

Daniel J Kliebenstein

List of Publications by Year in descending order

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179
papers

17,812
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10986

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209
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209
times ranked

14813
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#	ARTICLE	IF	CITATIONS
1	Genetic Control of Natural Variation in Arabidopsis Glucosinolate Accumulation. <i>Plant Physiology</i> , 2001, 126, 811-825.	4.8	607
2	Superoxide Dismutase in Arabidopsis: An Eclectic Enzyme Family with Disparate Regulation and Protein Localization. <i>Plant Physiology</i> , 1998, 118, 637-650.	4.8	558
3	Plant Secondary Metabolites as Defenses, Regulators, and Primary Metabolites: The Blurred Functional Trichotomy. <i>Plant Physiology</i> , 2020, 184, 39-52.	4.8	549
4	Disarming the mustard oil bomb. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11223-11228.	7.1	498
5	A UV-B-specific signaling component orchestrates plant UV protection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18225-18230.	7.1	495
6	Gene Duplication in the Diversification of Secondary Metabolism: Tandem 2-Oxoglutarate-Dependent Dioxygenases Control Glucosinolate Biosynthesis in Arabidopsis. <i>Plant Cell</i> , 2001, 13, 681-693.	6.6	447
7	The Arabidopsis Epithiospecifier Protein Promotes the Hydrolysis of Glucosinolates to Nitriles and Influences <i>Trichoplusia ni</i> Herbivory. <i>Plant Cell</i> , 2001, 13, 2793-2807.	6.6	400
8	Retrograde Signaling by the Plastidial Metabolite MEcPP Regulates Expression of Nuclear Stress-Response Genes. <i>Cell</i> , 2012, 149, 1525-1535.	28.9	368
9	Global eQTL Mapping Reveals the Complex Genetic Architecture of Transcript-Level Variation in Arabidopsis. <i>Genetics</i> , 2007, 175, 1441-1450.	2.9	352
10	<i>Arabidopsis</i> Defense against <i>Botrytis cinerea</i> : Chronology and Regulation Deciphered by High-Resolution Temporal Transcriptomic Analysis. <i>Plant Cell</i> , 2012, 24, 3530-3557.	6.6	337
11	Secondary metabolites and plant/environment interactions: a view through <i>Arabidopsis thaliana</i> tinted glasses. <i>Plant, Cell and Environment</i> , 2004, 27, 675-684.	5.7	335
12	Arabidopsis UVR8 Regulates Ultraviolet-B Signal Transduction and Tolerance and Contains Sequence Similarity to Human Regulator of Chromatin Condensation 1. <i>Plant Physiology</i> , 2002, 130, 234-243.	4.8	328
13	A Systems Biology Approach Identifies a R2R3 MYB Gene Subfamily with Distinct and Overlapping Functions in Regulation of Aliphatic Glucosinolates. <i>PLoS ONE</i> , 2007, 2, e1322.	2.5	321
14	Natural Enemies Drive Geographic Variation in Plant Defenses. <i>Science</i> , 2012, 338, 116-119.	12.6	286
15	Linking Metabolic QTLs with Network and cis-eQTLs Controlling Biosynthetic Pathways. <i>PLoS Genetics</i> , 2007, 3, e162.	3.5	275
16	Secondary metabolites influence Arabidopsis/Botrytis interactions: variation in host production and pathogen sensitivity. <i>Plant Journal</i> , 2005, 44, 25-36.	5.7	269
17	The Arabidopsis Epithiospecifier Protein Promotes the Hydrolysis of Glucosinolates to Nitriles and Influences <i>Trichoplusia ni</i> Herbivory. <i>Plant Cell</i> , 2001, 13, 2793-2807.	6.6	254
18	Combining Genome-Wide Association Mapping and Transcriptional Networks to Identify Novel Genes Controlling Glucosinolates in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2011, 9, e1001125.	5.6	246

