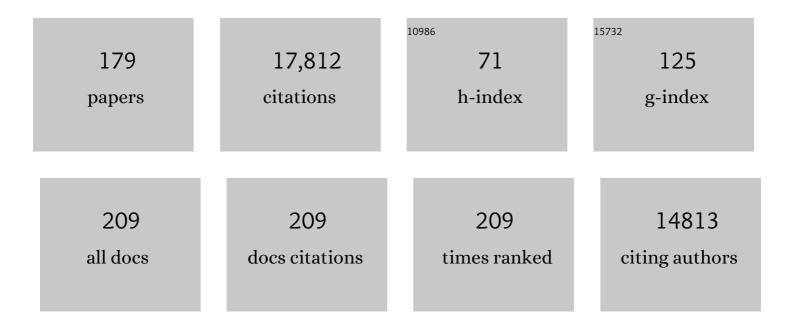
Daniel J Kliebenstein

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	OUP accepted manuscript. Environmental Entomology, 2022, 51, 52-62.	1.4	Ο
2	Mutation bias reflects natural selection in Arabidopsis thaliana. Nature, 2022, 602, 101-105.	27.8	206
3	A plant balancing act: Meshing new and existing metabolic pathways towards an optimized system. Current Opinion in Plant Biology, 2022, 66, 102173.	7.1	5
4	Exciting times in plant biotic interactions. Plant Cell, 2022, 34, 1421-1424.	6.6	3
5	The ease and complexity of identifying and using specialized metabolites for crop engineering. Emerging Topics in Life Sciences, 2022, 6, 153-162.	2.6	3
6	A keystone gene underlies the persistence of an experimental food web. Science, 2022, 376, 70-73.	12.6	23
7	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
8	Red-light is an environmental effector for mutualism between begomovirus and its vector whitefly. PLoS Pathogens, 2021, 17, e1008770.	4.7	26
9	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
10	Fine mapping identifies <i>NADâ€ME1</i> as a candidate underlying a major locus controlling temporal variation in primary and specialized metabolism in Arabidopsis. Plant Journal, 2021, 106, 454-467.	5.7	9
11	The <i>Arabidopsis thaliana</i> nucleotide sugar transporter GONST2 is a functional homolog of GONST1. Plant Direct, 2021, 5, e00309.	1.9	7
12	Quantitative interactions: the disease outcome of <i>Botrytis cinerea</i> across the plant kingdom. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	20
13	Genetic variation, environment and demography intersect to shape Arabidopsis defense metabolite variation across Europe. ELife, 2021, 10, .	6.0	33
14	Innovation, conservation, and repurposing of gene function in root cell type development. Cell, 2021, 184, 3333-3348.e19.	28.9	48
15	A reevaluation of the role of the <i>ASIL</i> trihelix transcription factors as repressors of the seed maturation program. Plant Direct, 2021, 5, e345.	1.9	2
16	A genomeâ€scale TF–DNA interaction network of transcriptional regulation of <i>Arabidopsis</i> primary and specialized metabolism. Molecular Systems Biology, 2021, 17, e10625.	7.2	15
17	Plant Responses Underlying Timely Specialized Metabolites Induction of Brassica Crops. Frontiers in Plant Science, 2021, 12, 807710.	3.6	7
18	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

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19	Using networks to identify and interpret natural variation. Current Opinion in Plant Biology, 2020, 54, 122-126.	7.1	5
20	flasher , a novel mutation in a glucosinolate modifying enzyme, conditions changes in plant architecture and hormone homeostasis. Plant Journal, 2020, 103, 1989-2006.	5.7	5
21	Plant Secondary Metabolites as Defenses, Regulators, and Primary Metabolites: The Blurred Functional Trichotomy. Plant Physiology, 2020, 184, 39-52.	4.8	549
22	Identification and stacking of crucial traits required for the domestication of pennycress. Nature Food, 2020, 1, 84-91.	14.0	54
23	Epistatic Transcription Factor Networks Differentially Modulate <i>Arabidopsis</i> Growth and Defense. Genetics, 2020, 214, 529-541.	2.9	12
24	FRS7 and FRS12 recruit NINJA to regulate expression of glucosinolate biosynthesis genes. New Phytologist, 2020, 227, 1124-1137.	7.3	17
25	Diverse Allyl Glucosinolate Catabolites Independently Influence Root Growth and Development. Plant Physiology, 2020, 183, 1376-1390.	4.8	34
26	mGWAS Uncovers Gln-Glucosinolate Seed-Specific Interaction and its Role in Metabolic Homeostasis. Plant Physiology, 2020, 183, 483-500.	4.8	24
