

Daniel S Nettleton

List of Publications by Year in descending order

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173
papers

13,402
citations

31976
53
h-index

24982
109
g-index

178
all docs

178
docs citations

178
times ranked

15869
citing authors

#	ARTICLE	IF	CITATIONS
1	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	12.6	3,612
2	Maize Inbreds Exhibit High Levels of Copy Number Variation (CNV) and Presence/Absence Variation (PAV) in Genome Content. <i>PLoS Genetics</i> , 2009, 5, e1000734.	3.5	484
3	All possible modes of gene action are observed in a global comparison of gene expression in a maize F1 hybrid and its inbred parents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6805-6810.	7.1	399
4	Gene Mapping via Bulk Segregant RNA-Seq (BSR-Seq). <i>PLoS ONE</i> , 2012, 7, e36406.	2.5	297
5	Detecting Differential Expression in RNA-sequence Data Using Quasi-likelihood with Shrunken Dispersion Estimates. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, .	0.6	282
6	Developmental Transcript Profiling of Cyst Nematode Feeding Cells in Soybean Roots. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 510-525.	2.6	240
7	Duplicate gene expression in allopolyploid <i>Gossypium</i> reveals two temporally distinct phases of expression evolution. <i>BMC Biology</i> , 2008, 6, 16.	3.8	235
8	Gene Expression Programs during Shoot, Root, and Callus Development in Arabidopsis Tissue Culture. <i>Plant Physiology</i> , 2006, 141, 620-637.	4.8	225
9	The Arabidopsis MicroRNA396-GRF1/GRF3 Regulatory Module Acts as a Developmental Regulator in the Reprogramming of Root Cells during Cyst Nematode Infection. <i>Plant Physiology</i> , 2012, 159, 321-335.	4.8	214
10	Interaction-Dependent Gene Expression in Mla-Specified Response to Barley Powdery Mildew [W]. <i>Plant Cell</i> , 2004, 16, 2514-2528.	6.6	204
11	Parallel Genome-Wide Expression Profiling of Host and Pathogen During Soybean Cyst Nematode Infection of Soybean. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 293-305.	2.6	197
12	Mu Transposon Insertion Sites and Meiotic Recombination Events Co-Localize with Epigenetic Marks for Open Chromatin across the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000733.	3.5	196
13	Transcriptional responses of <i>Pseudomonas syringae</i> to growth in epiphytic versus apoplastic leaf sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E425-34.	7.1	190
14	Host-Induced Gene Silencing in Barley Powdery Mildew Reveals a Class of Ribonuclease-Like Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 633-642.	2.6	190
15	Arabidopsis gene expression changes during cyst nematode parasitism revealed by statistical analyses of microarray expression profiles. <i>Plant Journal</i> , 2003, 33, 911-921.	5.7	180
16	Isolation, Characterization, and Pericycle-Specific Transcriptome Analyses of the Novel Maize Lateral and Seminal Root Initiation Mutant rum1. <i>Plant Physiology</i> , 2005, 139, 1255-1267.	4.8	179
17	Complementation contributes to transcriptome complexity in maize (<i>Zea mays</i> L.) hybrids relative to their inbred parents. <i>Genome Research</i> , 2012, 22, 2445-2454.	5.5	154
18	Transcriptomic and Proteomic Analyses of Pericycle Cells of the Maize Primary Root. <i>Plant Physiology</i> , 2007, 145, 575-588.	4.8	144

