Joseph R Nery

List of Publications by Year
in descending order

55 papers	**20,583** citations	57719 **44** h-index	133188 **59** g-index
86 all docs	**86** docs citations	**86** times ranked	**26890** citing authors

#	Article	IF	Citations
1	Human DNA methylomes at base resolution show widespread epigenomic differences. Nature, 2009, 462, 315-322.	13.7	4,063
2	Global Epigenomic Reconfiguration During Mammalian Brain Development. Science, 2013, 341, 1237905.	6.0	1,609
3	Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. Nature, 2011, 471, 68-73.	13.7	1,442
4	Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. Cell, 2016, 165, 1280-1292.	13.5	1,078
5	Widespread dynamic DNA methylation in response to biotic stress. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2183-91.	3.3	878
6	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. Cell, 2013, 153, 1134-1148.	13.5	689
7	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. Neuron, 2015, 86, 1369-1384.	3.8	640
8	Human body epigenome maps reveal noncanonical DNA methylation variation. Nature, 2015, 523, 212-216.	13.7	605
9	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. Cell, 2016, 166, 492-505.	13.5	594
10	Patterns of population epigenomic diversity. Nature, 2013, 495, 193-198.	13.7	543
11	Cryptochromes Interact Directly with PIFs to Control Plant Growth in Limiting Blue Light. Cell, 2016, 164, 233-245.	13.5	445
12	Single-cell methylomes identify neuronal subtypes and regulatory elements in mammalian cortex. Science, 2017, 357, 600-604.	6.0	445
13	Molecular Criteria for Defining the Naive Human Pluripotent State. Cell Stem Cell, 2016, 19, 502-515.	5.2	415
14	Integration of omic networks in a developmental atlas of maize. Science, 2016, 353, 814-818.	6.0	411
15	A transcription factor hierarchy defines an environmental stress response network. Science, 2016, 354, .	6.0	394
16	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. ELife, 2013, 2, e00675.	2.8	379
17	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	13.7	361
18	Comparison of the transcriptional landscapes between human and mouse tissues. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17224-17229.	3.3	337

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19	Mapping genome-wide transcription-factor binding sites using DAP-seq. Nature Protocols, 2017, 12, 1659-1672.	5.5	330
20	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	13.7	316
21	Abnormalities in human pluripotent cells due to reprogramming mechanisms. Nature, 2014, 511, 177-183.	13.7	307
22	Cerebral Organoids Recapitulate Epigenomic Signatures of the Human Fetal Brain. Cell Reports, 2016, 17, 3369-3384.	2.9	296
23	MethylC-seq library preparation for base-resolution whole-genome bisulfite sequencing. Nature Protocols, 2015, 10, 475-483.	5.5	250
24	Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. Genome Research, 2013, 23, 1663-1674.	2.4	227
25	Dynamic DNA methylation reconfiguration during seed development and germination. Genome Biology, 2017, 18, 171.	3.8	218
26	An alternative pluripotent state confers interspecies chimaeric competency. Nature, 2015, 521, 316-321.	13.7	215
27	Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. Nature Methods, 2019, 16, 999-1006.	9.0	200
28	Mobile small RNAs regulate genome-wide DNA methylation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E801-10.	3.3	192
29	Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. ELife, 2018, 7, .	2.8	180
30	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	13.7	166
31	Unique cell-type-specific patterns of DNA methylation in the root meristem. Nature Plants, 2016, 2, 16058.	4.7	159
32	CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. Nature Methods, 2017, 14, 819-825.	9.0	157
33	Integrated multi-omics framework of the plant response to jasmonic acid. Nature Plants, 2020, 6, 290-302.	4.7	145
34	Robust single-cell DNA methylome profiling with snmC-seq2. Nature Communications, 2018, 9, 3824.	5.8	138
35	The Developmental Potential of iPSCs Is Greatly Influenced by Reprogramming Factor Selection. Cell Stem Cell, 2014, 15, 295-309.	5.2	137
36	DNA methylation atlas of the mouse brain at single-cell resolution. Nature, 2021, 598, 120-128.	13.7	135

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37	The complex architecture and epigenomic impact of plant T-DNA insertions. PLoS Genetics, 2019, 15, e1007819.	1.5	109
38	Epigenomic landscapes of retinal rods and cones. ELife, 2016, 5, e11613.	2.8	106
39	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. Nature, 2020, 583, 752-759.	13.7	84
40	Improved regulatory element prediction based on tissue-specific local epigenomic signatures. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1633-E1640.	3.3	78
41	Functional Human Oocytes Generated by Transfer of Polar Body Genomes. Cell Stem Cell, 2017, 20, 112-119.	5.2	76
42	Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons. ELife, 2019, 8, .	2.8	64
43	The emergence of the brain non-CpG methylation system in vertebrates. Nature Ecology and Evolution, 2021, 5, 369-378.	3.4	63
44	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. Cell Genomics, 2022, 2, 100107.	3.0	58
45	PHYTOCHROME-INTERACTING FACTORs trigger environmentally responsive chromatin dynamics in plants. Nature Genetics, 2021, 53, 955-961.	9.4	54
46	Iterative single-cell multi-omic integration using online learning. Nature Biotechnology, 2021, 39, 1000-1007.	9.4	53
47	Surveillance of 3′ Noncoding Transcripts Requires FIERY1 and XRN3 in <i>Arabidopsis</i>. G3: Genes, Genomes, Genetics, 2012, 2, 487-498.	0.8	47
48	Epigenomic diversity of cortical projection neurons in the mouse brain. Nature, 2021, 598, 167-173.	13.7	47
49	OGT binds a conserved C-terminal domain of TET1 to regulate TET1 activity and function in development. ELife, 2018, 7, .	2.8	46
50	Allele-specific non-CG DNA methylation marks domains of active chromatin in female mouse brain. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2882-E2890.	3.3	45
51	Losing Dnmt3a dependent methylation in inhibitory neurons impairs neural function by a mechanism impacting Rett syndrome. ELife, 2020, 9, .	2.8	44
52	Single nucleus multi-omics regulatory landscape of the murine pituitary. Nature Communications, 2021, 12, 2677.	5.8	38
53	Leaf cell-specific and single-cell transcriptional profiling reveals a role for the palisade layer in UV light protection. Plant Cell, 2022, 34, 3261-3279.	3.1	31
54	Epigenetic silencing of a multifunctional plant stress regulator. ELife, 2019, 8, .	2.8	28

#	Article	IF	Citations
55	CrY2H-seq interactome screening. Protocol Exchange, 0, , .	0.3	1