

Ryan Lister

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/783688/publications.pdf>

Version: 2024-02-01

92
papers

28,753
citations

31976
53
h-index

43889
91
g-index

115
all docs

115
docs citations

115
times ranked

41451
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenome plasticity in plants. Nature Reviews Genetics, 2022, 23, 55-68.	16.3	73
2	Comprehensive evaluation of deconvolution methods for human brain gene expression. Nature Communications, 2022, 13, 1358.	12.8	32
3	Intestinal stem cell aging signature reveals a reprogramming strategy to enhance regenerative potential. Npj Regenerative Medicine, 2022, 7, .	5.2	4
4	Synthetic memory circuits for stable cell reprogramming in plants. Nature Biotechnology, 2022, 40, 1862-1872.	17.5	35
5	Cerebrospinal fluid liquid biopsy for detecting somatic mosaicism in brain. Brain Communications, 2021, 3, fcaa235.	3.3	42
6	The emergence of the brain non-CpG methylation system in vertebrates. Nature Ecology and Evolution, 2021, 5, 369-378.	7.8	63
7	Modelling human blastocysts by reprogramming fibroblasts into iBlastoids. Nature, 2021, 591, 627-632.	27.8	211
8	Transcriptional signature in microglia associated with A β plaque phagocytosis. Nature Communications, 2021, 12, 3015.	12.8	142
9	Genomic Targeting of TET Activity for Targeted Demethylation Using. Methods in Molecular Biology, 2021, 2272, 181-194.	0.9	6
10	Evolution of DNA Methylome Diversity in Eukaryotes. Journal of Molecular Biology, 2020, 432, 1687-1705.	4.2	82
11	schex avoids overplotting for large single-cell RNA-sequencing datasets. Bioinformatics, 2020, 36, 2291-2292.	4.1	10
12	Tracing animal genomic evolution with the chromosomal-level assembly of the freshwater sponge Ephydatia muelleri. Nature Communications, 2020, 11, 3676.	12.8	72
13	Reprogramming roadmap reveals route to human induced trophoblast stem cells. Nature, 2020, 586, 101-107.	27.8	131
14	Genomic adaptations to aquatic and aerial life in mayflies and the origin of insect wings. Nature Communications, 2020, 11, 2631.	12.8	57
15	Systematic assessment of tissue dissociation and storage biases in single-cell and single-nucleus RNA-seq workflows. Genome Biology, 2020, 21, 130.	8.8	342
16	Mitochondrial CLPP2 Assists Coordination and Homeostasis of Respiratory Complexes. Plant Physiology, 2020, 184, 148-164.	4.8	26
17	TINCâ€” A Method to Dissect Regulatory Complexes at Single-Locus Resolutionâ€” Reveals an Extensive Protein Complex at the Nanog Promoter. Stem Cell Reports, 2020, 15, 1246-1259.	4.8	12
18	Depletion of Foxk transcription factors causes genome-wide transcriptional misregulation and developmental arrest in zebrafish embryos. MicroPublication Biology, 2020, 2020, .	0.1	0

