

Joseph R Ecker

List of Publications by Year in descending order

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284
papers

101,231
citations

246

143
h-index

319

288
g-index

335
all docs

335
docs citations

335
times ranked

84510
citing authors

#	ARTICLE	IF	CITATIONS
1	The role of ATXR6 expression in modulating genome stability and transposable element repression in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
2	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. Cell Genomics, 2022, 2, 100107.	3.0	58
3	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
4	The emergence of the brain non-CpG methylation system in vertebrates. Nature Ecology and Evolution, 2021, 5, 369-378.	3.4	63
5	Comprehensive analysis of single cell ATAC-seq data with SnapATAC. Nature Communications, 2021, 12, 1337.	5.8	253
6	Iterative single-cell multi-omic integration using online learning. Nature Biotechnology, 2021, 39, 1000-1007.	9.4	53
7	Single nucleus multi-omics regulatory landscape of the murine pituitary. Nature Communications, 2021, 12, 2677.	5.8	38
8	PHYTOCHROME-INTERACTING FACTORs trigger environmentally responsive chromatin dynamics in plants. Nature Genetics, 2021, 53, 955-961.	9.4	54
9	A plant-specific syntaxin-6 protein contributes to the intracytoplasmic route for the begomovirus CabLCV. Plant Physiology, 2021, 187, 158-173.	2.3	12
10	Activity-dependent modulation of synapse-regulating genes in astrocytes. ELife, 2021, 10, .	2.8	58
11	Genome and time-of-day transcriptome of <i>Wolffia australiana</i> link morphological minimization with gene loss and less growth control. Genome Research, 2021, 31, 225-238.	2.4	56
12	An atlas of gene regulatory elements in adult mouse cerebrum. Nature, 2021, 598, 129-136.	13.7	95
13	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	13.7	166
14	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	13.7	361
15	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	13.7	316
16	DNA methylation atlas of the mouse brain at single-cell resolution. Nature, 2021, 598, 120-128.	13.7	135
17	Epigenomic diversity of cortical projection neurons in the mouse brain. Nature, 2021, 598, 167-173.	13.7	47
18	The biology of time: dynamic responses of cell types to developmental, circadian, and environmental cues. Plant Journal, 2021, , .	2.8	8

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19	The JA pathway MYC transcription factors regulate photomorphogenic responses by targeting HY5 gene expression. <i>Plant Journal</i> , 2020, 102, 138-152.	2.8	47
20	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	13.7	257
21	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. <i>Nature</i> , 2020, 583, 752-759.	13.7	84
22	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
23	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
24	A massively parallel barcoded sequencing pipeline enables generation of the first ORFeome and interactome map for rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11836-11842.	3.3	16
25	Extraction of Distinct Neuronal Cell Types from within a Genetically Continuous Population. <i>Neuron</i> , 2020, 107, 274-282.e6.	3.8	88
26	Integrated multi-omics framework of the plant response to jasmonic acid. <i>Nature Plants</i> , 2020, 6, 290-302.	4.7	145
27	Chimeric Activators and Repressors Define HY5 Activity and Reveal a Light-Regulated Feedback Mechanism. <i>Plant Cell</i> , 2020, 32, 967-983.	3.1	96
28	Losing Dnmt3a dependent methylation in inhibitory neurons impairs neural function by a mechanism impacting Rett syndrome. <i>ELife</i> , 2020, 9, .	2.8	44
29	A MYC2/MYC3/MYC4-dependent transcription factor network regulates water spray-responsive gene expression and jasmonate levels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23345-23356.	3.3	95
30	Auxin-sensitive Aux/IAA proteins mediate drought tolerance in Arabidopsis by regulating glucosinolate levels. <i>Nature Communications</i> , 2019, 10, 4021.	5.8	155
31	Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. <i>Nature Methods</i> , 2019, 16, 999-1006.	9.0	200
32	Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons. <i>ELife</i> , 2019, 8, .	2.8	64
33	Genomic Decoding of Neuronal Depolarization by Stimulus-Specific NPAS4 Heterodimers. <i>Cell</i> , 2019, 179, 373-391.e27.	13.5	73
34	The complex architecture and epigenomic impact of plant T-DNA insertions. <i>PLoS Genetics</i> , 2019, 15, e1007819.	1.5	109
35	Robust single-cell Hi-C clustering by convolution- and random-walk-based imputation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14011-14018.	3.3	101
36	Diversity and dynamics of DNA methylation: epigenomic resources and tools for crop breeding. <i>Breeding Science</i> , 2019, 69, 191-204.	0.9	30

