and theragnostic target of an age-related hypertension endotype. <i>PLoS Biology</i> , 2020, 18, e3000885.   | 2.6 | 23        |
| 75 | Classification of breast cancer subtypes by combining gene expression and DNA methylation data. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 236.   | 1.0 | 23        |
| 76 | Federated Random Forests can improve local performance of predictive models for various healthcare applications. <i>Bioinformatics</i> , 2022, 38, 2278-2286.   | 1.8 | 23        |
| 77 | CoryneRegNet 7, the reference database and analysis platform for corynebacterial gene regulatory networks. <i>Scientific Data</i> , 2020, 7, 142.   | 2.4 | 22        |
| 78 | Cluster Editing. <i>Lecture Notes in Computer Science</i> , 2013, , 33-44.  | 1.0 | 22        |
| 79 | Towards the integrated analysis, visualization and reconstruction of microbial gene regulatory networks. <i>Briefings in Bioinformatics</i> , 2008, 10, 75-83.  | 3.2 | 21        |
| 80 | Mature Epitope Density - A strategy for target selection based on immunoinformatics and exported prokaryotic proteins. <i>BMC Genomics</i> , 2013, 14, S4.  | 1.2 | 21        |
| 81 | 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> , 2007, 4, 186-197.                           | 1.0 | 20        |
| 82 | Differentially Methylated Genomic Regions in Birth-Weight Discordant Twin Pairs. <i>Annals of Human Genetics</i> , 2016, 80, 81-87.   | 0.3 | 19        |
| 83 | A global network for network medicine. <i>Npj Systems Biology and Applications</i> , 2020, 6, 29.   | 1.4 | 19        |
| 84 | Carotta: Revealing Hidden Confounder Markers in Metabolic Breath Profiles. <i>Metabolites</i> , 2015, 5, 344-363.   | 1.3 | 18        |
| 85 | 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> , 2020, 3, 67-90.                        | 2.7 | 18        |
| 86 | sPLINK: a hybrid federated tool as a robust alternative to meta-analysis in genome-wide association studies. <i>Genome Biology</i> , 2022, 23, 32.  | 3.8 | 18        |
| 87 | Density parameter estimation for finding clusters of homologous proteins – tracing actinobacterial pathogenicity lifestyles. <i>Bioinformatics</i> , 2013, 29, 215-222.   | 1.8 | 17        |
| 88 | Bi-Force: large-scale bicluster editing and its application to gene expression data biclustering. <i>Nucleic Acids Research</i> , 2014, 42, e78-e78.  | 6.5 | 17        |
| 89 | 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> , 2014, 6, 1058-1068. | 0.6 | 17        |
| 90 | Comprehensive analysis of high-throughput screens with HiTSeekR. <i>Nucleic Acids Research</i> , 2016, 44, 6639-6648.   | 6.5 | 17        |

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|-----|--|-----|-----------|
| 91  | The epigenetic factor BORIS (CTCF) controls the androgen receptor regulatory network in ovarian cancer. <i>Oncogenesis</i> , 2019, 8, 41.  | 2.1 | 17        |
| 92  | Increased Levels of Genomic Instability and Mutations in Homologous Recombination Genes in Locally Advanced Rectal Carcinomas. <i>Frontiers in Oncology</i> , 2019, 9, 395.                          | 1.3 | 17        |
| 93  | DNA methylome profiling in identical twin pairs discordant for body mass index. <i>International Journal of Obesity</i> , 2019, 43, 2491-2499.   | 1.6 | 16        |
| 94  | Community effort endorsing multiscale modelling, multiscale data science and multiscale computing for systems medicine. <i>Briefings in Bioinformatics</i> , 2019, 20, 1057-1062.                    | 3.2 | 15        |
| 95  | Inflammatory Breast Cancer: Clinical Implications of Genomic Alterations and Mutational Profiling. <i>Cancers</i> , 2020, 12, 2816.  | 1.7 | 15        |
| 96  | BiCoN: network-constrained biclustering of patients and omics data. <i>Bioinformatics</i> , 2021, 37, 2398-2404.   | 1.8 | 15        |
| 97  | Efficient Sample Tracking With OpenLabFramework. <i>Scientific Reports</i> , 2015, 4, 4278.  | 1.6 | 14        |
| 98  | Time-Resolved Systems Medicine Reveals Viral Infection-Modulating Host Targets. <i>Systems Medicine (New Rochelle, N Y)</i> , 2019, 2, 1-9.  | 1.4 | 14        |
| 99  | SPONGEdb: a pan-cancer resource for competing endogenous RNA interactions. <i>NAR Cancer</i> , 2021, 3, zcaa042.   | 1.6 | 14        |