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19	Comparative Analysis of Quantitative Trait Loci Controlling Glucosinolates, Myrosinase and Insect Resistance in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2002, 161, 325-332.	2.9	243
20	The Gene Controlling the Quantitative Trait Locus EPITHIOSPECIFIER MODIFIER1 Alters Glucosinolate Hydrolysis and Insect Resistance in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2006, 18, 1524-1536.	6.6	230
21	Benzoic acid glucosinolate esters and other glucosinolates from <i>Arabidopsis thaliana</i> . <i>Phytochemistry</i> , 2002, 59, 663-671.	2.9	226
22	A Complex Interplay of Three R2R3 MYB Transcription Factors Determines the Profile of Aliphatic Glucosinolates in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2010, 153, 348-363.	4.8	226
23	A Global Coexpression Network Approach for Connecting Genes to Specialized Metabolic Pathways in Plants. <i>Plant Cell</i> , 2017, 29, 944-959.	6.6	225
24	Transcriptional regulation of nitrogen-associated metabolism and growth. <i>Nature</i> , 2018, 563, 259-264.	27.8	222
25	Identification of a flavin-monooxygenase as the S-oxygenating enzyme in aliphatic glucosinolate biosynthesis in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2007, 50, 902-910.	5.7	219
26	Biochemical Networks and Epistasis Shape the <i>Arabidopsis thaliana</i> Metabolome. <i>Plant Cell</i> , 2008, 20, 1199-1216.	6.6	218
27	Comparative Quantitative Trait Loci Mapping of Aliphatic, Indolic and Benzylic Glucosinolate Production in <i>Arabidopsis thaliana</i> Leaves and Seeds. <i>Genetics</i> , 2001, 159, 359-370.	2.9	217
28	Mutation bias reflects natural selection in <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2022, 602, 101-105.	27.8	206
29	Understanding the Evolution of Defense Metabolites in <i>Arabidopsis thaliana</i> Using Genome-wide Association Mapping. <i>Genetics</i> , 2010, 185, 991-1007.	2.9	184
30	High-density haplotyping with microarray-based expression and single feature polymorphism markers in <i>Arabidopsis</i> . <i>Genome Research</i> , 2006, 16, 787-795.	5.5	179
31	Quantitative Resistance: More Than Just Perception of a Pathogen. <i>Plant Cell</i> , 2017, 29, 655-665.	6.6	179
32	LSD1 Regulates Salicylic Acid Induction of Copper Zinc Superoxide Dismutase in <i>Arabidopsis thaliana</i> . <i>Molecular Plant-Microbe Interactions</i> , 1999, 12, 1022-1026.	2.6	163
33	Quantitative Genomics: Analyzing Intraspecific Variation Using Global Gene Expression Polymorphisms or eQTLs. <i>Annual Review of Plant Biology</i> , 2009, 60, 93-114.	18.7	159
34	Auxin-sensitive Aux/IAA proteins mediate drought tolerance in <i>Arabidopsis</i> by regulating glucosinolate levels. <i>Nature Communications</i> , 2019, 10, 4021.	12.8	155
35	Subclade of Flavin-Monooxygenases Involved in Aliphatic Glucosinolate Biosynthesis. <i>Plant Physiology</i> , 2008, 148, 1721-1733.	4.8	150
36	Genetic Architecture of Plastic Methyl Jasmonate Responses in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2002, 161, 1685-1696.	2.9	149