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19	Paternal Dominance of Trans-eQTL Influences Gene Expression Patterns in Maize Hybrids. <i>Science</i> , 2009, 326, 1118-1120.	12.6	137
20	Code-Assisted Discovery of TAL Effector Targets in Bacterial Leaf Streak of Rice Reveals Contrast with Bacterial Blight and a Novel Susceptibility Gene. <i>PLoS Pathogens</i> , 2014, 10, e1003972.	4.7	137
21	Genetic Regulation of Gene Expression During Shoot Development in Arabidopsis. <i>Genetics</i> , 2006, 172, 1155-1164.	2.9	131
22	Soybean Homologs of MPK4 Negatively Regulate Defense Responses and Positively Regulate Growth and Development. <i>Plant Physiology</i> , 2011, 157, 1363-1378.	4.8	130
23	Spatial Analysis of Arabidopsis thaliana Gene Expression in Response to Turnip mosaic virus Infection. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 358-370.	2.6	129
24	Global gene expression analysis of the shoot apical meristem of maize (<i>Zea mays</i> L.). <i>Plant Journal</i> , 2007, 52, 391-404.	5.7	123
25	Identification of the novel protein QQS as a component of the starch metabolic network in Arabidopsis leaves. <i>Plant Journal</i> , 2009, 58, 485-498.	5.7	118
26	Transcriptional profiling of myostatin knockout mice implicates Wnt signaling in postnatal skeletal muscle growth and hypertrophy. <i>FASEB Journal</i> , 2006, 20, 580-582.	0.5	115
27	Distinct Biphasic mRNA Changes in Response to Asian Soybean Rust Infection. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 887-899.	2.6	112
28	QQS orphan gene regulates carbon and nitrogen partitioning across species via NF-YC interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14734-14739.	7.1	109
29	Estimating the number of true null hypotheses from a histogram of p values. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2006, 11, 337-356.	1.4	107
30	Loss of RNA-Dependent RNA Polymerase 2 (RDR2) Function Causes Widespread and Unexpected Changes in the Expression of Transposons, Genes, and 24-nt Small RNAs. <i>PLoS Genetics</i> , 2009, 5, e1000737.	3.5	106
31	The Soybean <i>Rhg1</i> Locus for Resistance to the Soybean Cyst Nematode <i>Heterodera glycines</i> Regulates the Expression of a Large Number of Stress- and Defense-Related Genes in Degenerating Feeding Cells. <i>Plant Physiology</i> , 2011, 155, 1960-1975.	4.8	102
32	Distinct genetic architectures for phenotype means and plasticities in <i>Zea mays</i> . <i>Nature Plants</i> , 2017, 3, 715-723.	9.3	98
33	The maize <i>brown midrib2</i> (<i>bm2</i>) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. <i>Plant Journal</i> , 2014, 77, 380-392.	5.7	94
34	Extreme phenotype genome-wide association study (XP-GWAS): a method for identifying trait-associated variants by sequencing pools of individuals selected from a diversity panel. <i>Plant Journal</i> , 2015, 84, 587-596.	5.7	93
35	Differential gene expression in the rat soleus muscle during early work overload-induced hypertrophy. <i>FASEB Journal</i> , 2002, 16, 1-21.	0.5	91
36	Stage-Specific Suppression of Basal Defense Discriminates Barley Plants Containing Fast- and Delayed-Acting Mla Powdery Mildew Resistance Alleles. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 939-947.	2.6	88