| 100 | Machine learning for deciphering cell heterogeneity and gene regulation. <i>Nature Computational Science</i> , 2021, 1, 183-191.   | 3.8 | 14        |
| 101 | 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> , 2017, 35, 1898-1912.                  | 1.4 | 13        |
| 102 | The Selection of a Hepatocyte Cell Line Susceptible to Plasmodium falciparum Sporozoite Invasion That Is Associated With Expression of Glypican-3. <i>Frontiers in Microbiology</i> , 2019, 10, 127. | 1.5 | 13        |
| 103 | DNA methylome profiling of all-cause mortality in comparison with age-associated methylation patterns. <i>Clinical Epigenetics</i> , 2019, 11, 23.   | 1.8 | 13        |
| 104 | Comprehensive Analysis of DNA Methylation and Prediction of Response to Neoadjuvant Therapy in Locally Advanced Rectal Cancer. <i>Cancers</i> , 2020, 12, 3079.                                      | 1.7 | 13        |
| 105 | Exact and heuristic algorithms for weighted cluster editing. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2007, 6, 391-401. | 0.4 | 13        |
| 106 | Massive fungal biodiversity data re-annotation with multi-level clustering. <i>Scientific Reports</i> , 2014, 4, 6837.   | 1.6 | 12        |
| 107 | Multiple Sclerosis Atlas: A Molecular Map of Brain Lesion Stages in Progressive Multiple Sclerosis. <i>Network and Systems Medicine</i> , 2020, 3, 122-129.  | 2.7 | 12        |
| 108 | Functional enrichment of alternative splicing events with NEASE reveals insights into tissue identity and diseases. <i>Genome Biology</i> , 2021, 22, 327.   | 3.8 | 12        |

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|-----|---|------|-----------|
| 109 | CoryneRegNet 2: An Integrative Bioinformatics Approach for Reconstruction and Comparison of Transcriptional Regulatory Networks in Prokaryotes. <i>Journal of Integrative Bioinformatics</i> , 2006, 3, 1-13.     | 1.0  | 11        |
| 110 | CoryneCenter – An online resource for the integrated analysis of corynebacterial genome and transcriptome data. <i>BMC Systems Biology</i> , 2007, 1, 55.   | 3.0  | 11        |
| 111 | On the limits of computational functional genomics for bacterial lifestyle prediction. <i>Briefings in Functional Genomics</i> , 2014, 13, 398-408.   | 1.3  | 11        |
| 112 | Mechanistic Modeling and Multiscale Applications for Precision Medicine: Theory and Practice. <i>Network and Systems Medicine</i> , 2020, 3, 36-56.   | 2.7  | 11        |
| 113 | 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> , 2013, 10, 35-47. | 1.0  | 10        |
| 114 | CSF proteome in multiple sclerosis subtypes related to brain lesion transcriptomes. <i>Scientific Reports</i> , 2021, 11, 4132.   | 1.6  | 10        |
| 115 | Value of a newly sequenced bacterial genome. <i>World Journal of Biological Chemistry</i> , 2014, 5, 161-8.   | 1.7  | 10        |
| 116 | Flimma: a federated and privacy-aware tool for differential gene expression analysis. <i>Genome Biology</i> , 2021, 22, 338.  | 3.8  | 10        |
| 117 | Robust disease module mining via enumeration of diverse prize-collecting Steiner trees. <i>Bioinformatics</i> , 2022, 38, 1600-1606.  | 1.8  | 10        |
| 118 | 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> , 2012, 4, 728-733.                         | 0.6  | 9         |
| 119 | NABEECO. , 2013, , .  |      | 9         |
| 120 | Efficient detection of differentially methylated regions using DiMmeR. <i>Bioinformatics</i> , 2017, 33, 549-551.   | 1.8  | 9         |
| 121 | An Early Stage Researcher's Primer on Systems Medicine Terminology. <i>Network and Systems Medicine</i> , 2021, 4, 2-50.  | 2.7  | 9         |
| 122 | Platelet Surface Protein Expression and Reactivity upon TRAP Stimulation after BNT162b2 Vaccination. <i>Thrombosis and Haemostasis</i> , 2022, 122, 1706-1711.  | 1.8  | 9         |
| 123 | De Novo and Supervised Endophenotyping Using Network-Guided Ensemble Learning. <i>Systems Medicine (New Rochelle, N Y)</i> , 2020, 3, 8-21.   | 1.4  | 9         |
| 124 | Cancer driver drug interaction explorer. <i>Nucleic Acids Research</i> , 2022, 50, W138-W144.   | 6.5  | 9         |