27	<scp>PMR</scp> 5, an acetylation protein at the intersection of pectin biosynthesis and defense against fungal pathogens. Plant Journal, 2019, 100, 1022-1035.	5.7	34
28	Viruses mobilize plant immunity to deter nonvector insect herbivores. Science Advances, 2019, 5, eaav9801.	10.3	57
29	Plant Networks as Traits and Hypotheses: Moving Beyond Description. Trends in Plant Science, 2019, 24, 840-852.	8.8	43
30	Auxin-sensitive Aux/IAA proteins mediate drought tolerance in Arabidopsis by regulating glucosinolate levels. Nature Communications, 2019, 10, 4021.	12.8	155
31	Questionomics: Using Big Data to Ask and Answer Big Questions. Plant Cell, 2019, 31, 1404-1405.	6.6	3
32	The effect of rhizosphere microbes outweighs host plant genetics in reducing insect herbivory. Molecular Ecology, 2019, 28, 1801-1811.	3.9	55
33	Interactions of Tomato and <i>Botrytis cinerea</i> Genetic Diversity: Parsing the Contributions of Host Differentiation, Domestication, and Pathogen Variation. Plant Cell, 2019, 31, 502-519.	6.6	49
34	Plant–necrotroph co-transcriptome networks illuminate a metabolic battlefield. ELife, 2019, 8, .	6.0	46
35	Network-Guided Discovery of Extensive Epistasis between Transcription Factors Involved in Aliphatic Glucosinolate Biosynthesis. Plant Cell, 2018, 30, 178-195.	6.6	40
36	Comparison of the Relative Potential for Epigenetic and Genetic Variation To Contribute to Trait Stability. G3: Genes, Genomes, Genetics, 2018, 8, 1733-1746.	1.8	25

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37	Digital Imaging Combined with Genome-Wide Association Mapping Links Loci to Plant-Pathogen Interaction Traits. Plant Physiology, 2018, 178, 1406-1422.	4.8	43
38	Transcriptional regulation of nitrogen-associated metabolism and growth. Nature, 2018, 563, 259-264.	27.8	222
39	Regulation of Root Angle and Gravitropism. G3: Genes, Genomes, Genetics, 2018, 8, 3841-3855.	1.8	24
40	Plant nutrient acquisition entices herbivore. Science, 2018, 361, 642-643.	12.6	4
41	The bHLH transcription factor ILR3 modulates multiple stress responses in Arabidopsis. Plant Molecular Biology, 2018, 97, 297-309.	3.9	60
42	A Global Coexpression Network Approach for Connecting Genes to Specialized Metabolic Pathways in Plants. Plant Cell, 2017, 29, 944-959.	6.6	225
43	Epistasis × environment interactions among <i>Arabidopsis thaliana</i> glucosinolate genes impact complex traits and fitness in the field. New Phytologist, 2017, 215, 1249-1263.	7.3	26
44	Quantitative Resistance: More Than Just Perception of a Pathogen. Plant Cell, 2017, 29, 655-665.	6.6	179
45	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
46	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
47	Initiation of ER Body Formation and Indole Clucosinolate Metabolism by the Plastidial Retrograde Signaling Metabolite, MEcPP. Molecular Plant, 2017, 10, 1400-1416.	8.3	26
48	An integrated RNAseq-1H NMR metabolomics approach to understand soybean primary metabolism regulation in response to Rhizoctonia foliar blight disease. BMC Plant Biology, 2017, 17, 84.	3.6	68
49	A novel Filamentous Flower mutant suppresses brevipedicellus developmental defects and modulates glucosinolate and auxin levels. PLoS ONE, 2017, 12, e0177045.	2.5	12
50	An evolutionarily young defense metabolite influences the root growth of plants via the ancient TOR signaling pathway. ELife, 2017, 6, .	6.0	84
51	The Quantitative Basis of the Arabidopsis Innate Immune System to Endemic Pathogens Depends on Pathogen Genetics. PLoS Genetics, 2016, 12, e1005789.	3.5	83
52	Isolate Dependency of Brassica rapa Resistance QTLs to Botrytis cinerea. Frontiers in Plant Science, 2016, 7, 161.	3.6	17