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37	The Genetic Basis of Constitutive and Herbivore-Induced ESP-Independent Nitrile Formation in <i>Arabidopsis</i> Å Å. <i>Plant Physiology</i> , 2009, 149, 561-574.	4.8	148
38	The Complex Genetic Architecture of the Metabolome. <i>PLoS Genetics</i> , 2010, 6, e1001198.	3.5	148
39	Identification of <i>Botrytis cinerea</i> susceptibility loci in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2004, 38, 473-486.	5.7	147
40	Pectin Biosynthesis Is Critical for Cell Wall Integrity and Immunity in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2016, 28, 537-556.	6.6	144
41	Deficiencies in Jasmonate-Mediated Plant Defense Reveal Quantitative Variation in <i>Botrytis cinerea</i> Pathogenesis. <i>PLoS Pathogens</i> , 2010, 6, e1000861.	4.7	141
42	Network Quantitative Trait Loci Mapping of Circadian Clock Outputs Identifies Metabolic Pathway-to-Clock Linkages in <i>Arabidopsis</i> Å Å. <i>Plant Cell</i> , 2011, 23, 471-485.	6.6	139
43	Fatty acids and early detection of pathogens. <i>Current Opinion in Plant Biology</i> , 2013, 16, 520-526.	7.1	137
44	Chapter five Glucosinolate hydrolysis and its impact on generalist and specialist insect herbivores. <i>Recent Advances in Phytochemistry</i> , 2003, , 101-125.	0.5	131
45	A Novel 2-Oxoacid-Dependent Dioxygenase Involved in the Formation of the Goiterogenic 2-Hydroxybut-3-enyl Glucosinolate and Generalist Insect Resistance in <i>Arabidopsis</i> Å Å. <i>Plant Physiology</i> , 2008, 148, 2096-2108.	4.8	131
46	The Chromatin Remodeler SPLAYED Regulates Specific Stress Signaling Pathways. <i>PLoS Pathogens</i> , 2008, 4, e1000237.	4.7	129
47	Geographic and evolutionary diversification of glucosinolates among near relatives of <i>Arabidopsis thaliana</i> (Brassicaceae). <i>Phytochemistry</i> , 2005, 66, 1321-1333.	2.9	126
48	Identification of QTLs controlling gene expression networks defined a priori. <i>BMC Bioinformatics</i> , 2006, 7, 308.	2.6	122
49	A Role for Gene Duplication and Natural Variation of Gene Expression in the Evolution of Metabolism. <i>PLoS ONE</i> , 2008, 3, e1838.	2.5	121
50	Making new molecules “ evolution of pathways for novel metabolites in plants. <i>Current Opinion in Plant Biology</i> , 2012, 15, 415-423.	7.1	121
51	Distinct Roles of Jasmonates and Aldehydes in Plant-Defense Responses. <i>PLoS ONE</i> , 2008, 3, e1904.	2.5	120
52	Convergence, constraint and the role of gene expression during adaptive radiation: floral anthocyanins in <i>Aquilegia</i> . <i>Molecular Ecology</i> , 2006, 15, 4645-4657.	3.9	119
53	Differential Levels of Insect Herbivory in the Field Associated with Genotypic Variation in Glucosinolates in <i>Arabidopsis thaliana</i> . <i>Journal of Chemical Ecology</i> , 2008, 34, 1026-1037.	1.8	118
54	Using knockout mutants to reveal the growth costs of defensive traits. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 2598-2603.	2.6	110