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37	BarleyBase—an expression profiling database for plant genomics. <i>Nucleic Acids Research</i> , 2004, 33, D614-D618.	14.5	86
38	Gene expression profiling of the short-term adaptive response to acute caloric restriction in liver and adipose tissues of pigs differing in feed efficiency. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2010, 298, R494-R507.	1.8	83
39	Nonsyntenic Genes Drive Highly Dynamic Complementation of Gene Expression in Maize Hybrids. <i>Plant Cell</i> , 2014, 26, 3939-3948.	6.6	80
40	Extensive tissue-specific transcriptomic plasticity in maize primary roots upon water deficit. <i>Journal of Experimental Botany</i> , 2016, 67, 1095-1107.	4.8	78
41	Transcriptomic and anatomical complexity of primary, seminal, and crown roots highlight root type-specific functional diversity in maize (<i>Zea mays</i> L.). <i>Journal of Experimental Botany</i> , 2016, 67, 1123-1135.	4.8	76
42	Copy number variation detection using next generation sequencing read counts. <i>BMC Bioinformatics</i> , 2014, 15, 109.	2.6	75
43	A Novel Approach for Characterizing Expression Levels of Genes Duplicated by Polyploidy. <i>Genetics</i> , 2006, 173, 1823-1827.	2.9	74
44	Laser Microdissection of Narrow Sheath Mutant Maize Uncovers Novel Gene Expression in the Shoot Apical Meristem. <i>PLoS Genetics</i> , 2007, 3, e101.	3.5	73
45	Microdissection of Shoot Meristem Functional Domains. <i>PLoS Genetics</i> , 2009, 5, e1000476.	3.5	73
46	Ontogeny of the Maize Shoot Apical Meristem. <i>Plant Cell</i> , 2012, 24, 3219-3234.	6.6	72
47	Accounting for Variability in the Use of Permutation Testing to Detect Quantitative Trait Loci. <i>Biometrics</i> , 2000, 56, 52-58.	1.4	69
48	Genomics, Prior Probability, and Statistical Tests of Multiple Hypotheses. <i>Genome Research</i> , 2004, 14, 997-1001.	5.5	68
49	Validation of a first-generation long-oligonucleotide microarray for transcriptional profiling in the pig. <i>Genomics</i> , 2005, 86, 618-625.	2.9	64
50	Unique genome-wide transcriptome profiles of chicken macrophages exposed to Salmonella-derived endotoxin. <i>BMC Genomics</i> , 2010, 11, 545.	2.8	64
51	A Discussion of Statistical Methods for Design and Analysis of Microarray Experiments for Plant Scientists. <i>Plant Cell</i> , 2006, 18, 2112-2121.	6.6	62
52	CmeR Functions as a Pleiotropic Regulator and Is Required for Optimal Colonization of <i>Campylobacter jejuni</i> In Vivo. <i>Journal of Bacteriology</i> , 2008, 190, 1879-1890.	2.2	60
53	Identification of differentially expressed gene categories in microarray studies using nonparametric multivariate analysis. <i>Bioinformatics</i> , 2008, 24, 192-201.	4.1	60
54	Biphasic Gene Expression Changes Elicited by <i>Phakopsora pachyrhizi</i> in Soybean Correlate with Fungal Penetration and Haustoria Formation. <i>Plant Physiology</i> , 2011, 157, 355-371.	4.8	59

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55	Transcriptional Profiling of <i>Mycoplasma hyopneumoniae</i> during Heat Shock Using Microarrays. <i>Infection and Immunity</i> , 2006, 74, 160-166.	2.2	57
56	Transcriptome analyses and virus induced gene silencing identify genes in the Rpp4-mediated Asian soybean rust resistance pathway. <i>Functional Plant Biology</i> , 2013, 40, 1029.	2.1	57
57	Substantial contribution of genetic variation in the expression of transcription factors to phenotypic variation revealed by eRD-GWAS. <i>Genome Biology</i> , 2017, 18, 192.	8.8	56
58	Transcriptional Analysis of the Global Regulatory Networks Active in <i>Pseudomonas syringae</i> during Leaf Colonization. <i>MBio</i> , 2014, 5, e01683-14.	4.1	55
59	SimSeq: a nonparametric approach to simulation of RNA-sequence datasets. <i>Bioinformatics</i> , 2015, 31, 2131-2140.	4.1	55
60	Post-weaning blood transcriptomic differences between Yorkshire pigs divergently selected for residual feed intake. <i>BMC Genomics</i> , 2016, 17, 73.	2.8	53
61	Root Type-Specific Reprogramming of Maize Pericycle Transcriptomes by Local High Nitrate Results in Disparate Lateral Root Branching Patterns. <i>Plant Physiology</i> , 2016, 170, 1783-1798.	4.8	53
62	Comparative gene expression profiles between heterotic and non-heterotic hybrids of tetraploid <i>Medicago sativa</i> . <i>BMC Plant Biology</i> , 2009, 9, 107.	3.6	51
63	<i>QQS</i> orphan gene and its interactor <i>NF-κB</i> reduce susceptibility to pathogens and pests. <i>Plant Biotechnology Journal</i> , 2019, 17, 252-263.	8.3	51
64	Single-Parent Expression Is a General Mechanism Driving Extensive Complementation of Non-syntenic Genes in Maize Hybrids. <i>Current Biology</i> , 2018, 28, 431-437.e4.	3.9	50
65	Crowdsourcing image analysis for plant phenomics to generate ground truth data for machine learning. <i>PLoS Computational Biology</i> , 2018, 14, e1006337.	3.2	48
66	Distinct Peripheral Blood RNA Responses to Salmonella in Pigs Differing in Salmonella Shedding Levels: Intersection of IFNG, TLR and miRNA Pathways. <i>PLoS ONE</i> , 2011, 6, e28768.	2.5	47
67	Random Forest Prediction Intervals. <i>American Statistician</i> , 2020, 74, 392-406.	1.6	46
68	Pooling mRNA in microarray experiments and its effect on power. <i>Bioinformatics</i> , 2007, 23, 1217-1224.	4.1	44
69	Microarray gene expression profiles of fasting induced changes in liver and adipose tissues of pigs expressing the melanocortin-4 receptor D298N variant. <i>Physiological Genomics</i> , 2009, 38, 98-111.	2.3	44
70	Adaptive and Dynamic Adaptive Procedures for False Discovery Rate Control and Estimation. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2012, 74, 163-182.	2.2	44
71	Spotted cotton oligonucleotide microarrays for gene expression analysis. <i>BMC Genomics</i> , 2007, 8, 81.	2.8	43
72	Sequence mining and transcript profiling to explore cyst nematode parasitism. <i>BMC Genomics</i> , 2009, 10, 58.	2.8	43