| 125 | MotifAdjuster: a tool for computational reassessment of transcription factor binding site annotations. <i>Genome Biology</i> , 2009, 10, R46.   | 13.9 | 8         |
| 126 | Extension and Robustness of Transitivity Clustering for Protein – Protein Interaction Network Analysis. <i>Internet Mathematics</i> , 2011, 7, 255-273.   | 0.7  | 8         |



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|-----|---|-----|-----------|
| 127 | Microarray R-based analysis of complex lysate experiments with MIRACLE. <i>Bioinformatics</i> , 2014, 30, i631-i638.  | 1.8 | 8         |
| 128 | Interactive microbial distribution analysis using BioAtlas. <i>Nucleic Acids Research</i> , 2017, 45, W509-W513.  | 6.5 | 8         |
| 129 | The End of Medicine as We Know It: Introduction to the New Journal, <i>Systems Medicine</i> . <i>Systems Medicine (New Rochelle, N Y)</i> , 2018, 1, 1-2.   | 1.4 | 8         |
| 130 | The Druggable Pocketome of <i>Corynebacterium diphtheriae</i> : A New Approach for in silico Putative Druggable Targets. <i>Frontiers in Genetics</i> , 2018, 9, 44.  | 1.1 | 8         |
| 131 | Enabling technologies towards personalization of scaffolds for large bone defect regeneration. <i>Current Opinion in Biotechnology</i> , 2022, 74, 263-270.   | 3.3 | 8         |
| 132 | Network Medicine-Based Unbiased Disease Modules for Drug and Diagnostic Target Identification in ROSopathies. <i>Handbook of Experimental Pharmacology</i> , 2020, 264, 49-68.                                | 0.9 | 7         |
| 133 | Novel DNA methylation marker discovery by assumption-free genome-wide association analysis of cognitive function in twins. <i>Aging Cell</i> , 2021, 20, e13293.  | 3.0 | 7         |
| 134 | ASimulatoR: splice-aware RNA-Seq data simulation. <i>Bioinformatics</i> , 2021, 37, 3008-3010.  | 1.8 | 7         |
| 135 | On the Consistency between Gene Expression and the Gene Regulatory Network of <i>Corynebacterium glutamicum</i> . <i>Network and Systems Medicine</i> , 2021, 4, 51-59.                                       | 2.7 | 7         |
| 136 | Parameter estimation of qualitative biological regulatory networks on high performance computing hardware. <i>BMC Systems Biology</i> , 2018, 12, 146.  | 3.0 | 6         |
| 137 | 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> , 2020, 18, 348-355. | 0.6 | 6         |
| 138 | EpiGEN: an epistasis simulation pipeline. <i>Bioinformatics</i> , 2020, 36, 4957-4959.  | 1.8 | 6         |
| 139 | Global Gene Expression Profiling and Transcription Factor Network Analysis of Cognitive Aging in Monozygotic Twins. <i>Frontiers in Genetics</i> , 2021, 12, 675587.  | 1.1 | 6         |
| 140 | Unbiased examination of genome-wide human endogenous retrovirus transcripts in MS brain lesions. <i>Multiple Sclerosis Journal</i> , 2021, 27, 1829-1837.   | 1.4 | 6         |
| 141 | Global Regulator of Rubber Degradation in <i>Gordonia polyisoprenivorans</i> VH2: Identification and Involvement in the Regulation Network. <i>Applied and Environmental Microbiology</i> , 2020, 86, .       | 1.4 | 6         |
| 142 | A systematic comparison of novel and existing differential analysis methods for CyTOF data. <i>Briefings in Bioinformatics</i> , 2022, 23, .  | 3.2 | 6         |
| 143 | A Systematic Review of Tissue and Single Cell Transcriptome/Proteome Studies of the Brain in Multiple Sclerosis. <i>Frontiers in Immunology</i> , 2022, 13, 761225.   | 2.2 | 6         |
| 144 | MoRAine--a web server for fast computational transcription factor binding motif re-annotation. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .  | 1.0 | 6         |

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|-----|---|-----|-----------|
| 145 | Consensus draft of the native mouse podocyte-ome. American Journal of Physiology - Renal Physiology, 2022, 323, F182-F197.  | 1.3 | 6         |
| 146 | MoRAine - A web server for fast computational transcription factor binding motif re-annotation. Journal of Integrative Bioinformatics, 2008, 5, .   | 1.0 | 5         |
| 147 | Efficient algorithms for extracting biological key pathways with global constraints. , 2012, , .  |     | 5         |
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