

Kamil Slowikowski

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

9,635
citations

257101

24
h-index

454577

30
g-index

44
all docs

44
docs citations

44
times ranked

19104
citing authors

#	ARTICLE	IF	CITATIONS
1	Urine Proteomics and Renal ^{Single-Cell} Transcriptomics Implicate Interleukin-16 in Lupus Nephritis. <i>Arthritis and Rheumatology</i> , 2022, 74, 829-839.	2.9	38
2	Single-cell meta-analysis of SARS-CoV-2 entry genes across tissues and demographics. <i>Nature Medicine</i> , 2021, 27, 546-559.	15.2	261
3	Single-cell transcriptomics in cancer: computational challenges and opportunities. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1452-1465.	3.2	108
4	A positively selected FBN1 missense variant reduces height in Peruvian individuals. <i>Nature</i> , 2020, 582, 234-239.	13.7	39
5	Using genetics to prioritize diagnoses for rheumatology outpatients with inflammatory arthritis. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	31
6	Synoviocyte-targeted therapy synergizes with TNF inhibition in arthritis reversal. <i>Science Advances</i> , 2020, 6, eaba4353.	4.7	43
7	CLUX1 and $\text{NF-}\kappa\text{B}$ mediate the synergistic inflammatory response to TNF and IL-17A in stromal fibroblasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5532-5541.	3.3	44
8	The immune cell landscape in kidneys of patients with lupus nephritis. <i>Nature Immunology</i> , 2019, 20, 902-914.	7.0	501
9	Tubular cell and keratinocyte single-cell transcriptomics applied to lupus nephritis reveal type I IFN and fibrosis relevant pathways. <i>Nature Immunology</i> , 2019, 20, 915-927.	7.0	275
10	Defining inflammatory cell states in rheumatoid arthritis joint synovial tissues by integrating single-cell transcriptomics and mass cytometry. <i>Nature Immunology</i> , 2019, 20, 928-942.	7.0	760
11	Lymphocyte innateness defined by transcriptional states reflects a balance between proliferation and effector functions. <i>Nature Communications</i> , 2019, 10, 687.	5.8	136
12	Fast, sensitive and accurate integration of single-cell data with Harmony. <i>Nature Methods</i> , 2019, 16, 1289-1296.	9.0	3,494
13	Functionally distinct disease-associated fibroblast subsets in rheumatoid arthritis. <i>Nature Communications</i> , 2018, 9, 789.	5.8	368
14	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. <i>Nature Genetics</i> , 2018, 50, 621-629.	9.4	807
15	Functional genomics of stromal cells in chronic inflammatory diseases. <i>Current Opinion in Rheumatology</i> , 2018, 30, 65-71.	2.0	10
16	Mixed-effects association of single cells identifies an expanded effector CD4 ⁺ T cell subset in rheumatoid arthritis. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	119
17	Discovering in vivo cytokine-eQTL interactions from a lupus clinical trial. <i>Genome Biology</i> , 2018, 19, 168.	3.8	36
18	Methods for high-dimensional analysis of cells dissociated from cryopreserved synovial tissue. <i>Arthritis Research and Therapy</i> , 2018, 20, 139.	1.6	93

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19	Pathologically expanded peripheral T helper cell subset drives B cells in rheumatoid arthritis. <i>Nature</i> , 2017, 542, 110-114.	13.7	767
20	Refining the role of de novo protein-truncating variants in neurodevelopmental disorders by using population reference samples. <i>Nature Genetics</i> , 2017, 49, 504-510.	9.4	298
21	A method to decipher pleiotropy by detecting underlying heterogeneity driven by hidden subgroups applied to autoimmune and neuropsychiatric diseases. <i>Nature Genetics</i> , 2016, 48, 803-810.	9.4	62
22	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
23	Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci. <i>American Journal of Human Genetics</i> , 2015, 97, 139-152.	2.6	122
24	Regulation of Gene Expression in Autoimmune Disease Loci and the Genetic Basis of Proliferation in CD4+ Effector Memory T Cells. <i>PLoS Genetics</i> , 2014, 10, e1004404.	1.5	46
25	SNPsea: an algorithm to identify cell types, tissues and pathways affected by risk loci. <i>Bioinformatics</i> , 2014, 30, 2496-2497.	1.8	60
26	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. <i>Science</i> , 2014, 343, 1246980.	6.0	391
27	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014, 46, 826-836.	9.4	281
28	Computational and experimental analyses of retrotransposon-associated minisatellite DNAs in the soybean genome. <i>BMC Bioinformatics</i> , 2012, 13, S13.	1.2	4