53	The Defense Metabolite, Allyl Glucosinolate, Modulates Arabidopsis thaliana Biomass Dependent upon the Endogenous Glucosinolate Pathway. Frontiers in Plant Science, 2016, 7, 774.	3.6	56
54	Genome Wide Association Mapping in Arabidopsis thaliana Identifies Novel Genes Involved in Linking Allyl Glucosinolate to Altered Biomass and Defense. Frontiers in Plant Science, 2016, 7, 1010.	3.6	62

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55	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
56	Observability of plant metabolic networks is reflected in the correlation of metabolic profiles Plant Physiology, 2016, 172, pp.00900.2016.	4.8	2
57	Expansive Phenotypic Landscape of <i>Botrytis cinerea</i> Shows Differential Contribution of Genetic Diversity and Plasticity. Molecular Plant-Microbe Interactions, 2016, 29, 287-298.	2.6	24
58	Pectin Biosynthesis Is Critical for Cell Wall Integrity and Immunity in <i>Arabidopsis thaliana</i> . Plant Cell, 2016, 28, 537-556.	6.6	144
59	False idolatry of the mythical growth versus immunity tradeoff in molecular systems plant pathology. Physiological and Molecular Plant Pathology, 2016, 95, 55-59.	2.5	63
60	Molecular mechanisms governing differential robustness of development and environmental responses in plants. Annals of Botany, 2016, 117, 795-809.	2.9	68
61	Macroevolutionary patterns of glucosinolate defense and tests of defenseâ€escalation and resource availability hypotheses. New Phytologist, 2015, 208, 915-927.	7.3	40
62	Whole genome resequencing of Botrytis cinerea isolates identifies high levels of standing diversity. Frontiers in Microbiology, 2015, 6, 996.	3.5	42
63	The conserved transcription factors, MYB115 and MYB118, control expression of the newly evolved benzoyloxy glucosinolate pathway in Arabidopsis thaliana. Frontiers in Plant Science, 2015, 6, 343.	3.6	52
64	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
65	Natural variation in cross-talk between glucosinolates and onset of flowering in Arabidopsis. Frontiers in Plant Science, 2015, 6, 697.	3.6	60
66	Investigation of the multifunctional gene AOP3 expands the regulatory network fine-tuning glucosinolate production in Arabidopsis. Frontiers in Plant Science, 2015, 6, 762.	3.6	14
67	The Plant CellIntroduces Breakthrough Reports: A New Forum for Cutting-Edge Plant Research. Plant Cell, 2015, , tpc.15.00862.	6.6	1
68	In Planta Variation of Volatile Biosynthesis: An Alternative Biosynthetic Route to the Formation of the Pathogen-Induced Volatile Homoterpene DMNT via Triterpene Degradation in Arabidopsis Roots. Plant Cell, 2015, 27, 874-890.	6.6	64
69	Reassess the <i>t</i> Test: Interact with All Your Data via ANOVA. Plant Cell, 2015, 27, 2088-2094.	6.6	48
70	Transcriptional networks governing plant metabolism. Current Plant Biology, 2015, 3-4, 56-64.	4.7	38
71	Genetic Variation in the Nuclear and Organellar Genomes Modulates Stochastic Variation in the Metabolome, Growth, and Defense. PLoS Genetics, 2015, 11, e1004779.	3.5	39
72	Keeping the rhythm: light/dark cycles during postharvest storage preserve the tissue integrity and nutritional content of leafy plants. BMC Plant Biology, 2015, 15, 92.	3.6	42

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73	The Glucosinolate Biosynthetic Gene AOP2 Mediates Feed-back Regulation of Jasmonic Acid Signaling in Arabidopsis. Molecular Plant, 2015, 8, 1201-1212.	8.3	62
74	Natural variation of plant metabolism: genetic mechanisms, interpretive caveats, evolutionary and mechanistic insights Plant Physiology, 2015, 169, pp.01108.2015.	4.8	55
75	Quantitative Variation in Responses to Root Spatial Constraint within <i>Arabidopsis thaliana</i> . Plant Cell, 2015, 27, 2227-2243.	6.6	11
