

Joseph R Nery

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7254211/publications.pdf>

Version: 2024-02-01

55
papers

20,583
citations

57631

44
h-index

133063

59
g-index

86
all docs

86
docs citations

86
times ranked

26890
citing authors

#	ARTICLE	IF	CITATIONS
1	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. <i>Cell Genomics</i> , 2022, 2, 100107.	3.0	58
2	Leaf cell-specific and single-cell transcriptional profiling reveals a role for the palisade layer in UV light protection. <i>Plant Cell</i> , 2022, 34, 3261-3279.	3.1	31
3	The emergence of the brain non-CpG methylation system in vertebrates. <i>Nature Ecology and Evolution</i> , 2021, 5, 369-378.	3.4	63
4	Iterative single-cell multi-omic integration using online learning. <i>Nature Biotechnology</i> , 2021, 39, 1000-1007.	9.4	53
5	Single nucleus multi-omics regulatory landscape of the murine pituitary. <i>Nature Communications</i> , 2021, 12, 2677.	5.8	38
6	PHYTOCHROME-INTERACTING FACTORs trigger environmentally responsive chromatin dynamics in plants. <i>Nature Genetics</i> , 2021, 53, 955-961.	9.4	54
7	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	13.7	166
8	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021, 598, 111-119.	13.7	361
9	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	13.7	316
10	DNA methylation atlas of the mouse brain at single-cell resolution. <i>Nature</i> , 2021, 598, 120-128.	13.7	135
11	Epigenomic diversity of cortical projection neurons in the mouse brain. <i>Nature</i> , 2021, 598, 167-173.	13.7	47
12	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. <i>Nature</i> , 2020, 583, 752-759.	13.7	84
13	Integrated multi-omics framework of the plant response to jasmonic acid. <i>Nature Plants</i> , 2020, 6, 290-302.	4.7	145
14	Losing Dnmt3a dependent methylation in inhibitory neurons impairs neural function by a mechanism impacting Rett syndrome. <i>ELife</i> , 2020, 9, .	2.8	44
15	Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. <i>Nature Methods</i> , 2019, 16, 999-1006.	9.0	200
16	Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons. <i>ELife</i> , 2019, 8, .	2.8	64
17	The complex architecture and epigenomic impact of plant T-DNA insertions. <i>PLoS Genetics</i> , 2019, 15, e1007819.	1.5	109
18	Epigenetic silencing of a multifunctional plant stress regulator. <i>ELife</i> , 2019, 8, .	2.8	28

#	ARTICLE	IF	CITATIONS
19	Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. <i>ELife</i> , 2018, 7, .	2.8	180
20	Robust single-cell DNA methylome profiling with snmC-seq2. <i>Nature Communications</i> , 2018, 9, 3824.	5.8	138
21	OGT binds a conserved C-terminal domain of TET1 to regulate TET1 activity and function in development. <i>ELife</i> , 2018, 7, .	2.8	46
22	Improved regulatory element prediction based on tissue-specific local epigenomic signatures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1633-E1640.	3.3	78
23	Allele-specific non-CG DNA methylation marks domains of active chromatin in female mouse brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2882-E2890.	3.3	45
24	Mapping genome-wide transcription-factor binding sites using DAP-seq. <i>Nature Protocols</i> , 2017, 12, 1659-1672.	5.5	330
25	Single-cell methylomes identify neuronal subtypes and regulatory elements in mammalian cortex. <i>Science</i> , 2017, 357, 600-604.	6.0	445
26	CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. <i>Nature Methods</i> , 2017, 14, 819-825.	9.0	157
27	Functional Human Oocytes Generated by Transfer of Polar Body Genomes. <i>Cell Stem Cell</i> , 2017, 20, 112-119.	5.2	76
28	Dynamic DNA methylation reconfiguration during seed development and germination. <i>Genome Biology</i> , 2017, 18, 171.	3.8	218
29	Cerebral Organoids Recapitulate Epigenomic Signatures of the Human Fetal Brain. <i>Cell Reports</i> , 2016, 17, 3369-3384.	2.9	296
30	Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. <i>Cell</i> , 2016, 165, 1280-1292.	13.5	1,078
31	Integration of omic networks in a developmental atlas of maize. <i>Science</i> , 2016, 353, 814-818.	6.0	411
32	Epigenomic Diversity in a Global Collection of <i>Arabidopsis thaliana</i> Accessions. <i>Cell</i> , 2016, 166, 492-505.	13.5	594
33	Molecular Criteria for Defining the Naive Human Pluripotent State. <i>Cell Stem Cell</i> , 2016, 19, 502-515.	5.2	415
34	Unique cell-type-specific patterns of DNA methylation in the root meristem. <i>Nature Plants</i> , 2016, 2, 16058.	4.7	159
35	A transcription factor hierarchy defines an environmental stress response network. <i>Science</i> , 2016, 354, .	6.0	394
36	Mobile small RNAs regulate genome-wide DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E801-10.	3.3	192

#	ARTICLE	IF	CITATIONS
37	Cryptochromes Interact Directly with PIFs to Control Plant Growth in Limiting Blue Light. <i>Cell</i> , 2016, 164, 233-245.	13.5	445
38	Epigenomic landscapes of retinal rods and cones. <i>ELife</i> , 2016, 5, e11613.	2.8	106
39	Human body epigenome maps reveal noncanonical DNA methylation variation. <i>Nature</i> , 2015, 523, 212-216.	13.7	605
40	MethylC-seq library preparation for base-resolution whole-genome bisulfite sequencing. <i>Nature Protocols</i> , 2015, 10, 475-483.	5.5	250
41	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. <i>Neuron</i> , 2015, 86, 1369-1384.	3.8	640
42	An alternative pluripotent state confers interspecies chimaeric competency. <i>Nature</i> , 2015, 521, 316-321.	13.7	215
43	Comparison of the transcriptional landscapes between human and mouse tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17224-17229.	3.3	337
44	The Developmental Potential of iPSCs Is Greatly Influenced by Reprogramming Factor Selection. <i>Cell Stem Cell</i> , 2014, 15, 295-309.	5.2	137
45	Abnormalities in human pluripotent cells due to reprogramming mechanisms. <i>Nature</i> , 2014, 511, 177-183.	13.7	307
46	Global Epigenomic Reconfiguration During Mammalian Brain Development. <i>Science</i> , 2013, 341, 1237905.	6.0	1,609
47	Patterns of population epigenomic diversity. <i>Nature</i> , 2013, 495, 193-198.	13.7	543
48	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	13.5	689
49	Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. <i>Genome Research</i> , 2013, 23, 1663-1674.	2.4	227
50	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in <i>Arabidopsis</i> . <i>ELife</i> , 2013, 2, e00675.	2.8	379
51	Surveillance of 3â€² Noncoding Transcripts Requires FIERY1 and XRN3 in <i>Arabidopsis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 487-498.	0.8	47
52	Widespread dynamic DNA methylation in response to biotic stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2183-91.	3.3	878
53	Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> , 2011, 471, 68-73.	13.7	1,442
54	Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> , 2009, 462, 315-322.	13.7	4,063

#	ARTICLE	IF	CITATIONS
55	CrY2H-seq interactome screening. Protocol Exchange, 0, , .	0.3	1