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37	Common alleles of CMT2 and NRPE1 are major determinants of CHH methylation variation in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2019, 15, e1008492.	1.5	68
38	Epigenetic silencing of a multifunctional plant stress regulator. <i>ELife</i> , 2019, 8, .	2.8	28
39	Title is missing!. , 2019, 15, e1008492.		0
40	Title is missing!. , 2019, 15, e1008492.		0
41	Title is missing!. , 2019, 15, e1008492.		0
42	Title is missing!. , 2019, 15, e1008492.		0
43	A B-ARR-mediated cytokinin transcriptional network directs hormone cross-regulation and shoot development. <i>Nature Communications</i> , 2018, 9, 1604.	5.8	130
44	High contiguity <i>Arabidopsis thaliana</i> genome assembly with a single nanopore flow cell. <i>Nature Communications</i> , 2018, 9, 541.	5.8	243
45	Piecing together cis-regulatory networks: insights from epigenomics studies in plants. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2018, 10, e1411.	6.6	13
46	Profiling Interactome Networks with the HaloTag-NAPPA In Situ Protein Array. <i>Current Protocols in Plant Biology</i> , 2018, 3, e20071.	2.8	8
47	Dynamic DNA methylation: In the right place at the right time. <i>Science</i> , 2018, 361, 1336-1340.	6.0	469
48	Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. <i>ELife</i> , 2018, 7, .	2.8	180
49	Robust single-cell DNA methylome profiling with snmC-seq2. <i>Nature Communications</i> , 2018, 9, 3824.	5.8	138
50	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
51	Plant Stress Tolerance Requires Auxin-Sensitive Aux/IAA Transcriptional Repressors. <i>Current Biology</i> , 2017, 27, 437-444.	1.8	148
52	Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <i>New Phytologist</i> , 2017, 214, 808-819.	3.5	75
53	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
54	Sequencing and functional validation of the JGI Brachypodium distachyon DNA collection. <i>Plant Journal</i> , 2017, 91, 361-370.	2.8	46

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55	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
56	<scp>JAZ</scp>2 controls stomata dynamics during bacterial invasion. New Phytologist, 2017, 213, 1378-1392.	3.5	124
57	The BRAIN Initiative Cell Census Consortium: Lessons Learned toward Generating a Comprehensive Brain Cell Atlas. Neuron, 2017, 96, 542-557.	3.8	235
58	Mapping genome-wide transcription-factor binding sites using DAP-seq. Nature Protocols, 2017, 12, 1659-1672.	5.5	330
59	Single-cell methylomes identify neuronal subtypes and regulatory elements in mammalian cortex. Science, 2017, 357, 600-604.	6.0	445
60	Challenges and recommendations for epigenomics in precision health. Nature Biotechnology, 2017, 35, 1128-1132.	9.4	19
61	CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. Nature Methods, 2017, 14, 819-825.	9.0	157
62	Functional Human Oocytes Generated by Transfer of Polar Body Genomes. Cell Stem Cell, 2017, 20, 112-119.	5.2	76
63	Dynamic and rapid changes in the transcriptome and epigenome during germination and in developing rice (<i>Oryza sativa</i>) coleoptiles under anoxia and reoxygenation. Plant Journal, 2017, 89, 805-824.	2.8	63
64	Dynamic DNA methylation reconfiguration during seed development and germination. Genome Biology, 2017, 18, 171.	3.8	218
65	An ABA-increased interaction of the PYL6 ABA receptor with MYC2 Transcription Factor: A putative link of ABA and JA signaling. Scientific Reports, 2016, 6, 28941.	1.6	155
66	Cerebral Organoids Recapitulate Epigenomic Signatures of the Human Fetal Brain. Cell Reports, 2016, 17, 3369-3384.	2.9	296
67	Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. Cell, 2016, 165, 1280-1292.	13.5	1,078
68	Integration of omic networks in a developmental atlas of maize. Science, 2016, 353, 814-818.	6.0	411
69	Profiling of Transcription Factor Binding Events by Chromatin Immunoprecipitation Sequencing (ChIP-seq). Current Protocols in Plant Biology, 2016, 1, 293-306.	2.8	24
70	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. Cell, 2016, 166, 492-505.	13.5	594
71	Molecular Criteria for Defining the Naive Human Pluripotent State. Cell Stem Cell, 2016, 19, 502-515.	5.2	415
72	Phased diploid genome assembly with single-molecule real-time sequencing. Nature Methods, 2016, 13, 1050-1054.	9.0	1,658

