

# Tom Michoel

## List of Publications by Year in descending order

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Version: 2024-02-01

71  
papers

2,869  
citations

279798

23  
h-index

197818

49  
g-index

83  
all docs

83  
docs citations

83  
times ranked

5719  
citing authors

#	ARTICLE	IF	CITATIONS
1	Microglial brain region~dependent diversity and selective regional sensitivities to aging. <i>Nature Neuroscience</i> , 2016, 19, 504-516.	14.8	919
2	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. <i>Science</i> , 2016, 353, 827-830.	12.6	241
3	Cross-Tissue Regulatory Gene Networks in Coronary Artery Disease. <i>Cell Systems</i> , 2016, 2, 196-208.	6.2	120
4	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	17.5	88
5	Integrative Multi-omics Module Network Inference with Lemon-Tree. <i>PLoS Computational Biology</i> , 2015, 11, e1003983.	3.2	86
6	Module networks revisited: computational assessment and prioritization of model predictions. <i>Bioinformatics</i> , 2009, 25, 490-496.	4.1	82
7	Plasma Cholesterol~Induced Lesion Networks Activated before Regression of Early, Mature, and Advanced Atherosclerosis. <i>PLoS Genetics</i> , 2014, 10, e1004201.	3.5	64
8	Analysis of a Gibbs sampler method for model-based clustering of gene expression data. <i>Bioinformatics</i> , 2008, 24, 176-183.	4.1	59
9	Comparative analysis of module-based versus direct methods for reverse-engineering transcriptional regulatory networks. <i>BMC Systems Biology</i> , 2009, 3, 49.	3.0	55
10	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
11	Predicting Gene Function from Uncontrolled Expression Variation among Individual Wild-Type <i>Arabidopsis</i> Plants. <i>Plant Cell</i> , 2013, 25, 2865-2877.	6.6	50
12	Alignment and integration of complex networks by hypergraph-based spectral clustering. <i>Physical Review E</i> , 2012, 86, 056111.	2.1	49
13	Module Network Inference from a Cancer Gene Expression Data Set Identifies MicroRNA Regulated Modules. <i>PLoS ONE</i> , 2010, 5, e10162.	2.5	46
14	Contribution of Gene Regulatory Networks to Heritability of Coronary~Artery Disease. <i>Journal of the American College of Cardiology</i> , 2019, 73, 2946-2957.	2.8	45
15	Human Validation of Genes Associated With a Murine Atherosclerotic Phenotype. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2016, 36, 1240-1246.	2.4	44
16	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. <i>Scientific Reports</i> , 2018, 8, 3434.	3.3	43
17	Variation in the SERPINA6/SERPINA1 locus alters morning plasma cortisol, hepatic corticosteroid binding globulin expression, gene expression in peripheral tissues, and risk of cardiovascular disease. <i>Journal of Human Genetics</i> , 2021, 66, 625-636.	2.3	40
18	kruX: matrix-based non-parametric eQTL discovery. <i>BMC Bioinformatics</i> , 2014, 15, 11.	2.6	39

