

Joseph R Ecker

List of Publications by Year in descending order

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284
papers

101,231
citations

246

143
h-index

322

288
g-index

335
all docs

335
docs citations

335
times ranked

84510
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
2	Genome-Wide Insertional Mutagenesis of <i>Arabidopsis thaliana</i> . <i>Science</i> , 2003, 301, 653-657.	12.6	4,667
3	Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> , 2009, 462, 315-322.	27.8	4,063
4	Highly Integrated Single-Base Resolution Maps of the Epigenome in <i>Arabidopsis</i> . <i>Cell</i> , 2008, 133, 523-536.	28.9	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.	28.9	1,841
6	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010, 28, 1045-1048.	17.5	1,705
7	Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , 2016, 13, 1050-1054.	19.0	1,658
8	Genome-wide association study of 107 phenotypes in <i>Arabidopsis thaliana</i> inbred lines. <i>Nature</i> , 2010, 465, 627-631.	27.8	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.	28.9	1,647
10	HIV-1 Integration in the Human Genome Favors Active Genes and Local Hotspots. <i>Cell</i> , 2002, 110, 521-529.	28.9	1,622
11	Global Epigenomic Reconfiguration During Mammalian Brain Development. <i>Science</i> , 2013, 341, 1237905.	12.6	1,609
12	Determination and Inference of Eukaryotic Transcription Factor Sequence Specificity. <i>Cell</i> , 2014, 158, 1431-1443.	28.9	1,515
13	Ethylene Biosynthesis and Signaling Networks. <i>Plant Cell</i> , 2002, 14, S131-S151.	6.6	1,488
14	Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> , 2011, 471, 68-73.	27.8	1,442
15	Chromatin architecture reorganization during stem cell differentiation. <i>Nature</i> , 2015, 518, 331-336.	27.8	1,442
16	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	1,252
17	EIN2, a Bifunctional Transducer of Ethylene and Stress Responses in <i>Arabidopsis</i> . <i>Science</i> , 1999, 284, 2148-2152.	12.6	1,172
18	1,135 Genomes Reveal the Global Pattern of Polymorphism in <i>Arabidopsis thaliana</i> . <i>Cell</i> , 2016, 166, 481-491.	28.9	1,107

