

Joseph R Ecker

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/382557/publications.pdf>

Version: 2024-02-01

284
papers

101,231
citations

246

143
h-index

322

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, .	7.1	11
2	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. Cell Genomics, 2022, 2, 100107.	6.5	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.	6.6	31
4	The emergence of the brain non-CpG methylation system in vertebrates. Nature Ecology and Evolution, 2021, 5, 369-378.	7.8	63
5	Comprehensive analysis of single cell ATAC-seq data with SnapATAC. Nature Communications, 2021, 12, 1337.	12.8	253
6	Iterative single-cell multi-omic integration using online learning. Nature Biotechnology, 2021, 39, 1000-1007.	17.5	53
7	Single nucleus multi-omics regulatory landscape of the murine pituitary. Nature Communications, 2021, 12, 2677.	12.8	38
8	PHYTOCHROME-INTERACTING FACTORs trigger environmentally responsive chromatin dynamics in plants. Nature Genetics, 2021, 53, 955-961.	21.4	54
9	A plant-specific syntaxin-6 protein contributes to the intracytoplasmic route for the begomovirus CabLCV. Plant Physiology, 2021, 187, 158-173.	4.8	12
10	Activity-dependent modulation of synapse-regulating genes in astrocytes. ELife, 2021, 10, .	6.0	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.	5.5	56
12	An atlas of gene regulatory elements in adult mouse cerebrum. Nature, 2021, 598, 129-136.	27.8	95
13	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	27.8	166
14	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	27.8	361
15	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	27.8	316
16	DNA methylation atlas of the mouse brain at single-cell resolution. Nature, 2021, 598, 120-128.	27.8	135
17	Epigenomic diversity of cortical projection neurons in the mouse brain. Nature, 2021, 598, 167-173.	27.8	47
18	The biology of time: dynamic responses of cell types to developmental, circadian, and environmental cues. Plant Journal, 2021, , .	5.7	8

#	ARTICLE	IF	CITATIONS
19	The JA pathway MYC transcription factors regulate photomorphogenic responses by targeting HY5 gene expression. <i>Plant Journal</i> , 2020, 102, 138-152.	5.7	47
20	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	27.8	257
21	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. <i>Nature</i> , 2020, 583, 752-759.	27.8	84
22	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
23	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	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.	7.1	16
25	Extraction of Distinct Neuronal Cell Types from within a Genetically Continuous Population. <i>Neuron</i> , 2020, 107, 274-282.e6.	8.1	88
26	Integrated multi-omics framework of the plant response to jasmonic acid. <i>Nature Plants</i> , 2020, 6, 290-302.	9.3	145
27	Chimeric Activators and Repressors Define HY5 Activity and Reveal a Light-Regulated Feedback Mechanism. <i>Plant Cell</i> , 2020, 32, 967-983.	6.6	96
28	Losing Dnmt3a dependent methylation in inhibitory neurons impairs neural function by a mechanism impacting Rett syndrome. <i>ELife</i> , 2020, 9, .	6.0	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.	7.1	95
30	Auxin-sensitive Aux/IAA proteins mediate drought tolerance in Arabidopsis by regulating glucosinolate levels. <i>Nature Communications</i> , 2019, 10, 4021.	12.8	155
31	Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. <i>Nature Methods</i> , 2019, 16, 999-1006.	19.0	200
32	Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons. <i>ELife</i> , 2019, 8, .	6.0	64
33	Genomic Decoding of Neuronal Depolarization by Stimulus-Specific NPAS4 Heterodimers. <i>Cell</i> , 2019, 179, 373-391.e27.	28.9	73
34	The complex architecture and epigenomic impact of plant T-DNA insertions. <i>PLoS Genetics</i> , 2019, 15, e1007819.	3.5	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.	7.1	101
36	Diversity and dynamics of DNA methylation: epigenomic resources and tools for crop breeding. <i>Breeding Science</i> , 2019, 69, 191-204.	1.9	30

#	ARTICLE	IF	CITATIONS
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.	3.5	68
38	Epigenetic silencing of a multifunctional plant stress regulator. <i>ELife</i> , 2019, 8, .	6.0	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.	12.8	130
44	High contiguity <i>Arabidopsis thaliana</i> genome assembly with a single nanopore flow cell. <i>Nature Communications</i> , 2018, 9, 541.	12.8	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.	12.6	469
48	Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. <i>ELife</i> , 2018, 7, .	6.0	180
49	Robust single-cell DNA methylome profiling with snmC-seq2. <i>Nature Communications</i> , 2018, 9, 3824.	12.8	138
50	OGT binds a conserved C-terminal domain of TET1 to regulate TET1 activity and function in development. <i>ELife</i> , 2018, 7, .	6.0	46
51	Plant Stress Tolerance Requires Auxin-Sensitive Aux/IAA Transcriptional Repressors. <i>Current Biology</i> , 2017, 27, 437-444.	3.9	148
52	Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <i>New Phytologist</i> , 2017, 214, 808-819.	7.3	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.	7.1	78
54	Sequencing and functional validation of the JGI Brachypodium distachyon DNA collection. <i>Plant Journal</i> , 2017, 91, 361-370.	5.7	46