76	Overexpression of Three Glucosinolate Biosynthesis Genes in Brassica napus Identifies Enhanced Resistance to Sclerotinia sclerotiorum and Botrytis cinerea. PLoS ONE, 2015, 10, e0140491.	2.5	57
77	Natural genetic variation in Arabidopsis thaliana defense metabolism genes modulates field fitness. ELife, 2015, 4, .	6.0	107
78	Evolution retraces its steps to advance. ELife, 2015, 4, .	6.0	0
79	The AT-hook motif-encoding gene METABOLIC NETWORK MODULATOR 1 underlies natural variation in Arabidopsis primary metabolism. Frontiers in Plant Science, 2014, 5, 415.	3.6	12
80	Meta-analysis of metabolome QTLs in Arabidopsis: trying to estimate the network size controlling genetic variation of the metabolome. Frontiers in Plant Science, 2014, 5, 461.	3.6	13
81	Promoter-Based Integration in Plant Defense Regulation Â. Plant Physiology, 2014, 166, 1803-1820.	4.8	89
82	Synthetic biology of metabolism: using natural variation to reverse engineer systems. Current Opinion in Plant Biology, 2014, 19, 20-26.	7.1	21
83	Interview with Daniel Kliebenstein. Trends in Plant Science, 2014, 19, 204-205.	8.8	Ο
84	Orchestration of plant defense systems: genes to populations. Trends in Plant Science, 2014, 19, 250-255.	8.8	18
85	Response of Turnip to Botrytis cinerea Infection and Their Relationship with Glucosinolate Profiles. Korean Journal of Plant Resources, 2014, 27, 371-379.	0.2	2
86	New Synthesis—Regulatory Evolution, the Veiled World of Chemical Diversification. Journal of Chemical Ecology, 2013, 39, 349-349.	1.8	5
87	Fatty acids and early detection of pathogens. Current Opinion in Plant Biology, 2013, 16, 520-526.	7.1	137
88	Making new molecules—evolution of structures for novel metabolites in plants. Current Opinion in Plant Biology, 2013, 16, 112-117.	7.1	49
89	Postharvest Circadian Entrainment Enhances Crop Pest Resistance and Phytochemical Cycling. Current Biology, 2013, 23, 1235-1241.	3.9	73
90	Hierarchical Nuclear and Cytoplasmic Genetic Architectures for Plant Growth and Defense within <i>Arabidopsis</i> Â. Plant Cell, 2013, 25, 1929-1945.	6.6	46

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91	Identification of Novel Loci Regulating Interspecific Variation in Root Morphology and Cellular Development in Tomato Â. Plant Physiology, 2013, 162, 755-768.	4.8	68
92	Cytoplasmic genetic variation and extensive cytonuclear interactions influence natural variation in the metabolome. ELife, 2013, 2, e00776.	6.0	76
93	Exploring the shallow end; estimating information content in transcriptomics studies. Frontiers in Plant Science, 2012, 3, 213.	3.6	13
94	What Can Causal Networks Tell Us about Metabolic Pathways?. PLoS Computational Biology, 2012, 8, e1002458.	3.2	20
95	Natural Enemies Drive Geographic Variation in Plant Defenses. Science, 2012, 338, 116-119.	12.6	286
96	<i>Arabidopsis</i> Defense against <i>Botrytis cinerea</i> : Chronology and Regulation Deciphered by High-Resolution Temporal Transcriptomic Analysis Â. Plant Cell, 2012, 24, 3530-3557.	6.6	337
97	Retrograde Signaling by the Plastidial Metabolite MEcPP Regulates Expression of Nuclear Stress-Response Genes. Cell, 2012, 149, 1525-1535.	28.9	368
98	Making new molecules – evolution of pathways for novel metabolites in plants. Current Opinion in Plant Biology, 2012, 15, 415-423.	7.1	121
99	Model Misinterpretation within Biology: Phenotypes, Statistics, Networks, and Inference. Frontiers in Plant Science, 2012, 3, 13.	3.6	3
100	Plant Defense Compounds: Systems Approaches to Metabolic Analysis. Annual Review of Phytopathology, 2012, 50, 155-173.	7.8	46
