

Mika Gustafsson

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

1,268
citations

471509

17
h-index

395702

33
g-index

45
all docs

45
docs citations

45
times ranked

2324
citing authors

#	ARTICLE	IF	CITATIONS
1	CD4 ⁺ T-cell DNA methylation changes during pregnancy significantly correlate with disease-associated methylation changes in autoimmune diseases. <i>Epigenetics</i> , 2022, 17, 1040-1055.	2.7	4
2	MODalyse—a novel software for inference of disease module hub regulators identified a putative multiple sclerosis regulator supported by independent eQTL data. <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	1
3	Progesterone Inhibits the Establishment of Activation-Associated Chromatin During TH1 Differentiation. <i>Frontiers in Immunology</i> , 2022, 13, 835625.	4.8	7
4	Deep neural network prediction of genome-wide transcriptome signatures “beyond the Black-box. <i>Npj Systems Biology and Applications</i> , 2022, 8, 9.	3.0	10
5	Multi-omics protein-coding units as massively parallel Bayesian networks: Empirical validation of causality structure. <i>IScience</i> , 2022, 25, 104048.	4.1	5
6	Hybrid modelling for stroke care: Review and suggestions of new approaches for risk assessment and simulation of scenarios. <i>NeuroImage: Clinical</i> , 2021, 31, 102694.	2.7	10
7	ComHub: Community predictions of hubs in gene regulatory networks. <i>BMC Bioinformatics</i> , 2021, 22, 58.	2.6	9
8	Progesterone Dampens Immune Responses in Vitro Activated CD4 ⁺ T Cells and Affects Genes Associated With Autoimmune Diseases That Improve During Pregnancy. <i>Frontiers in Immunology</i> , 2021, 12, 672168.	4.8	22
9	Combined prenatal <i>Lactobacillus reuteri</i> and ω -3 supplementation synergistically modulates DNA methylation in neonatal T helper cells. <i>Clinical Epigenetics</i> , 2021, 13, 135.	4.1	9
10	Differential effects of estradiol and progesterone on human T cell activation <i>in vitro</i> . <i>European Journal of Immunology</i> , 2021, 51, 2430-2440.	2.9	12
11	TET2 as a tumor suppressor and therapeutic target in T-cell acute lymphoblastic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	29
12	Using high-throughput multi-omics data to investigate structural balance in elementary gene regulatory network motifs. <i>Bioinformatics</i> , 2021, 38, 173-178.	4.1	5
13	A validated generally applicable approach using the systematic assessment of disease modules by GWAS reveals a multi-omic module strongly associated with risk factors in multiple sclerosis. <i>BMC Genomics</i> , 2021, 22, 631.	2.8	5
14	Digital twins to personalize medicine. <i>Genome Medicine</i> , 2020, 12, 4.	8.2	158
15	LiPLike: towards gene regulatory network predictions of high certainty. <i>Bioinformatics</i> , 2020, 36, 2522-2529.	4.1	16
16	Whole-genome sequencing and gene network modules predict gemcitabine/carboplatin-induced myelosuppression in non-small cell lung cancer patients. <i>Npj Systems Biology and Applications</i> , 2020, 6, 25.	3.0	9
17	Pre- and postnatal <i>Lactobacillus reuteri</i> treatment alters DNA methylation of infant T helper cells. <i>Pediatric Allergy and Immunology</i> , 2020, 31, 544-553.	2.6	17
18	Deriving disease modules from the compressed transcriptional space embedded in a deep autoencoder. <i>Nature Communications</i> , 2020, 11, 856.	12.8	37

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19	MODifier: an Ensemble R Package for Inference of Disease Modules from Transcriptomics Networks. <i>Bioinformatics</i> , 2020, 36, 3918-3919.	4.1	14
20	Therapeutic efficacy of dimethyl fumarate in relapsing-remitting multiple sclerosis associates with ROS pathway in monocytes. <i>Nature Communications</i> , 2019, 10, 3081.	12.8	97
21	A validated single-cell-based strategy to identify diagnostic and therapeutic targets in complex diseases. <i>Genome Medicine</i> , 2019, 11, 47.	8.2	68
22	Identification of DNA methylation patterns predisposing for an efficient response to BCG vaccination in healthy BCG-naïve subjects. <i>Epigenetics</i> , 2019, 14, 589-601.	2.7	35
23	ModuleDiscoverer: Identification of regulatory modules in protein-protein interaction networks. <i>Scientific Reports</i> , 2018, 8, 433.	3.3	57
24	Cross-talks via mTORC2 can explain enhanced activation in response to insulin in diabetic patients. <i>Bioscience Reports</i> , 2017, 37, .	2.4	10
25	LASSIMâ€”A network inference toolbox for genome-wide mechanistic modeling. <i>PLoS Computational Biology</i> , 2017, 13, e1005608.	3.2	6
26	Potential Involvement of Type I Interferon Signaling in Immunotherapy in Seasonal Allergic Rhinitis. <i>Journal of Immunology Research</i> , 2016, 2016, 1-6.	2.2	4
27	5-Hydroxymethylcytosine Remodeling Precedes Lineage Specification during Differentiation of Human CD4+ T Cells. <i>Cell Reports</i> , 2016, 16, 559-570.	6.4	56
28	Cancer network activity associated with therapeutic response and synergism. <i>Genome Medicine</i> , 2016, 8, 88.	8.2	7
29	Dynamic Response Genes in CD4+ T Cells Reveal a Network of Interactive Proteins that Classifies Disease Activity in Multiple Sclerosis. <i>Cell Reports</i> , 2016, 16, 2928-2939.	6.4	38
30	A validated gene regulatory network and GWAS identifies early regulators of T cellâ€”associated diseases. <i>Science Translational Medicine</i> , 2015, 7, 313ra178.	12.4	66
31	Modules, networks and systems medicine for understanding disease and aiding diagnosis. <i>Genome Medicine</i> , 2014, 6, 82.	8.2	169
32	DNA Methylation Changes Separate Allergic Patients from Healthy Controls and May Reflect Altered CD4+ T-Cell Population Structure. <i>PLoS Genetics</i> , 2014, 10, e1004059.	3.5	70
33	Integrated genomic and prospective clinical studies show the importance of modular pleiotropy for disease susceptibility, diagnosis and treatment. <i>Genome Medicine</i> , 2014, 6, 17.	8.2	27
34	A Generally Applicable Translational Strategy Identifies S100A4 as a Candidate Gene in Allergy. <i>Science Translational Medicine</i> , 2014, 6, 218ra4.	12.4	54
35	Targeted omics and systems medicine: personalising care. <i>Lancet Respiratory Medicine</i> , 2014, 2, 785-787.	10.7	20
36	Reverse Engineering of Gene Networks with LASSO and Nonlinear Basis Functions. <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 265-275.	3.8	27

#	ARTICLE	IF	CITATIONS
37	Constructing and Analyzing a Large-Scale Gene-to-Gene Regulatory Network-Lasso-Constrained Inference and Biological Validation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 254-261.	3.0	74