#	ARTICLE	IF	CITATIONS
19	Retention of paternal DNA methylome in the developing zebrafish germline. Nature Communications, 2019, 10, 3054.	12.8	99
20	LINE-1 Evasion of Epigenetic Repression in Humans. Molecular Cell, 2019, 75, 590-604.e12.	9.7	106
21	Capture of a functionally active methyl-CpG binding domain by an arthropod retrotransposon family. Genome Research, 2019, 29, 1277-1286.	5.5	19
22	HOME: a histogram based machine learning approach for effective identification of differentially methylated regions. BMC Bioinformatics, 2019, 20, 253.	2.6	45
23	Convergent evolution of a vertebrate-like methylome in a marine sponge. Nature Ecology and Evolution, 2019, 3, 1464-1473.	7.8	47
24	A single-cell atlas of entorhinal cortex from individuals with Alzheimer's disease reveals cell-type-specific gene expression regulation. Nature Neuroscience, 2019, 22, 2087-2097.	14.8	591
25	Harnessing targeted DNA methylation and demethylation using dCas9. Essays in Biochemistry, 2019, 63, 813-825.	4.7	10
26	Recurrent acquisition of cytosine methyltransferases into eukaryotic retrotransposons. Nature Communications, 2018, 9, 1341.	12.8	42
27	Generation of Whole Genome Bisulfite Sequencing Libraries for Comprehensive DNA Methylome Analysis. Methods in Molecular Biology, 2018, 1767, 291-298.	0.9	4
28	Approaches for the Analysis and Interpretation of Whole Genome Bisulfite Sequencing Data. Methods in Molecular Biology, 2018, 1767, 299-310.	0.9	6
29	Amphioxus functional genomics and the origins of vertebrate gene regulation. Nature, 2018, 564, 64-70.	27.8	224
30	A modular dCas9-SunTag DNMT3A epigenome editing system overcomes pervasive off-target activity of direct fusion dCas9-DNMT3A constructs. Genome Research, 2018, 28, 1193-1206.	5.5	123
31	Synthetically controlling dendrimer flexibility improves delivery of large plasmid DNA. Chemical Science, 2017, 8, 2923-2930.	7.4	101
32	Nutrient stress-induced chromatin changes in plants. Current Opinion in Plant Biology, 2017, 39, 1-7.	7.1	57
33	Comprehensive characterization of distinct states of human naive pluripotency generated by reprogramming. Nature Methods, 2017, 14, 1055-1062.	19.0	128
34	Rapid Recovery Gene Downregulation during Excess-Light Stress and Recovery in Arabidopsis. Plant Cell, 2017, 29, 1836-1863.	6.6	90
35	Epigenomic Landscapes of hESC-Derived Neural Rosettes: Modeling Neural Tube Formation and Diseases. Cell Reports, 2017, 20, 1448-1462.	6.4	28
36	Cell Type of Origin Dictates the Route to Pluripotency. Cell Reports, 2017, 21, 2649-2660.	6.4	49

#	ARTICLE	IF	CITATIONS
37	Transient and Permanent Reconfiguration of Chromatin and Transcription Factor Occupancy Drive Reprogramming. <i>Cell Stem Cell</i> , 2017, 21, 834-845.e6.	11.1	95
38	DNA methylation and the preservation of cell identity. <i>Current Opinion in Genetics and Development</i> , 2017, 46, 9-14.	3.3	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.	5.7	63
40	Extensive transcriptomic and epigenomic remodelling occurs during <i>Arabidopsis thaliana</i> germination. <i>Genome Biology</i> , 2017, 18, 172.	8.8	163
41	Regulatory remodeling in the allo-tetraploid frog <i>Xenopus laevis</i> . <i>Genome Biology</i> , 2017, 18, 198.	8.8	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.	5.5	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.	5.7	66
45	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 2016, 538, 336-343.	27.8	849
46	Unique cell-type-specific patterns of DNA methylation in the root meristem. <i>Nature Plants</i> , 2016, 2, 16058.	9.3	159
47	Active DNA demethylation at enhancers during the vertebrate phylotypic period. <i>Nature Genetics</i> , 2016, 48, 417-426.	21.4	210
48	Epigenomic landscapes of retinal rods and cones. <i>ELife</i> , 2016, 5, e11613.	6.0	106
49	Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation. <i>ELife</i> , 2016, 5, .	6.0	181
50	methylPipe and compEpiTools: a suite of R packages for the integrative analysis of epigenomics data. <i>BMC Bioinformatics</i> , 2015, 16, 313.	2.6	68
51	Stress induced gene expression drives transient DNA methylation changes at adjacent repetitive elements. <i>ELife</i> , 2015, 4, .	6.0	285
52	Turning over DNA methylation in the mind. <i>Frontiers in Neuroscience</i> , 2015, 9, 252.	2.8	49
53	Embryonic transcription is controlled by maternally defined chromatin state. <i>Nature Communications</i> , 2015, 6, 10148.	12.8	103
54	MethylC-seq library preparation for base-resolution whole-genome bisulfite sequencing. <i>Nature Protocols</i> , 2015, 10, 475-483.	12.0	250