101	The Quantitative Genetics of Phenotypic Error or Uniformity. Frontiers in Genetics, 2011, 2, 59.	2.3	2
102	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
103	Chemically mediated tritrophic interactions: opposing effects of glucosinolates on a specialist herbivore and its predators. Journal of Applied Ecology, 2011, 48, 880-887.	4.0	57
104	Cofactome analyses reveal enhanced flux of carbon into oil for potential biofuel production. Plant Journal, 2011, 67, 1018-1028.	5.7	28
105	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
106	Using knockout mutants to reveal the growth costs of defensive traits. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 2598-2603.	2.6	110
107	Network Quantitative Trait Loci Mapping of Circadian Clock Outputs Identifies Metabolic Pathway-to-Clock Linkages in <i>Arabidopsis</i> Â Â. Plant Cell, 2011, 23, 471-485.	6.6	139
108	Biosynthesis and Defensive Function of <i>N</i> ÂΔ-Acetylornithine, a Jasmonate-Induced <i>Arabidopsis</i> Metabolite Â. Plant Cell, 2011, 23, 3303-3318.	6.6	80

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109	Intronic T-DNA Insertion Renders Arabidopsis <i>opr3</i> a Conditional Jasmonic Acid-Producing Mutant Â. Plant Physiology, 2011, 156, 770-778.	4.8	93
110	Combining Genome-Wide Association Mapping and Transcriptional Networks to Identify Novel Genes Controlling Glucosinolates in Arabidopsis thaliana. PLoS Biology, 2011, 9, e1001125.	5.6	246
111	Genomic Analysis of QTLs and Genes Altering Natural Variation in Stochastic Noise. PLoS Genetics, 2011, 7, e1002295.	3.5	107
112	Regulatory networks of glucosinolates shape Arabidopsis thaliana fitness. Current Opinion in Plant Biology, 2010, 13, 347-352.	7.1	81
113	A new method for measuring relative growth rate can uncover the costs of defensive compounds in <i>Arabidopsis thaliana</i> . New Phytologist, 2010, 187, 1102-1111.	7.3	74
114	Deficiencies in Jasmonate-Mediated Plant Defense Reveal Quantitative Variation in Botrytis cinerea Pathogenesis. PLoS Pathogens, 2010, 6, e1000861.	4.7	141
115	A Complex Interplay of Three R2R3 MYB Transcription Factors Determines the Profile of Aliphatic Glucosinolates in Arabidopsis Â. Plant Physiology, 2010, 153, 348-363.	4.8	226
116	The Complex Genetic Architecture of the Metabolome. PLoS Genetics, 2010, 6, e1001198.	3.5	148
117	Systems Biology Uncovers the Foundation of Natural Genetic Diversity. Plant Physiology, 2010, 152, 480-486.	4.8	24
118	All Mold Is Not Alike: The Importance of Intraspecific Diversity in Necrotrophic Plant Pathogens. PLoS Pathogens, 2010, 6, e1000759.	4.7	23
119	Understanding the Evolution of Defense Metabolites in <i>Arabidopsis thaliana</i> Using Genome-wide Association Mapping. Genetics, 2010, 185, 991-1007.	2.9	184
120	The Genetic Basis of Constitutive and Herbivore-Induced ESP-Independent Nitrile Formation in Arabidopsis Â. Plant Physiology, 2009, 149, 561-574.	4.8	148
121	MODIFIED VACUOLE PHENOTYPE1 Is an Arabidopsis Myrosinase-Associated Protein Involved in Endomembrane Protein Trafficking Â. Plant Physiology, 2009, 152, 120-132.	4.8	57
122	Advancing Genetic Theory and Application by Metabolic Quantitative Trait Loci Analysis. Plant Cell, 2009, 21, 1637-1646.	6.6	66
123	A quantitative genetics and ecological model system: understanding the aliphatic glucosinolate biosynthetic network via QTLs. Phytochemistry Reviews, 2009, 8, 243-254.	6.5	46
124	Competition, herbivory and genetics interact to determine the accumulation and fitness consequences of a defence metabolite. Journal of Ecology, 2009, 97, 78-88.	4.0	75
125	Quantification of Variation in Expression Networks. Methods in Molecular Biology, 2009, 553, 227-245.	0.9	14

