

# Joseph R Ecker

## List of Publications by Year in descending order

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284  
papers

101,231  
citations

300

143  
h-index

374

288  
g-index

335  
all docs

335  
docs citations

335  
times ranked

93821  
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 <sup>2+</sup> - 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 $\hat{\Gamma}^2$ -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 <sup>2+</sup> /H <sup>+</sup> 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
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