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19	Expression Quantitative Trait Loci Acting Across Multiple Tissues Are Enriched in Inherited Risk for Coronary Artery Disease. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 305-315.	5.1	39
20	Human Y Chromosome Exerts Pleiotropic Effects on Susceptibility to Atherosclerosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019, 39, 2386-2401.	2.4	36
21	Efficient and accurate causal inference with hidden confounders from genome-transcriptome variation data. <i>PLoS Computational Biology</i> , 2017, 13, e1005703.	3.2	36
22	Validating module network learning algorithms using simulated data. <i>BMC Bioinformatics</i> , 2007, 8, S5.	2.6	34
23	SNAIL1 combines competitive displacement of ASCL2 and epigenetic mechanisms to rapidly silence the EPHB3 tumor suppressor in colorectal cancer. <i>Molecular Oncology</i> , 2015, 9, 335-354.	4.6	34
24	Silencing of the EPHB3 tumor-suppressor gene in human colorectal cancer through decommissioning of a transcriptional enhancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4886-4891.	7.1	32
25	Prediction of a gene regulatory network linked to prostate cancer from gene expression, microRNA and clinical data. <i>Bioinformatics</i> , 2010, 26, i638-i644.	4.1	30
26	Application of long read sequencing to determine expressed antigen diversity in <i>Trypanosoma brucei</i> infections. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007262.	3.0	25
27	Transcription regulatory networks in <i>Caenorhabditis elegans</i> inferred through reverse-engineering of gene expression profiles constitute biological hypotheses for metazoan development. <i>Molecular BioSystems</i> , 2009, 5, 1817.	2.9	23
28	Structural and functional organization of RNA regulons in the post-transcriptional regulatory network of yeast. <i>Nucleic Acids Research</i> , 2011, 39, 9108-9117.	14.5	23
29	MotifSuite: workflow for probabilistic motif detection and assessment. <i>Bioinformatics</i> , 2012, 28, 1931-1932.	4.1	23
30	Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. <i>Journal of Leukocyte Biology</i> , 2015, 97, 985-995.	3.3	23
31	Smoking is Associated to DNA Methylation in Atherosclerotic Carotid Lesions. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002030.	3.6	23
32	Variants in ALOX5, ALOX5AP and LTA4H are not associated with atherosclerotic plaque phenotypes: The Athero-Express Genomics Study. <i>Atherosclerosis</i> , 2015, 239, 528-538.	0.8	22
33	Post-transcriptional regulatory networks play a key role in noise reduction that is conserved from microorganisms to mammals. <i>FEBS Journal</i> , 2012, 279, 3501-3512.	4.7	20
34	The Index-Based Subgraph Matching Algorithm with General Symmetries (ISMAGS): Exploiting Symmetry for Faster Subgraph Enumeration. <i>PLoS ONE</i> , 2014, 9, e97896.	2.5	19
35	Enhancer decommissioning by Snail1-induced competitive displacement of TCF7L2 and down-regulation of transcriptional activators results in EPHB2 silencing. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 1353-1367.	1.9	18
36	The Index-Based Subgraph Matching Algorithm (ISMA): Fast Subgraph Enumeration in Large Networks Using Optimized Search Trees. <i>PLoS ONE</i> , 2013, 8, e61183.	2.5	17

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37	Lim Domain Binding 2. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014, 34, 2068-2077.	2.4	17
38	Functional transcription factor target discovery via compendia of binding and expression profiles. <i>Scientific Reports</i> , 2016, 6, 20649.	3.3	16
39	Enrichment and aggregation of topological motifs are independent organizational principles of integrated interaction networks. <i>Molecular BioSystems</i> , 2011, 7, 2769.	2.9	15
40	Multi-Species Network Inference Improves Gene Regulatory Network Reconstruction for Early Embryonic Development in <i>Drosophila</i> . <i>Journal of Computational Biology</i> , 2015, 22, 253-265.	1.6	15
41	Carbonyl reductase 1 catalyzes $20\beta$ -reduction of glucocorticoids, modulating receptor activation and metabolic complications of obesity. <i>Scientific Reports</i> , 2017, 7, 10633.	3.3	15
42	High-Dimensional Bayesian Network Inference From Systems Genetics Data Using Genetic Node Ordering. <i>Frontiers in Genetics</i> , 2019, 10, 1196.	2.3	14
43	CyClus3D: a Cytoscape plugin for clustering network motifs in integrated networks. <i>Bioinformatics</i> , 2011, 27, 1587-1588.	4.1	13
44	Model-based clustering of multi-tissue gene expression data. <i>Bioinformatics</i> , 2020, 36, 1807-1813.	4.1	13
45	Helicoidal transfer matrix model for inhomogeneous DNA melting. <i>Physical Review E</i> , 2006, 73, 011908.	2.1	12
46	Context-specific transcriptional regulatory network inference from global gene expression maps using double two-way t-tests. <i>Bioinformatics</i> , 2012, 28, 2325-2332.	4.1	12
47	Variable reproducibility in genome-scale public data: A case study using ENCODE ChIP sequencing resource. <i>FEBS Letters</i> , 2015, 589, 3866-3870.	2.8	12
48	Characterizing regulatory path motifs in integrated networks using perturbational data. <i>Genome Biology</i> , 2010, 11, R32.	9.6	10
49	Changes in the gene expression profile during spontaneous migraine attacks. <i>Scientific Reports</i> , 2021, 11, 8294.	3.3	10
50	Goldstone Boson Normal Coordinates. <i>Communications in Mathematical Physics</i> , 2001, 216, 461-490.	2.2	9
51	Detection of Regulator Genes and eQTLs in Gene Networks. , 2016, , 1-23.		9
52	A Graph Feature Auto-Encoder for the prediction of unobserved node features on biological networks. <i>BMC Bioinformatics</i> , 2021, 22, 525.	2.6	8
53	An Algorithm to Automatically Generate the Combinatorial Orbit Counting Equations. <i>PLoS ONE</i> , 2016, 11, e0147078.	2.5	7
54	Central limit theorems for the large-spin asymptotics of quantum spins. <i>Probability Theory and Related Fields</i> , 2004, 130, 493-517.	1.8	6

