

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	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	13.7	5,653
2	Genome-Wide Insertional Mutagenesis of <i>Arabidopsis thaliana</i> . <i>Science</i> , 2003, 301, 653-657.	6.0	4,667
3	Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> , 2009, 462, 315-322.	13.7	4,063
4	Highly Integrated Single-Base Resolution Maps of the Epigenome in <i>Arabidopsis</i> . <i>Cell</i> , 2008, 133, 523-536.	13.5	2,229
5	CTR1, a negative regulator of the ethylene response pathway in <i>Arabidopsis</i> , encodes a member of the Raf family of protein kinases. <i>Cell</i> , 1993, 72, 427-441.	13.5	1,841
6	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010, 28, 1045-1048.	9.4	1,705
7	Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , 2016, 13, 1050-1054.	9.0	1,658
8	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
9	Genome-wide High-Resolution Mapping and Functional Analysis of DNA Methylation in <i>Arabidopsis</i> . <i>Cell</i> , 2006, 126, 1189-1201.	13.5	1,647
10	HIV-1 Integration in the Human Genome Favors Active Genes and Local Hotspots. <i>Cell</i> , 2002, 110, 521-529.	13.5	1,622
11	Global Epigenomic Reconfiguration During Mammalian Brain Development. <i>Science</i> , 2013, 341, 1237905.	6.0	1,609
12	Determination and Inference of Eukaryotic Transcription Factor Sequence Specificity. <i>Cell</i> , 2014, 158, 1431-1443.	13.5	1,515
13	Ethylene Biosynthesis and Signaling Networks. <i>Plant Cell</i> , 2002, 14, S131-S151.	3.1	1,488
14	Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> , 2011, 471, 68-73.	13.7	1,442
15	Chromatin architecture reorganization during stem cell differentiation. <i>Nature</i> , 2015, 518, 331-336.	13.7	1,442
16	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
17	EIN2, a Bifunctional Transducer of Ethylene and Stress Responses in <i>Arabidopsis</i> . <i>Science</i> , 1999, 284, 2148-2152.	6.0	1,172
18	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

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19	Assignment of 30 Microsatellite Loci to the Linkage Map of Arabidopsis. <i>Genomics</i> , 1994, 19, 137-144.	1.3	1,105
20	Mitogen-activated protein kinase cascades in plants: a new nomenclature. <i>Trends in Plant Science</i> , 2002, 7, 301-308.	4.3	1,080
21	Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. <i>Cell</i> , 2016, 165, 1280-1292.	13.5	1,078
22	Functional Genomic Analysis of the AUXIN RESPONSE FACTOR Gene Family Members in Arabidopsis thaliana: Unique and Overlapping Functions of ARF7 and ARF19. <i>Plant Cell</i> , 2005, 17, 444-463.	3.1	933
23	Activation of the Ethylene Gas Response Pathway in Arabidopsis by the Nuclear Protein ETHYLENE-INSENSITIVE3 and Related Proteins. <i>Cell</i> , 1997, 89, 1133-1144.	13.5	928
24	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.	3.3	878
25	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
26	Empirical Analysis of Transcriptional Activity in the Arabidopsis Genome. <i>Science</i> , 2003, 302, 842-846.	6.0	853
27	Arabidopsis RIN4 Is a Target of the Type III Virulence Effector AvrRpt2 and Modulates RPS2-Mediated Resistance. <i>Cell</i> , 2003, 112, 379-389.	13.5	852
28	Evidence for Network Evolution in an Arabidopsis Interactome Map. <i>Science</i> , 2011, 333, 601-607.	6.0	838
29	The ethylene signaling pathway: new insights. <i>Current Opinion in Plant Biology</i> , 2004, 7, 40-49.	3.5	834
30	Retroviral DNA Integration: ASLV, HIV, and MLV Show Distinct Target Site Preferences. <i>PLoS Biology</i> , 2004, 2, e234.	2.6	830
31	Plant Responses to Ethylene Gas Are Mediated by SCFEBF1/EBF2-Dependent Proteolysis of EIN3 Transcription Factor. <i>Cell</i> , 2003, 115, 667-677.	13.5	827
32	Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. <i>Science</i> , 2011, 333, 596-601.	6.0	776
33	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. <i>Cell Stem Cell</i> , 2010, 6, 479-491.	5.2	747
34	Genome-wide mapping of 5-hydroxymethylcytosine in embryonic stem cells. <i>Nature</i> , 2011, 473, 394-397.	13.7	738
35	Common Sequence Polymorphisms Shaping Genetic Diversity in Arabidopsis thaliana. <i>Science</i> , 2007, 317, 338-342.	6.0	689
36	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	13.5	689