#	ARTICLE	IF	CITATIONS
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.	7.1	45
56	<sc>JAZ</sc>2 controls stomata dynamics during bacterial invasion. New Phytologist, 2017, 213, 1378-1392.	7.3	124
57	The BRAIN Initiative Cell Census Consortium: Lessons Learned toward Generating a Comprehensive Brain Cell Atlas. Neuron, 2017, 96, 542-557.	8.1	235
58	Mapping genome-wide transcription-factor binding sites using DAP-seq. Nature Protocols, 2017, 12, 1659-1672.	12.0	330
59	Single-cell methylomes identify neuronal subtypes and regulatory elements in mammalian cortex. Science, 2017, 357, 600-604.	12.6	445
60	Challenges and recommendations for epigenomics in precision health. Nature Biotechnology, 2017, 35, 1128-1132.	17.5	19
61	CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. Nature Methods, 2017, 14, 819-825.	19.0	157
62	Functional Human Oocytes Generated by Transfer of Polar Body Genomes. Cell Stem Cell, 2017, 20, 112-119.	11.1	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.	5.7	63
64	Dynamic DNA methylation reconfiguration during seed development and germination. Genome Biology, 2017, 18, 171.	8.8	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.	3.3	155
66	Cerebral Organoids Recapitulate Epigenomic Signatures of the Human Fetal Brain. Cell Reports, 2016, 17, 3369-3384.	6.4	296
67	Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. Cell, 2016, 165, 1280-1292.	28.9	1,078
68	Integration of omic networks in a developmental atlas of maize. Science, 2016, 353, 814-818.	12.6	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.	28.9	594
71	Molecular Criteria for Defining the Naive Human Pluripotent State. Cell Stem Cell, 2016, 19, 502-515.	11.1	415
72	Phased diploid genome assembly with single-molecule real-time sequencing. Nature Methods, 2016, 13, 1050-1054.	19.0	1,658

#	ARTICLE	IF	CITATIONS
73	Unique cell-type-specific patterns of DNA methylation in the root meristem. <i>Nature Plants</i> , 2016, 2, 16058.	9.3	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.	12.8	125
75	A transcription factor hierarchy defines an environmental stress response network. <i>Science</i> , 2016, 354, .	12.6	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.	1.8	89
77	1,135 Genomes Reveal the Global Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2016, 166, 481-491.	28.9	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.	7.1	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.	7.1	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.	6.6	31
81	Active DNA demethylation at enhancers during the vertebrate phylotypic period. <i>Nature Genetics</i> , 2016, 48, 417-426.	21.4	210
82	Cryptochromes Interact Directly with PIFs to Control Plant Growth in Limiting Blue Light. <i>Cell</i> , 2016, 164, 233-245.	28.9	445
83	Epigenomic landscapes of retinal rods and cones. <i>ELife</i> , 2016, 5, e11613.	6.0	106
84	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
85	Stress induced gene expression drives transient DNA methylation changes at adjacent repetitive elements. <i>ELife</i> , 2015, 4, .	6.0	285
86	Exceptional epigenetics in the brain. <i>Science</i> , 2015, 348, 1094-1095.	12.6	11
87	Human body epigenome maps reveal noncanonical DNA methylation variation. <i>Nature</i> , 2015, 523, 212-216.	27.8	605
88	MethylC-seq library preparation for base-resolution whole-genome bisulfite sequencing. <i>Nature Protocols</i> , 2015, 10, 475-483.	12.0	250
89	Integrative analysis of haplotype-resolved epigenomes across human tissues. <i>Nature</i> , 2015, 518, 350-354.	27.8	201
90	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653

#	ARTICLE	IF	CITATIONS
91	Chromatin architecture reorganization during stem cell differentiation. <i>Nature</i> , 2015, 518, 331-336.	27.8	1,442
92	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. <i>Neuron</i> , 2015, 86, 1369-1384.	8.1	640
93	Non-CG Methylation in the Human Genome. <i>Annual Review of Genomics and Human Genetics</i> , 2015, 16, 55-77.	6.2	210
94	An alternative pluripotent state confers interspecies chimaeric competency. <i>Nature</i> , 2015, 521, 316-321.	27.8	215
95	ERRs Mediate a Metabolic Switch Required for Somatic Cell Reprogramming to Pluripotency. <i>Cell Stem Cell</i> , 2015, 16, 547-555.	11.1	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.	7.1	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.	0.9	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.	5.5	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.	3.5	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.	7.1	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.	7.1	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.	0.8	11
103	The Developmental Potential of iPSCs Is Greatly Influenced by Reprogramming Factor Selection. <i>Cell Stem Cell</i> , 2014, 15, 295-309.	11.1	137
104	A Genome-Scale Resource for the Functional Characterization of <i>Arabidopsis</i> Transcription Factors. <i>Cell Reports</i> , 2014, 8, 622-632.	6.4	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.	6.6	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.	11.0	367
107	Determination and Inference of Eukaryotic Transcription Factor Sequence Specificity. <i>Cell</i> , 2014, 158, 1431-1443.	28.9	1,515
108	Abnormalities in human pluripotent cells due to reprogramming mechanisms. <i>Nature</i> , 2014, 511, 177-183.	27.8	307