126 Anti-Rust Antitrust. Science, 2009, 323, 1301-1302.

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127	Quantitative Genomics: Analyzing Intraspecific Variation Using Global Gene Expression Polymorphisms or eQTLs. Annual Review of Plant Biology, 2009, 60, 93-114.	18.7	159
128	Use of Secondary Metabolite Variation in Crop Improvement. , 2009, , 83-95.		8
129	Differential Levels of Insect Herbivory in the Field Associated with Genotypic Variation in Glucosinolates in Arabidopsis thaliana. Journal of Chemical Ecology, 2008, 34, 1026-1037.	1.8	118
130	ESP and ESM1 mediate indol-3-acetonitrile production from indol-3-ylmethyl glucosinolate in Arabidopsis. Phytochemistry, 2008, 69, 663-671.	2.9	90
131	Determination of the absolute configuration of the glucosinolate methyl sulfoxide group reveals a stereospecific biosynthesis of the side chain. Phytochemistry, 2008, 69, 2737-2742.	2.9	30
132	Identifying the molecular basis of QTLs: eQTLs add a new dimension. Trends in Plant Science, 2008, 13, 72-77.	8.8	104
133	Ecological costs of biotrophic versus necrotrophic pathogen resistance, the hypersensitive response and signal transduction. Plant Science, 2008, 174, 551-556.	3.6	63
134	Complex Genetics Control Natural Variation in <i>Arabidopsis thaliana</i> Resistance to <i>Botrytis cinerea</i> . Genetics, 2008, 180, 2237-2250.	2.9	104
135	Genotype, Age, Tissue, and Environment Regulate the Structural Outcome of Glucosinolate Activation Â Â. Plant Physiology, 2008, 147, 415-428.	4.8	100
136	The Chromatin Remodeler SPLAYED Regulates Specific Stress Signaling Pathways. PLoS Pathogens, 2008, 4, e1000237.	4.7	129
137	Genetic Networks Controlling Structural Outcome of Glucosinolate Activation across Development. PLoS Genetics, 2008, 4, e1000234.	3.5	26
138	Subclade of Flavin-Monooxygenases Involved in Aliphatic Glucosinolate Biosynthesis. Plant Physiology, 2008, 148, 1721-1733.	4.8	150
139	A Novel 2-Oxoacid-Dependent Dioxygenase Involved in the Formation of the Goiterogenic 2-Hydroxybut-3-enyl Glucosinolate and Generalist Insect Resistance in Arabidopsis À. Plant Physiology, 2008, 148, 2096-2108.	4.8	131
140	Biochemical Networks and Epistasis Shape the <i>Arabidopsis thaliana</i> Metabolome. Plant Cell, 2008, 20, 1199-1216.	6.6	218
141	Distinct Roles of Jasmonates and Aldehydes in Plant-Defense Responses. PLoS ONE, 2008, 3, e1904.	2.5	120
142	A Role for Gene Duplication and Natural Variation of Gene Expression in the Evolution of Metabolism. PLoS ONE, 2008, 3, e1838.	2.5	121
143	Global eQTL Mapping Reveals the Complex Genetic Architecture of Transcript-Level Variation in Arabidopsis. Genetics, 2007, 175, 1441-1450.	2.9	352
144	Linking Metabolic QTLs with Network and cis-eQTLs Controlling Biosynthetic Pathways. PLoS Genetics, 2007, 3, e162.	3.5	275

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145	Natural Variation among Arabidopsis thaliana Accessions for Transcriptome Response to Exogenous Salicylic Acid. Plant Cell, 2007, 19, 2099-2110.	6.6	101
146	Elevated Genetic Variation Within Virulence-Associated <i>Botrytis cinerea</i> Polygalacturonase Loci. Molecular Plant-Microbe Interactions, 2007, 20, 1126-1137.	2.6	56
147	Identification of a flavin-monooxygenase as the S-oxygenating enzyme in aliphatic glucosinolate biosynthesis in Arabidopsis. Plant Journal, 2007, 50, 902-910.	5.7	219
148	Characterization of seedâ€specific benzoyloxyglucosinolate mutations in <i>Arabidopsis thaliana</i> . Plant Journal, 2007, 51, 1062-1076.	5.7	90
149	Metabolomics and Plant Quantitative Trait Locus Analysis – The Optimum Genetical Genomics Platform?. , 2007, , 29-44.		13
150	A Systems Biology Approach Identifies a R2R3 MYB Gene Subfamily with Distinct and Overlapping Functions in Regulation of Aliphatic Glucosinolates. PLoS ONE, 2007, 2, e1322.	2.5	321