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37	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.	3.1	650
38	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
39	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. <i>Neuron</i> , 2015, 86, 1369-1384.	3.8	640
40	Transgenerational Epigenetic Instability Is a Source of Novel Methylation Variants. <i>Science</i> , 2011, 334, 369-373.	6.0	635
41	Type-A Arabidopsis Response Regulators Are Partially Redundant Negative Regulators of Cytokinin Signaling[W]. <i>Plant Cell</i> , 2004, 16, 658-671.	3.1	631
42	Localization of Iron in Arabidopsis Seed Requires the Vacuolar Membrane Transporter VIT1. <i>Science</i> , 2006, 314, 1295-1298.	6.0	614
43	Auxin response factors ARF6 and ARF8 promote jasmonic acid production and flower maturation. <i>Development (Cambridge)</i> , 2005, 132, 4107-4118.	1.2	608
44	Human body epigenome maps reveal noncanonical DNA methylation variation. <i>Nature</i> , 2015, 523, 212-216.	13.7	605
45	Trp-dependent auxin biosynthesis in Arabidopsis: involvement of cytochrome P450s CYP79B2 and CYP79B3. <i>Genes and Development</i> , 2002, 16, 3100-3112.	2.7	598
46	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. <i>Cell</i> , 2016, 166, 492-505.	13.5	594
47	A role for LEDGF/p75 in targeting HIV DNA integration. <i>Nature Medicine</i> , 2005, 11, 1287-1289.	15.2	583
48	EIN4 and ERS2 Are Members of the Putative Ethylene Receptor Gene Family in Arabidopsis. <i>Plant Cell</i> , 1998, 10, 1321-1332.	3.1	546
49	Patterns of population epigenomic diversity. <i>Nature</i> , 2013, 495, 193-198.	13.7	543
50	Chloroplast to nucleus communication triggered by accumulation of Mg-protoporphyrinIX. <i>Nature</i> , 2003, 421, 79-83.	13.7	534
51	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.	2.6	523
52	DELLA Proteins and Gibberellin-Regulated Seed Germination and Floral Development in Arabidopsis. <i>Plant Physiology</i> , 2004, 135, 1008-1019.	2.3	521
53	ABA-Activated SnRK2 Protein Kinase is Required for Dehydration Stress Signaling in Arabidopsis. <i>Plant and Cell Physiology</i> , 2002, 43, 1473-1483.	1.5	520
54	CBF2/DREB1C is a negative regulator of CBF1/DREB1B and CBF3/DREB1A expression and plays a central role in stress tolerance in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 3985-3990.	3.3	519

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55	Recombination and linkage disequilibrium in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2007, 39, 1151-1155.	9.4	497
56	THE ETHYLENE GAS SIGNAL TRANSDUCTION PATHWAY: A Molecular Perspective. <i>Annual Review of Genetics</i> , 1998, 32, 227-254.	3.2	490
57	GUN4, a Regulator of Chlorophyll Synthesis and Intracellular Signaling. <i>Science</i> , 2003, 299, 902-906.	6.0	478
58	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
59	Involvement of NRAMP1 from <i>Arabidopsis thaliana</i> in iron transport. <i>Biochemical Journal</i> , 2000, 347, 749-755.	1.7	474
60	Dynamic DNA methylation: In the right place at the right time. <i>Science</i> , 2018, 361, 1336-1340.	6.0	469
61	Processing and Subcellular Trafficking of ER-Tethered EIN2 Control Response to Ethylene Gas. <i>Science</i> , 2012, 338, 390-393.	6.0	461
62	Linking photoreceptor excitation to changes in plant architecture. <i>Genes and Development</i> , 2012, 26, 785-790.	2.7	460
63	<i>Arabidopsis</i> 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
64	Phototropin-related NPL1 controls chloroplast relocation induced by blue light. <i>Nature</i> , 2001, 410, 952-954.	13.7	448
65	Cryptochromes Interact Directly with PIFs to Control Plant Growth in Limiting Blue Light. <i>Cell</i> , 2016, 164, 233-245.	13.5	445
66	Single-cell methylomes identify neuronal subtypes and regulatory elements in mammalian cortex. <i>Science</i> , 2017, 357, 600-604.	6.0	445
67	HOKLESS1, an Ethylene Response Gene, Is Required for Differential Cell Elongation in the <i>Arabidopsis</i> Hypocotyl. <i>Cell</i> , 1996, 85, 183-194.	13.5	433
68	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
69	NPH4/ARF7 and ARF19 promote leaf expansion and auxin-induced lateral root formation. <i>Plant Journal</i> , 2005, 43, 118-130.	2.8	415
70	Molecular Criteria for Defining the Naive Human Pluripotent State. <i>Cell Stem Cell</i> , 2016, 19, 502-515.	5.2	415
71	Enhanced Fitness Conferred by Naturally Occurring Variation in the Circadian Clock. <i>Science</i> , 2003, 302, 1049-1053.	6.0	411
72	Integration of omic networks in a developmental atlas of maize. <i>Science</i> , 2016, 353, 814-818.	6.0	411