#	ARTICLE	IF	CITATIONS
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.	5.5	83
110	Global Epigenomic Reconfiguration During Mammalian Brain Development. <i>Science</i> , 2013, 341, 1237905.	12.6	1,609
111	Sigma factor-mediated plastid retrograde signals control nuclear gene expression. <i>Plant Journal</i> , 2013, 73, 1-13.	5.7	145
112	Patterns of population epigenomic diversity. <i>Nature</i> , 2013, 495, 193-198.	27.8	543
113	Epigenetic trigger for tomato ripening. <i>Nature Biotechnology</i> , 2013, 31, 119-120.	17.5	21
114	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	28.9	689
115	STAR: an integrated solution to management and visualization of sequencing data. <i>Bioinformatics</i> , 2013, 29, 3204-3210.	4.1	13
116	Functional Characterization of Type-B Response Regulators in the Arabidopsis Cytokinin Response. <i>Plant Physiology</i> , 2013, 162, 212-224.	4.8	82
117	Response to Perspective. <i>Plant Signaling and Behavior</i> , 2013, 8, e25037.	2.4	5
118	Basic Helix-Loop-Helix Transcription Factors MYC2, MYC3, and MYC4 Regulate Glucosinolate Biosynthesis, Insect Performance, and Feeding Behavior in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 25, 3117-3132.	6.6	453
119	Epigenomic programming contributes to the genomic drift evolution of the F-Box protein superfamily in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16927-16932.	7.1	25
120	Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. <i>Genome Research</i> , 2013, 23, 1663-1674.	5.5	227
121	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in <i>Arabidopsis</i> . <i>ELife</i> , 2013, 2, e00675.	6.0	379
122	Detection of allele-specific methylation through a generalized heterogeneous epigenome model. <i>Bioinformatics</i> , 2012, 28, i163-i171.	4.1	21
123	Surveillance of Noncoding Transcripts Requires FIERY1 and XRN3 in <i>Arabidopsis</i> . <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 487-498.	1.8	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.	0.9	22
125	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
126	Circadian Oscillations of Protein-Coding and Regulatory RNAs in a Highly Dynamic Mammalian Liver Epigenome. <i>Cell Metabolism</i> , 2012, 16, 833-845.	16.2	230

#	ARTICLE	IF	CITATIONS
127	Linking photoreceptor excitation to changes in plant architecture. <i>Genes and Development</i> , 2012, 26, 785-790.	5.9	460
128	Release Factor One Is Nonessential in <i>Escherichia coli</i> . <i>ACS Chemical Biology</i> , 2012, 7, 1337-1344.	3.4	100
129	Epigenetic and epigenomic variation in <i>Arabidopsis thaliana</i> . <i>Trends in Plant Science</i> , 2012, 17, 149-154.	8.8	92
130	Processing and Subcellular Trafficking of ER-Tethered EIN2 Control Response to Ethylene Gas. <i>Science</i> , 2012, 338, 390-393.	12.6	461
131	ENCODE explained. <i>Nature</i> , 2012, 489, 52-54.	27.8	245
132	“Leveling” the playing field for analyses of single-base resolution DNA methylomes. <i>Trends in Genetics</i> , 2012, 28, 583-585.	6.7	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.	5.5	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.	7.1	878
135	Evidence for Network Evolution in an <i>Arabidopsis</i> Interactome Map. <i>Science</i> , 2011, 333, 601-607.	12.6	838
136	RF1 knockout allows ribosomal incorporation of unnatural amino acids at multiple sites. <i>Nature Chemical Biology</i> , 2011, 7, 779-786.	8.0	286
137	Transgenerational Epigenetic Instability Is a Source of Novel Methylation Variants. <i>Science</i> , 2011, 334, 369-373.	12.6	635
138	Forward and Reverse Genetics through Derivation of Haploid Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2011, 9, 563-574.	11.1	208
139	Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. <i>Science</i> , 2011, 333, 596-601.	12.6	776
140	Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> , 2011, 471, 68-73.	27.8	1,442
141	Genome-wide mapping of 5-hydroxymethylcytosine in embryonic stem cells. <i>Nature</i> , 2011, 473, 394-397.	27.8	738
142	The DNA methylome. <i>FEBS Letters</i> , 2011, 585, 1994-2000.	2.8	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.	1.8	71
144	Linking genotype to phenotype using the <i>Arabidopsis</i> unimutant collection. <i>Plant Journal</i> , 2010, 61, 928-940.	5.7	171

