

Joseph R Ecker

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

299 papers	77,320 citations	135 h-index	277 g-index
335 ext. papers	92,247 ext. citations	19.6 avg, IF	7.57 L-index

#	Paper	IF	Citations
299	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity.. <i>Cell Genomics</i> , 2022 , 2,		4
298	The biology of time: dynamic responses of cell types to developmental, circadian and environmental cues. <i>Plant Journal</i> , 2021 ,	6.9	1
297	An atlas of gene regulatory elements in adult mouse cerebrum. <i>Nature</i> , 2021 , 598, 129-136	50.4	8
296	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021 , 598, 103-110	50.4	23
295	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021 , 598, 111-119	50.4	31
294	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021 , 598, 86-102	50.4	44
293	DNA methylation atlas of the mouse brain at single-cell resolution. <i>Nature</i> , 2021 , 598, 120-128	50.4	14
292	Epigenomic diversity of cortical projection neurons in the mouse brain. <i>Nature</i> , 2021 , 598, 167-173	50.4	9
291	Iterative single-cell multi-omic integration using online learning. <i>Nature Biotechnology</i> , 2021 , 39, 1000-1007	47.5	12
290	Single nucleus multi-omics regulatory landscape of the murine pituitary. <i>Nature Communications</i> , 2021 , 12, 2677	17.4	8
289	PHYTOCHROME-INTERACTING FACTORs trigger environmentally responsive chromatin dynamics in plants. <i>Nature Genetics</i> , 2021 , 53, 955-961	36.3	11
288	A plant-specific syntaxin-6 protein contributes to the intracytoplasmic route for the begomovirus CabLCV. <i>Plant Physiology</i> , 2021 , 187, 158-173	6.6	2
287	The emergence of the brain non-CpG methylation system in vertebrates. <i>Nature Ecology and Evolution</i> , 2021 , 5, 369-378	12.3	19
286	Comprehensive analysis of single cell ATAC-seq data with SnapATAC. <i>Nature Communications</i> , 2021 , 12, 1337	17.4	61
285	Activity-dependent modulation of synapse-regulating genes in astrocytes. <i>ELife</i> , 2021 , 10,	8.9	11
284	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	11.5	6
283	Extraction of Distinct Neuronal Cell Types from within a Genetically Continuous Population. <i>Neuron</i> , 2020 , 107, 274-282.e6	13.9	41

282	Integrated multi-omics framework of the plant response to jasmonic acid. <i>Nature Plants</i> , 2020 , 6, 290-302	11.5	59
281	Chimeric Activators and Repressors Define HY5 Activity and Reveal a Light-Regulated Feedback Mechanism. <i>Plant Cell</i> , 2020 , 32, 967-983	11.6	52
280	Losing Dnmt3a dependent methylation in inhibitory neurons impairs neural function by a mechanism impacting Rett syndrome. <i>ELife</i> , 2020 , 9,	8.9	19
279	Genome and time-of-day transcriptome of link morphological minimization with gene loss and less growth control. <i>Genome Research</i> , 2020 ,	9.7	17
278	The JA-pathway MYC transcription factors regulate photomorphogenic responses by targeting HY5 gene expression. <i>Plant Journal</i> , 2020 , 102, 138-152	6.9	24
277	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020 , 583, 744-751	50.4	76
276	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. <i>Nature</i> , 2020 , 583, 752-759	50.4	35
275	Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698	50.4	61
274	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020 , 583, 699-710	50.4	360
273	Auxin-sensitive Aux/IAA proteins mediate drought tolerance in Arabidopsis by regulating glucosinolate levels. <i>Nature Communications</i> , 2019 , 10, 4021	17.4	78
272	Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. <i>Nature Methods</i> , 2019 , 16, 999-1006	21.6	84
271	Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons. <i>ELife</i> , 2019 , 8,	8.9	41
270	Genomic Decoding of Neuronal Depolarization by Stimulus-Specific NPAS4 Heterodimers. <i>Cell</i> , 2019 , 179, 373-391.e27	56.2	31
269	The complex architecture and epigenomic impact of plant T-DNA insertions. <i>PLoS Genetics</i> , 2019 , 15, e1007819	6	61
268	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	11.5	32
267	Diversity and dynamics of DNA methylation: epigenomic resources and tools for crop breeding. <i>Breeding Science</i> , 2019 , 69, 191-204	2	18
266	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	11.5	38
265	Epigenetic silencing of a multifunctional plant stress regulator. <i>ELife</i> , 2019 , 8,	8.9	16

