Mikael Benson

List of Publications by Year in descending order

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361045 329751 1,636 36 20 37 citations h-index g-index papers 41 41 41 3589 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	CD4 ⁺ T-cell DNA methylation changes during pregnancy significantly correlate with disease-associated methylation changes in autoimmune diseases. Epigenetics, 2022, 17, 1040-1055.	1.3	4
2	A dynamic single cell-based framework for digital twins to prioritize disease genes and drug targets. Genome Medicine, 2022, 14, 48.	3.6	16
3	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, .	3.3	29
4	Cell type identification for single cell RNA data by bulk data reference projection. , 2021, , .		0
5	Bulk and single cell transcriptomic data indicate that a dichotomy between inflammatory pathways in peripheral blood and arthritic joints complicates biomarker discovery. Cytokine, 2020, 127, 154960.	1.4	22
6	Digital twins to personalize medicine. Genome Medicine, 2020, 12, 4.	3.6	158
7	Meta-Analysis of Expression Profiling Data Indicates Need for Combinatorial Biomarkers in Pediatric Ulcerative Colitis. Journal of Immunology Research, 2020, 2020, 1-11.	0.9	10
8	A validated single-cell-based strategy to identify diagnostic and therapeutic targets in complex diseases. Genome Medicine, 2019, 11, 47.	3.6	68
9	An algorithm-based meta-analysis of genome- and proteome-wide data identifies a combination of potential plasma biomarkers for colorectal cancer. Scientific Reports, 2019, 9, 15575.	1.6	10
10	Translating genomic medicine to the clinic: challenges and opportunities. Genome Medicine, 2019, 11, 9.	3.6	18
11	Estimating heritability and genetic correlations from large health datasets in the absence of genetic data. Nature Communications, 2019, 10, 5508.	5.8	17
12	A reassessment of DNA-immunoprecipitation-based genomic profiling. Nature Methods, 2018, 15, 499-504.	9.0	92
13	Single-cell analyses to tailor treatments. Science Translational Medicine, 2017, 9, .	5.8	116
14	GAB2 regulates type 2 T helper cell differentiation in humans. Cytokine, 2017, 96, 234-237.	1.4	3
15	Roles of piRNAs in microcystin-leucine-arginine (MC-LR) induced reproductive toxicity in testis on male offspring. Food and Chemical Toxicology, 2017, 105, 177-185.	1.8	11
16	LASSIM—A network inference toolbox for genome-wide mechanistic modeling. PLoS Computational Biology, 2017, 13, e1005608.	1.5	6
17	Potential Involvement of Type I Interferon Signaling in Immunotherapy in Seasonal Allergic Rhinitis. Journal of Immunology Research, 2016, 2016, 1-6.	0.9	4
18	5-Hydroxymethylcytosine Remodeling Precedes Lineage Specification during Differentiation of Human CD4+ T Cells. Cell Reports, 2016, 16, 559-570.	2.9	56

#	Article	IF	Citations
19	Cancer network activity associated with therapeutic response and synergism. Genome Medicine, 2016, 8, 88.	3.6	7
20	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.	2.9	38
21	Making sense of big data in health research: Towards an EU action plan. Genome Medicine, 2016, 8, 71.	3.6	190
22	Rapid reprogramming of epigenetic and transcriptional profiles in mammalian culture systems. Genome Biology, 2015, 16, 11.	3.8	137
23	Roles of miRNAs in microcystin-LR-induced Sertoli cell toxicity. Toxicology and Applied Pharmacology, 2015, 287, 1-8.	1.3	24
24	A validated gene regulatory network and GWAS identifies early regulators of T cell–associated diseases. Science Translational Medicine, 2015, 7, 313ra178.	5.8	66
25	Modules, networks and systems medicine for understanding disease and aiding diagnosis. Genome Medicine, 2014, 6, 82.	3.6	169
26	DNA Methylation Changes Separate Allergic Patients from Healthy Controls and May Reflect Altered CD4+ T-Cell Population Structure. PLoS Genetics, 2014, 10, e1004059.	1.5	70
27	Integrated genomic and prospective clinical studies show the importance of modular pleiotropy for disease susceptibility, diagnosis and treatment. Genome Medicine, 2014, 6, 17.	3.6	27
28	A Generally Applicable Translational Strategy Identifies S100A4 as a Candidate Gene in Allergy. Science Translational Medicine, 2014, 6, 218ra4.	5.8	54
29	Targeted omics and systems medicine: personalising care. Lancet Respiratory Medicine, the, 2014, 2, 785-787.	5.2	20
30	Differential Shannon entropy and differential coefficient of variation: alternatives and augmentations to differential expression in the search for disease-related genes. International Journal of Computational Biology and Drug Design, 2014, 7, 183.	0.3	12
31	Altered Levels of the Soluble IL-1, IL-4 and TNF Receptors, as well as the IL-1 Receptor Antagonist, in Intermittent Allergic Rhinitis. International Archives of Allergy and Immunology, 2004, 134, 227-232.	0.9	18
32	DNA microarray analysis of chromosomal susceptibility regions to identify candidate genes for allergic disease: A pilot study. Acta Oto-Laryngologica, 2004, 124, 813-819.	0.3	4
33	Gene profiling reveals increased expression of uteroglobin and other anti-inflammatory genes in glucocorticoid-treated nasal polyps. Journal of Allergy and Clinical Immunology, 2004, 113, 1137-1143.	1.5	60
34	Epithelial Cells in Nasal Fluids from Patients with Allergic Rhinitis: How do they Relate to Epidermal Growth Factor, Eosinophils and Eosinophil Cationic Protein?. Acta Oto-Laryngologica, 2002, 122, 202-205.	0.3	6
35	DNA MICROARRAY ANALYSIS OF TRANSFORMING GROWTH FACTOR-Î ² AND RELATED TRANSCRIPTS IN NASAL BIOPSIES FROM PATIENTS WITH ALLERGIC RHINITIS. Cytokine, 2002, 18, 20-25.	1.4	30
36	INCREASED EXPRESSION OF VASCULAR ENDOTHELIAL GROWTH FACTOR-A IN SEASONAL ALLERGIC RHINITIS. Cytokine, 2002, 20, 268-273.	1.4	29