#	ARTICLE	IF	CITATIONS
145	Genome-wide association study of 107 phenotypes in <i>Arabidopsis thaliana</i> inbred lines. <i>Nature</i> , 2010, 465, 627-631.	27.8	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.	17.5	647
147	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010, 28, 1045-1048.	17.5	1,705
148	Zeroing in on DNA methylomes with no BS. <i>Nature Methods</i> , 2010, 7, 435-437.	19.0	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.	7.1	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.	4.7	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.	11.1	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.	6.6	432
154	Finding the fifth base: Genome-wide sequencing of cytosine methylation. <i>Genome Research</i> , 2009, 19, 959-966.	5.5	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.	3.4	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.	2.9	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.	5.9	297
158	Regulation of membrane trafficking and organ separation by the NEVERSHED ARF-GAP protein. <i>Development (Cambridge)</i> , 2009, 136, 1909-1918.	2.5	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.	7.1	261
160	Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> , 2009, 462, 315-322.	27.8	4,063
161	Prepublication data sharing. <i>Nature</i> , 2009, 461, 168-170.	27.8	243
162	Literature-curated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 39-46.	19.0	288

#	ARTICLE	IF	CITATIONS
163	Exploring the transcriptional landscape of plant circadian rhythms using genome tiling arrays. <i>Genome Biology</i> , 2009, 10, R17.	9.6	103
164	Utilizing tiling microarrays for whole-genome analysis in plants. <i>Plant Journal</i> , 2008, 53, 636-644.	5.7	44
165	Highly Integrated Single-Base Resolution Maps of the Epigenome in <i>Arabidopsis</i> . <i>Cell</i> , 2008, 133, 523-536.	28.9	2,229
166	A Link between RNA Metabolism and Silencing Affecting <i>Arabidopsis</i> Development. <i>Developmental Cell</i> , 2008, 14, 854-866.	7.0	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.	6.6	334
168	Potential Sites of Bioactive Gibberellin Production during Reproductive Growth in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2008, 20, 320-336.	6.6	209
169	The phosphatase laforin crosses evolutionary boundaries and links carbohydrate metabolism to neuronal disease. <i>FASEB Journal</i> , 2008, 22, 102.2.	0.5	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.	7.1	157
171	The phosphatase laforin crosses evolutionary boundaries and links carbohydrate metabolism to neuronal disease. <i>Journal of Cell Biology</i> , 2007, 178, 477-488.	5.2	140
172	Small RNA-mediated chromatin silencing directed to the 3' region of the <i>Arabidopsis</i> gene encoding the developmental regulator, FLC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3633-3638.	7.1	116
173	Higher plants possess two different types of ATX1-like copper chaperones. <i>Biochemical and Biophysical Research Communications</i> , 2007, 354, 385-390.	2.1	92
174	Genome-Wide High-Resolution Mapping of Exosome Substrates Reveals Hidden Features in the <i>Arabidopsis</i> Transcriptome. <i>Cell</i> , 2007, 131, 1340-1353.	28.9	298
175	A WD40 Domain Cyclophilin Interacts with Histone H3 and Functions in Gene Repression and Organogenesis in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2007, 19, 2403-2416.	6.6	66
176	Common Sequence Polymorphisms Shaping Genetic Diversity in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007, 317, 338-342.	12.6	689
177	Recombination and linkage disequilibrium in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2007, 39, 1151-1155.	21.4	497
178	An adapter ligation-mediated PCR method for high-throughput mapping of T-DNA inserts in the <i>Arabidopsis</i> genome. <i>Nature Protocols</i> , 2007, 2, 2910-2917.	12.0	111
179	Mapping the genome landscape using tiling array technology. <i>Current Opinion in Plant Biology</i> , 2007, 10, 534-542.	7.1	61
180	The phosphatase laforin crosses evolutionary boundaries and links carbohydrate metabolism to neuronal disease. <i>Journal of Experimental Medicine</i> , 2007, 204, i22-i22.	8.5	0