264	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	6	19
263	Common alleles of CMT2 and NRPE1 are major determinants of CHH methylation variation in <i>Arabidopsis thaliana</i> 2019 , 15, e1008492		
262	Common alleles of CMT2 and NRPE1 are major determinants of CHH methylation variation in <i>Arabidopsis thaliana</i> 2019 , 15, e1008492		
261	Common alleles of CMT2 and NRPE1 are major determinants of CHH methylation variation in <i>Arabidopsis thaliana</i> 2019 , 15, e1008492		
260	Common alleles of CMT2 and NRPE1 are major determinants of CHH methylation variation in <i>Arabidopsis thaliana</i> 2019 , 15, e1008492		
259	A B-ARR-mediated cytokinin transcriptional network directs hormone cross-regulation and shoot development. <i>Nature Communications</i> , 2018 , 9, 1604	17.4	75
258	High contiguity <i>Arabidopsis thaliana</i> genome assembly with a single nanopore flow cell. <i>Nature Communications</i> , 2018 , 9, 541	17.4	164
257	OGT binds a conserved C-terminal domain of TET1 to regulate TET1 activity and function in development. <i>ELife</i> , 2018 , 7,	8.9	27
256	Author response: Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells 2018 ,		7
255	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	9
254	Profiling Interactome Networks with the HaloTag-NAPPA In Situ Protein Array. <i>Current Protocols in Plant Biology</i> , 2018 , 3, e20071	2.8	6
253	Dynamic DNA methylation: In the right place at the right time. <i>Science</i> , 2018 , 361, 1336-1340	33.3	246
252	Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. <i>ELife</i> , 2018 , 7,	8.9	114
251	Robust single-cell DNA methylome profiling with snmC-seq2. <i>Nature Communications</i> , 2018 , 9, 3824	17.4	66
250	Plant Stress Tolerance Requires Auxin-Sensitive Aux/IAA Transcriptional Repressors. <i>Current Biology</i> , 2017 , 27, 437-444	6.3	80
249	Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <i>New Phytologist</i> , 2017 , 214, 808-819	9.8	49
248	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	11.5	60
247	Sequencing and functional validation of the JGI <i>Brachypodium distachyon</i> T-DNA collection. <i>Plant Journal</i> , 2017 , 91, 361-370	6.9	29

