

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
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178
all docs

178
docs citations

178
times ranked

15869
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-parent expression complementation contributes to phenotypic heterosis in maize hybrids. <i>Plant Physiology</i> , 2022, , .	4.8	6
2	A residual-based approach for robust random forest regression. <i>Statistics and Its Interface</i> , 2021, 14, 389-402.	0.3	2
3	KAT4IA: K-Means Assisted Training for Image Analysis of Field-Grown Plant Phenotypes. <i>Plant Phenomics</i> , 2021, 2021, 9805489.	5.9	5
4	Variable importance assessments and backward variable selection for multi-sample problems. <i>Journal of Multivariate Analysis</i> , 2021, 186, 104807.	1.0	0
5	Random Forest Prediction Intervals. <i>American Statistician</i> , 2020, 74, 392-406.	1.6	46
6	Tree aggregation for random forest class probability estimation. <i>Statistical Analysis and Data Mining</i> , 2020, 13, 134-150.	2.8	19
7	rmRNAseq: differential expression analysis for repeated-measures RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 4432-4439.	4.1	10
8	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
9	Adjusting for Spatial Effects in Genomic Prediction. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2020, 25, 699-718.	1.4	10
10	<i>QQS</i> orphan gene and its interactor <i>NFYC4</i> reduce susceptibility to pathogens and pests. <i>Plant Biotechnology Journal</i> , 2019, 17, 252-263.	8.3	51
11	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
12	Small RNA discovery in the interaction between barley and the powdery mildew pathogen. <i>BMC Genomics</i> , 2019, 20, 610.	2.8	37
13	Assessing plant performance in the Envirotron. <i>Plant Methods</i> , 2019, 15, 117.	4.3	13
14	Stress response to CO ₂ deprivation by <i>Arabidopsis thaliana</i> in plant cultures. <i>PLoS ONE</i> , 2019, 14, e0212462.	2.5	14
15	Sparse model identification and learning for ultra-high-dimensional additive partially linear models. <i>Journal of Multivariate Analysis</i> , 2019, 173, 204-228.	1.0	2
16	Additive partially linear models for ultra-high-dimensional regression. <i>Stat</i> , 2019, 8, e223.	0.4	4
17	Detecting rare and faint signals via thresholding maximum likelihood estimators. <i>Annals of Statistics</i> , 2018, 46, .	2.6	5
18	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

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19	A hidden Markov tree model for testing multiple hypotheses corresponding to Gene Ontology gene sets. BMC Bioinformatics, 2018, 19, 107.	2.6	2
20	Nested Hierarchical Functional Data Modeling and Inference for the Analysis of Functional Plant Phenotypes. Journal of the American Statistical Association, 2018, 113, 593-606.	3.1	21
21	Empirical Comparisons of Different Statistical Models To Identify and Validate Kernel Row Number-Associated Variants from Structured Multi-parent Mapping Populations of Maize. G3: Genes, Genomes, Genetics, 2018, 8, 3567-3575.	1.8	19
22	Crowdsourcing image analysis for plant phenomics to generate ground truth data for machine learning. PLoS Computational Biology, 2018, 14, e1006337.	3.2	48
23	From Arabidopsis to Crops: The Arabidopsis QQS Orphan Gene Modulates Nitrogen Allocation Across Species. , 2018, , 95-117.		13
24	Non-syntenic genes drive RTCS-dependent regulation of the embryo transcriptome during formation of seminal root primordia in maize (<i>Zea mays</i> L.). Journal of Experimental Botany, 2017, 68, erw422.	4.8	11
25	Discovery and Characterization of the 3-Hydroxyacyl-ACP Dehydratase Component of the Plant Mitochondrial Fatty Acid Synthase System. Plant Physiology, 2017, 173, 2010-2028.	4.8	21
26	Stability of Single-Parent Gene Expression Complementation in Maize Hybrids upon Water Deficit Stress. Plant Physiology, 2017, 173, 1247-1257.	4.8	36
27	Interchromosomal Transfer of Immune Regulation During Infection of Barley with the Powdery Mildew Pathogen. G3: Genes, Genomes, Genetics, 2017, 7, 3317-3329.	1.8	6
28	Microbial community sequencing analysis of the calf eye microbiota and relationship to infectious bovine keratoconjunctivitis. Veterinary Microbiology, 2017, 207, 267-279.	1.9	17
29	Substantial contribution of genetic variation in the expression of transcription factors to phenotypic variation revealed by eRD-GWAS. Genome Biology, 2017, 18, 192.	8.8	56
30	Complexity and specificity of the maize (<i>Zea mays</i> L.) root hair transcriptome. Journal of Experimental Botany, 2017, 68, 2175-2185.	4.8	19
31	Distinct genetic architectures for phenotype means and plasticities in <i>Zea mays</i> . Nature Plants, 2017, 3, 715-723.	9.3	98
32	A Clade-Specific Arabidopsis Gene Connects Primary Metabolism and Senescence. Frontiers in Plant Science, 2016, 7, 983.	3.6	24
33	Post-weaning blood transcriptomic differences between Yorkshire pigs divergently selected for residual feed intake. BMC Genomics, 2016, 17, 73.	2.8	53
34	Accounting for host cell protein behavior in anion-exchange chromatography. Biotechnology Progress, 2016, 32, 1453-1463.	2.6	2
35	Genes and Small RNA Transcripts Exhibit Dosage-Dependent Expression Pattern in Maize Copy-Number Alterations. Genetics, 2016, 203, 1133-1147.	2.9	12
36	Root Type-Specific Reprogramming of Maize Pericycle Transcriptomes by Local High Nitrate Results in Disparate Lateral Root Branching Patterns. Plant Physiology, 2016, 170, 1783-1798.	4.8	53