#	ARTICLE	IF	CITATIONS
181	Localization of Iron in Arabidopsis Seed Requires the Vacuolar Membrane Transporter VIT1. <i>Science</i> , 2006, 314, 1295-1298.	12.6	614
182	Genome-wide High-Resolution Mapping and Functional Analysis of DNA Methylation in Arabidopsis. <i>Cell</i> , 2006, 126, 1189-1201.	28.9	1,647
183	CDPKs CPK6 and CPK3 Function in ABA Regulation of Guard Cell S-Type Anion- and Ca ²⁺ - Permeable Channels and Stomatal Closure. <i>PLoS Biology</i> , 2006, 4, e327.	5.6	523
184	The Arabidopsis heavy metal P-type ATPase HMA5 interacts with metallochaperones and functions in copper detoxification of roots. <i>Plant Journal</i> , 2006, 45, 225-236.	5.7	290
185	Moving forward in reverse: genetic technologies to enable genome-wide phenomic screens in Arabidopsis. <i>Nature Reviews Genetics</i> , 2006, 7, 524-536.	16.3	230
186	The ACC synthase TOE sequence is required for interaction with ETO1 family proteins and destabilization of target proteins. <i>Plant Molecular Biology</i> , 2006, 62, 427-437.	3.9	67
187	The Arabidopsis Histidine Phosphotransfer Proteins Are Redundant Positive Regulators of Cytokinin Signaling. <i>Plant Cell</i> , 2006, 18, 3073-3087.	6.6	392
188	The POLARIS Peptide of Arabidopsis Regulates Auxin Transport and Root Growth via Effects on Ethylene Signaling. <i>Plant Cell</i> , 2006, 18, 3058-3072.	6.6	146
189	Retroviral DNA Integration: Viral and Cellular Determinants of Target-Site Selection. <i>PLoS Pathogens</i> , 2006, 2, e60.	4.7	310
190	PHYTOCHROME KINASE SUBSTRATE 1 is a phototropin 1 binding protein required for phototropism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10134-10139.	7.1	176
191	HIV Integration Site Selection: Targeting in Macrophages and the Effects of Different Routes of Viral Entry. <i>Molecular Therapy</i> , 2006, 14, 218-225.	8.2	83
192	ETHYLENE-INSENSITIVE5 encodes a 5'→3' exoribonuclease required for regulation of the EIN3-targeting F-box proteins EBF1/2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13286-13293.	7.1	163
193	Integration Site Selection by HIV-Based Vectors in Dividing and Growth-Arrested IMR-90 Lung Fibroblasts. <i>Molecular Therapy</i> , 2006, 13, 366-373.	8.2	57
194	RACK1 mediates multiple hormone responsiveness and developmental processes in Arabidopsis. <i>Journal of Experimental Botany</i> , 2006, 57, 2697-2708.	4.8	128
195	Downregulation of ClpR2 Leads to Reduced Accumulation of the ClpPRS Protease Complex and Defects in Chloroplast Biogenesis in Arabidopsis. <i>Plant Cell</i> , 2006, 18, 1704-1721.	6.6	110
196	Arabidopsis ETO1 specifically interacts with and negatively regulates type 2 1-aminocyclopropane-1-carboxylate synthases. <i>BMC Plant Biology</i> , 2005, 5, 14.	3.6	148
197	NPH4/ARF7 and ARF19 promote leaf expansion and auxin-induced lateral root formation. <i>Plant Journal</i> , 2005, 43, 118-130.	5.7	415
198	A role for LEDGF/p75 in targeting HIV DNA integration. <i>Nature Medicine</i> , 2005, 11, 1287-1289.	30.7	583