246	Allele-specific non-CG DNA methylation marks domains of active chromatin in female mouse brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E2882-E2890	11.5	35
245	JAZ2 controls stomata dynamics during bacterial invasion. <i>New Phytologist</i> , 2017 , 213, 1378-1392	9.8	80
244	The BRAIN Initiative Cell Census Consortium: Lessons Learned toward Generating a Comprehensive Brain Cell Atlas. <i>Neuron</i> , 2017 , 96, 542-557	13.9	159
243	Dynamic DNA methylation reconfiguration during seed development and germination. <i>Genome Biology</i> , 2017 , 18, 171	18.3	132
242	Mapping genome-wide transcription-factor binding sites using DAP-seq. <i>Nature Protocols</i> , 2017 , 12, 1659-1672	18.7	142
241	Single-cell methylomes identify neuronal subtypes and regulatory elements in mammalian cortex. <i>Science</i> , 2017 , 357, 600-604	33.3	279
240	Challenges and recommendations for epigenomics in precision health. <i>Nature Biotechnology</i> , 2017 , 35, 1128-1132	44.5	16
239	CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. <i>Nature Methods</i> , 2017 , 14, 819-825	21.6	86
238	Functional Human Oocytes Generated by Transfer of Polar Body Genomes. <i>Cell Stem Cell</i> , 2017 , 20, 112-119	18.9	57
237	Dynamic and rapid changes in the transcriptome and epigenome during germination and in developing rice (<i>Oryza sativa</i>) coleoptiles under anoxia and re-oxygenation. <i>Plant Journal</i> , 2017 , 89, 805-824	6.9	43
236	Integration of omic networks in a developmental atlas of maize. <i>Science</i> , 2016 , 353, 814-8	33.3	232
235	Profiling of transcription factor binding events by chromatin immunoprecipitation sequencing (ChIP-seq). <i>Current Protocols in Plant Biology</i> , 2016 , 1, 293-306	2.8	16
234	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. <i>Cell</i> , 2016 , 166, 492-505	56.2	353
233	Molecular Criteria for Defining the Naive Human Pluripotent State. <i>Cell Stem Cell</i> , 2016 , 19, 502-515	18	291
232	Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , 2016 , 13, 1050-1054	21.6	1015
231	Unique cell-type-specific patterns of DNA methylation in the root meristem. <i>Nature Plants</i> , 2016 , 2, 16058	11.5	125
230	EIN2-dependent regulation of acetylation of histone H3K14 and non-canonical histone H3K23 in ethylene signalling. <i>Nature Communications</i> , 2016 , 7, 13018	17.4	58
229	A transcription factor hierarchy defines an environmental stress response network. <i>Science</i> , 2016 , 354,	33.3	241

228	The Arabidopsis 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, 1383-90	3.2	54
227	1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. <i>Cell</i> , 2016 , 166, 481-491	40.1	620
226	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	11.5	52
225	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	11.5	153
224	A Proposal Regarding Best Practices for Validating the Identity of Genetic Stocks and the Effects of Genetic Variants. <i>Plant Cell</i> , 2016 , 28, 606-9	11.6	25
223	Active DNA demethylation at enhancers during the vertebrate phylotypic period. <i>Nature Genetics</i> , 2016 , 48, 417-26	36.3	157
222	Cryptochromes Interact Directly with PIFs to Control Plant Growth in Limiting Blue Light. <i>Cell</i> , 2016 , 164, 233-245	56.2	295
221	Epigenomic landscapes of retinal rods and cones. <i>ELife</i> , 2016 , 5, e11613	8.9	83
220	An ABA-increased interaction of the PYL6 ABA receptor with MYC2 Transcription Factor: A putative link of ABA and JA signaling. <i>Scientific Reports</i> , 2016 , 6, 28941	4.9	103
219	Cerebral Organoids Recapitulate Epigenomic Signatures of the Human Fetal Brain. <i>Cell Reports</i> , 2016 , 17, 3369-3384	10.6	207
218	Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. <i>Cell</i> , 2016 , 165, 1280-1292	56.2	528
217	Chromatin architecture reorganization during stem cell differentiation. <i>Nature</i> , 2015 , 518, 331-6	50.4	988
216	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. <i>Neuron</i> , 2015 , 86, 1369-84	13.9	430
215	Non-CG Methylation in the Human Genome. <i>Annual Review of Genomics and Human Genetics</i> , 2015 , 16, 55-77	9.7	154
214	An alternative pluripotent state confers interspecies chimaeric competency. <i>Nature</i> , 2015 , 521, 316-21	50.4	167
213	ERRs Mediate a Metabolic Switch Required for Somatic Cell Reprogramming to Pluripotency. <i>Cell Stem Cell</i> , 2015 , 16, 547-55	18	87
212	Genome-wide identification of CCA1 targets uncovers an expanded clock network in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E4802-10	11.5	156
211	methylPipe and compEpiTools: a suite of R packages for the integrative analysis of epigenomics data. <i>BMC Bioinformatics</i> , 2015 , 16, 313	3.6	48

