

Ryan Lister

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

28,753
citations

31902

53
h-index

43802

91
g-index

115
all docs

115
docs citations

115
times ranked

41451
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenome plasticity in plants. <i>Nature Reviews Genetics</i> , 2022, 23, 55-68.	7.7	73
2	Comprehensive evaluation of deconvolution methods for human brain gene expression. <i>Nature Communications</i> , 2022, 13, 1358.	5.8	32
3	Intestinal stem cell aging signature reveals a reprogramming strategy to enhance regenerative potential. <i>Npj Regenerative Medicine</i> , 2022, 7, .	2.5	4
4	Synthetic memory circuits for stable cell reprogramming in plants. <i>Nature Biotechnology</i> , 2022, 40, 1862-1872.	9.4	35
5	Cerebrospinal fluid liquid biopsy for detecting somatic mosaicism in brain. <i>Brain Communications</i> , 2021, 3, fcaa235.	1.5	42
6	The emergence of the brain non-CpG methylation system in vertebrates. <i>Nature Ecology and Evolution</i> , 2021, 5, 369-378.	3.4	63
7	Modelling human blastocysts by reprogramming fibroblasts into iBlastoids. <i>Nature</i> , 2021, 591, 627-632.	13.7	211
8	Transcriptional signature in microglia associated with A β 2 plaque phagocytosis. <i>Nature Communications</i> , 2021, 12, 3015.	5.8	142
9	Genomic Targeting of TET Activity for Targeted Demethylation Using. <i>Methods in Molecular Biology</i> , 2021, 2272, 181-194.	0.4	6
10	Evolution of DNA Methylome Diversity in Eukaryotes. <i>Journal of Molecular Biology</i> , 2020, 432, 1687-1705.	2.0	82
11	schex avoids overplotting for large single-cell RNA-sequencing datasets. <i>Bioinformatics</i> , 2020, 36, 2291-2292.	1.8	10
12	Tracing animal genomic evolution with the chromosomal-level assembly of the freshwater sponge <i>Ephydatia muelleri</i> . <i>Nature Communications</i> , 2020, 11, 3676.	5.8	72
13	Reprogramming roadmap reveals route to human induced trophoblast stem cells. <i>Nature</i> , 2020, 586, 101-107.	13.7	131
14	Genomic adaptations to aquatic and aerial life in mayflies and the origin of insect wings. <i>Nature Communications</i> , 2020, 11, 2631.	5.8	57
15	Systematic assessment of tissue dissociation and storage biases in single-cell and single-nucleus RNA-seq workflows. <i>Genome Biology</i> , 2020, 21, 130.	3.8	342
16	Mitochondrial CLPP2 Assists Coordination and Homeostasis of Respiratory Complexes. <i>Plant Physiology</i> , 2020, 184, 148-164.	2.3	26
17	TINCâ€” A Method to Dissect Regulatory Complexes at Single-Locus Resolutionâ€” Reveals an Extensive Protein Complex at the Nanog Promoter. <i>Stem Cell Reports</i> , 2020, 15, 1246-1259.	2.3	12
18	Depletion of Foxk transcription factors causes genome-wide transcriptional misregulation and developmental arrest in zebrafish embryos. <i>MicroPublication Biology</i> , 2020, 2020, .	0.1	0

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19	Retention of paternal DNA methylome in the developing zebrafish germline. <i>Nature Communications</i> , 2019, 10, 3054.	5.8	99
20	LINE-1 Evasion of Epigenetic Repression in Humans. <i>Molecular Cell</i> , 2019, 75, 590-604.e12.	4.5	106
21	Capture of a functionally active methyl-CpG binding domain by an arthropod retrotransposon family. <i>Genome Research</i> , 2019, 29, 1277-1286.	2.4	19
22	HOME: a histogram based machine learning approach for effective identification of differentially methylated regions. <i>BMC Bioinformatics</i> , 2019, 20, 253.	1.2	45
23	Convergent evolution of a vertebrate-like methylome in a marine sponge. <i>Nature Ecology and Evolution</i> , 2019, 3, 1464-1473.	3.4	47
24	A single-cell atlas of entorhinal cortex from individuals with Alzheimer's disease reveals cell-type-specific gene expression regulation. <i>Nature Neuroscience</i> , 2019, 22, 2087-2097.	7.1	591
25	Harnessing targeted DNA methylation and demethylation using dCas9. <i>Essays in Biochemistry</i> , 2019, 63, 813-825.	2.1	10
26	Recurrent acquisition of cytosine methyltransferases into eukaryotic retrotransposons. <i>Nature Communications</i> , 2018, 9, 1341.	5.8	42
27	Generation of Whole Genome Bisulfite Sequencing Libraries for Comprehensive DNA Methylome Analysis. <i>Methods in Molecular Biology</i> , 2018, 1767, 291-298.	0.4	4
28	Approaches for the Analysis and Interpretation of Whole Genome Bisulfite Sequencing Data. <i>Methods in Molecular Biology</i> , 2018, 1767, 299-310.	0.4	6
29	Amphioxus functional genomics and the origins of vertebrate gene regulation. <i>Nature</i> , 2018, 564, 64-70.	13.7	224
30	A modular dCas9-SunTag DNMT3A epigenome editing system overcomes pervasive off-target activity of direct fusion dCas9-DNMT3A constructs. <i>Genome Research</i> , 2018, 28, 1193-1206.	2.4	123
31	Synthetically controlling dendrimer flexibility improves delivery of large plasmid DNA. <i>Chemical Science</i> , 2017, 8, 2923-2930.	3.7	101
32	Nutrient stress-induced chromatin changes in plants. <i>Current Opinion in Plant Biology</i> , 2017, 39, 1-7.	3.5	57
33	Comprehensive characterization of distinct states of human naive pluripotency generated by reprogramming. <i>Nature Methods</i> , 2017, 14, 1055-1062.	9.0	128
34	Rapid Recovery Gene Downregulation during Excess-Light Stress and Recovery in Arabidopsis. <i>Plant Cell</i> , 2017, 29, 1836-1863.	3.1	90
35	Epigenomic Landscapes of hESC-Derived Neural Rosettes: Modeling Neural Tube Formation and Diseases. <i>Cell Reports</i> , 2017, 20, 1448-1462.	2.9	28
36	Cell Type of Origin Dictates the Route to Pluripotency. <i>Cell Reports</i> , 2017, 21, 2649-2660.	2.9	49