#	ARTICLE	IF	CITATIONS
199	FRIGIDA-Independent Variation in Flowering Time of Natural Arabidopsis thaliana Accessions. <i>Genetics</i> , 2005, 170, 1197-1207.	2.9	138
200	Class III Homeodomain-Leucine Zipper Gene Family Members Have Overlapping, Antagonistic, and Distinct Roles in Arabidopsis Development. <i>Plant Cell</i> , 2005, 17, 61-76.	6.6	650
201	Functional Genomic Analysis of the AUXIN/INDOLE-3-ACETIC ACID Gene Family Members in Arabidopsis thaliana [W]. <i>Plant Cell</i> , 2005, 17, 3282-3300.	6.6	331
202	LUX ARRHYTHMO encodes a Myb domain protein essential for circadian rhythms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10387-10392.	7.1	381
203	Auxin response factors ARF6 and ARF8 promote jasmonic acid production and flower maturation. <i>Development (Cambridge)</i> , 2005, 132, 4107-4118.	2.5	608
204	Multiple Type-B Response Regulators Mediate Cytokinin Signal Transduction in Arabidopsis [W]. <i>Plant Cell</i> , 2005, 17, 3007-3018.	6.6	397
205	Rapid Array Mapping of Circadian Clock and Developmental Mutations in Arabidopsis. <i>Plant Physiology</i> , 2005, 138, 990-997.	4.8	85
206	Genome-wide analysis of cAMP-response element binding protein occupancy, phosphorylation, and target gene activation in human tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4459-4464.	7.1	878
207	Functional Genomic Analysis of the AUXIN RESPONSE FACTOR Gene Family Members in Arabidopsis thaliana: Unique and Overlapping Functions of ARF7 and ARF19 [W]. <i>Plant Cell</i> , 2005, 17, 444-463.	6.6	933
208	Quantitative trait locus mapping and DNA array hybridization identify an FLM deletion as a cause for natural flowering-time variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2460-2465.	7.1	174
209	Phytochrome-Specific Type 5 Phosphatase Controls Light Signal Flux by Enhancing Phytochrome Stability and Affinity for a Signal Transducer. <i>Cell</i> , 2005, 120, 395-406.	28.9	148
210	Applications of DNA tiling arrays for whole-genome analysis. <i>Genomics</i> , 2005, 85, 1-15.	2.9	376
211	A Homolog of Prokaryotic Thiol Disulfide Transporter CcdA Is Required for the Assembly of the Cytochrome <i>bc</i> ₁ Complex in Arabidopsis Chloroplasts. <i>Journal of Biological Chemistry</i> , 2004, 279, 32474-32482.	3.4	90
212	The phytochrome-interacting transcription factor, PIF3, acts early, selectively, and positively in light-induced chloroplast development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16091-16098.	7.1	275
213	Retroviral DNA Integration: ASLV, HIV, and MLV Show Distinct Target Site Preferences. <i>PLoS Biology</i> , 2004, 2, e234.	5.6	830
214	Type-A Arabidopsis Response Regulators Are Partially Redundant Negative Regulators of Cytokinin Signaling[W]. <i>Plant Cell</i> , 2004, 16, 658-671.	6.6	631
215	Reentry of the Ethylene MPK6 Module. <i>Plant Cell</i> , 2004, 16, 3169-3173.	6.6	58
216	GCR1 Can Act Independently of Heterotrimeric G-Protein in Response to Brassinosteroids and Gibberellins in Arabidopsis Seed Germination. <i>Plant Physiology</i> , 2004, 135, 907-915.	4.8	160

#	ARTICLE	IF	CITATIONS
217	Light-Response Quantitative Trait Loci Identified with Composite Interval and eXtreme Array Mapping in <i>Arabidopsis thaliana</i> . Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY394847 and AY466496. <i>Genetics</i> , 2004, 167, 907-917.	2.9	83
218	Short-Term Growth Responses to Ethylene in <i>Arabidopsis</i> Seedlings Are EIN3/EIL1 Independent. <i>Plant Physiology</i> , 2004, 136, 2921-2927.	4.8	140
219	Regulation of flowering time in <i>Arabidopsis</i> by K homology domain proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12759-12764.	7.1	150
220	CBF2/DREB1C is a negative regulator of CBF1/DREB1B and CBF3/DREB1A expression and plays a central role in stress tolerance in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 3985-3990.	7.1	519
221	An <i>Arabidopsis</i> NPR1-like gene, NPR4, is required for disease resistance. <i>Plant Journal</i> , 2004, 41, 304-318.	5.7	148
222	Regulation of ethylene gas biosynthesis by the <i>Arabidopsis</i> ETO1 protein. <i>Nature</i> , 2004, 428, 945-950.	27.8	362
223	The ethylene signaling pathway: new insights. <i>Current Opinion in Plant Biology</i> , 2004, 7, 40-49.	7.1	834
224	The Central Role of PhEIN2 in Ethylene Responses throughout Plant Development in <i>Petunia</i> . <i>Plant Physiology</i> , 2004, 136, 2900-2912.	4.8	126
225	DELLA Proteins and Gibberellin-Regulated Seed Germination and Floral Development in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2004, 135, 1008-1019.	4.8	521
226	PLANT GENOMICS: The Third Wave. <i>Annual Review of Genomics and Human Genetics</i> , 2004, 5, 443-477.	6.2	68
227	Flagellin Is Not a Major Defense Elicitor in <i>Ralstonia solanacearum</i> Cells or Extracts Applied to <i>Arabidopsis thaliana</i> . <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 696-706.	2.6	111
228	Convergence of Signaling Pathways in the Control of Differential Cell Growth in <i>Arabidopsis</i> . <i>Developmental Cell</i> , 2004, 7, 193-204.	7.0	289
229	Chloroplast to nucleus communication triggered by accumulation of Mg-protoporphyrinIX. <i>Nature</i> , 2003, 421, 79-83.	27.8	534
230	GUN4, a Regulator of Chlorophyll Synthesis and Intracellular Signaling. <i>Science</i> , 2003, 299, 902-906.	12.6	478
231	Empirical Analysis of Transcriptional Activity in the <i>Arabidopsis</i> Genome. <i>Science</i> , 2003, 302, 842-846.	12.6	853
232	<i>Arabidopsis</i> RIN4 Is a Target of the Type III Virulence Effector AvrRpt2 and Modulates RPS2-Mediated Resistance. <i>Cell</i> , 2003, 112, 379-389.	28.9	852
233	Plant Responses to Ethylene Gas Are Mediated by SCFEBF1/EBF2-Dependent Proteolysis of EIN3 Transcription Factor. <i>Cell</i> , 2003, 115, 667-677.	28.9	827
234	Genome-Wide Insertional Mutagenesis of <i>Arabidopsis thaliana</i> . <i>Science</i> , 2003, 301, 653-657.	12.6	4,667