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37	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
38	Case-Specific Random Forests. <i>Journal of Computational and Graphical Statistics</i> , 2016, 25, 49-65.	1.7	25
39	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
40	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
41	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
42	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
43	Hierarchical Modeling and Differential Expression Analysis for RNA-seq Experiments with Inbred and Hybrid Genotypes. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2015, 20, 598-613.	1.4	4
44	Guest Editors' Introduction to the Special Issue on "Statistical Genomics and Transcriptomics in Agriculture". <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2015, 20, 439-441.	1.4	0
45	A systems biology approach toward understanding seed composition in soybean. <i>BMC Genomics</i> , 2015, 16, S9.	2.8	39
46	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
47	SimSeq: a nonparametric approach to simulation of RNA-sequence datasets. <i>Bioinformatics</i> , 2015, 31, 2131-2140.	4.1	55
48	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
49	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
50	Salmonella enterica 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
51	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
52	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
53	<i>QQS</i> 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
54	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

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55	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
56	Nonsyntenic Genes Drive Highly Dynamic Complementation of Gene Expression in Maize Hybrids. <i>Plant Cell</i> , 2014, 26, 3939-3948.	6.6	80
57	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
58	Flor Revisited (Again): eQTL and Mutational Analysis of NB-LRR Mediated Immunity to Powdery Mildew in Barley. <i>Journal of Integrative Agriculture</i> , 2014, 13, 237-243.	3.5	1
59	Significant Variation for Bio-oil Compounds After Pyrolysis/Gas Chromatographyâ€‘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
60	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
61	An improved method for computing q-values when the distribution of effect sizes is asymmetric. <i>Bioinformatics</i> , 2014, 30, 3044-3053.	4.1	3
62	Estimation and Testing of Gene Expression Heterosis. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2014, 19, 319-337.	1.4	5
63	Copy number variation detection using next generation sequencing read counts. <i>BMC Bioinformatics</i> , 2014, 15, 109.	2.6	75
64	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
65	Design of RNA Sequencing Experiments. , 2014, , 93-113.		2
66	Predictor augmentation in random forests. <i>Statistics and Its Interface</i> , 2014, 7, 177-186.	0.3	1
67	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
68	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
69	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
70	Reverse engineering and analysis of large genome-scale gene networks. <i>Nucleic Acids Research</i> , 2013, 41, e24-e24.	14.5	34
71	Estimation of False Discovery Rate Using Sequential Permutation <i>p</i> -Values. <i>Biometrics</i> , 2013, 69, 1-7.	1.4	14
72	Does My Baby Really Look Like Me? Using Tests For Resemblance Between Parent and Child to Teach Topics in Categorical Data Analysis. <i>Journal of Statistics Education</i> , 2013, 21, .	1.4	1