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73	Unique cell-type-specific patterns of DNA methylation in the root meristem. <i>Nature Plants</i> , 2016, 2, 16058.	4.7	159
74	EIN2-dependent regulation of acetylation of histone H3K14 and non-canonical histone H3K23 in ethylene signalling. <i>Nature Communications</i> , 2016, 7, 13018.	5.8	125
75	A transcription factor hierarchy defines an environmental stress response network. <i>Science</i> , 2016, 354, .	6.0	394
76	The <i>Arabidopsis</i> Auxin Receptor F-Box Proteins AFB4 and AFB5 Are Required for Response to the Synthetic Auxin Picloram. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1383-1390.	0.8	89
77	1,135 Genomes Reveal the Global Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2016, 166, 481-491.	13.5	1,107
78	Mapping transcription factor interactome networks using HaloTag protein arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4238-47.	3.3	67
79	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
80	A Proposal Regarding Best Practices for Validating the Identity of Genetic Stocks and the Effects of Genetic Variants. <i>Plant Cell</i> , 2016, 28, 606-609.	3.1	31
81	Active DNA demethylation at enhancers during the vertebrate phylotypic period. <i>Nature Genetics</i> , 2016, 48, 417-426.	9.4	210
82	Cryptochromes Interact Directly with PIFs to Control Plant Growth in Limiting Blue Light. <i>Cell</i> , 2016, 164, 233-245.	13.5	445
83	Epigenomic landscapes of retinal rods and cones. <i>ELife</i> , 2016, 5, e11613.	2.8	106
84	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
85	Stress induced gene expression drives transient DNA methylation changes at adjacent repetitive elements. <i>ELife</i> , 2015, 4, .	2.8	285
86	Exceptional epigenetics in the brain. <i>Science</i> , 2015, 348, 1094-1095.	6.0	11
87	Human body epigenome maps reveal noncanonical DNA methylation variation. <i>Nature</i> , 2015, 523, 212-216.	13.7	605
88	MethylC-seq library preparation for base-resolution whole-genome bisulfite sequencing. <i>Nature Protocols</i> , 2015, 10, 475-483.	5.5	250
89	Integrative analysis of haplotype-resolved epigenomes across human tissues. <i>Nature</i> , 2015, 518, 350-354.	13.7	201
90	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	13.7	5,653

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91	Chromatin architecture reorganization during stem cell differentiation. <i>Nature</i> , 2015, 518, 331-336.	13.7	1,442
92	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. <i>Neuron</i> , 2015, 86, 1369-1384.	3.8	640
93	Non-CG Methylation in the Human Genome. <i>Annual Review of Genomics and Human Genetics</i> , 2015, 16, 55-77.	2.5	210
94	An alternative pluripotent state confers interspecies chimaeric competency. <i>Nature</i> , 2015, 521, 316-321.	13.7	215
95	ERRs Mediate a Metabolic Switch Required for Somatic Cell Reprogramming to Pluripotency. <i>Cell Stem Cell</i> , 2015, 16, 547-555.	5.2	109
96	Genome-wide identification of CCA1 targets uncovers an expanded clock network in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4802-10.	3.3	230
97	A User's Guide to the <i>Arabidopsis</i> T-DNA Insertion Mutant Collections. <i>Methods in Molecular Biology</i> , 2015, 1284, 323-342.	0.4	91
98	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
99	DNA Topoisomerase I Promotes Transcriptional Silencing of Transposable Elements through DNA Methylation and Histone Lysine 9 Dimethylation in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2014, 10, e1004446.	1.5	26
100	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
101	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
102	Genotypic variation of gene expression during the soybean innate immunity response. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S27-S30.	0.4	11
103	The Developmental Potential of iPSCs Is Greatly Influenced by Reprogramming Factor Selection. <i>Cell Stem Cell</i> , 2014, 15, 295-309.	5.2	137
104	A Genome-Scale Resource for the Functional Characterization of <i>Arabidopsis</i> Transcription Factors. <i>Cell Reports</i> , 2014, 8, 622-632.	2.9	164
105	The <i>Arabidopsis</i> 14-3-3 Protein RARE COLD INDUCIBLE 1A Links Low-Temperature Response and Ethylene Biosynthesis to Regulate Freezing Tolerance and Cold Acclimation. <i>Plant Cell</i> , 2014, 26, 3326-3342.	3.1	178
106	Convergent Targeting of a Common Host Protein-Network by Pathogen Effectors from Three Kingdoms of Life. <i>Cell Host and Microbe</i> , 2014, 16, 364-375.	5.1	367
107	Determination and Inference of Eukaryotic Transcription Factor Sequence Specificity. <i>Cell</i> , 2014, 158, 1431-1443.	13.5	1,515
108	Abnormalities in human pluripotent cells due to reprogramming mechanisms. <i>Nature</i> , 2014, 511, 177-183.	13.7	307