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55	Genomic Analysis of QTLs and Genes Altering Natural Variation in Stochastic Noise. PLoS Genetics, 2011, 7, e1002295.	3.5	107
56	Natural genetic variation in Arabidopsis thaliana defense metabolism genes modulates field fitness. ELife, 2015, 4, .	6.0	107
57	Genomic Survey of Gene Expression Diversity in Arabidopsis thaliana. Genetics, 2006, 172, 1179-1189.	2.9	104
58	Identifying the molecular basis of QTLs: eQTLs add a new dimension. Trends in Plant Science, 2008, 13, 72-77.	8.8	104
59	Complex Genetics Control Natural Variation in <i>Arabidopsis thaliana</i> Resistance to <i>Botrytis cinerea</i> . Genetics, 2008, 180, 2237-2250.	2.9	104
60	Natural Variation among Arabidopsis thaliana Accessions for Transcriptome Response to Exogenous Salicylic Acid. Plant Cell, 2007, 19, 2099-2110.	6.6	101
61	An ecological genomic approach challenging the paradigm of differential plant responses to specialist versus generalist insect herbivores. Oecologia, 2011, 167, 677-689.	2.0	101
62	Genotype, Age, Tissue, and Environment Regulate the Structural Outcome of Glucosinolate Activation. Plant Physiology, 2008, 147, 415-428.	4.8	100
63	Intronic T-DNA Insertion Renders Arabidopsis <i>opr3</i> a Conditional Jasmonic Acid-Producing Mutant. Plant Physiology, 2011, 156, 770-778.	4.8	93
64	Characterization of seed-specific benzoyloxyglucosinolate mutations in <i>Arabidopsis thaliana</i> . Plant Journal, 2007, 51, 1062-1076.	5.7	90
65	ESP and ESM1 mediate indol-3-acetonitrile production from indol-3-ylmethyl glucosinolate in Arabidopsis. Phytochemistry, 2008, 69, 663-671.	2.9	90
66	Promoter-Based Integration in Plant Defense Regulation. Plant Physiology, 2014, 166, 1803-1820.	4.8	89
67	Plastic Transcriptomes Stabilize Immunity to Pathogen Diversity: The Jasmonic Acid and Salicylic Acid Networks within the Arabidopsis/ <i>Botrytis</i> Pathosystem. Plant Cell, 2017, 29, 2727-2752.	6.6	84
68	An evolutionarily young defense metabolite influences the root growth of plants via the ancient TOR signaling pathway. ELife, 2017, 6, .	6.0	84
69	The Quantitative Basis of the Arabidopsis Innate Immune System to Endemic Pathogens Depends on Pathogen Genetics. PLoS Genetics, 2016, 12, e1005789.	3.5	83
70	Regulatory networks of glucosinolates shape Arabidopsis thaliana fitness. Current Opinion in Plant Biology, 2010, 13, 347-352.	7.1	81
71	Arctic Mustard Flower Color Polymorphism Controlled by Petal-Specific Downregulation at the Threshold of the Anthocyanin Biosynthetic Pathway. PLoS ONE, 2011, 6, e18230.	2.5	80
72	Biosynthesis and Defensive Function of <i>N</i> -Acetylornithine, a Jasmonate-Induced Arabidopsis Metabolite. Plant Cell, 2011, 23, 3303-3318.	6.6	80

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73	Cytoplasmic genetic variation and extensive cytonuclear interactions influence natural variation in the metabolome. <i>ELife</i> , 2013, 2, e00776.	6.0	76
74	Competition, herbivory and genetics interact to determine the accumulation and fitness consequences of a defence metabolite. <i>Journal of Ecology</i> , 2009, 97, 78-88.	4.0	75
75	A new method for measuring relative growth rate can uncover the costs of defensive compounds in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2010, 187, 1102-1111.	7.3	74
76	Postharvest Circadian Entrainment Enhances Crop Pest Resistance and Phytochemical Cycling. <i>Current Biology</i> , 2013, 23, 1235-1241.	3.9	73
77	Identification of Novel Loci Regulating Interspecific Variation in Root Morphology and Cellular Development in Tomato. <i>Plant Physiology</i> , 2013, 162, 755-768.	4.8	68
78	Molecular mechanisms governing differential robustness of development and environmental responses in plants. <i>Annals of Botany</i> , 2016, 117, 795-809.	2.9	68
79	An integrated RNAseq-1H NMR metabolomics approach to understand soybean primary metabolism regulation in response to <i>Rhizoctonia</i> foliar blight disease. <i>BMC Plant Biology</i> , 2017, 17, 84.	3.6	68
80	Advancing Genetic Theory and Application by Metabolic Quantitative Trait Loci Analysis. <i>Plant Cell</i> , 2009, 21, 1637-1646.	6.6	66
81	In Planta Variation of Volatile Biosynthesis: An Alternative Biosynthetic Route to the Formation of the Pathogen-Induced Volatile Homoterpene DMNT via Triterpene Degradation in <i>Arabidopsis</i> Roots. <i>Plant Cell</i> , 2015, 27, 874-890.	6.6	64
82	Ecological costs of biotrophic versus necrotrophic pathogen resistance, the hypersensitive response and signal transduction. <i>Plant Science</i> , 2008, 174, 551-556.	3.6	63
83	False idolatry of the mythical growth versus immunity tradeoff in molecular systems plant pathology. <i>Physiological and Molecular Plant Pathology</i> , 2016, 95, 55-59.	2.5	63
84	The Glucosinolate Biosynthetic Gene AOP2 Mediates Feed-back Regulation of Jasmonic Acid Signaling in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2015, 8, 1201-1212.	8.3	62
85	Genome Wide Association Mapping in <i>Arabidopsis thaliana</i> Identifies Novel Genes Involved in Linking Allyl Glucosinolate to Altered Biomass and Defense. <i>Frontiers in Plant Science</i> , 2016, 7, 1010.	3.6	62
86	Natural variation in cross-talk between glucosinolates and onset of flowering in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 697.	3.6	60
87	The bHLH transcription factor ILR3 modulates multiple stress responses in <i>Arabidopsis</i> . <i>Plant Molecular Biology</i> , 2018, 97, 297-309.	3.9	60
88	MODIFIED VACUOLE PHENOTYPE1 Is an <i>Arabidopsis</i> Myrosinase-Associated Protein Involved in Endomembrane Protein Trafficking. <i>Plant Physiology</i> , 2009, 152, 120-132.	4.8	57
89	Chemically mediated tritrophic interactions: opposing effects of glucosinolates on a specialist herbivore and its predators. <i>Journal of Applied Ecology</i> , 2011, 48, 880-887.	4.0	57
90	Viruses mobilize plant immunity to deter nonvector insect herbivores. <i>Science Advances</i> , 2019, 5, eaav9801.	10.3	57

