

Joshua Z Levin

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

30,670
citations

87843

38
h-index

243529

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.	13.7	180
2	The evolution, evolvability and engineering of gene regulatory DNA. <i>Nature</i> , 2022, 603, 455-463.	13.7	126
3	Pluripotent stem cell-derived models of neurological diseases reveal early transcriptional heterogeneity. <i>Genome Biology</i> , 2021, 22, 73.	3.8	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, .	3.3	36
5	Distinct subnetworks of the thalamic reticular nucleus. <i>Nature</i> , 2020, 583, 819-824.	13.7	104
6	In vivo Perturb-Seq reveals neuronal and glial abnormalities associated with autism risk genes. <i>Science</i> , 2020, 370, .	6.0	155
7	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , 2020, 38, 747-755.	9.4	313
8	Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. <i>Nature Biotechnology</i> , 2020, 38, 737-746.	9.4	527
9	Individual brain organoids reproducibly form cell diversity of the human cerebral cortex. <i>Nature</i> , 2019, 570, 523-527.	13.7	649
10	Single-cell transcriptomic profiling of the aging mouse brain. <i>Nature Neuroscience</i> , 2019, 22, 1696-1708.	7.1	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.	11.6	78
12	TBK1 Suppresses RIPK1-Driven Apoptosis and Inflammation during Development and in Aging. <i>Cell</i> , 2018, 174, 1477-1491.e19.	13.5	291
13	Comprehensive comparative analysis of 5' end RNA-sequencing methods. <i>Nature Methods</i> , 2018, 15, 505-511.	9.0	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.	0.8	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.	3.3	265
16	Comprehensive Classification of Retinal Bipolar Neurons by Single-Cell Transcriptomics. <i>Cell</i> , 2016, 166, 1308-1323.e30.	13.5	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.	5.8	153
18	Transcriptomic Characterization of SF3B1 Mutation Reveals Its Pleiotropic Effects in Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2016, 30, 750-763.	7.7	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. <i>Rna</i> , 2016, 22, 660-666.	1.6	53
20	Structure of the germline genome of <i>Tetrahymena thermophila</i> and relationship to the massively rearranged somatic genome. <i>ELife</i> , 2016, 5, .	2.8	130
21	Genome Sequences of Three Phytopathogenic Species of the Magnaporthaceae Family of Fungi. G3: Genes, Genomes, Genetics, 2015, 5, 2539-2545.	0.8	33
22	Transcriptional Consequences of 16p11.2 Deletion and Duplication in Mouse Cortex and Multiplex Autism Families. <i>American Journal of Human Genetics</i> , 2014, 94, 870-883.	2.6	116
23	Chemoproteomic Discovery of Cysteine-Containing Human Short Open Reading Frames. <i>Journal of the American Chemical Society</i> , 2013, 135, 16750-16753.	6.6	34
24	Peptidomic discovery of short open reading frame-encoded peptides in human cells. <i>Nature Chemical Biology</i> , 2013, 9, 59-64.	3.9	529
25	Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells. <i>Nature</i> , 2013, 498, 236-240.	13.7	1,103
26	Comparative analysis of RNA sequencing methods for degraded or low-input samples. <i>Nature Methods</i> , 2013, 10, 623-629.	9.0	419
27	Distinctive Expansion of Potential Virulence Genes in the Genome of the Oomycete Fish Pathogen <i>Saprolegnia parasitica</i> . <i>PLoS Genetics</i> , 2013, 9, e1003272.	1.5	221
28	Complete viral RNA genome sequencing of ultra-low copy samples by sequence-independent amplification. <i>Nucleic Acids Research</i> , 2013, 41, e13-e13.	6.5	75
29	Efficient and robust RNA-seq process for cultured bacteria and complex community transcriptomes. <i>Genome Biology</i> , 2012, 13, r23.	13.9	197
30	Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. <i>Genome Research</i> , 2012, 22, 577-591.	2.4	809
31	Microsporidian genome analysis reveals evolutionary strategies for obligate intracellular growth. <i>Genome Research</i> , 2012, 22, 2478-2488.	2.4	235
32	De novo assembly of highly diverse viral populations. <i>BMC Genomics</i> , 2012, 13, 475.	1.2	183
33	RNA-SeQC: RNA-seq metrics for quality control and process optimization. <i>Bioinformatics</i> , 2012, 28, 1530-1532.	1.8	746
34	Comparative Functional Genomics of the Fission Yeasts. <i>Science</i> , 2011, 332, 930-936.	6.0	458
35	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652.	9.4	17,264
36	Metabolic labeling of RNA uncovers principles of RNA production and degradation dynamics in mammalian cells. <i>Nature Biotechnology</i> , 2011, 29, 436-442.	9.4	524

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37	Ab initio reconstruction of cell type-specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. <i>Nature Biotechnology</i> , 2010, 28, 503-510.	9.4	1,251
38	Comprehensive comparative analysis of strand-specific RNA sequencing methods. <i>Nature Methods</i> , 2010, 7, 709-715.	9.0	662
39	Integrative analysis of the melanoma transcriptome. <i>Genome Research</i> , 2010, 20, 413-427.	2.4	248
40	Strand-specific RNA sequencing reveals extensive regulated long antisense transcripts that are conserved across yeast species. <i>Genome Biology</i> , 2010, 11, R87.	13.9	122
41	Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3264-3269.	3.3	201
42	Targeted next-generation sequencing of a cancer transcriptome enhances detection of sequence variants and novel fusion transcripts. <i>Genome Biology</i> , 2009, 10, R115.	13.9	172