

# 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	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
2	Restricted maximum-likelihood method for learning latent variance components in gene expression data with known and unknown confounders. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	3
3	Changes in the gene expression profile during spontaneous migraine attacks. Scientific Reports, 2021, 11, 8294.	3.3	10
4	Comparison between instrumental variable and mediation-based methods for reconstructing causal gene networks in yeast. Molecular Omics, 2021, 17, 241-251.	2.8	4
5	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. Journal of Human Genetics, 2021, 66, 625-636.	2.3	40
6	A Graph Feature Auto-Encoder for the prediction of unobserved node features on biological networks. BMC Bioinformatics, 2021, 22, 525.	2.6	8
7	Model-based clustering of multi-tissue gene expression data. Bioinformatics, 2020, 36, 1807-1813.	4.1	13
8	OR09-04 Common Genetic Variants Associated with SERPINA6 Expression in Liver Influence Cortisol-Responsive Transcriptional Networks in Human Adipose Tissue. Journal of the Endocrine Society, 2020, 4, .	0.2	0
9	Accurate wisdom of the crowd from unsupervised dimension reduction. Royal Society Open Science, 2019, 6, 181806.	2.4	1
10	Human Y Chromosome Exerts Pleiotropic Effects on Susceptibility to Atherosclerosis. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 2386-2401.	2.4	36
11	Contribution of Gene Regulatory Networks to Heritability of Coronary Artery Disease. Journal of the American College of Cardiology, 2019, 73, 2946-2957.	2.8	45
12	Application of long read sequencing to determine expressed antigen diversity in Trypanosoma brucei infections. PLoS Neglected Tropical Diseases, 2019, 13, e0007262.	3.0	25
13	High-Dimensional Bayesian Network Inference From Systems Genetics Data Using Genetic Node Ordering. Frontiers in Genetics, 2019, 10, 1196.	2.3	14
14	Whole-Transcriptome Causal Network Inference with Genomic and Transcriptomic Data. Methods in Molecular Biology, 2019, 1883, 95-109.	0.9	1
15	Learning Differential Module Networks Across Multiple Experimental Conditions. Methods in Molecular Biology, 2019, 1883, 303-321.	0.9	6
16	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. Scientific Reports, 2018, 8, 3434.	3.3	43
17	Causal Transcription Regulatory Network Inference Using Enhancer Activity as a Causal Anchor. International Journal of Molecular Sciences, 2018, 19, 3609.	4.1	5
18	Smoking is Associated to DNA Methylation in Atherosclerotic Carotid Lesions. Circulation Genomic and Precision Medicine, 2018, 11, e002030.	3.6	23

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19	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
20	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
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	An Algorithm to Automatically Generate the Combinatorial Orbit Counting Equations. <i>PLoS ONE</i> , 2016, 11, e0147078.	2.5	7
23	Human Validation of Genes Associated With a Murine Atherosclerotic Phenotype. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2016, 36, 1240-1246.	2.4	44
24	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
25	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. <i>Science</i> , 2016, 353, 827-830.	12.6	241
26	Detection of Regulator Genes and eQTLs in Gene Networks. , 2016, , 1-23.		9
27	Functional transcription factor target discovery via compendia of binding and expression profiles. <i>Scientific Reports</i> , 2016, 6, 20649.	3.3	16
28	Cross-Tissue Regulatory Gene Networks in Coronary Artery Disease. <i>Cell Systems</i> , 2016, 2, 196-208.	6.2	120
29	Microglial brain region $\hat{a}$ dependent diversity and selective regional sensitivities to aging. <i>Nature Neuroscience</i> , 2016, 19, 504-516.	14.8	919
30	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
31	Variable reproducibility in genome $\hat{a}$ scale public data: A case study using ENCODE CHIP sequencing resource. <i>FEBS Letters</i> , 2015, 589, 3866-3870.	2.8	12
32	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	17.5	88
33	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
34	SNAIL1 combines competitive displacement of ASCL2 and $\hat{A}$ epigenetic mechanisms to rapidly silence the EPHB3 tumor suppressor in colorectal cancer. <i>Molecular Oncology</i> , 2015, 9, 335-354.	4.6	34
35	Integrative Multi-omics Module Network Inference with Lemon-Tree. <i>PLoS Computational Biology</i> , 2015, 11, e1003983.	3.2	86
36	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

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37	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
38	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
39	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
40	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
41	Plasma Cholesterol-Induced Lesion Networks Activated before Regression of Early, Mature, and Advanced Atherosclerosis. <i>PLoS Genetics</i> , 2014, 10, e1004201.	3.5	64
42	kruX: matrix-based non-parametric eQTL discovery. <i>BMC Bioinformatics</i> , 2014, 15, 11.	2.6	39
43	Lim Domain Binding 2. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014, 34, 2068-2077.	2.4	17
44	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
45	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
46	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
47	MotifSuite: workflow for probabilistic motif detection and assessment. <i>Bioinformatics</i> , 2012, 28, 1931-1932.	4.1	23
48	Alignment and integration of complex networks by hypergraph-based spectral clustering. <i>Physical Review E</i> , 2012, 86, 056111.	2.1	49
49	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
50	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
51	Enrichment and aggregation of topological motifs are independent organizational principles of integrated interaction networks. <i>Molecular BioSystems</i> , 2011, 7, 2769.	2.9	15
52	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
53	CyClus3D: a Cytoscape plugin for clustering network motifs in integrated networks. <i>Bioinformatics</i> , 2011, 27, 1587-1588.	4.1	13
54	An integrative approach to infer regulation programs in a transcription regulatory module network. , 2011, , .		0

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55	Module Network Inference from a Cancer Gene Expression Data Set Identifies MicroRNA Regulated Modules. <i>PLoS ONE</i> , 2010, 5, e10162.	2.5	46
56	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
57	Implementing quantum gates using the ferromagnetic spin-JXXZ chain with kink boundary conditions. <i>New Journal of Physics</i> , 2010, 12, 025003.	2.9	3
58	Characterizing regulatory path motifs in integrated networks using perturbational data. <i>Genome Biology</i> , 2010, 11, R32.	9.6	10
59	A regression tree-based Gibbs sampler to learn the regulation programs in a transcription regulatory module network. , 2010, , .		4
60	Module networks revisited: computational assessment and prioritization of model predictions. <i>Bioinformatics</i> , 2009, 25, 490-496.	4.1	82
61	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
62	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
63	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
64	Analysis of a Gibbs sampler method for model-based clustering of gene expression data. <i>Bioinformatics</i> , 2008, 24, 176-183.	4.1	59
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	Validating module network learning algorithms using simulated data. <i>BMC Bioinformatics</i> , 2007, 8, S5.	2.6	34
67	Helicoidal transfer matrix model for inhomogeneous DNA melting. <i>Physical Review E</i> , 2006, 73, 011908.	2.1	12
68	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
69	Goldstone Boson Normal Coordinates. <i>Communications in Mathematical Physics</i> , 2001, 216, 461-490.	2.2	9
70	Interferencing in Coupled Bose-Einstein Condensates. <i>Journal of Statistical Physics</i> , 2001, 102, 1383-1405.	1.2	0
71	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