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19	Assignment of 30 Microsatellite Loci to the Linkage Map of Arabidopsis. <i>Genomics</i> , 1994, 19, 137-144.	2.9	1,105
20	Mitogen-activated protein kinase cascades in plants: a new nomenclature. <i>Trends in Plant Science</i> , 2002, 7, 301-308.	8.8	1,080
21	Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. <i>Cell</i> , 2016, 165, 1280-1292.	28.9	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.	6.6	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.	28.9	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.	7.1	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.	7.1	878
26	Empirical Analysis of Transcriptional Activity in the Arabidopsis Genome. <i>Science</i> , 2003, 302, 842-846.	12.6	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.	28.9	852
28	Evidence for Network Evolution in an Arabidopsis Interactome Map. <i>Science</i> , 2011, 333, 601-607.	12.6	838
29	The ethylene signaling pathway: new insights. <i>Current Opinion in Plant Biology</i> , 2004, 7, 40-49.	7.1	834
30	Retroviral DNA Integration: ASLV, HIV, and MLV Show Distinct Target Site Preferences. <i>PLoS Biology</i> , 2004, 2, e234.	5.6	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.	28.9	827
32	Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network. <i>Science</i> , 2011, 333, 596-601.	12.6	776
33	Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. <i>Cell Stem Cell</i> , 2010, 6, 479-491.	11.1	747
34	Genome-wide mapping of 5-hydroxymethylcytosine in embryonic stem cells. <i>Nature</i> , 2011, 473, 394-397.	27.8	738
35	Common Sequence Polymorphisms Shaping Genetic Diversity in Arabidopsis thaliana. <i>Science</i> , 2007, 317, 338-342.	12.6	689
36	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	28.9	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.	6.6	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.	17.5	647
39	Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. <i>Neuron</i> , 2015, 86, 1369-1384.	8.1	640
40	Transgenerational Epigenetic Instability Is a Source of Novel Methylation Variants. <i>Science</i> , 2011, 334, 369-373.	12.6	635
41	Type-A Arabidopsis Response Regulators Are Partially Redundant Negative Regulators of Cytokinin Signaling[W]. <i>Plant Cell</i> , 2004, 16, 658-671.	6.6	631
42	Localization of Iron in Arabidopsis Seed Requires the Vacuolar Membrane Transporter VIT1. <i>Science</i> , 2006, 314, 1295-1298.	12.6	614
43	Auxin response factors ARF6 and ARF8 promote jasmonic acid production and flower maturation. <i>Development (Cambridge)</i> , 2005, 132, 4107-4118.	2.5	608
44	Human body epigenome maps reveal noncanonical DNA methylation variation. <i>Nature</i> , 2015, 523, 212-216.	27.8	605
45	Trp-dependent auxin biosynthesis in Arabidopsis: involvement of cytochrome P450s CYP79B2 and CYP79B3. <i>Genes and Development</i> , 2002, 16, 3100-3112.	5.9	598
46	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. <i>Cell</i> , 2016, 166, 492-505.	28.9	594
47	A role for LEDGF/p75 in targeting HIV DNA integration. <i>Nature Medicine</i> , 2005, 11, 1287-1289.	30.7	583
48	EIN4 and ERS2 Are Members of the Putative Ethylene Receptor Gene Family in Arabidopsis. <i>Plant Cell</i> , 1998, 10, 1321-1332.	6.6	546
49	Patterns of population epigenomic diversity. <i>Nature</i> , 2013, 495, 193-198.	27.8	543
50	Chloroplast to nucleus communication triggered by accumulation of Mg-protoporphyrinIX. <i>Nature</i> , 2003, 421, 79-83.	27.8	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.	5.6	523
52	DELLA Proteins and Gibberellin-Regulated Seed Germination and Floral Development in Arabidopsis. <i>Plant Physiology</i> , 2004, 135, 1008-1019.	4.8	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.	3.1	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.	7.1	519