#	ARTICLE	IF	CITATIONS
235	A Growth Regulatory Loop That Provides Homeostasis to Phytochrome A Signaling[W]. Plant Cell, 2003, 15, 2966-2978.	6.6	67
236	The $\hat{\gamma}$ -Subunit of the Arabidopsis G Protein Negatively Regulates Auxin-Induced Cell Division and Affects Multiple Developmental Processes[W]. Plant Cell, 2003, 15, 393-409.	6.6	310
237	A Reevaluation of the Role of the Heterotrimeric G Protein in Coupling Light Responses in Arabidopsis. Plant Physiology, 2003, 131, 1623-1627.	4.8	124
238	Mutations in the Ca ²⁺ /H ⁺ Transporter CAX1 Increase CBF/DREB1 Expression and the Cold-Acclimation Response in Arabidopsis. Plant Cell, 2003, 15, 2940-2951.	6.6	170
239	Enhanced Fitness Conferred by Naturally Occurring Variation in the Circadian Clock. Science, 2003, 302, 1049-1053.	12.6	411
240	Five components of the ethylene-response pathway identified in a screen for weak ethylene-insensitive mutants in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2992-2997.	7.1	380
241	Isolation and Characterization of phyC Mutants in Arabidopsis Reveals Complex Crosstalk between Phytochrome Signaling Pathways. Plant Cell, 2003, 15, 1962-1980.	6.6	190
242	ABA-Activated SnRK2 Protein Kinase is Required for Dehydration Stress Signaling in Arabidopsis. Plant and Cell Physiology, 2002, 43, 1473-1483.	3.1	520
243	Ethylene Biosynthesis and Signaling Networks. Plant Cell, 2002, 14, S131-S151.	6.6	1,488
244	NPSN11 Is a Cell Plate-Associated SNARE Protein That Interacts with the Syntaxin KNOLLE. Plant Physiology, 2002, 129, 530-539.	4.8	84
245	Trp-dependent auxin biosynthesis in Arabidopsis: involvement of cytochrome P450s CYP79B2 and CYP79B3. Genes and Development, 2002, 16, 3100-3112.	5.9	598
246	HIV-1 Integration in the Human Genome Favors Active Genes and Local Hotspots. Cell, 2002, 110, 521-529.	28.9	1,622
247	Mitogen-activated protein kinase cascades in plants: a new nomenclature. Trends in Plant Science, 2002, 7, 301-308.	8.8	1,080
248	De-Etiolated 1 and Damaged DNA Binding Protein 1 Interact to Regulate Arabidopsis Photomorphogenesis. Current Biology, 2002, 12, 1462-1472.	3.9	203
249	Divergent perspectives on GM food. Nature Biotechnology, 2002, 20, 1195-1196.	17.5	11
250	Three Redundant Brassinosteroid Early Response Genes Encode Putative bHLH Transcription Factors Required for Normal Growth. Genetics, 2002, 162, 1445-1456.	2.9	259
251	An Arabidopsis circadian clock component interacts with both CRY1 and phyB. Nature, 2001, 410, 487-490.	27.8	199
252	Phototropin-related NPL1 controls chloroplast relocation induced by blue light. Nature, 2001, 410, 952-954.	27.8	448