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91	Overexpression of Three Glucosinolate Biosynthesis Genes in <i>Brassica napus</i> Identifies Enhanced Resistance to <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS ONE</i> , 2015, 10, e0140491.	2.5	57
92	Elevated Genetic Variation Within Virulence-Associated <i>Botrytis cinerea</i> Polygalacturonase Loci. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 1126-1137.	2.6	56
93	The Defense Metabolite, Allyl Glucosinolate, Modulates <i>Arabidopsis thaliana</i> Biomass Dependent upon the Endogenous Glucosinolate Pathway. <i>Frontiers in Plant Science</i> , 2016, 7, 774.	3.6	56
94	Natural variation of plant metabolism: genetic mechanisms, interpretive caveats, evolutionary and mechanistic insights.. <i>Plant Physiology</i> , 2015, 169, pp.01108.2015.	4.8	55
95	The effect of rhizosphere microbes outweighs host plant genetics in reducing insect herbivory. <i>Molecular Ecology</i> , 2019, 28, 1801-1811.	3.9	55
96	Identification and stacking of crucial traits required for the domestication of pennycress. <i>Nature Food</i> , 2020, 1, 84-91.	14.0	54
97	Antisense RNA inhibition of Rubisco activase expression. <i>Plant Journal</i> , 1994, 5, 787-798.	5.7	53
98	The conserved transcription factors, MYB115 and MYB118, control expression of the newly evolved benzoxy glucosinolate pathway in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 343.	3.6	52
99	Making new molecules—evolution of structures for novel metabolites in plants. <i>Current Opinion in Plant Biology</i> , 2013, 16, 112-117.	7.1	49
100	Interactions of Tomato and <i>Botrytis cinerea</i> Genetic Diversity: Parsing the Contributions of Host Differentiation, Domestication, and Pathogen Variation. <i>Plant Cell</i> , 2019, 31, 502-519.	6.6	49
101	Reassess the <i>t</i> -Test: Interact with All Your Data via ANOVA. <i>Plant Cell</i> , 2015, 27, 2088-2094.	6.6	48
102	Innovation, conservation, and repurposing of gene function in root cell type development. <i>Cell</i> , 2021, 184, 3333-3348.e19.	28.9	48
103	A quantitative genetics and ecological model system: understanding the aliphatic glucosinolate biosynthetic network via QTLs. <i>Phytochemistry Reviews</i> , 2009, 8, 243-254.	6.5	46
104	Plant Defense Compounds: Systems Approaches to Metabolic Analysis. <i>Annual Review of Phytopathology</i> , 2012, 50, 155-173.	7.8	46
105	Hierarchical Nuclear and Cytoplasmic Genetic Architectures for Plant Growth and Defense within <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 25, 1929-1945.	6.6	46
106	Plant—necrotroph co-transcriptome networks illuminate a metabolic battlefield. <i>ELife</i> , 2019, 8, .	6.0	46
107	Digital Imaging Combined with Genome-Wide Association Mapping Links Loci to Plant-Pathogen Interaction Traits. <i>Plant Physiology</i> , 2018, 178, 1406-1422.	4.8	43
108	Plant Networks as Traits and Hypotheses: Moving Beyond Description. <i>Trends in Plant Science</i> , 2019, 24, 840-852.	8.8	43