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73	Multiple Type-B Response Regulators Mediate Cytokinin Signal Transduction in Arabidopsis. <i>Plant Cell</i> , 2005, 17, 3007-3018.	3.1	397
74	A Link between RNA Metabolism and Silencing Affecting Arabidopsis Development. <i>Developmental Cell</i> , 2008, 14, 854-866.	3.1	394
75	A transcription factor hierarchy defines an environmental stress response network. <i>Science</i> , 2016, 354, .	6.0	394
76	The Arabidopsis Histidine Phosphotransfer Proteins Are Redundant Positive Regulators of Cytokinin Signaling. <i>Plant Cell</i> , 2006, 18, 3073-3087.	3.1	392
77	RESPONSIVE-TO-ANTAGONIST1, a Menkes/Wilson Disease-Related Copper Transporter, Is Required for Ethylene Signaling in Arabidopsis. <i>Cell</i> , 1999, 97, 383-393.	13.5	385
78	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.	3.3	381
79	Five components of the ethylene-response pathway identified in a screen for weak ethylene-insensitive mutants in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2992-2997.	3.3	380
80	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. <i>ELife</i> , 2013, 2, e00675.	2.8	379
81	Applications of DNA tiling arrays for whole-genome analysis. <i>Genomics</i> , 2005, 85, 1-15.	1.3	376
82	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
83	Regulation of ethylene gas biosynthesis by the Arabidopsis ETO1 protein. <i>Nature</i> , 2004, 428, 945-950.	13.7	362
84	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021, 598, 111-119.	13.7	361
85	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
86	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
87	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.	3.1	331
88	Mapping genome-wide transcription-factor binding sites using DAP-seq. <i>Nature Protocols</i> , 2017, 12, 1659-1672.	5.5	330
89	Finding the fifth base: Genome-wide sequencing of cytosine methylation. <i>Genome Research</i> , 2009, 19, 959-966.	2.4	323
90	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	13.7	316

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91	The $\hat{\rho}^2$ -Subunit of the Arabidopsis G Protein Negatively Regulates Auxin-Induced Cell Division and Affects Multiple Developmental Processes[W]. <i>Plant Cell</i> , 2003, 15, 393-409.	3.1	310
92	Retroviral DNA Integration: Viral and Cellular Determinants of Target-Site Selection. <i>PLoS Pathogens</i> , 2006, 2, e60.	2.1	310
93	Abnormalities in human pluripotent cells due to reprogramming mechanisms. <i>Nature</i> , 2014, 511, 177-183.	13.7	307
94	Genome-Wide High-Resolution Mapping of Exosome Substrates Reveals Hidden Features in the Arabidopsis Transcriptome. <i>Cell</i> , 2007, 131, 1340-1353.	13.5	298
95	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
96	Cerebral Organoids Recapitulate Epigenomic Signatures of the Human Fetal Brain. <i>Cell Reports</i> , 2016, 17, 3369-3384.	2.9	296
97	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.	2.8	290
98	Convergence of Signaling Pathways in the Control of Differential Cell Growth in Arabidopsis. <i>Developmental Cell</i> , 2004, 7, 193-204.	3.1	289
99	Literature-curated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 39-46.	9.0	288
100	RF1 knockout allows ribosomal incorporation of unnatural amino acids at multiple sites. <i>Nature Chemical Biology</i> , 2011, 7, 779-786.	3.9	286
101	Stress induced gene expression drives transient DNA methylation changes at adjacent repetitive elements. <i>ELife</i> , 2015, 4, .	2.8	285
102	â€˜Levelingâ€™ the playing field for analyses of single-base resolution DNA methylomes. <i>Trends in Genetics</i> , 2012, 28, 583-585.	2.9	276
103	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.	3.3	275
104	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
105	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
106	Three Redundant Brassinosteroid Early Response Genes Encode Putative bHLH Transcription Factors Required for Normal Growth. <i>Genetics</i> , 2002, 162, 1445-1456.	1.2	259
107	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	13.7	257
108	Comprehensive analysis of single cell ATAC-seq data with SnapATAC. <i>Nature Communications</i> , 2021, 12, 1337.	5.8	253