#	ARTICLE	IF	CITATIONS
253	The Ethylene Pathway: A Paradigm for Plant Hormone Signaling and Interaction. <i>Science Signaling</i> , 2001, 2001, re1-re1.	3.6	38
254	Involvement of NRAMP1 from <i>Arabidopsis thaliana</i> in iron transport. <i>Biochemical Journal</i> , 2000, 347, 749.	3.7	125
255	Involvement of NRAMP1 from <i>Arabidopsis thaliana</i> in iron transport. <i>Biochemical Journal</i> , 2000, 347, 749-755.	3.7	474
256	Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 816-820.	27.8	234
257	Ethylene signaling: from mutants to molecules. <i>Current Opinion in Plant Biology</i> , 2000, 3, 353-360.	7.1	166
258	A complete BAC-based physical map of the <i>Arabidopsis thaliana</i> genome. <i>Nature Genetics</i> , 1999, 22, 271-275.	21.4	155
259	EIN2, a Bifunctional Transducer of Ethylene and Stress Responses in <i>Arabidopsis</i> . <i>Science</i> , 1999, 284, 2148-2152.	12.6	1,172
260	RESPONSIVE-TO-ANTAGONIST1, a Menkes/Wilson Disease-Related Copper Transporter, Is Required for Ethylene Signaling in <i>Arabidopsis</i> . <i>Cell</i> , 1999, 97, 383-393.	28.9	385
261	Genes blossom from a weed. <i>Nature</i> , 1998, 391, 438-439.	27.8	18
262	Cell signalling and gene regulation: piecing the puzzle together. <i>Current Opinion in Plant Biology</i> , 1998, 1, 375-377.	7.1	0
263	Ethylene gas: perception, signaling and response. <i>Current Opinion in Plant Biology</i> , 1998, 1, 393-398.	7.1	85
264	Ethylene signaling in <i>Arabidopsis</i> : Events from the membrane to the nucleus. <i>Plant Physiology and Biochemistry</i> , 1998, 36, 103-113.	5.8	31
265	THE ETHYLENE GAS SIGNAL TRANSDUCTION PATHWAY: A Molecular Perspective. <i>Annual Review of Genetics</i> , 1998, 32, 227-254.	7.6	490
266	EIN4 and ERS2 Are Members of the Putative Ethylene Receptor Gene Family in <i>Arabidopsis</i> . <i>Plant Cell</i> , 1998, 10, 1321-1332.	6.6	546
267	<i>Arabidopsis</i> Homologs of a c-Jun Coactivator Are Present Both in Monomeric Form and in the COP9 Complex, and Their Abundance Is Differentially Affected by the Pleiotropic <i>cop/det/fus</i> Mutations. <i>Plant Cell</i> , 1998, 10, 1779-1790.	6.6	156
268	EIN4 and ERS2 Are Members of the Putative Ethylene Receptor Gene Family in <i>Arabidopsis</i> . <i>Plant Cell</i> , 1998, 10, 1321.	6.6	44
269	Activation of the Ethylene Gas Response Pathway in <i>Arabidopsis</i> by the Nuclear Protein ETHYLENE-INSENSITIVE3 and Related Proteins. <i>Cell</i> , 1997, 89, 1133-1144.	28.9	928
270	BRIghtening the Pathway to Steroid Hormone Signaling Events in Plants. <i>Cell</i> , 1997, 90, 825-827.	28.9	19

#	ARTICLE	IF	CITATIONS
271	HOOKLESS1, an Ethylene Response Gene, Is Required for Differential Cell Elongation in the Arabidopsis Hypocotyl. <i>Cell</i> , 1996, 85, 183-194.	28.9	433
272	Assignment of 30 Microsatellite Loci to the Linkage Map of Arabidopsis. <i>Genomics</i> , 1994, 19, 137-144.	2.9	1,105
273	Ethylene gas: it's not just for ripening any more!. <i>Trends in Genetics</i> , 1993, 9, 356-362.	6.7	80
274	Mutant analysis as an experimental approach towards understanding plant hormone action. <i>Seminars in Developmental Biology</i> , 1993, 4, 3-13.	1.3	12
275	CTR1, a negative regulator of the ethylene response pathway in arabidopsis, encodes a member of the Raf family of protein kinases. <i>Cell</i> , 1993, 72, 427-441.	28.9	1,841
276	Genetic and physical linkage of the Arabidopsis genome: Methods for anchoring Yeast Artificial Chromosomes. , 1992, , 144-169.		22
277	Exploiting the Triple Response of Arabidopsis to Identify Ethylene-Related Mutants. <i>Plant Cell</i> , 1990, 2, 513.	6.6	16
278	PFGE and YAC analysis of the Arabidopsis genome. <i>Methods</i> , 1990, 1, 186-194.	3.8	69
279	Chromosomal mapping of the ubiquitin gene family in <i>Saccharomyces cerevisiae</i> by pulsed field gel electrophoresis. <i>Nucleic Acids Research</i> , 1989, 17, 3611-3612.	14.5	10
280	Development of large DNA methods for plants: molecular cloning of large segments of Arabidopsis and carrot DNA into yeast. <i>Nucleic Acids Research</i> , 1988, 16, 11091-11105.	14.5	99
281	Variation in the Structure of Varicella-Zoster Virus DNA. <i>Intervirology</i> , 1984, 21, 25-37.	2.8	20
282	Analysis of interruptions in the phosphodiester backbone of herpes simplex virus DNA. <i>Virology</i> , 1981, 110, 213-216.	2.4	12
283	CrY2H-seq interactome screening. <i>Protocol Exchange</i> , 0, , .	0.3	1
284	Dnmt3a knockout in excitatory neurons impairs postnatal synapse maturation and increases the repressive histone modification H3K27me3. <i>ELife</i> , 0, 11, .	6.0	10