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109	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.	2.4	83
110	Global Epigenomic Reconfiguration During Mammalian Brain Development. <i>Science</i> , 2013, 341, 1237905.	6.0	1,609
111	Sigma factor-mediated plastid retrograde signals control nuclear gene expression. <i>Plant Journal</i> , 2013, 73, 1-13.	2.8	145
112	Patterns of population epigenomic diversity. <i>Nature</i> , 2013, 495, 193-198.	13.7	543
113	Epigenetic trigger for tomato ripening. <i>Nature Biotechnology</i> , 2013, 31, 119-120.	9.4	21
114	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	13.5	689
115	STAR: an integrated solution to management and visualization of sequencing data. <i>Bioinformatics</i> , 2013, 29, 3204-3210.	1.8	13
116	Functional Characterization of Type-B Response Regulators in the Arabidopsis Cytokinin Response. <i>Plant Physiology</i> , 2013, 162, 212-224.	2.3	82
117	Response to Perspective. <i>Plant Signaling and Behavior</i> , 2013, 8, e25037.	1.2	5
118	Basic Helix-Loop-Helix Transcription Factors MYC2, MYC3, and MYC4 Regulate Glucosinolate Biosynthesis, Insect Performance, and Feeding Behavior. <i>Plant Cell</i> , 2013, 25, 3117-3132.	3.1	453
119	Epigenomic programming contributes to the genomic drift evolution of the F-Box protein superfamily in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16927-16932.	3.3	25
120	Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. <i>Genome Research</i> , 2013, 23, 1663-1674.	2.4	227
121	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. <i>ELife</i> , 2013, 2, e00675.	2.8	379
122	Detection of allele-specific methylation through a generalized heterogeneous epigenome model. <i>Bioinformatics</i> , 2012, 28, i163-i171.	1.8	21
123	Surveillance of Noncoding Transcripts Requires FIERY1 and XRN3 in Arabidopsis. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 487-498.	0.8	47
124	A Blueprint for an International Cancer Epigenome Consortium. A Report from the AACR Cancer Epigenome Task Force. <i>Cancer Research</i> , 2012, 72, 6319-6324.	0.4	22
125	Spatial and functional relationships among Pol V-associated loci, Pol IV-dependent siRNAs, and cytosine methylation in the Arabidopsis epigenome. <i>Genes and Development</i> , 2012, 26, 1825-1836.	2.7	137
126	Circadian Oscillations of Protein-Coding and Regulatory RNAs in a Highly Dynamic Mammalian Liver Epigenome. <i>Cell Metabolism</i> , 2012, 16, 833-845.	7.2	230

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127	Linking photoreceptor excitation to changes in plant architecture. <i>Genes and Development</i> , 2012, 26, 785-790.	2.7	460
128	Release Factor One Is Nonessential in <i>Escherichia coli</i> . <i>ACS Chemical Biology</i> , 2012, 7, 1337-1344.	1.6	100
129	Epigenetic and epigenomic variation in <i>Arabidopsis thaliana</i> . <i>Trends in Plant Science</i> , 2012, 17, 149-154.	4.3	92
130	Processing and Subcellular Trafficking of ER-Tethered EIN2 Control Response to Ethylene Gas. <i>Science</i> , 2012, 338, 390-393.	6.0	461
131	ENCODE explained. <i>Nature</i> , 2012, 489, 52-54.	13.7	245
132	“Leveling” the playing field for analyses of single-base resolution DNA methylomes. <i>Trends in Genetics</i> , 2012, 28, 583-585.	2.9	276
133	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
134	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
135	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. <i>Science</i> , 2011, 333, 601-607.	6.0	838
136	RF1 knockout allows ribosomal incorporation of unnatural amino acids at multiple sites. <i>Nature Chemical Biology</i> , 2011, 7, 779-786.	3.9	286
137	Transgenerational Epigenetic Instability Is a Source of Novel Methylation Variants. <i>Science</i> , 2011, 334, 369-373.	6.0	635
138	Forward and Reverse Genetics through Derivation of Haploid Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2011, 9, 563-574.	5.2	208
139	Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. <i>Science</i> , 2011, 333, 596-601.	6.0	776
140	Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> , 2011, 471, 68-73.	13.7	1,442
141	Genome-wide mapping of 5-hydroxymethylcytosine in embryonic stem cells. <i>Nature</i> , 2011, 473, 394-397.	13.7	738
142	The DNA methylome. <i>FEBS Letters</i> , 2011, 585, 1994-2000.	1.3	80
143	Unexpected Diversity of Chloroplast Noncoding RNAs as Revealed by Deep Sequencing of the <i>Arabidopsis</i> Transcriptome. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 559-570.	0.8	71
144	Linking genotype to phenotype using the <i>Arabidopsis</i> unimutant collection. <i>Plant Journal</i> , 2010, 61, 928-940.	2.8	171