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109	MethylC-seq library preparation for base-resolution whole-genome bisulfite sequencing. <i>Nature Protocols</i> , 2015, 10, 475-483.	5.5	250
110	ENCODE explained. <i>Nature</i> , 2012, 489, 52-54.	13.7	245
111	Prepublication data sharing. <i>Nature</i> , 2009, 461, 168-170.	13.7	243
112	High contiguity <i>Arabidopsis thaliana</i> genome assembly with a single nanopore flow cell. <i>Nature Communications</i> , 2018, 9, 541.	5.8	243
113	The BRAIN Initiative Cell Census Consortium: Lessons Learned toward Generating a Comprehensive Brain Cell Atlas. <i>Neuron</i> , 2017, 96, 542-557.	3.8	235
114	Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 816-820.	13.7	234
115	Moving forward in reverse: genetic technologies to enable genome-wide phenomic screens in <i>Arabidopsis</i> . <i>Nature Reviews Genetics</i> , 2006, 7, 524-536.	7.7	230
116	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
117	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
118	Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. <i>Genome Research</i> , 2013, 23, 1663-1674.	2.4	227
119	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
120	Dynamic DNA methylation reconfiguration during seed development and germination. <i>Genome Biology</i> , 2017, 18, 171.	3.8	218
121	An alternative pluripotent state confers interspecies chimaeric competency. <i>Nature</i> , 2015, 521, 316-321.	13.7	215
122	Non-CG Methylation in the Human Genome. <i>Annual Review of Genomics and Human Genetics</i> , 2015, 16, 55-77.	2.5	210
123	Active DNA demethylation at enhancers during the vertebrate phylotypic period. <i>Nature Genetics</i> , 2016, 48, 417-426.	9.4	210
124	Potential Sites of Bioactive Gibberellin Production during Reproductive Growth in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2008, 20, 320-336.	3.1	209
125	Forward and Reverse Genetics through Derivation of Haploid Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2011, 9, 563-574.	5.2	208
126	De-Etiolated 1 and Damaged DNA Binding Protein 1 Interact to Regulate <i>Arabidopsis</i> Photomorphogenesis. <i>Current Biology</i> , 2002, 12, 1462-1472.	1.8	203