#	ARTICLE	IF	CITATIONS
55	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
56	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. <i>Neuron</i> , 2015, 86, 1369-1384.	8.1	640
57	Of Mice and Man: Differential DNMT Dependence in Mammalian ESCs. <i>Cell Stem Cell</i> , 2015, 16, 459-460.	11.1	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.	5.5	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.	7.1	39
60	Analysis of an artificial zinc finger epigenetic modulator: widespread binding but limited regulation. <i>Nucleic Acids Research</i> , 2014, 42, 10856-10868.	14.5	56
61	Genome-wide DNA methylation patterns in LSH mutant reveals de-repression of repeat elements and redundant epigenetic silencing pathways. <i>Genome Research</i> , 2014, 24, 1613-1623.	5.5	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.	4.4	23
63	Global Epigenomic Reconfiguration During Mammalian Brain Development. <i>Science</i> , 2013, 341, 1237905.	12.6	1,609
64	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	28.9	689
65	STAR: an integrated solution to management and visualization of sequencing data. <i>Bioinformatics</i> , 2013, 29, 3204-3210.	4.1	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.	5.9	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.	5.5	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.	7.1	878
69	Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> , 2011, 471, 68-73.	27.8	1,442
70	Genome-wide mapping of 5-hydroxymethylcytosine in embryonic stem cells. <i>Nature</i> , 2011, 473, 394-397.	27.8	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.	17.5	647
72	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. <i>Cell Stem Cell</i> , 2010, 6, 479-491.	11.1	747

#	ARTICLE	IF	CITATIONS
73	Finding the fifth base: Genome-wide sequencing of cytosine methylation. <i>Genome Research</i> , 2009, 19, 959-966.	5.5	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.	7.1	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.	5.7	237
76	Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> , 2009, 462, 315-322.	27.8	4,063
77	Highly Integrated Single-Base Resolution Maps of the Epigenome in Arabidopsis. <i>Cell</i> , 2008, 133, 523-536.	28.9	2,229
78	A Link between RNA Metabolism and Silencing Affecting Arabidopsis Development. <i>Developmental Cell</i> , 2008, 14, 854-866.	7.0	394
79	Identification of Regulatory Pathways Controlling Gene Expression of Stress-Responsive Mitochondrial Proteins in Arabidopsis. <i>Plant Physiology</i> , 2008, 147, 1858-1873.	4.8	140
80	Characterization of the Preprotein and Amino Acid Transporter Gene Family in Arabidopsis. <i>Plant Physiology</i> , 2007, 143, 199-212.	4.8	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.	4.8	50
82	Functional Definition of Outer Membrane Proteins Involved in Preprotein Import into Mitochondria. <i>Plant Cell</i> , 2007, 19, 3739-3759.	6.6	146
83	Mitochondrial Protein Import: Convergent Solutions for Receptor Structure. <i>Current Biology</i> , 2006, 16, R197-R199.	3.9	28
84	Stress-induced co-expression of alternative respiratory chain components in Arabidopsis thaliana. <i>Plant Molecular Biology</i> , 2005, 58, 193-212.	3.9	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.	4.8	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.	2.8	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.	4.8	71
90	The Mitochondrial Protein Import Machinery of Plants (MPIMP) database. <i>Nucleic Acids Research</i> , 2003, 31, 325-327.	14.5	35

#	ARTICLE	IF	CITATIONS
91	Zinc-dependent intermembrane space proteins stimulate import of carrier proteins into plant mitochondria. Plant Journal, 2002, 30, 555-566.	5.7	38
92	Arabidopsis thaliana ferrochelatase-I and -II are not imported into Arabidopsis mitochondria. FEBS Letters, 2001, 506, 291-295.	2.8	70