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145	Genome-wide association study of 107 phenotypes in <i>Arabidopsis thaliana</i> inbred lines. <i>Nature</i> , 2010, 465, 627-631.	13.7	1,651
146	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
147	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010, 28, 1045-1048.	9.4	1,705
148	Zeroing in on DNA methylomes with no BS. <i>Nature Methods</i> , 2010, 7, 435-437.	9.0	8
149	Direct transcriptional control of the <i>Arabidopsis</i> immune receptor FLS2 by the ethylene-dependent transcription factors EIN3 and EIL1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14502-14507.	3.3	218
150	Two Plant Viral Suppressors of Silencing Require the Ethylene-Inducible Host Transcription Factor RAV2 to Block RNA Silencing. <i>PLoS Pathogens</i> , 2010, 6, e1000729.	2.1	124
151	Ethylene Responses in Seedling Growth and Development. , 2010, , 358-376.		2
152	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. <i>Cell Stem Cell</i> , 2010, 6, 479-491.	5.2	747
153	Ethylene-Induced Stabilization of ETHYLENE INSENSITIVE3 and EIN3-LIKE1 Is Mediated by Proteasomal Degradation of EIN3 Binding F-Box 1 and 2 That Requires EIN2 in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2010, 22, 2384-2401.	3.1	432
154	Finding the fifth base: Genome-wide sequencing of cytosine methylation. <i>Genome Research</i> , 2009, 19, 959-966.	2.4	323
155	A Family of Bacterial Cysteine Protease Type III Effectors Utilizes Acylation-dependent and -independent Strategies to Localize to Plasma Membranes. <i>Journal of Biological Chemistry</i> , 2009, 284, 15867-15879.	1.6	92
156	A Combinatorial Interplay Among the 1-Aminocyclopropane-1-Carboxylate Isoforms Regulates Ethylene Biosynthesis in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2009, 183, 979-1003.	1.2	263
157	Interplay between ethylene, ETP1/ETP2 F-box proteins, and degradation of EIN2 triggers ethylene responses in <i>Arabidopsis</i> . <i>Genes and Development</i> , 2009, 23, 512-521.	2.7	297
158	Regulation of membrane trafficking and organ separation by the NEVERSHED ARF-GAP protein. <i>Development (Cambridge)</i> , 2009, 136, 1909-1918.	1.2	106
159	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
160	Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> , 2009, 462, 315-322.	13.7	4,063
161	Prepublication data sharing. <i>Nature</i> , 2009, 461, 168-170.	13.7	243
162	Literature-curated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 39-46.	9.0	288

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163	Exploring the transcriptional landscape of plant circadian rhythms using genome tiling arrays. <i>Genome Biology</i> , 2009, 10, R17.	13.9	103
164	Utilizing tiling microarrays for whole-genome analysis in plants. <i>Plant Journal</i> , 2008, 53, 636-644.	2.8	44
165	Highly Integrated Single-Base Resolution Maps of the Epigenome in <i>Arabidopsis</i> . <i>Cell</i> , 2008, 133, 523-536.	13.5	2,229
166	A Link between RNA Metabolism and Silencing Affecting <i>Arabidopsis</i> Development. <i>Developmental Cell</i> , 2008, 14, 854-866.	3.1	394
167	The <i>Arabidopsis</i> Phytochrome-Interacting Factor PIF7, Together with PIF3 and PIF4, Regulates Responses to Prolonged Red Light by Modulating phyB Levels. <i>Plant Cell</i> , 2008, 20, 337-352.	3.1	334
168	Potential Sites of Bioactive Gibberellin Production during Reproductive Growth in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2008, 20, 320-336.	3.1	209
169	The phosphatase laforin crosses evolutionary boundaries and links carbohydrate metabolism to neuronal disease. <i>FASEB Journal</i> , 2008, 22, 102.2.	0.2	0
170	Genome-wide patterns of single-feature polymorphism in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12057-12062.	3.3	157
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