

# Nikolaos Barkas

## List of Publications by Year in descending order

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Version: 2024-02-01

25  
papers

2,557  
citations

623734

14  
h-index

677142

22  
g-index

30  
all docs

30  
docs citations

30  
times ranked

4908  
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of 6.4 million SARS-CoV-2 genomes identifies mutations associated with fitness. <i>Science</i> , 2022, 376, 1327-1332.	12.6	172
2	Spliceosome mutations are common in persons with myeloproliferative neoplasm-associated myelofibrosis with RBC-transfusion-dependence and correlate with response to pomalidomide. <i>Leukemia</i> , 2021, 35, 1197-1202.	7.2	9
3	Single cell transcriptomics of primate sensory neurons identifies cell types associated with chronic pain. <i>Nature Communications</i> , 2021, 12, 1510.	12.8	121
4	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , 2021, 595, 107-113.	27.8	537
5	Imprinted Gene Expression and Function of the Dopa Decarboxylase Gene in the Developing Heart. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 676543.	3.7	9
6	Human prostate cancer bone metastases have an actionable immunosuppressive microenvironment. <i>Cancer Cell</i> , 2021, 39, 1464-1478.e8.	16.8	98
7	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	27.8	316
8	Distinct evolutionary paths in chronic lymphocytic leukemia during resistance to the graft-versus-leukemia effect. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	17
9	Transcription of intragenic CpG islands influences spatiotemporal host gene pre-mRNA processing. <i>Nucleic Acids Research</i> , 2020, 48, 8349-8359.	14.5	10
10	Joint analysis of heterogeneous single-cell RNA-seq dataset collections. <i>Nature Methods</i> , 2019, 16, 695-698.	19.0	219
11	Myocardial differentiation is dependent upon endocardial signaling during early cardiogenesis <i>in vitro</i> . <i>Development (Cambridge)</i> , 2019, 146, .	2.5	9
12	Unravelling Intratumoral Heterogeneity through High-Sensitivity Single-Cell Mutational Analysis and Parallel RNA Sequencing. <i>Molecular Cell</i> , 2019, 73, 1292-1305.e8.	9.7	218
13	Thymus Regeneration Is Dependent on Distinct Mesenchymal Stromal Cell Populations. <i>Blood</i> , 2019, 134, 586-586.	1.4	1
14	Distinct Evolutionary Patterns in Chronic Lymphocytic Leukemia (CLL) during Resistance to Graft-Versus-Leukemia (GvL). <i>Blood</i> , 2019, 134, 516-516.	1.4	0
15	Ezh2 and Runx1 Mutations Collaborate to Initiate Lympho-Myeloid Leukemia in Early Thymic Progenitors. <i>Cancer Cell</i> , 2018, 33, 274-291.e8.	16.8	58
16	Perivascular Niche Cells Sense Thrombocytopenia and Activate Platelet-Biased Hscs in an IL-1 Dependent Manner. <i>Experimental Hematology</i> , 2018, 64, S44.	0.4	2
17	Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data. <i>Genome Research</i> , 2018, 28, 1217-1227.	5.5	172
18	Clonal and Single Cell Dynamics of Resistance to Graft-Versus-Leukemia (GvL) in Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2018, 132, 820-820.	1.4	0

#	ARTICLE	IF	CITATIONS
19	Single-cell transcriptomics uncovers distinct molecular signatures of stem cells in chronic myeloid leukemia. <i>Nature Medicine</i> , 2017, 23, 692-702.	30.7	336
20	Niche-mediated depletion of the normal hematopoietic stem cell reservoir by Flt3-ITD-induced myeloproliferation. <i>Journal of Experimental Medicine</i> , 2017, 214, 2005-2021.	8.5	43
21	Unravelling Cell Cycle and Ontogeny Transcriptional Heterogeneity in Hematopoietic Stem Cells through Integrated Single Cell RNA-Seq. <i>Blood</i> , 2017, 130, 769-769.	1.4	1
22	Single-cell profiling of human megakaryocyte-erythroid progenitors identifies distinct megakaryocyte and erythroid differentiation pathways. <i>Genome Biology</i> , 2016, 17, 83.	8.8	124
23	Single Cell Whole Transcriptome Analysis Reveals Distinct Molecular Signatures of Therapy-Resistant Chronic Myeloid Leukemia Stem Cells. <i>Blood</i> , 2015, 126, 13-13.	1.4	2
24	Ezh2 and Runx1 Mutations Targeted to Early Lymphoid Progenitors Collaborate to Promote Early Thymic Progenitor Leukemia. <i>Blood</i> , 2015, 126, 846-846.	1.4	0
25	Genome-wide and parental allele-specific analysis of CTCF and cohesin DNA binding in mouse brain reveals a tissue-specific binding pattern and an association with imprinted differentially methylated regions. <i>Genome Research</i> , 2013, 23, 1624-1635.	5.5	55