

# Kedar Nath Natarajan

## List of Publications by Year in descending order

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Version: 2024-02-01

21  
papers

5,351  
citations

471509

17  
h-index

642732

23  
g-index

34  
all docs

34  
docs citations

34  
times ranked

9921  
citing authors

#	ARTICLE	IF	CITATIONS
1	TENET: gene network reconstruction using transfer entropy reveals key regulatory factors from single cell transcriptomic data. <i>Nucleic Acids Research</i> , 2021, 49, e1-e1.	14.5	26
2	Transcriptional Dynamics of Hepatic Sinusoidal-Associated Cells After Liver Injury. <i>Hepatology</i> , 2020, 72, 2119-2133.	7.3	62
3	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. <i>Nature Communications</i> , 2020, 11, 810.	12.8	235
4	Single-cell transcriptomics identifies CD44 as a marker and regulator of endothelial to haematopoietic transition. <i>Nature Communications</i> , 2020, 11, 586.	12.8	69
5	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
6	Predicting gene regulatory networks from cell atlases. <i>Life Science Alliance</i> , 2020, 3, e202000658.	2.8	7
7	The Malaria Cell Atlas: Single parasite transcriptomes across the complete <i>Plasmodium</i> life cycle. <i>Science</i> , 2019, 365, .	12.6	198
8	Single-Cell Tagged Reverse Transcription (STRT-Seq). <i>Methods in Molecular Biology</i> , 2019, 1979, 133-153.	0.9	21
9	Comparative analysis of sequencing technologies for single-cell transcriptomics. <i>Genome Biology</i> , 2019, 20, 70.	8.8	82
10	A rapid and robust method for single cell chromatin accessibility profiling. <i>Nature Communications</i> , 2018, 9, 5345.	12.8	188
11	Distinctive features of lincRNA gene expression suggest widespread RNA-independent functions. <i>Life Science Alliance</i> , 2018, 1, e201800124.	2.8	32
12	Power analysis of single-cell RNA-sequencing experiments. <i>Nature Methods</i> , 2017, 14, 381-387.	19.0	496
13	SC3: consensus clustering of single-cell RNA-seq data. <i>Nature Methods</i> , 2017, 14, 483-486.	19.0	1,203
14	Flipping between Polycomb repressed and active transcriptional states introduces noise in gene expression. <i>Nature Communications</i> , 2017, 8, 36.	12.8	62
15	Single cell transcriptomics of pluripotent stem cells: reprogramming and differentiation. <i>Current Opinion in Genetics and Development</i> , 2017, 46, 66-76.	3.3	17
16	The systems biology format converter. <i>BMC Bioinformatics</i> , 2016, 17, 154.	2.6	30
17	Single-cell analysis of CD4+ T-cell differentiation reveals three major cell states and progressive acceleration of proliferation. <i>Genome Biology</i> , 2016, 17, 103.	8.8	65
18	BioModels: ten-year anniversary. <i>Nucleic Acids Research</i> , 2015, 43, D542-D548.	14.5	334

#	ARTICLE	IF	CITATIONS
19	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. <i>Nature Biotechnology</i> , 2015, 33, 155-160.	17.5	1,068
20	Computational assignment of cell-cycle stage from single-cell transcriptome data. <i>Methods</i> , 2015, 85, 54-61.	3.8	381
21	Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. <i>Cell Stem Cell</i> , 2015, 17, 471-485.	11.1	505