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73	The maize <i>brown midrib4</i> (<i>bm4</i>) gene encodes a functional folylpolyglutamate synthase. <i>Plant Journal</i> , 2015, 81, 493-504.	5.7	42
74	Gene expression profiling in <i>Salmonella</i> <i>Choleraesuis</i> -infected porcine lung using a long oligonucleotide microarray. <i>Mammalian Genome</i> , 2006, 17, 777-789.	2.2	41
75	Analysis of Porcine Transcriptional Response to <i>Salmonella enterica</i> serovar <i>Choleraesuis</i> suggests novel targets of NFκB are activated in the Mesenteric Lymph Node. <i>BMC Genomics</i> , 2008, 9, 437.	2.8	41
76	ArcA Controls Metabolism, Chemotaxis, and Motility Contributing to the Pathogenicity of Avian Pathogenic <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2015, 83, 3545-3554.	2.2	41
77	Multiple Marginal Independence Testing for Pick Any/C Variables. <i>Communications in Statistics Part B: Simulation and Computation</i> , 2000, 29, 1285-1316.	1.2	40
78	Transcriptional profiling of <i>Mycoplasma hyopneumoniae</i> during iron depletion using microarrays. <i>Microbiology (United Kingdom)</i> , 2006, 152, 937-944.	1.8	40
79	Divergent evolution of arrested development in the dauer stage of <i>Caenorhabditis elegans</i> and the infective stage of <i>Heterodera glycines</i> . <i>Genome Biology</i> , 2007, 8, R211.	9.6	40
80	Endometrial gene expression profiling in pregnant Meishan and Yorkshire pigs on day 12 of gestation. <i>BMC Genomics</i> , 2014, 15, 156.	2.8	40
81	A systems biology approach toward understanding seed composition in soybean. <i>BMC Genomics</i> , 2015, 16, S9.	2.8	39
82	Convergence properties of the EM algorithm in constrained parameter spaces. <i>Canadian Journal of Statistics</i> , 1999, 27, 639-648.	0.9	38
83	Microarray analysis of vegetative phase change in maize. <i>Plant Journal</i> , 2008, 56, 1045-1057.	5.7	37
84	<i>Salmonella enterica</i> serovar Typhimurium-infected pigs with different shedding levels exhibit distinct clinical, peripheral cytokine and transcriptomic immune response phenotypes. <i>Innate Immunity</i> , 2015, 21, 227-241.	2.4	37
85	Small RNA discovery in the interaction between barley and the powdery mildew pathogen. <i>BMC Genomics</i> , 2019, 20, 610.	2.8	37
86	Global transcriptional response of porcine mesenteric lymph nodes to <i>Salmonella enterica</i> serovar Typhimurium. <i>Genomics</i> , 2007, 90, 72-84.	2.9	36
87	Exploring the Information in p-Values for the Analysis and Planning of Multiple-Test Experiments. <i>Biometrics</i> , 2007, 63, 483-495.	1.4	36
88	Stability of Single-Parent Gene Expression Complementation in Maize Hybrids upon Water Deficit Stress. <i>Plant Physiology</i> , 2017, 173, 1247-1257.	4.8	36
89	Reverse engineering and analysis of large genome-scale gene networks. <i>Nucleic Acids Research</i> , 2013, 41, e24-e24.	14.5	34
90	Using Random Forests to distinguish gahnite compositions as an exploration guide to Broken Hill-type Pb-Zn-Ag deposits in the Broken Hill domain, Australia. <i>Journal of Geochemical Exploration</i> , 2015, 149, 74-86.	3.2	34