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73	Gene expression in intestinal mucosal biopsy specimens obtained from dogs with chronic enteropathy. American Journal of Veterinary Research, 2012, 73, 1219-1229.	0.6	22
74	The Arabidopsis MicroRNA396-GRF1/GRF3 Regulatory Module Acts as a Developmental Regulator in the Reprogramming of Root Cells during Cyst Nematode Infection. Plant Physiology, 2012, 159, 321-335.	4.8	214
75	Complementation contributes to transcriptome complexity in maize (<i>Zea mays</i> L.) hybrids relative to their inbred parents. Genome Research, 2012, 22, 2445-2454.	5.5	154
76	Borrowing Information Across Genes and Experiments for Improved Error Variance Estimation in Microarray Data Analysis. Statistical Applications in Genetics and Molecular Biology, 2012, 11, Article 12.	0.6	5
77	Ontogeny of the Maize Shoot Apical Meristem. Plant Cell, 2012, 24, 3219-3234.	6.6	72
78	The importance of distinct modeling strategies for gene and gene-specific treatment effects in hierarchical models for microarray data. Annals of Applied Statistics, 2012, 6, .	1.1	2
79	A Hierarchical Semiparametric Model for Incorporating Intergene Information for Analysis of Genomic Data. Biometrics, 2012, 68, 1168-1177.	1.4	2
80	Changes in genome content generated via segregation of nonallelic homologs. Plant Journal, 2012, 72, 390-399.	5.7	24
81	Detecting Differential Expression in RNA-sequence Data Using Quasi-likelihood with Shrunken Dispersion Estimates. Statistical Applications in Genetics and Molecular Biology, 2012, 11, .	0.6	282
82	Estimating the Number of Genes That Are Differentially Expressed in Both of Two Independent Experiments. Journal of Agricultural, Biological, and Environmental Statistics, 2012, 17, 583-600.	1.4	1
83	Proteomics-based, multivariate random forest method for prediction of protein separation behavior during cation-exchange chromatography. Journal of Chromatography A, 2012, 1249, 103-114.	3.7	11
84	Adaptive and Dynamic Adaptive Procedures for False Discovery Rate Control and Estimation. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2012, 74, 163-182.	2.2	44
85	Improved Estimation of the Noncentrality Parameter Distribution from a Large Number of Statistics, with Applications to False Discovery Rate Estimation in Microarray Data Analysis. Biometrics, 2012, 68, 1178-1187.	1.4	4
86	Gene Mapping via Bulk Segregant RNA-Seq (BSR-Seq). PLoS ONE, 2012, 7, e36406.	2.5	297
87	An Efficient and Scalable Implementation of SNP-Pair Interaction Testing for Genetic Association Studies. , 2011, , .		4
88	Distinct Peripheral Blood RNA Responses to Salmonella in Pigs Differing in Salmonella Shedding Levels: Intersection of IFNG, TLR and miRNA Pathways. PLoS ONE, 2011, 6, e28768.	2.5	47
89	Quantitative and Temporal Definition of the <i>Mla</i> Transcriptional Regulon During Barley-Powdery Mildew Interactions. Molecular Plant-Microbe Interactions, 2011, 24, 694-705.	2.6	24
90	Helicobacter bilis Colonization Enhances Susceptibility to Typhlocolitis Following an Inflammatory Trigger. Digestive Diseases and Sciences, 2011, 56, 2838-2848.	2.3	26