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109	Whole genome resequencing of <i>Botrytis cinerea</i> isolates identifies high levels of standing diversity. <i>Frontiers in Microbiology</i> , 2015, 6, 996.	3.5	42
110	Keeping the rhythm: light/dark cycles during postharvest storage preserve the tissue integrity and nutritional content of leafy plants. <i>BMC Plant Biology</i> , 2015, 15, 92.	3.6	42
111	Macroevolutionary patterns of glucosinolate defense and tests of defense–escalation and resource availability hypotheses. <i>New Phytologist</i> , 2015, 208, 915-927.	7.3	40
112	Network-Guided Discovery of Extensive Epistasis between Transcription Factors Involved in Aliphatic Glucosinolate Biosynthesis. <i>Plant Cell</i> , 2018, 30, 178-195.	6.6	40
113	Genetic Variation in the Nuclear and Organellar Genomes Modulates Stochastic Variation in the Metabolome, Growth, and Defense. <i>PLoS Genetics</i> , 2015, 11, e1004779.	3.5	39
114	Transcriptional networks governing plant metabolism. <i>Current Plant Biology</i> , 2015, 3-4, 56-64.	4.7	38
115	<scp>PMR</scp>5, an acetylation protein at the intersection of pectin biosynthesis and defense against fungal pathogens. <i>Plant Journal</i> , 2019, 100, 1022-1035.	5.7	34
116	Diverse Allyl Glucosinolate Catabolites Independently Influence Root Growth and Development. <i>Plant Physiology</i> , 2020, 183, 1376-1390.	4.8	34
117	Genetic variation, environment and demography intersect to shape <i>Arabidopsis</i> defense metabolite variation across Europe. <i>ELife</i> , 2021, 10, .	6.0	33
118	Determination of the absolute configuration of the glucosinolate methyl sulfoxide group reveals a stereospecific biosynthesis of the side chain. <i>Phytochemistry</i> , 2008, 69, 2737-2742.	2.9	30
119	Cofactome analyses reveal enhanced flux of carbon into oil for potential biofuel production. <i>Plant Journal</i> , 2011, 67, 1018-1028.	5.7	28
120	Genetic Networks Controlling Structural Outcome of Glucosinolate Activation across Development. <i>PLoS Genetics</i> , 2008, 4, e1000234.	3.5	26
121	Epistasis – environment interactions among <i>Arabidopsis thaliana</i> glucosinolate genes impact complex traits and fitness in the field. <i>New Phytologist</i> , 2017, 215, 1249-1263.	7.3	26
122	Initiation of ER Body Formation and Indole Glucosinolate Metabolism by the Plastidial Retrograde Signaling Metabolite, MEcPP. <i>Molecular Plant</i> , 2017, 10, 1400-1416.	8.3	26
123	Red-light is an environmental effector for mutualism between begomovirus and its vector whitefly. <i>PLoS Pathogens</i> , 2021, 17, e1008770.	4.7	26
124	Comparison of the Relative Potential for Epigenetic and Genetic Variation To Contribute to Trait Stability. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1733-1746.	1.8	25
125	Systems Biology Uncovers the Foundation of Natural Genetic Diversity. <i>Plant Physiology</i> , 2010, 152, 480-486.	4.8	24
126	Expansive Phenotypic Landscape of <i>Botrytis cinerea</i> Shows Differential Contribution of Genetic Diversity and Plasticity. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 287-298.	2.6	24