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55	Recombination and linkage disequilibrium in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2007, 39, 1151-1155.	21.4	497
56	THE ETHYLENE GAS SIGNAL TRANSDUCTION PATHWAY: A Molecular Perspective. <i>Annual Review of Genetics</i> , 1998, 32, 227-254.	7.6	490
57	GUN4, a Regulator of Chlorophyll Synthesis and Intracellular Signaling. <i>Science</i> , 2003, 299, 902-906.	12.6	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.	5.5	476
59	Involvement of NRAMP1 from <i>Arabidopsis thaliana</i> in iron transport. <i>Biochemical Journal</i> , 2000, 347, 749-755.	3.7	474
60	Dynamic DNA methylation: In the right place at the right time. <i>Science</i> , 2018, 361, 1336-1340.	12.6	469
61	Processing and Subcellular Trafficking of ER-Tethered EIN2 Control Response to Ethylene Gas. <i>Science</i> , 2012, 338, 390-393.	12.6	461
62	Linking photoreceptor excitation to changes in plant architecture. <i>Genes and Development</i> , 2012, 26, 785-790.	5.9	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.	6.6	453
64	Phototropin-related NPL1 controls chloroplast relocation induced by blue light. <i>Nature</i> , 2001, 410, 952-954.	27.8	448
65	Cryptochromes Interact Directly with PIFs to Control Plant Growth in Limiting Blue Light. <i>Cell</i> , 2016, 164, 233-245.	28.9	445
66	Single-cell methylomes identify neuronal subtypes and regulatory elements in mammalian cortex. <i>Science</i> , 2017, 357, 600-604.	12.6	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.	28.9	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.	6.6	432
69	NPH4/ARF7 and ARF19 promote leaf expansion and auxin-induced lateral root formation. <i>Plant Journal</i> , 2005, 43, 118-130.	5.7	415
70	Molecular Criteria for Defining the Naive Human Pluripotent State. <i>Cell Stem Cell</i> , 2016, 19, 502-515.	11.1	415
71	Enhanced Fitness Conferred by Naturally Occurring Variation in the Circadian Clock. <i>Science</i> , 2003, 302, 1049-1053.	12.6	411
72	Integration of omic networks in a developmental atlas of maize. <i>Science</i> , 2016, 353, 814-818.	12.6	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.	6.6	397
74	A Link between RNA Metabolism and Silencing Affecting Arabidopsis Development. <i>Developmental Cell</i> , 2008, 14, 854-866.	7.0	394
75	A transcription factor hierarchy defines an environmental stress response network. <i>Science</i> , 2016, 354, .	12.6	394
76	The Arabidopsis Histidine Phosphotransfer Proteins Are Redundant Positive Regulators of Cytokinin Signaling. <i>Plant Cell</i> , 2006, 18, 3073-3087.	6.6	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.	28.9	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.	7.1	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.	7.1	380
80	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. <i>ELife</i> , 2013, 2, e00675.	6.0	379
81	Applications of DNA tiling arrays for whole-genome analysis. <i>Genomics</i> , 2005, 85, 1-15.	2.9	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.	11.0	367
83	Regulation of ethylene gas biosynthesis by the Arabidopsis ETO1 protein. <i>Nature</i> , 2004, 428, 945-950.	27.8	362
84	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021, 598, 111-119.	27.8	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.	7.1	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.	6.6	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.	6.6	331
88	Mapping genome-wide transcription-factor binding sites using DAP-seq. <i>Nature Protocols</i> , 2017, 12, 1659-1672.	12.0	330
89	Finding the fifth base: Genome-wide sequencing of cytosine methylation. <i>Genome Research</i> , 2009, 19, 959-966.	5.5	323
90	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	27.8	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.	6.6	310
92	Retroviral DNA Integration: Viral and Cellular Determinants of Target-Site Selection. <i>PLoS Pathogens</i> , 2006, 2, e60.	4.7	310
93	Abnormalities in human pluripotent cells due to reprogramming mechanisms. <i>Nature</i> , 2014, 511, 177-183.	27.8	307
94	Genome-Wide High-Resolution Mapping of Exosome Substrates Reveals Hidden Features in the Arabidopsis Transcriptome. <i>Cell</i> , 2007, 131, 1340-1353.	28.9	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.	5.9	297
96	Cerebral Organoids Recapitulate Epigenomic Signatures of the Human Fetal Brain. <i>Cell Reports</i> , 2016, 17, 3369-3384.	6.4	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.	5.7	290
98	Convergence of Signaling Pathways in the Control of Differential Cell Growth in Arabidopsis. <i>Developmental Cell</i> , 2004, 7, 193-204.	7.0	289
99	Literature-curated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 39-46.	19.0	288
100	RF1 knockout allows ribosomal incorporation of unnatural amino acids at multiple sites. <i>Nature Chemical Biology</i> , 2011, 7, 779-786.	8.0	286
101	Stress induced gene expression drives transient DNA methylation changes at adjacent repetitive elements. <i>ELife</i> , 2015, 4, .	6.0	285
102	â€˜Levelingâ€™ the playing field for analyses of single-base resolution DNA methylomes. <i>Trends in Genetics</i> , 2012, 28, 583-585.	6.7	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.	7.1	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.	2.9	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.	7.1	261
106	Three Redundant Brassinosteroid Early Response Genes Encode Putative bHLH Transcription Factors Required for Normal Growth. <i>Genetics</i> , 2002, 162, 1445-1456.	2.9	259
107	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	27.8	257
108	Comprehensive analysis of single cell ATAC-seq data with SnapATAC. <i>Nature Communications</i> , 2021, 12, 1337.	12.8	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.	12.0	250
110	ENCODE explained. <i>Nature</i> , 2012, 489, 52-54.	27.8	245
111	Prepublication data sharing. <i>Nature</i> , 2009, 461, 168-170.	27.8	243
112	High contiguity <i>Arabidopsis thaliana</i> genome assembly with a single nanopore flow cell. <i>Nature Communications</i> , 2018, 9, 541.	12.8	243
113	The BRAIN Initiative Cell Census Consortium: Lessons Learned toward Generating a Comprehensive Brain Cell Atlas. <i>Neuron</i> , 2017, 96, 542-557.	8.1	235
114	Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 816-820.	27.8	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.	16.3	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.	16.2	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.	7.1	230
118	Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. <i>Genome Research</i> , 2013, 23, 1663-1674.	5.5	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.	7.1	218
120	Dynamic DNA methylation reconfiguration during seed development and germination. <i>Genome Biology</i> , 2017, 18, 171.	8.8	218
121	An alternative pluripotent state confers interspecies chimaeric competency. <i>Nature</i> , 2015, 521, 316-321.	27.8	215
122	Non-CC Methylation in the Human Genome. <i>Annual Review of Genomics and Human Genetics</i> , 2015, 16, 55-77.	6.2	210
123	Active DNA demethylation at enhancers during the vertebrate phylotypic period. <i>Nature Genetics</i> , 2016, 48, 417-426.	21.4	210
124	Potential Sites of Bioactive Gibberellin Production during Reproductive Growth in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2008, 20, 320-336.	6.6	209
125	Forward and Reverse Genetics through Derivation of Haploid Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2011, 9, 563-574.	11.1	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.	3.9	203