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91	Quantitative Trait Loci Associated With Adventitious Shoot Formation in Tissue Culture and the Program of Shoot Development in Arabidopsis. <i>Genetics</i> , 2004, 167, 1883-1892.	2.9	33
92	Broadly Conserved Fungal Effector BEC1019 Suppresses Host Cell Death and Enhances Pathogen Virulence in Powdery Mildew of Barley (<i>Hordeum vulgare</i> L.) (Retracted). <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 968-983.	2.6	33
93	Principal Components Regression With Data Chosen Components and Related Methods. <i>Technometrics</i> , 2003, 45, 70-79.	1.9	29
94	Transformation of maize with the p1 transcription factor directs production of silk maysin, a corn earworm resistance factor, in concordance with a hierarchy of floral organ pigmentation. <i>Plant Biotechnology Journal</i> , 2005, 3, 225-235.	8.3	28
95	Scanning microarrays at multiple intensities enhances discovery of differentially expressed genes. <i>Bioinformatics</i> , 2006, 22, 1863-1870.	4.1	28
96	Transcript-Based Cloning of <i>RRP46</i> , a Regulator of rRNA Processing and <i>R</i> Gene-Independent Cell Death in Barley-Powdery Mildew Interactions. <i>Plant Cell</i> , 2009, 21, 3280-3295.	6.6	26
97	<i>Helicobacter bilis</i> Colonization Enhances Susceptibility to Typhlocolitis Following an Inflammatory Trigger. <i>Digestive Diseases and Sciences</i> , 2011, 56, 2838-2848.	2.3	26
98	Using random forests to estimate win probability before each play of an NFL game. <i>Journal of Quantitative Analysis in Sports</i> , 2014, 10, .	1.0	25
99	Case-Specific Random Forests. <i>Journal of Computational and Graphical Statistics</i> , 2016, 25, 49-65.	1.7	25
100	Quantitative and Temporal Definition of the <i>Mla</i> Transcriptional Regulon During Barley-Powdery Mildew Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 694-705.	2.6	24
101	Changes in genome content generated via segregation of non-allelic homologs. <i>Plant Journal</i> , 2012, 72, 390-399.	5.7	24
102	A Clade-Specific Arabidopsis Gene Connects Primary Metabolism and Senescence. <i>Frontiers in Plant Science</i> , 2016, 7, 983.	3.6	24
103	Gene expression in intestinal mucosal biopsy specimens obtained from dogs with chronic enteropathy. <i>American Journal of Veterinary Research</i> , 2012, 73, 1219-1229.	0.6	22
104	Testing the equality of distributions of random vectors with categorical components. <i>Computational Statistics and Data Analysis</i> , 2001, 37, 195-208.	1.2	21
105	A Hidden Markov Model Approach to Testing Multiple Hypotheses on a Tree-Transformed Gene Ontology Graph. <i>Journal of the American Statistical Association</i> , 2010, 105, 1444-1454.	3.1	21
106	Discovery and Characterization of the 3-Hydroxyacyl-ACP Dehydratase Component of the Plant Mitochondrial Fatty Acid Synthase System. <i>Plant Physiology</i> , 2017, 173, 2010-2028.	4.8	21
107	Nested Hierarchical Functional Data Modeling and Inference for the Analysis of Functional Plant Phenotypes. <i>Journal of the American Statistical Association</i> , 2018, 113, 593-606.	3.1	21
108	Transcriptional profiling using a novel cDNA array identifies differential gene expression during porcine embryo elongation. <i>Molecular Reproduction and Development</i> , 2005, 71, 129-139.	2.0	19