210	Stress induced gene expression drives transient DNA methylation changes at adjacent repetitive elements. <i>ELife</i> , 2015 , 4,	8.9	208
209	Epigenetics. Exceptional epigenetics in the brain. <i>Science</i> , 2015 , 348, 1094-5	33.3	9
208	Human body epigenome maps reveal noncanonical DNA methylation variation. <i>Nature</i> , 2015 , 523, 212-6	50.4	442
207	MethylC-seq library preparation for base-resolution whole-genome bisulfite sequencing. <i>Nature Protocols</i> , 2015 , 10, 475-83	18.8	190
206	Integrative analysis of haplotype-resolved epigenomes across human tissues. <i>Nature</i> , 2015 , 518, 350-354	50.4	155
205	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015 , 518, 317-30	50.4	3849
204	Author response: Stress induced gene expression drives transient DNA methylation changes at adjacent repetitive elements 2015 ,		5
203	A user guide to the Arabidopsis T-DNA insertion mutant collections. <i>Methods in Molecular Biology</i> , 2015 , 1284, 323-42	1.4	52
202	The developmental potential of iPSCs is greatly influenced by reprogramming factor selection. <i>Cell Stem Cell</i> , 2014 , 15, 295-309	18	112
201	A genome-scale resource for the functional characterization of Arabidopsis transcription factors. <i>Cell Reports</i> , 2014 , 8, 622-32	10.6	116
200	The Arabidopsis 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, 3326-42	11.6	122
199	Convergent targeting of a common host protein-network by pathogen effectors from three kingdoms of life. <i>Cell Host and Microbe</i> , 2014 , 16, 364-75	23.4	242
198	Determination and inference of eukaryotic transcription factor sequence specificity. <i>Cell</i> , 2014 , 158, 1431-1443	56.2	866
197	Abnormalities in human pluripotent cells due to reprogramming mechanisms. <i>Nature</i> , 2014 , 511, 177-83	50.4	255
196	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, 1613-23	9.7	67
195	Systematic mapping of occluded genes by cell fusion reveals prevalence and stability of cis-mediated silencing in somatic cells. <i>Genome Research</i> , 2014 , 24, 267-80	9.7	5
194	DNA topoisomerase 1 promotes transcriptional silencing of transposable elements through DNA methylation and histone lysine 9 dimethylation in Arabidopsis. <i>PLoS Genetics</i> , 2014 , 10, e1004446	6	16
193	CG hypomethylation in Lsh ^{-/-} 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, 5890-5	11.5	37

192	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, 17224-9	11.5	239
191	Genotypic variation of gene expression during the soybean innate immunity response. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014 , 12, S27-S30	1	6
190	Global epigenomic reconfiguration during mammalian brain development. <i>Science</i> , 2013 , 341, 1237905	33.3	1283
189	Sigma factor-mediated plastid retrograde signals control nuclear gene expression. <i>Plant Journal</i> , 2013 , 73, 1-13	6.9	117
188	Patterns of population epigenomic diversity. <i>Nature</i> , 2013 , 495, 193-8	50.4	406
187	Epigenomic analysis of multilineage differentiation of human embryonic stem cells. <i>Cell</i> , 2013 , 153, 1134-48	54.8	550
186	STAR: an integrated solution to management and visualization of sequencing data. <i>Bioinformatics</i> , 2013 , 29, 3204-10	7.2	9
185	Functional characterization of type-B response regulators in the Arabidopsis cytokinin response. <i>Plant Physiology</i> , 2013 , 162, 212-24	6.6	63
184	Response to perspective: "separation anxiety: an analysis of ethylene-induced cleavage of EIN2". <i>Plant Signaling and Behavior</i> , 2013 , 8,	2.5	4
183	Arabidopsis basic helix-loop-helix transcription factors MYC2, MYC3, and MYC4 regulate glucosinolate biosynthesis, insect performance, and feeding behavior. <i>Plant Cell</i> , 2013 , 25, 3117-32	11.6	313
182	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, 16927-32	11.5	20
181	Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. <i>Genome Research</i> , 2013 , 23, 1663-74	9.7	189
180	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. <i>ELife</i> , 2013 , 2, e00675	8.9	265
179	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, 1825-36	12.6	115
178	Circadian oscillations of protein-coding and regulatory RNAs in a highly dynamic mammalian liver epigenome. <i>Cell Metabolism</i> , 2012 , 16, 833-45	24.6	199
177	Linking photoreceptor excitation to changes in plant architecture. <i>Genes and Development</i> , 2012 , 26, 785-90	12.6	334
176	Release factor one is nonessential in Escherichia coli. <i>ACS Chemical Biology</i> , 2012 , 7, 1337-44	4.9	85
175	Epigenetic and epigenomic variation in Arabidopsis thaliana. <i>Trends in Plant Science</i> , 2012 , 17, 149-54	13.1	76