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127	Integrative analysis of haplotype-resolved epigenomes across human tissues. <i>Nature</i> , 2015, 518, 350-354.	27.8	201
128	Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. <i>Nature Methods</i> , 2019, 16, 999-1006.	19.0	200
129	An <i>Arabidopsis</i> circadian clock component interacts with both CRY1 and phyB. <i>Nature</i> , 2001, 410, 487-490.	27.8	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.	7.1	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.	6.6	190
132	Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. <i>ELife</i> , 2018, 7, .	6.0	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.	6.6	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.	7.1	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.	7.1	174
136	Linking genotype to phenotype using the <i>Arabidopsis</i> unimutant collection. <i>Plant Journal</i> , 2010, 61, 928-940.	5.7	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.	6.6	170
138	Ethylene signaling: from mutants to molecules. <i>Current Opinion in Plant Biology</i> , 2000, 3, 353-360.	7.1	166
139	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	27.8	166
140	A Genome-Scale Resource for the Functional Characterization of <i>Arabidopsis</i> Transcription Factors. <i>Cell Reports</i> , 2014, 8, 622-632.	6.4	164
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.	7.1	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.	4.8	160
143	Unique cell-type-specific patterns of DNA methylation in the root meristem. <i>Nature Plants</i> , 2016, 2, 16058.	9.3	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.	7.1	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.	19.0	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.	6.6	156
147	A complete BAC-based physical map of the Arabidopsis thaliana genome. <i>Nature Genetics</i> , 1999, 22, 271-275.	21.4	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.	3.3	155
149	Auxin-sensitive Aux/IAA proteins mediate drought tolerance in Arabidopsis by regulating glucosinolate levels. <i>Nature Communications</i> , 2019, 10, 4021.	12.8	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.	7.1	150
151	An Arabidopsis NPR1-like gene, NPR4, is required for disease resistance. <i>Plant Journal</i> , 2004, 41, 304-318.	5.7	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.	3.6	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.	28.9	148
154	Plant Stress Tolerance Requires Auxin-Sensitive Aux/IAA Transcriptional Repressors. <i>Current Biology</i> , 2017, 27, 437-444.	3.9	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.	6.6	146
156	Sigma factor-mediated plastid retrograde signals control nuclear gene expression. <i>Plant Journal</i> , 2013, 73, 1-13.	5.7	145
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