Mika Gustafsson

List of Publications by Year in descending order

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	Modules, networks and systems medicine for understanding disease and aiding diagnosis. Genome Medicine, 2014, 6, 82.	8.2	169
2	Digital twins to personalize medicine. Genome Medicine, 2020, 12, 4.	8.2	158
3	Therapeutic efficacy of dimethyl fumarate in relapsing-remitting multiple sclerosis associates with ROS pathway in monocytes. Nature Communications, 2019, 10, 3081.	12.8	97
4	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
5	DNA Methylation Changes Separate Allergic Patients from Healthy Controls and May Reflect Altered CD4+ T-Cell Population Structure. PLoS Genetics, 2014, 10, e1004059.	3.5	70
6	A validated single-cell-based strategy to identify diagnostic and therapeutic targets in complex diseases. Genome Medicine, 2019, 11, 47.	8.2	68
7	A validated gene regulatory network and GWAS identifies early regulators of T cell–associated diseases. Science Translational Medicine, 2015, 7, 313ra178.	12.4	66
8	ModuleDiscoverer: Identification of regulatory modules in protein-protein interaction networks. Scientific Reports, 2018, 8, 433.	3.3	57
9	5-Hydroxymethylcytosine Remodeling Precedes Lineage Specification during Differentiation of Human CD4+ T Cells. Cell Reports, 2016, 16, 559-570.	6.4	56
10	A Generally Applicable Translational Strategy Identifies S100A4 as a Candidate Gene in Allergy. Science Translational Medicine, 2014, 6, 218ra4.	12.4	54
11	Dynamic Response Genes in CD4+ T Cells Reveal a Network of Interactive Proteins that Classifies Disease Activity in Multiple Sclerosis. Cell Reports, 2016, 16, 2928-2939.	6.4	38
12	Deriving disease modules from the compressed transcriptional space embedded in a deep autoencoder. Nature Communications, 2020, 11, 856.	12.8	37
13	Identification of DNA methylation patterns predisposing for an efficient response to BCG vaccination in healthy BCG-naïve subjects. Epigenetics, 2019, 14, 589-601.	2.7	35
14	TET2 as a tumor suppressor and therapeutic target in T-cell acute lymphoblastic leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	29
15	Reverse Engineering of Gene Networks with LASSO and Nonlinear Basis Functions. Annals of the New York Academy of Sciences, 2009, 1158, 265-275.	3.8	27
16	Integrated genomic and prospective clinical studies show the importance of modular pleiotropy for disease susceptibility, diagnosis and treatment. Genome Medicine, 2014, 6, 17.	8.2	27
17	Progesterone Dampens Immune ResponsesÂinÂIn VitroÂActivated CD4+ÂT CellsÂand Affects Genes Associated With Autoimmune DiseasesÂThat Improve During Pregnancy. Frontiers in Immunology, 2021, 12, 672168.	4.8	22
18	Targeted omics and systems medicine: personalising care. Lancet Respiratory Medicine,the, 2014, 2, 785-787.	10.7	20

#	Article	IF	Citations
19	Preâ€•and postnatal *Lactobacillus reuteri* treatment alters DNA methylation of infant T helper cells. Pediatric Allergy and Immunology, 2020, 31, 544-553.	2.6	17
20	LiPLike: towards gene regulatory network predictions of high certainty. Bioinformatics, 2020, 36, 2522-2529.	4.1	16
21	MODifieR: an Ensemble R Package for Inference of Disease Modules from Transcriptomics Networks. Bioinformatics, 2020, 36, 3918-3919.	4.1	14
22	Differential effects of estradiol and progesterone on human T cell activation *in vitro*. European Journal of Immunology, 2021, 51, 2430-2440.	2.9	12
23	Cross-talks via mTORC2 can explain enhanced activation in response to insulin in diabetic patients. Bioscience Reports, 2017, 37, .	2.4	10
24	Hybrid modelling for stroke care: Review and suggestions of new approaches for risk assessment and simulation of scenarios. NeuroImage: Clinical, 2021, 31, 102694.	2.7	10
25	Deep neural network prediction of genome-wide transcriptome signatures â€" beyond the Black-box. Npj Systems Biology and Applications, 2022, 8, 9.	3.0	10
26	Whole-genome sequencing and gene network modules predict gemcitabine/carboplatin-induced myelosuppression in non-small cell lung cancer patients. Npj Systems Biology and Applications, 2020, 6, 25.	3.0	9
27	ComHub: Community predictions of hubs in gene regulatory networks. BMC Bioinformatics, 2021, 22, 58.	2.6	9
28	Combined prenatal Lactobacillus reuteri and Ï‰-3 supplementation synergistically modulates DNA methylation in neonatal T helper cells. Clinical Epigenetics, 2021, 13, 135.	4.1	9
29	Cancer network activity associated with therapeutic response and synergism. Genome Medicine, 2016, 8, 88.	8.2	7
30	Progesterone Inhibits the Establishment of Activation-Associated Chromatin During TH1 Differentiation. Frontiers in Immunology, 2022, 13, 835625.	4.8	7
31	LASSIMâ€"A network inference toolbox for genome-wide mechanistic modeling. PLoS Computational Biology, 2017, 13, e1005608.	3.2	6
32	Using high-throughput multi-omics data to investigate structural balance in elementary gene regulatory network motifs. Bioinformatics, 2021, 38, 173-178.	4.1	5
33	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. BMC Genomics, 2021, 22, 631.	2.8	5
34	Multi-omics protein-coding units as massively parallel Bayesian networks: Empirical validation of causality structure. IScience, 2022, 25, 104048.	4.1	5
35	Potential Involvement of Type I Interferon Signaling in Immunotherapy in Seasonal Allergic Rhinitis. Journal of Immunology Research, 2016, 2016, 1-6.	2.2	4
36	CD4$^+$ T-cell DNA methylation changes during pregnancy significantly correlate with disease-associated methylation changes in autoimmune diseases. Epigenetics, 2022, 17, 1040-1055.	2.7	4

#	Article	IF	Citations
37	MODalyseR—a novel software for inference of disease module hub regulators identified a putative multiple sclerosis regulator supported by independent eQTL data. Bioinformatics Advances, 2022, 2, .	2.4	1