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37	Transient and Permanent Reconfiguration of Chromatin and Transcription Factor Occupancy Drive Reprogramming. <i>Cell Stem Cell</i> , 2017, 21, 834-845.e6.	5.2	95
38	DNA methylation and the preservation of cell identity. <i>Current Opinion in Genetics and Development</i> , 2017, 46, 9-14.	1.5	114
39	Dynamic and rapid changes in the transcriptome and epigenome during germination and in developing rice (<i>Oryza sativa</i>) coleoptiles under anoxia and reoxygenation. <i>Plant Journal</i> , 2017, 89, 805-824.	2.8	63
40	Extensive transcriptomic and epigenomic remodelling occurs during <i>Arabidopsis thaliana</i> germination. <i>Genome Biology</i> , 2017, 18, 172.	3.8	163
41	Regulatory remodeling in the allo-tetraploid frog <i>Xenopus laevis</i> . <i>Genome Biology</i> , 2017, 18, 198.	3.8	34
42	Beyond mCG. , 2017, , 81-94.		0
43	DNA methylation profiles of diverse <i>Brachypodium distachyon</i> align with underlying genetic diversity. <i>Genome Research</i> , 2016, 26, 1520-1531.	2.4	34
44	Retrograde signalling caused by heritable mitochondrial dysfunction is partially mediated by ANAC017 and improves plant performance. <i>Plant Journal</i> , 2016, 88, 542-558.	2.8	66
45	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 2016, 538, 336-343.	13.7	849
46	Unique cell-type-specific patterns of DNA methylation in the root meristem. <i>Nature Plants</i> , 2016, 2, 16058.	4.7	159
47	Active DNA demethylation at enhancers during the vertebrate phylotypic period. <i>Nature Genetics</i> , 2016, 48, 417-426.	9.4	210
48	Epigenomic landscapes of retinal rods and cones. <i>ELife</i> , 2016, 5, e11613.	2.8	106
49	Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation. <i>ELife</i> , 2016, 5, .	2.8	181
50	methylPipe and compEpiTools: a suite of R packages for the integrative analysis of epigenomics data. <i>BMC Bioinformatics</i> , 2015, 16, 313.	1.2	68
51	Stress induced gene expression drives transient DNA methylation changes at adjacent repetitive elements. <i>ELife</i> , 2015, 4, .	2.8	285
52	Turning over DNA methylation in the mind. <i>Frontiers in Neuroscience</i> , 2015, 9, 252.	1.4	49
53	Embryonic transcription is controlled by maternally defined chromatin state. <i>Nature Communications</i> , 2015, 6, 10148.	5.8	103
54	MethylC-seq library preparation for base-resolution whole-genome bisulfite sequencing. <i>Nature Protocols</i> , 2015, 10, 475-483.	5.5	250