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127	Integrative analysis of haplotype-resolved epigenomes across human tissues. <i>Nature</i> , 2015, 518, 350-354.	13.7	201
128	Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. <i>Nature Methods</i> , 2019, 16, 999-1006.	9.0	200
129	An <i>Arabidopsis</i> circadian clock component interacts with both CRY1 and phyB. <i>Nature</i> , 2001, 410, 487-490.	13.7	199
130	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
131	Isolation and Characterization of phyC Mutants in <i>Arabidopsis</i> Reveals Complex Crosstalk between Phytochrome Signaling Pathways. <i>Plant Cell</i> , 2003, 15, 1962-1980.	3.1	190
132	Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. <i>ELife</i> , 2018, 7, .	2.8	180
133	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
134	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.	3.3	176
135	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.	3.3	174
136	Linking genotype to phenotype using the <i>Arabidopsis</i> unimutant collection. <i>Plant Journal</i> , 2010, 61, 928-940.	2.8	171
137	Mutations in the Ca ²⁺ /H ⁺ Transporter CAX1 Increase CBF/DREB1 Expression and the Cold-Acclimation Response in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2003, 15, 2940-2951.	3.1	170
138	Ethylene signaling: from mutants to molecules. <i>Current Opinion in Plant Biology</i> , 2000, 3, 353-360.	3.5	166
139	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	13.7	166
140	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
141	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.	3.3	163
142	GCR1 Can Act Independently of Heterotrimeric G-Protein in Response to Brassinosteroids and Gibberellins in <i>Arabidopsis</i> Seed Germination. <i>Plant Physiology</i> , 2004, 135, 907-915.	2.3	160
143	Unique cell-type-specific patterns of DNA methylation in the root meristem. <i>Nature Plants</i> , 2016, 2, 16058.	4.7	159
144	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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145	CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. <i>Nature Methods</i> , 2017, 14, 819-825.	9.0	157
146	Arabidopsis 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 cop/det/fus Mutations. <i>Plant Cell</i> , 1998, 10, 1779-1790.	3.1	156
147	A complete BAC-based physical map of the Arabidopsis thaliana genome. <i>Nature Genetics</i> , 1999, 22, 271-275.	9.4	155
148	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.	1.6	155
149	Auxin-sensitive Aux/IAA proteins mediate drought tolerance in Arabidopsis by regulating glucosinolate levels. <i>Nature Communications</i> , 2019, 10, 4021.	5.8	155
150	Regulation of flowering time in Arabidopsis by K homology domain proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12759-12764.	3.3	150
151	An Arabidopsis NPR1-like gene, NPR4, is required for disease resistance. <i>Plant Journal</i> , 2004, 41, 304-318.	2.8	148
152	Arabidopsis ETO1 specifically interacts with and negatively regulates type 2 1-aminocyclopropane-1-carboxylate synthases. <i>BMC Plant Biology</i> , 2005, 5, 14.	1.6	148
153	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.	13.5	148
154	Plant Stress Tolerance Requires Auxin-Sensitive Aux/IAA Transcriptional Repressors. <i>Current Biology</i> , 2017, 27, 437-444.	1.8	148
155	The POLARIS Peptide of Arabidopsis Regulates Auxin Transport and Root Growth via Effects on Ethylene Signaling. <i>Plant Cell</i> , 2006, 18, 3058-3072.	3.1	146
156	Sigma factor-mediated plastid retrograde signals control nuclear gene expression. <i>Plant Journal</i> , 2013, 73, 1-13.	2.8	145
157	Integrated multi-omics framework of the plant response to jasmonic acid. <i>Nature Plants</i> , 2020, 6, 290-302.	4.7	145
158	Short-Term Growth Responses to Ethylene in Arabidopsis Seedlings Are EIN3/EIL1 Independent. <i>Plant Physiology</i> , 2004, 136, 2921-2927.	2.3	140
159	The phosphatase laforin crosses evolutionary boundaries and links carbohydrate metabolism to neuronal disease. <i>Journal of Cell Biology</i> , 2007, 178, 477-488.	2.3	140
160	FRIGIDA-Independent Variation in Flowering Time of Natural Arabidopsis thaliana Accessions. <i>Genetics</i> , 2005, 170, 1197-1207.	1.2	138
161	Robust single-cell DNA methylome profiling with snmC-seq2. <i>Nature Communications</i> , 2018, 9, 3824.	5.8	138
162	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

#	ARTICLE	IF	CITATIONS
163	The Developmental Potential of iPSCs Is Greatly Influenced by Reprogramming Factor Selection. <i>Cell Stem Cell</i> , 2014, 15, 295-309.	5.2	137
164	DNA methylation atlas of the mouse brain at single-cell resolution. <i>Nature</i> , 2021, 598, 120-128.	13.7	135
165	A B-ARR-mediated cytokinin transcriptional network directs hormone cross-regulation and shoot development. <i>Nature Communications</i> , 2018, 9, 1604.	5.8	130
166	RACK1 mediates multiple hormone responsiveness and developmental processes in Arabidopsis. <i>Journal of Experimental Botany</i> , 2006, 57, 2697-2708.	2.4	128
167	The Central Role of PhEIN2 in Ethylene Responses throughout Plant Development in Petunia. <i>Plant Physiology</i> , 2004, 136, 2900-2912.	2.3	126
168	Involvement of NRAMP1 from Arabidopsis thaliana in iron transport. <i>Biochemical Journal</i> , 2000, 347, 749.	1.7	125
169	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
170	A Reevaluation of the Role of the Heterotrimeric G Protein in Coupling Light Responses in Arabidopsis. <i>Plant Physiology</i> , 2003, 131, 1623-1627.	2.3	124
171	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
172	<scp>JAZ</scp>2 controls stomata dynamics during bacterial invasion. <i>New Phytologist</i> , 2017, 213, 1378-1392.	3.5	124
173	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
174	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, 3633-3638.	3.3	116
175	Flagellin Is Not a Major Defense Elicitor in Ralstonia solanacearum Cells or Extracts Applied to Arabidopsis thaliana. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 696-706.	1.4	111
176	An adapter ligation-mediated PCR method for high-throughput mapping of T-DNA inserts in the Arabidopsis genome. <i>Nature Protocols</i> , 2007, 2, 2910-2917.	5.5	111
177	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.	3.1	110
178	ERRs Mediate a Metabolic Switch Required for Somatic Cell Reprogramming to Pluripotency. <i>Cell Stem Cell</i> , 2015, 16, 547-555.	5.2	109
179	The complex architecture and epigenomic impact of plant T-DNA insertions. <i>PLoS Genetics</i> , 2019, 15, e1007819.	1.5	109
180	Regulation of membrane trafficking and organ separation by the NEVERSHED ARF-GAP protein. <i>Development (Cambridge)</i> , 2009, 136, 1909-1918.	1.2	106