174	Processing and subcellular trafficking of ER-tethered EIN2 control response to ethylene gas. <i>Science</i> , 2012 , 338, 390-3	33.3	333
173	Genomics: ENCODE explained. <i>Nature</i> , 2012 , 489, 52-5	50.4	191
172	Leveling the playing field for analyses of single-base resolution DNA methylomes. <i>Trends in Genetics</i> , 2012 , 28, 583-5	8.5	182
171	Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. <i>Genome Research</i> , 2012 , 22, 246-58	9.7	385
170	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	11.5	640
169	Detection of allele-specific methylation through a generalized heterogeneous epigenome model. <i>Bioinformatics</i> , 2012 , 28, i163-71	7.2	19
168	Surveillance of 3' Noncoding Transcripts Requires FIERY1 and XRN3 in Arabidopsis. <i>G3: Genes, Genomes, Genetics</i> , 2012 , 2, 487-98	3.2	33
167	A blueprint for an international cancer epigenome consortium. A report from the AACR Cancer Epigenome Task Force. <i>Cancer Research</i> , 2012 , 72, 6319-24	10.1	21
166	RF1 knockout allows ribosomal incorporation of unnatural amino acids at multiple sites. <i>Nature Chemical Biology</i> , 2011 , 7, 779-86	11.7	255
165	Transgenerational epigenetic instability is a source of novel methylation variants. <i>Science</i> , 2011 , 334, 369-73	33.3	485
164	Forward and reverse genetics through derivation of haploid mouse embryonic stem cells. <i>Cell Stem Cell</i> , 2011 , 9, 563-74	18	180
163	Independently evolved virulence effectors converge onto hubs in a plant immune system network. <i>Science</i> , 2011 , 333, 596-601	33.3	601
162	Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> , 2011 , 471, 68-73	50.4	1241
161	Genome-wide mapping of 5-hydroxymethylcytosine in embryonic stem cells. <i>Nature</i> , 2011 , 473, 394-7	50.4	653
160	The DNA methylome. <i>FEBS Letters</i> , 2011 , 585, 1994-2000	3.8	63
159	Evidence for network evolution in an Arabidopsis interactome map. <i>Science</i> , 2011 , 333, 601-7	33.3	689
158	Unexpected Diversity of Chloroplast Noncoding RNAs as Revealed by Deep Sequencing of the Arabidopsis Transcriptome. <i>G3: Genes, Genomes, Genetics</i> , 2011 , 1, 559-70	3.2	58
157	Linking genotype to phenotype using the Arabidopsis unimutant collection. <i>Plant Journal</i> , 2010 , 61, 928-40	40	141