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55	Learning Differential Module Networks Across Multiple Experimental Conditions. <i>Methods in Molecular Biology</i> , 2019, 1883, 303-321.	0.9	6
56	Reverse-Engineering Transcriptional Modules from Gene Expression Data. <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 36-43.	3.8	5
57	Causal Transcription Regulatory Network Inference Using Enhancer Activity as a Causal Anchor. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3609.	4.1	5
58	A regression tree-based Gibbs sampler to learn the regulation programs in a transcription regulatory module network. , 2010, , .		4
59	An Integrative Approach to Infer Regulation Programs in a Transcription Regulatory Module Network. <i>Journal of Biomedicine and Biotechnology</i> , 2012, 2012, 1-8.	3.0	4
60	Natural coordinate descent algorithm for L1-penalised regression in generalised linear models. <i>Computational Statistics and Data Analysis</i> , 2016, 97, 60-70.	1.2	4
61	Comparison between instrumental variable and mediation-based methods for reconstructing causal gene networks in yeast. <i>Molecular Omics</i> , 2021, 17, 241-251.	2.8	4
62	Implementing quantum gates using the ferromagnetic spin-1XXZ chain with kink boundary conditions. <i>New Journal of Physics</i> , 2010, 12, 025003.	2.9	3
63	Meta-analysis of Liver and Heart Transcriptomic Data for Functional Annotation Transfer in Mammalian Orthologs. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 425-432.	4.1	3
64	Restricted maximum-likelihood method for learning latent variance components in gene expression data with known and unknown confounders. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	3
65	Transport of interface states in the Heisenberg chain. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2008, 41, 492001.	2.1	2
66	Accurate wisdom of the crowd from unsupervised dimension reduction. <i>Royal Society Open Science</i> , 2019, 6, 181806.	2.4	1
67	Whole-Transcriptome Causal Network Inference with Genomic and Transcriptomic Data. <i>Methods in Molecular Biology</i> , 2019, 1883, 95-109.	0.9	1
68	Interferencing in Coupled Bose-Einstein Condensates. <i>Journal of Statistical Physics</i> , 2001, 102, 1383-1405.	1.2	0
69	An integrative approach to infer regulation programs in a transcription regulatory module network. , 2011, , .		0
70	Common variants in the gene encoding corticosteroid binding globulin influence cortisol-responsive gene networks in human adipose tissue. <i>Endocrine Abstracts</i> , 0, , .	0.0	0
71	OR09-04 Common Genetic Variants Associated with SERPINA6 Expression in Liver Influence Cortisol-Responsive Transcriptional Networks in Human Adipose Tissue. <i>Journal of the Endocrine Society</i> , 2020, 4, .	0.2	0