#	ARTICLE	IF	CITATIONS
181	Epigenomic landscapes of retinal rods and cones. <i>ELife</i> , 2016, 5, e11613.	2.8	106
182	Exploring the transcriptional landscape of plant circadian rhythms using genome tiling arrays. <i>Genome Biology</i> , 2009, 10, R17.	13.9	103
183	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
184	Release Factor One Is Nonessential in <i>Escherichia coli</i> . <i>ACS Chemical Biology</i> , 2012, 7, 1337-1344.	1.6	100
185	Development of large DNA methods for plants: molecular cloning of large segments of <i>Arabidopsis</i> and carrot DNA into yeast. <i>Nucleic Acids Research</i> , 1988, 16, 11091-11105.	6.5	99
186	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
187	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
188	An atlas of gene regulatory elements in adult mouse cerebrum. <i>Nature</i> , 2021, 598, 129-136.	13.7	95
189	Higher plants possess two different types of ATX1-like copper chaperones. <i>Biochemical and Biophysical Research Communications</i> , 2007, 354, 385-390.	1.0	92
190	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
191	Epigenetic and epigenomic variation in <i>Arabidopsis thaliana</i> . <i>Trends in Plant Science</i> , 2012, 17, 149-154.	4.3	92
192	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
193	A Homolog of Prokaryotic Thiol Disulfide Transporter CcdA Is Required for the Assembly of the Cytochrome <i>bc</i> Complex in <i>Arabidopsis</i> Chloroplasts. <i>Journal of Biological Chemistry</i> , 2004, 279, 32474-32482.	1.6	90
194	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
195	Extraction of Distinct Neuronal Cell Types from within a Genetically Continuous Population. <i>Neuron</i> , 2020, 107, 274-282.e6.	3.8	88
196	Ethylene gas: perception, signaling and response. <i>Current Opinion in Plant Biology</i> , 1998, 1, 393-398.	3.5	85
197	Rapid Array Mapping of Circadian Clock and Developmental Mutations in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2005, 138, 990-997.	2.3	85
198	NPSN11 Is a Cell Plate-Associated SNARE Protein That Interacts with the Syntaxin KNOLLE. <i>Plant Physiology</i> , 2002, 129, 530-539.	2.3	84

#	ARTICLE	IF	CITATIONS
199	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. <i>Nature</i> , 2020, 583, 752-759.	13.7	84
200	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.	1.2	83
201	HIV Integration Site Selection: Targeting in Macrophages and the Effects of Different Routes of Viral Entry. <i>Molecular Therapy</i> , 2006, 14, 218-225.	3.7	83
202	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
203	Functional Characterization of Type-B Response Regulators in the <i>Arabidopsis</i> Cytokinin Response. <i>Plant Physiology</i> , 2013, 162, 212-224.	2.3	82
204	Ethylene gas: it's not just for ripening any more!. <i>Trends in Genetics</i> , 1993, 9, 356-362.	2.9	80
205	The DNA methylome. <i>FEBS Letters</i> , 2011, 585, 1994-2000.	1.3	80
206	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
207	Functional Human Oocytes Generated by Transfer of Polar Body Genomes. <i>Cell Stem Cell</i> , 2017, 20, 112-119.	5.2	76
208	Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <i>New Phytologist</i> , 2017, 214, 808-819.	3.5	75
209	Genomic Decoding of Neuronal Depolarization by Stimulus-Specific NPAS4 Heterodimers. <i>Cell</i> , 2019, 179, 373-391.e27.	13.5	73
210	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
211	PFGE and YAC analysis of the <i>Arabidopsis</i> genome. <i>Methods</i> , 1990, 1, 186-194.	1.9	69
212	PLANT GENOMICS: The Third Wave. <i>Annual Review of Genomics and Human Genetics</i> , 2004, 5, 443-477.	2.5	68
213	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
214	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
215	A Growth Regulatory Loop That Provides Homeostasis to Phytochrome A Signaling[W]. <i>Plant Cell</i> , 2003, 15, 2966-2978.	3.1	67
216	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.	2.0	67