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109	Complexity and specificity of the maize (<i>Zea mays</i> L.) root hair transcriptome. <i>Journal of Experimental Botany</i> , 2017, 68, 2175-2185.	4.8	19
110	Empirical Comparisons of Different Statistical Models To Identify and Validate Kernel Row Number-Associated Variants from Structured Multi-parent Mapping Populations of Maize. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3567-3575.	1.8	19
111	Tree aggregation for random forest class probability estimation. <i>Statistical Analysis and Data Mining</i> , 2020, 13, 134-150.	2.8	19
112	Microbial community sequencing analysis of the calf eye microbiota and relationship to infectious bovine keratoconjunctivitis. <i>Veterinary Microbiology</i> , 2017, 207, 267-279.	1.9	17
113	Mucosal gene expression profiles following the colonization of immunocompetent defined-flora C3H mice with <i>Helicobacter bilis</i> : a prelude to typhlocolitis. <i>Microbes and Infection</i> , 2009, 11, 374-383.	1.9	15
114	Identifying Genes Associated with a Quantitative Trait or Quantitative Trait Locus via Selective Transcriptional Profiling. <i>Biometrics</i> , 2006, 62, 504-514.	1.4	14
115	Array-Based Genomic Comparative Hybridization Analysis of Field Strains of <i>Mycoplasma hyopneumoniae</i> . <i>Journal of Bacteriology</i> , 2007, 189, 7977-7982.	2.2	14
116	Floret-specific differences in gene expression and support for the hypothesis that tapetal degeneration of <i>Zea mays</i> L. occurs via programmed cell death. <i>Journal of Genetics and Genomics</i> , 2008, 35, 603-616.	3.9	14
117	Estimation of False Discovery Rate Using Sequential Permutation p -Values. <i>Biometrics</i> , 2013, 69, 1-7.	1.4	14
118	The knottin-like Blufensin family regulates genes involved in nuclear import and the secretory pathway in barley-powdery mildew interactions. <i>Frontiers in Plant Science</i> , 2015, 6, 409.	3.6	14
119	Stress response to CO ₂ deprivation by <i>Arabidopsis thaliana</i> in plant cultures. <i>PLoS ONE</i> , 2019, 14, e0212462.	2.5	14
120	From <i>Arabidopsis</i> to Crops: The <i>Arabidopsis</i> QQS Orphan Gene Modulates Nitrogen Allocation Across Species. , 2018,, 95-117.		13
121	Assessing plant performance in the Enviratron. <i>Plant Methods</i> , 2019, 15, 117.	4.3	13
122	Comparison of Transcript Profiles in Wild-type and $\alpha 2$ Maize Endosperm in Different Genetic Backgrounds. <i>Crop Science</i> , 2007, 47, S-45.	1.8	12
123	Genes and Small RNA Transcripts Exhibit Dosage-Dependent Expression Pattern in Maize Copy-Number Alterations. <i>Genetics</i> , 2016, 203, 1133-1147.	2.9	12
124	Proteomics-based, multivariate random forest method for prediction of protein separation behavior during cation-exchange chromatography. <i>Journal of Chromatography A</i> , 2012, 1249, 103-114.	3.7	11
125	Non-syntenic genes drive RTCS-dependent regulation of the embryo transcriptome during formation of seminal root primordia in maize (<i>Zea mays</i> L.). <i>Journal of Experimental Botany</i> , 2017, 68, erw422.	4.8	11
126	High-Resolution Genotyping via Whole Genome Hybridizations to Microarrays Containing Long Oligonucleotide Probes. <i>PLoS ONE</i> , 2010, 5, e14178.	2.5	11