156	Genome-wide association study of 107 phenotypes in Arabidopsis thaliana inbred lines. <i>Nature</i> , 2010 , 465, 627-31	50.4	1257
155	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010 , 28, 1097-105	44.5	570
154	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010 , 28, 1045-8	44.5	1284
153	Direct transcriptional control of the Arabidopsis 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, 14502-7	11.5	177
152	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	7.6	107
151	Ethylene Responses in Seedling Growth and Development 2010 , 358-376		2
150	Distinct epigenomic landscapes of pluripotent and lineage-committed human cells. <i>Cell Stem Cell</i> , 2010 , 6, 479-91	18	630
149	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 Arabidopsis. <i>Plant Cell</i> , 2010 , 22, 2384-401	11.6	328
148	Finding the fifth base: genome-wide sequencing of cytosine methylation. <i>Genome Research</i> , 2009 , 19, 959-66	9.7	271
147	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, 15867-79	5.4	73
146	A combinatorial interplay among the 1-aminocyclopropane-1-carboxylate isoforms regulates ethylene biosynthesis in Arabidopsis thaliana. <i>Genetics</i> , 2009 , 183, 979-1003	4	208
145	Interplay between ethylene, ETP1/ETP2 F-box proteins, and degradation of EIN2 triggers ethylene responses in Arabidopsis. <i>Genes and Development</i> , 2009 , 23, 512-21	12.6	238
144	Regulation of membrane trafficking and organ separation by the NEVERSHED ARF-GAP protein. <i>Development (Cambridge)</i> , 2009 , 136, 1909-18	6.6	89
143	Next is now: new technologies for sequencing of genomes, transcriptomes, and beyond. <i>Current Opinion in Plant Biology</i> , 2009 , 12, 107-18	9.9	238
142	Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> , 2009 , 462, 315-22	50.4	3401
141	Prepublication data sharing. <i>Nature</i> , 2009 , 461, 168-70	50.4	197
140	Literature-curated protein interaction datasets. <i>Nature Methods</i> , 2009 , 6, 39-46	21.6	237
139	Exploring the transcriptional landscape of plant circadian rhythms using genome tiling arrays. <i>Genome Biology</i> , 2009 , 10, R17	18.3	93

138	Highly integrated single-base resolution maps of the epigenome in Arabidopsis. <i>Cell</i> , 2008 , 133, 523-36	56.2	1896
137	A link between RNA metabolism and silencing affecting Arabidopsis development. <i>Developmental Cell</i> , 2008 , 14, 854-66	10.2	328
136	The Arabidopsis 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, 337-52	11.6	261
135	Potential sites of bioactive gibberellin production during reproductive growth in Arabidopsis. <i>Plant Cell</i> , 2008 , 20, 320-36	11.6	175
134	Utilizing tiling microarrays for whole-genome analysis in plants. <i>Plant Journal</i> , 2008 , 53, 636-44	6.9	38
133	The phosphatase laforin crosses evolutionary boundaries and links carbohydrate metabolism to neuronal disease. <i>FASEB Journal</i> , 2008 , 22, 102.2	0.9	
132	A WD40 domain cyclophilin interacts with histone H3 and functions in gene repression and organogenesis in Arabidopsis. <i>Plant Cell</i> , 2007 , 19, 2403-16	11.6	53
131	Common sequence polymorphisms shaping genetic diversity in Arabidopsis thaliana. <i>Science</i> , 2007 , 317, 338-42	33.3	596
130	Recombination and linkage disequilibrium in Arabidopsis thaliana. <i>Nature Genetics</i> , 2007 , 39, 1151-5	36.3	400
129	An adapter ligation-mediated PCR method for high-throughput mapping of T-DNA inserts in the Arabidopsis genome. <i>Nature Protocols</i> , 2007 , 2, 2910-7	18.8	96
128	Mapping the genome landscape using tiling array technology. <i>Current Opinion in Plant Biology</i> , 2007 , 10, 534-42	9.9	54
127	Genome-wide patterns of single-feature polymorphism in Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 12057-62	11.5	147
126	The phosphatase laforin crosses evolutionary boundaries and links carbohydrate metabolism to neuronal disease. <i>Journal of Cell Biology</i> , 2007 , 178, 477-88	7.3	127
125	Small RNA-mediated chromatin silencing directed to the 3' region of the Arabidopsis gene encoding the developmental regulator, FLC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 3633-8	11.5	102
124	Higher plants possess two different types of ATX1-like copper chaperones. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 354, 385-90	3.4	66
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