#	ARTICLE	IF	CITATIONS
217	Mapping transcription factor interactome networks using HaloTag protein arrays. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4238-47.	3.3	67
218	A WD40 Domain Cyclophilin Interacts with Histone H3 and Functions in Gene Repression and Organogenesis in Arabidopsis. Plant Cell, 2007, 19, 2403-2416.	3.1	66
219	Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons. ELife, 2019, 8, .	2.8	64
220	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
221	The emergence of the brain non-CpG methylation system in vertebrates. Nature Ecology and Evolution, 2021, 5, 369-378.	3.4	63
222	Mapping the genome landscape using tiling array technology. Current Opinion in Plant Biology, 2007, 10, 534-542.	3.5	61
223	Reentry of the Ethylene MPK6 Module. Plant Cell, 2004, 16, 3169-3173.	3.1	58
224	Activity-dependent modulation of synapse-regulating genes in astrocytes. ELife, 2021, 10, .	2.8	58
225	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. Cell Genomics, 2022, 2, 100107.	3.0	58
226	Integration Site Selection by HIV-Based Vectors in Dividing and Growth-Arrested IMR-90 Lung Fibroblasts. Molecular Therapy, 2006, 13, 366-373.	3.7	57
227	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
228	PHYTOCHROME-INTERACTING FACTORS trigger environmentally responsive chromatin dynamics in plants. Nature Genetics, 2021, 53, 955-961.	9.4	54
229	Iterative single-cell multi-omic integration using online learning. Nature Biotechnology, 2021, 39, 1000-1007.	9.4	53
230	Surveillance of 3â€² Noncoding Transcripts Requires FIERY1 and XRN3 in <i>Arabidopsis</i> . G3: Genes, Genomes, Genetics, 2012, 2, 487-498.	0.8	47
231	The JA pathway MYC transcription factors regulate photomorphogenic responses by targeting HY5 gene expression. Plant Journal, 2020, 102, 138-152.	2.8	47
232	Epigenomic diversity of cortical projection neurons in the mouse brain. Nature, 2021, 598, 167-173.	18.7	47
233	Sequencing and functional validation of the JGI <i>Brachypodium distachyon</i> DNA collection. Plant Journal, 2017, 91, 361-370.	2.8	46
234	OGT binds a conserved C-terminal domain of TET1 to regulate TET1 activity and function in development. ELife, 2018, 7, .	2.8	46

#	ARTICLE	IF	CITATIONS
235	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.	3.3	45
236	EIN4 and ERS2 Are Members of the Putative Ethylene Receptor Gene Family in Arabidopsis. <i>Plant Cell</i> , 1998, 10, 1321.	3.1	44
237	Utilizing tiling microarrays for whole-genome analysis in plants. <i>Plant Journal</i> , 2008, 53, 636-644.	2.8	44
238	Losing Dnmt3a dependent methylation in inhibitory neurons impairs neural function by a mechanism impacting Rett syndrome. <i>ELife</i> , 2020, 9, .	2.8	44
239	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, 5890-5895.	3.3	39
240	The Ethylene Pathway: A Paradigm for Plant Hormone Signaling and Interaction. <i>Science Signaling</i> , 2001, 2001, re1-re1.	1.6	38
241	Single nucleus multi-omics regulatory landscape of the murine pituitary. <i>Nature Communications</i> , 2021, 12, 2677.	5.8	38
242	Ethylene signaling in Arabidopsis : Events from the membrane to the nucleus. <i>Plant Physiology and Biochemistry</i> , 1998, 36, 103-113.	2.8	31
243	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
244	Leaf cell-specific and single-cell transcriptional profiling reveals a role for the palisade layer in UV light protection. <i>Plant Cell</i> , 2022, 34, 3261-3279.	3.1	31
245	Diversity and dynamics of DNA methylation: epigenomic resources and tools for crop breeding. <i>Breeding Science</i> , 2019, 69, 191-204.	0.9	30
246	Epigenetic silencing of a multifunctional plant stress regulator. <i>ELife</i> , 2019, 8, .	2.8	28
247	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.	1.5	26
248	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
249	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	24
250	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
251	Genetic and physical linkage of the Arabidopsis genome: Methods for anchoring Yeast Artificial Chromosomes. , 1992, , 144-169.		22
252	Detection of allele-specific methylation through a generalized heterogeneous epigenome model. <i>Bioinformatics</i> , 2012, 28, i163-i171.	1.8	21