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55	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	13.7	5,653
56	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. <i>Neuron</i> , 2015, 86, 1369-1384.	3.8	640
57	Of Mice and Man: Differential DNMT Dependence in Mammalian ESCs. <i>Cell Stem Cell</i> , 2015, 16, 459-460.	5.2	3
58	Systematic mapping of occluded genes by cell fusion reveals prevalence and stability of <i>cis</i> -mediated silencing in somatic cells. <i>Genome Research</i> , 2014, 24, 267-280.	2.4	12
59	CG hypomethylation in <i>Lsh</i> ^{-/-} mouse embryonic fibroblasts is associated with de novo H3K4me1 formation and altered cellular plasticity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5890-5895.	3.3	39
60	Analysis of an artificial zinc finger epigenetic modulator: widespread binding but limited regulation. <i>Nucleic Acids Research</i> , 2014, 42, 10856-10868.	6.5	56
61	Genome-wide DNA methylation patterns in <i>LSH</i> mutant reveals de-repression of repeat elements and redundant epigenetic silencing pathways. <i>Genome Research</i> , 2014, 24, 1613-1623.	2.4	83
62	Epigenomics and the control of fate, form and function in social insects. <i>Current Opinion in Insect Science</i> , 2014, 1, 31-38.	2.2	23
63	Global Epigenomic Reconfiguration During Mammalian Brain Development. <i>Science</i> , 2013, 341, 1237905.	6.0	1,609
64	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	13.5	689
65	STAR: an integrated solution to management and visualization of sequencing data. <i>Bioinformatics</i> , 2013, 29, 3204-3210.	1.8	13
66	Spatial and functional relationships among Pol V-associated loci, Pol IV-dependent siRNAs, and cytosine methylation in the <i>Arabidopsis</i> epigenome. <i>Genes and Development</i> , 2012, 26, 1825-1836.	2.7	137
67	Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. <i>Genome Research</i> , 2012, 22, 246-258.	2.4	476
68	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
69	Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> , 2011, 471, 68-73.	13.7	1,442
70	Genome-wide mapping of 5-hydroxymethylcytosine in embryonic stem cells. <i>Nature</i> , 2011, 473, 394-397.	13.7	738
71	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010, 28, 1097-1105.	9.4	647
72	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. <i>Cell Stem Cell</i> , 2010, 6, 479-491.	5.2	747

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73	Finding the fifth base: Genome-wide sequencing of cytosine methylation. <i>Genome Research</i> , 2009, 19, 959-966.	2.4	323
74	Next is now: new technologies for sequencing of genomes, transcriptomes, and beyond. <i>Current Opinion in Plant Biology</i> , 2009, 12, 107-118.	3.5	261
75	The Arabidopsis glutathione transferase gene family displays complex stress regulation and co-silencing multiple genes results in altered metabolic sensitivity to oxidative stress. <i>Plant Journal</i> , 2009, 58, 53-68.	2.8	237
76	Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> , 2009, 462, 315-322.	13.7	4,063
77	Highly Integrated Single-Base Resolution Maps of the Epigenome in Arabidopsis. <i>Cell</i> , 2008, 133, 523-536.	13.5	2,229
78	A Link between RNA Metabolism and Silencing Affecting Arabidopsis Development. <i>Developmental Cell</i> , 2008, 14, 854-866.	3.1	394
79	Identification of Regulatory Pathways Controlling Gene Expression of Stress-Responsive Mitochondrial Proteins in Arabidopsis. <i>Plant Physiology</i> , 2008, 147, 1858-1873.	2.3	140
80	Characterization of the Preprotein and Amino Acid Transporter Gene Family in Arabidopsis. <i>Plant Physiology</i> , 2007, 143, 199-212.	2.3	94
81	Characterization of the Regulatory and Expression Context of an Alternative Oxidase Gene Provides Insights into Cyanide-Insensitive Respiration during Growth and Development. <i>Plant Physiology</i> , 2007, 143, 1519-1533.	2.3	50
82	Functional Definition of Outer Membrane Proteins Involved in Preprotein Import into Mitochondria. <i>Plant Cell</i> , 2007, 19, 3739-3759.	3.1	146
83	Mitochondrial Protein Import: Convergent Solutions for Receptor Structure. <i>Current Biology</i> , 2006, 16, R197-R199.	1.8	28
84	Stress-induced co-expression of alternative respiratory chain components in Arabidopsis thaliana. <i>Plant Molecular Biology</i> , 2005, 58, 193-212.	2.0	302
85	Protein import into mitochondria: origins and functions today (Review). <i>Molecular Membrane Biology</i> , 2005, 22, 87-100.	2.0	76
86	A Transcriptomic and Proteomic Characterization of the Arabidopsis Mitochondrial Protein Import Apparatus and Its Response to Mitochondrial Dysfunction. <i>Plant Physiology</i> , 2004, 134, 777-789.	2.3	148
87	A plant outer mitochondrial membrane protein with high amino acid sequence identity to a chloroplast protein import receptor. <i>FEBS Letters</i> , 2004, 557, 109-114.	1.3	126
88	Expression Analysis of Mitochondrial Components in a Variety of Plant Species Using Real-Time Quantitative PCR. , 2004, , 61-72.		0
89	Identification, Expression, and Import of Components 17 and 23 of the Inner Mitochondrial Membrane Translocase from Arabidopsis. <i>Plant Physiology</i> , 2003, 131, 1737-1747.	2.3	71
90	The Mitochondrial Protein Import Machinery of Plants (MPIMP) database. <i>Nucleic Acids Research</i> , 2003, 31, 325-327.	6.5	35

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91	Zinc-dependent intermembrane space proteins stimulate import of carrier proteins into plant mitochondria. <i>Plant Journal</i> , 2002, 30, 555-566.	2.8	38
92	<i>Arabidopsis thaliana</i> ferrochelatase-I and -II are not imported into <i>Arabidopsis</i> mitochondria. <i>FEBS Letters</i> , 2001, 506, 291-295.	1.3	70