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127	Regulation of Root Angle and Gravitropism. G3: Genes, Genomes, Genetics, 2018, 8, 3841-3855.	1.8	24
128	mGWAS Uncovers Gln-Glucosinolate Seed-Specific Interaction and its Role in Metabolic Homeostasis. Plant Physiology, 2020, 183, 483-500.	4.8	24
129	All Mold Is Not Alike: The Importance of Intraspecific Diversity in Necrotrophic Plant Pathogens. PLoS Pathogens, 2010, 6, e1000759.	4.7	23
130	A keystone gene underlies the persistence of an experimental food web. Science, 2022, 376, 70-73.	12.6	23
131	Acetylation of cell wall is required for structural integrity of the leaf surface and exerts a global impact on plant stress responses. Frontiers in Plant Science, 2015, 6, 550.	3.6	22
132	Synthetic biology of metabolism: using natural variation to reverse engineer systems. Current Opinion in Plant Biology, 2014, 19, 20-26.	7.1	21
133	What Can Causal Networks Tell Us about Metabolic Pathways?. PLoS Computational Biology, 2012, 8, e1002458.	3.2	20
134	Quantitative interactions: the disease outcome of <i>Botrytis cinerea</i> across the plant kingdom. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	20
135	Glucosinolate Survey of Cultivated and Feral Mashua (<i>Tropaeolum tuberosum</i> Ruiz & Pavón) in the Cuzco Region of Peru. Economic Botany, 2006, 60, 254-264.	1.7	18
136	Orchestration of plant defense systems: genes to populations. Trends in Plant Science, 2014, 19, 250-255.	8.8	18
137	Pathogen Genetic Control of Transcriptome Variation in the <i>Arabidopsis thaliana</i> <i>Botrytis cinerea</i> Pathosystem. Genetics, 2020, 215, 253-266.	2.9	18
138	Integrated omics reveal novel functions and underlying mechanisms of the receptor kinase FERONIA in <i>Arabidopsis thaliana</i> . Plant Cell, 2022, 34, 2594-2614.	6.6	18
139	Isolate Dependency of Brassica rapa Resistance QTLs to Botrytis cinerea. Frontiers in Plant Science, 2016, 7, 161.	3.6	17
140	An Integrative Genetic Study of Rice Metabolism, Growth and Stochastic Variation Reveals Potential C/N Partitioning Loci. Scientific Reports, 2016, 6, 30143.	3.3	17
141	FRS7 and FRS12 recruit NINJA to regulate expression of glucosinolate biosynthesis genes. New Phytologist, 2020, 227, 1124-1137.	7.3	17
142	Destabilization of rbcS sense transcripts by antisense RNA. Plant Molecular Biology, 1994, 25, 569-576.	3.9	16
143	Genome size evolution is associated with climate seasonality and glucosinolates, but not life history, soil nutrients or range size, across a clade of mustards. Annals of Botany, 2021, 127, 887-902.	2.9	16
144	Using RNA-Seq for Genomic Scaffold Placement, Correcting Assemblies, and Genetic Map Creation in a Common <i>Brassica rapa</i> Mapping Population. G3: Genes, Genomes, Genetics, 2017, 7, 2259-2270.	1.8	15

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145	A genome-scale TF-DNA interaction network of transcriptional regulation of <i>Arabidopsis</i> primary and specialized metabolism. <i>Molecular Systems Biology</i> , 2021, 17, e10625.	7.2	15
146	Quantification of Variation in Expression Networks. <i>Methods in Molecular Biology</i> , 2009, 553, 227-245.	0.9	14
147	Investigation of the multifunctional gene AOP3 expands the regulatory network fine-tuning glucosinolate production in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 762.	3.6	14
148	Exploring the shallow end; estimating information content in transcriptomics studies. <i>Frontiers in Plant Science</i> , 2012, 3, 213.	3.6	13
149	Meta-analysis of metabolome QTLs in <i>Arabidopsis</i> : trying to estimate the network size controlling genetic variation of the metabolome. <i>Frontiers in Plant Science</i> , 2014, 5, 461.	3.6	13
150	Metabolomics and Plant Quantitative Trait Locus Analysis – The Optimum Genetical Genomics Platform?. , 2007, , 29-44.		13
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