

# Joshua Z Levin

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

30,670  
citations

87888

38  
h-index

243625

44  
g-index

58  
all docs

58  
docs citations

58  
times ranked

48510  
citing authors

#	ARTICLE	IF	CITATIONS
1	Autism genes converge on asynchronous development of shared neuron classes. <i>Nature</i> , 2022, 602, 268-273.	27.8	180
2	The evolution, evolvability and engineering of gene regulatory DNA. <i>Nature</i> , 2022, 603, 455-463.	27.8	126
3	Pluripotent stem cell-derived models of neurological diseases reveal early transcriptional heterogeneity. <i>Genome Biology</i> , 2021, 22, 73.	8.8	6
4	A RIPK1-regulated inflammatory microglial state in amyotrophic lateral sclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	36
5	Distinct subnetworks of the thalamic reticular nucleus. <i>Nature</i> , 2020, 583, 819-824.	27.8	104
6	In vivo Perturb-Seq reveals neuronal and glial abnormalities associated with autism risk genes. <i>Science</i> , 2020, 370, .	12.6	155
7	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , 2020, 38, 747-755.	17.5	313
8	Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. <i>Nature Biotechnology</i> , 2020, 38, 737-746.	17.5	527
9	Individual brain organoids reproducibly form cell diversity of the human cerebral cortex. <i>Nature</i> , 2019, 570, 523-527.	27.8	649
10	Single-cell transcriptomic profiling of the aging mouse brain. <i>Nature Neuroscience</i> , 2019, 22, 1696-1708.	14.8	432
11	Effects of 3D culturing conditions on the transcriptomic profile of stem-cell-derived neurons. <i>Nature Biomedical Engineering</i> , 2018, 2, 540-554.	22.5	78
12	TBK1 Suppresses RIPK1-Driven Apoptosis and Inflammation during Development and in Aging. <i>Cell</i> , 2018, 174, 1477-1491.e19.	28.9	291
13	Comprehensive comparative analysis of 5' end RNA-sequencing methods. <i>Nature Methods</i> , 2018, 15, 505-511.	19.0	90
14	Comparative Analysis Highlights Variable Genome Content of Wheat Rusts and Divergence of the Mating Loci. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 361-376.	1.8	127
15	RIPK1 mediates a disease-associated microglial response in Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8788-E8797.	7.1	265
16	Comprehensive Classification of Retinal Bipolar Neurons by Single-Cell Transcriptomics. <i>Cell</i> , 2016, 166, 1308-1323.e30.	28.9	1,010
17	Genome analysis of three <i>Pneumocystis</i> species reveals adaptation mechanisms to life exclusively in mammalian hosts. <i>Nature Communications</i> , 2016, 7, 10740.	12.8	153
18	Transcriptomic Characterization of SF3B1 Mutation Reveals Its Pleiotropic Effects in Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2016, 30, 750-763.	16.8	173

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19	Use of the MS2 aptamer and coat protein for RNA localization in yeast: A response to “MS2 coat proteins bound to yeast mRNAs block 5’ to 3’ degradation and trap mRNA decay products: implications for the localization of mRNAs by MS2-MCP system” Rna, 2016, 22, 660-666.	3.5	53
20	Structure of the germline genome of <i>Tetrahymena thermophila</i> and relationship to the massively rearranged somatic genome. ELife, 2016, 5, .	6.0	130
21	Genome Sequences of Three Phytopathogenic Species of the Magnaporthaceae Family of Fungi. G3: Genes, Genomes, Genetics, 2015, 5, 2539-2545.	1.8	33
22	Transcriptional Consequences of 16p11.2 Deletion and Duplication in Mouse Cortex and Multiplex Autism Families. American Journal of Human Genetics, 2014, 94, 870-883.	6.2	116
23	Chemoproteomic Discovery of Cysteine-Containing Human Short Open Reading Frames. Journal of the American Chemical Society, 2013, 135, 16750-16753.	13.7	34
24	Peptidomic discovery of short open reading frame–encoded peptides in human cells. Nature Chemical Biology, 2013, 9, 59-64.	8.0	529
25	Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells. Nature, 2013, 498, 236-240.	27.8	1,103
26	Comparative analysis of RNA sequencing methods for degraded or low-input samples. Nature Methods, 2013, 10, 623-629.	19.0	419
27	Distinctive Expansion of Potential Virulence Genes in the Genome of the Oomycete Fish Pathogen <i>Saprolegnia parasitica</i> . PLoS Genetics, 2013, 9, e1003272.	3.5	221
28	Complete viral RNA genome sequencing of ultra-low copy samples by sequence-independent amplification. Nucleic Acids Research, 2013, 41, e13-e13.	14.5	75
29	Efficient and robust RNA-seq process for cultured bacteria and complex community transcriptomes. Genome Biology, 2012, 13, r23.	9.6	197
30	Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. Genome Research, 2012, 22, 577-591.	5.5	809
31	Microsporidian genome analysis reveals evolutionary strategies for obligate intracellular growth. Genome Research, 2012, 22, 2478-2488.	5.5	235
32	De novo assembly of highly diverse viral populations. BMC Genomics, 2012, 13, 475.	2.8	183
33	RNA-SeQC: RNA-seq metrics for quality control and process optimization. Bioinformatics, 2012, 28, 1530-1532.	4.1	746
34	Comparative Functional Genomics of the Fission Yeasts. Science, 2011, 332, 930-936.	12.6	458
35	Full-length transcriptome assembly from RNA-Seq data without a reference genome. Nature Biotechnology, 2011, 29, 644-652.	17.5	17,264
36	Metabolic labeling of RNA uncovers principles of RNA production and degradation dynamics in mammalian cells. Nature Biotechnology, 2011, 29, 436-442.	17.5	524

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37	Ab initio reconstruction of cell type-specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. Nature Biotechnology, 2010, 28, 503-510.	17.5	1,251
38	Comprehensive comparative analysis of strand-specific RNA sequencing methods. Nature Methods, 2010, 7, 709-715.	19.0	662
39	Integrative analysis of the melanoma transcriptome. Genome Research, 2010, 20, 413-427.	5.5	248
40	Strand-specific RNA sequencing reveals extensive regulated long antisense transcripts that are conserved across yeast species. Genome Biology, 2010, 11, R87.	9.6	122
41	Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3264-3269.	7.1	201
42	Targeted next-generation sequencing of a cancer transcriptome enhances detection of sequence variants and novel fusion transcripts. Genome Biology, 2009, 10, R115.	9.6	172