#	ARTICLE	IF	CITATIONS
253	Epigenetic trigger for tomato ripening. <i>Nature Biotechnology</i> , 2013, 31, 119-120.	9.4	21
254	Variation in the Structure of Varicella-Zoster Virus DNA. <i>Intervirology</i> , 1984, 21, 25-37.	1.2	20
255	BRI-ghtening the Pathway to Steroid Hormone Signaling Events in Plants. <i>Cell</i> , 1997, 90, 825-827.	13.5	19
256	Challenges and recommendations for epigenomics in precision health. <i>Nature Biotechnology</i> , 2017, 35, 1128-1132.	9.4	19
257	Genes blossom from a weed. <i>Nature</i> , 1998, 391, 438-439.	13.7	18
258	Exploiting the Triple Response of Arabidopsis to Identify Ethylene-Related Mutants. <i>Plant Cell</i> , 1990, 2, 513.	3.1	16
259	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
260	STAR: an integrated solution to management and visualization of sequencing data. <i>Bioinformatics</i> , 2013, 29, 3204-3210.	1.8	13
261	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
262	Analysis of interruptions in the phosphodiester backbone of herpes simplex virus DNA. <i>Virology</i> , 1981, 110, 213-216.	1.1	12
263	Mutant analysis as an experimental approach towards understanding plant hormone action. <i>Seminars in Developmental Biology</i> , 1993, 4, 3-13.	1.3	12
264	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, 267-280.	2.4	12
265	A plant-specific syntaxin-6 protein contributes to the intracytoplasmic route for the begomovirus CabLCV. <i>Plant Physiology</i> , 2021, 187, 158-173.	2.3	12
266	Divergent perspectives on GM food. <i>Nature Biotechnology</i> , 2002, 20, 1195-1196.	9.4	11
267	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
268	Exceptional epigenetics in the brain. <i>Science</i> , 2015, 348, 1094-1095.	6.0	11
269	The role of ATXR6 expression in modulating genome stability and transposable element repression in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	11
270	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.	6.5	10

#	ARTICLE	IF	CITATIONS
271	Dnmt3a knockout in excitatory neurons impairs postnatal synapse maturation and increases the repressive histone modification H3K27me3. <i>ELife</i> , 0, 11, .	2.8	10
272	Zeroing in on DNA methylomes with no BS. <i>Nature Methods</i> , 2010, 7, 435-437.	9.0	8
273	Profiling Interactome Networks with the HaloTagâ€NAPPA <i>In Situ</i> Protein Array. <i>Current Protocols in Plant Biology</i> , 2018, 3, e20071.	2.8	8
274	The biology of time: dynamic responses of cell types to developmental, circadian, and environmental cues. <i>Plant Journal</i> , 2021, , .	2.8	8
275	Response to Perspective. <i>Plant Signaling and Behavior</i> , 2013, 8, e25037.	1.2	5
276	Ethylene Responses in Seedling Growth and Development. , 2010, , 358-376.		2
277	CrY2H-seq interactome screening. <i>Protocol Exchange</i> , 0, , .	0.3	1
278	Cell signalling and gene regulation: piecing the puzzle together. <i>Current Opinion in Plant Biology</i> , 1998, 1, 375-377.	3.5	0
279	The phosphatase laforin crosses evolutionary boundaries and links carbohydrate metabolism to neuronal disease. <i>Journal of Experimental Medicine</i> , 2007, 204, i22-i22.	4.2	0
280	The phosphatase laforin crosses evolutionary boundaries and links carbohydrate metabolism to neuronal disease. <i>FASEB Journal</i> , 2008, 22, 102.2.	0.2	0
281	Title is missing!. , 2019, 15, e1008492.		0
282	Title is missing!. , 2019, 15, e1008492.		0
283	Title is missing!. , 2019, 15, e1008492.		0
284	Title is missing!. , 2019, 15, e1008492.		0