151	Convergence, constraint and the role of gene expression during adaptive radiation: floral anthocyanins in Aquilegia. Molecular Ecology, 2006, 15, 4645-4657.	3.9	119
152	Glucosinolate Survey of Cultivated and Feral Mashua (Tropaeolum tuberosum RuÃz & Pavón) in the Cuzco Region of Peru. Economic Botany, 2006, 60, 254-264.	1.7	18
153	Identification of QTLs controlling gene expression networks defined a priori. BMC Bioinformatics, 2006, 7, 308.	2.6	122
154	High-density haplotyping with microarray-based expression and single feature polymorphism markers in Arabidopsis. Genome Research, 2006, 16, 787-795.	5.5	179
155	The Gene Controlling the Quantitative Trait Locus EPITHIOSPECIFIER MODIFIER1 Alters Glucosinolate Hydrolysis and Insect Resistance in Arabidopsis. Plant Cell, 2006, 18, 1524-1536.	6.6	230
156	Genomic Survey of Gene Expression Diversity in Arabidopsis thaliana. Genetics, 2006, 172, 1179-1189.	2.9	104
157	Geographic and evolutionary diversification of glucosinolates among near relatives of Arabidopsis thaliana (Brassicaceae). Phytochemistry, 2005, 66, 1321-1333.	2.9	126
158	Secondary metabolites influence Arabidopsis/Botrytis interactions: variation in host production and pathogen sensitivity. Plant Journal, 2005, 44, 25-36.	5.7	269
159	A constitutivePR-1::luciferaseexpression screen identifies Arabidopsis mutants with differential disease resistance to both biotrophic and necrotrophic pathogens. Molecular Plant Pathology, 2005, 6, 31-41.	4.2	8
160	A UV-B-specific signaling component orchestrates plant UV protection. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 18225-18230.	7.1	495
161	Linking Metabolic QTL with Network and cis-eQTL Controlling Biosynthetic Pathways. PLoS Genetics, 2005, preprint, e162.	3.5	7
162	Identification ofBotrytis cinereasusceptibility loci inArabidopsis thaliana. Plant Journal, 2004, 38, 473-486.	5.7	147

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163	Secondary metabolites and plant/environment interactions: a view through Arabidopsis thaliana tinged glasses. Plant, Cell and Environment, 2004, 27, 675-684.	5.7	335
164	Chapter five Glucosinolate hydrolysis and its impact on generalist and specialist insect herbivores. Recent Advances in Phytochemistry, 2003, , 101-125.	0.5	131
165	Arabidopsis UVR8 Regulates Ultraviolet-B Signal Transduction and Tolerance and Contains Sequence Similarity to Human Regulator of Chromatin Condensation 1. Plant Physiology, 2002, 130, 234-243.	4.8	328
166	Disarming the mustard oil bomb. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11223-11228.	7.1	498
167	Benzoic acid glucosinolate esters and other glucosinolates from Arabidopsis thaliana. Phytochemistry, 2002, 59, 663-671.	2.9	226
168	Comparative Analysis of Quantitative Trait Loci Controlling Glucosinolates, Myrosinase and Insect Resistance in <i>Arabidopsis thaliana</i> . Genetics, 2002, 161, 325-332.	2.9	243
169	Genetic Architecture of Plastic Methyl Jasmonate Responses in <i>Arabidopsis thaliana</i> . Genetics, 2002, 161, 1685-1696.	2.9	149
170	Genetic Control of Natural Variation in Arabidopsis Glucosinolate Accumulation. Plant Physiology, 2001, 126, 811-825.	4.8	607
171	The Arabidopsis Epithiospecifier Protein Promotes the Hydrolysis of Glucosinolates to Nitriles and Influences <i>Trichoplusia ni</i> Herbivory. Plant Cell, 2001, 13, 2793-2807.	6.6	400
172	Gene Duplication in the Diversification of Secondary Metabolism: Tandem 2-Oxoglutarate–Dependent Dioxygenases Control Glucosinolate Biosynthesis in Arabidopsis. Plant Cell, 2001, 13, 681-693.	6.6	447
173	The Arabidopsis Epithiospecifier Protein Promotes the Hydrolysis of Glucosinolates to Nitriles and Influences Trichoplusia ni Herbivory. Plant Cell, 2001, 13, 2793.	6.6	6
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