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127	Selective transcriptional profiling for trait-based eQTL mapping. <i>Animal Genetics</i> , 2006, 37, 13-17.	1.7	10
128	Testing for the Supremacy of a Multinomial Cell Probability. <i>Journal of the American Statistical Association</i> , 2009, 104, 1052-1059.	3.1	10
129	rmRNAseq: differential expression analysis for repeated-measures RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 4432-4439.	4.1	10
130	Adjusting for Spatial Effects in Genomic Prediction. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2020, 25, 699-718.	1.4	10
131	Empirical Bayes Analysis of RNA-seq Data for Detection of Gene Expression Heterosis. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2015, 20, 614-628.	1.4	9
132	Metabolomic Profiling of <i>Nicotiana</i> Spp. Nectars Indicate That Pollinator Feeding Preference Is a Stronger Determinant Than Plant Phylogenetics in Shaping Nectar Diversity. <i>Metabolites</i> , 2020, 10, 214.	2.9	8
133	Significant Variation for Bio-oil Compounds After Pyrolysis/Gas Chromatography–Mass Spectrometry of Cobs and Stover Among Five Near-Isogenic Brown Midrib Hybrids in Maize. <i>Bioenergy Research</i> , 2014, 7, 693-701.	3.9	7
134	Detecting Differentially Expressed Genes with RNA-seq Data Using Backward Selection to Account for the Effects of Relevant Covariates. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2015, 20, 577-597.	1.4	7
135	Fully Bayesian Analysis of RNA-seq Counts for the Detection of Gene Expression Heterosis. <i>Journal of the American Statistical Association</i> , 2019, 114, 610-621.	3.1	7
136	Linear Mixed Model Selection for False Discovery Rate Control in Microarray Data Analysis. <i>Biometrics</i> , 2010, 66, 621-629.	1.4	6
137	Interchromosomal Transfer of Immune Regulation During Infection of Barley with the Powdery Mildew Pathogen. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3317-3329.	1.8	6
138	Single-parent expression complementation contributes to phenotypic heterosis in maize hybrids. <i>Plant Physiology</i> , 2022, , .	4.8	6
139	Interval Mapping of Quantitative Trait Loci through Order-Restricted Inference. <i>Biometrics</i> , 1998, 54, 74.	1.4	5
140	Order-restricted hypothesis testing in a variation of the normal mixture model. <i>Canadian Journal of Statistics</i> , 1999, 27, 383-394.	0.9	5
141	Borrowing Information Across Genes and Experiments for Improved Error Variance Estimation in Microarray Data Analysis. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, Article 12.	0.6	5
142	Estimation and Testing of Gene Expression Heterosis. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2014, 19, 319-337.	1.4	5
143	Detecting rare and faint signals via thresholding maximum likelihood estimators. <i>Annals of Statistics</i> , 2018, 46, .	2.6	5
144	KAT4IA: K-Means Assisted Training for Image Analysis of Field-Grown Plant Phenotypes. <i>Plant Phenomics</i> , 2021, 2021, 9805489.	5.9	5

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145	Identifying differentially expressed genes in unreplicated multiple-treatment microarray timecourse experiments. Computational Statistics and Data Analysis, 2006, 50, 518-532.	1.2	4
146	An Efficient and Scalable Implementation of SNP-Pair Interaction Testing for Genetic Association Studies. , 2011, , .		4
147	Accounting for spot matching uncertainty in the analysis of proteomics data from two-dimensional gel electrophoresis. Sankhya B, 2011, 73, 123-143.	0.9	4
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