

# James Zou

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11546287/publications.pdf>

Version: 2024-02-01

30  
papers

13,656  
citations

331670

21  
h-index

526287

27  
g-index

31  
all docs

31  
docs citations

31  
times ranked

34706  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular hallmarks of heterochronic parabiosis at single-cell resolution. Nature, 2022, 603, 309-314.	27.8	51
2	Shifting machine learning for healthcare from development to deployment and from models to data. Nature Biomedical Engineering, 2022, 6, 1330-1345.	22.5	69
3	National Cancer Institute Workshop on Artificial Intelligence in Radiation Oncology: Training the Next Generation. Practical Radiation Oncology, 2021, 11, 74-83.	2.1	16
4	Deep learning for biomedical videos: perspective and recommendations. , 2021, , 37-48.		1
5	Mouse aging cell atlas analysis reveals global and cell type-specific aging signatures. ELife, 2021, 10, .	6.0	64
6	Ensuring that biomedical AI benefits diverse populations. EBioMedicine, 2021, 67, 103358.	6.1	39
7	Who's Responsible? Jointly Quantifying the Contribution of the Learning Algorithm and Data. , 2021, , .		4
8	Comprehensive analysis of 2.4 million patent-to-research citations maps the biomedical innovation and translation landscape. Nature Biotechnology, 2021, 39, 678-683.	17.5	10
9	Quantification of Gender Bias and Sentiment Toward Political Leaders Over 20 Years of Kenyan News Using Natural Language Processing. Frontiers in Psychology, 2021, 12, 712646.	2.1	1
10	How Much Does Your Data Exploration Overfit? Controlling Bias via Information Usage. IEEE Transactions on Information Theory, 2020, 66, 302-323.	2.4	45
11	A single-cell transcriptomic atlas characterizes ageing tissues in the mouse. Nature, 2020, 583, 590-595.	27.8	683
12	Ageing hallmarks exhibit organ-specific temporal signatures. Nature, 2020, 583, 596-602.	27.8	317
13	RNA-GPS predicts high-resolution RNA subcellular localization and highlights the role of splicing. Rna, 2020, 26, 851-865.	3.5	15
14	Integrating spatial gene expression and breast tumour morphology via deep learning. Nature Biomedical Engineering, 2020, 4, 827-834.	22.5	208
15	An online platform for interactive feedback in biomedical machine learning. Nature Machine Intelligence, 2020, 2, 86-88.	16.0	7
16	Sex and gender analysis improves science and engineering. Nature, 2019, 575, 137-146.	27.8	336
17	Multiaccuracy. , 2019, , .		81
18	Interpretation of Neural Networks Is Fragile. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 3681-3688.	4.9	251

#	ARTICLE	IF	CITATIONS
19	A primer on deep learning in genomics. <i>Nature Genetics</i> , 2019, 51, 12-18.	21.4	542
20	Word embeddings quantify 100 years of gender and ethnic stereotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3635-E3644.	7.1	480
21	DeepTag: inferring diagnoses from veterinary clinical notes. <i>Npj Digital Medicine</i> , 2018, 1, 60.	10.9	17
22	The clinical imperative for inclusivity: Race, ethnicity, and ancestry (REA) in genomics. <i>Human Mutation</i> , 2018, 39, 1713-1720.	2.5	102
23	AI can be sexist and racist – it’s time to make it fair. <i>Nature</i> , 2018, 559, 324-326.	27.8	386
24	Correcting for cell-type heterogeneity in DNA methylation: a comprehensive evaluation. <i>Nature Methods</i> , 2017, 14, 218-219.	19.0	33
25	Analysis of protein-coding genetic variation in 60,706 humans. <i>Nature</i> , 2016, 536, 285-291.	27.8	9,051
26	Quantifying unobserved protein-coding variants in human populations provides a roadmap for large-scale sequencing projects. <i>Nature Communications</i> , 2016, 7, 13293.	12.8	35
27	Sparse PCA corrects for cell type heterogeneity in epigenome-wide association studies. <i>Nature Methods</i> , 2016, 13, 443-445.	19.0	205
28	Epigenome-wide association studies without the need for cell-type composition. <i>Nature Methods</i> , 2014, 11, 309-311.	19.0	205
29	Epstein-Barr virus exploits intrinsic B-lymphocyte transcription programs to achieve immortal cell growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14902-14907.	7.1	180
30	Genome-wide analysis reveals conserved and divergent features of Notch1/RBPJ binding in human and murine T-lymphoblastic leukemia cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14908-14913.	7.1	221