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91	Accounting for spot matching uncertainty in the analysis of proteomics data from two-dimensional gel electrophoresis. <i>Sankhya B</i> , 2011, 73, 123-143.	0.9	4
92	Soybean Homologs of MPK4 Negatively Regulate Defense Responses and Positively Regulate Growth and Development Â Â. <i>Plant Physiology</i> , 2011, 157, 1363-1378.	4.8	130
93	Biphasic Gene Expression Changes Elicited by<i>Phakopsora pachyrhizi</i> in Soybean Correlate with Fungal Penetration and Haustoria Formation Â Â. <i>Plant Physiology</i> , 2011, 157, 355-371.	4.8	59
94	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 Â Â. <i>Plant Physiology</i> , 2011, 155, 1960-1975.	4.8	102
95	Unique genome-wide transcriptome profiles of chicken macrophages exposed to Salmonella-derived endotoxin. <i>BMC Genomics</i> , 2010, 11, 545.	2.8	64
96	Linear Mixed Model Selection for False Discovery Rate Control in Microarray Data Analysis. <i>Biometrics</i> , 2010, 66, 621-629.	1.4	6
97	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
98	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
99	High-Resolution Genotyping via Whole Genome Hybridizations to Microarrays Containing Long Oligonucleotide Probes. <i>PLoS ONE</i> , 2010, 5, e14178.	2.5	11
100	Variance model selection with application to joint analysis of multiple microarray datasets under false discovery rate control. <i>Statistics and Its Interface</i> , 2010, 3, 477-491.	0.3	4
101	Differentially expressed microRNAs in dystrophinâ€deficient muscle.. <i>FASEB Journal</i> , 2010, 24, 989.1.	0.5	0
102	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
103	Microdissection of Shoot Meristem Functional Domains. <i>PLoS Genetics</i> , 2009, 5, e1000476.	3.5	73
104	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
105	Loss of RNAâ€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
106	Transcript-Based Cloning of<i>RRP46</i>, a Regulator of rRNA Processing and<i>R</i>Geneâ€Independent Cell Death in Barleyâ€Powdery Mildew Interactions Â. <i>Plant Cell</i> , 2009, 21, 3280-3295.	6.6	26
107	Paternal Dominance of Trans-eQTL Influences Gene Expression Patterns in Maize Hybrids. <i>Science</i> , 2009, 326, 1118-1120.	12.6	137
108	Sequence mining and transcript profiling to explore cyst nematode parasitism. <i>BMC Genomics</i> , 2009, 10, 58.	2.8	43

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109	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
110	Identification of the novel protein QQS as a component of the starch metabolic network in <i>Arabidopsis</i> leaves. <i>Plant Journal</i> , 2009, 58, 485-498.	5.7	118
111	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
112	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	12.6	3,612
113	Testing for the Supremacy of a Multinomial Cell Probability. <i>Journal of the American Statistical Association</i> , 2009, 104, 1052-1059.	3.1	10
114	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
115	Leptin mediates discriminate response to feed restriction in feed efficient pigs. <i>FASEB Journal</i> , 2009, 23, 1022.3.	0.5	0
116	Combining classical trait and microarray data to dissect transcriptional regulation: a case study. <i>Theoretical and Applied Genetics</i> , 2008, 116, 683-690.	3.6	2
117	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
118	Microarray analysis of vegetative phase change in maize. <i>Plant Journal</i> , 2008, 56, 1045-1057.	5.7	37
119	Analysis of Porcine Transcriptional Response to <i>Salmonella enterica</i> serovar <i>Choleraesuis</i> suggests novel targets of NFkappaB are activated in the Mesenteric Lymph Node. <i>BMC Genomics</i> , 2008, 9, 437.	2.8	41
120	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
121	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
122	Identification of differentially expressed gene categories in microarray studies using nonparametric multivariate analysis. <i>Bioinformatics</i> , 2008, 24, 192-201.	4.1	60
123	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
124	Pooling mRNA in microarray experiments and its effect on power. <i>Bioinformatics</i> , 2007, 23, 1217-1224.	4.1	44
125	Transcriptomic and Proteomic Analyses of Pericycle Cells of the Maize Primary Root. <i>Plant Physiology</i> , 2007, 145, 575-588.	4.8	144
126	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

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127	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
128	Developmental Transcript Profiling of Cyst Nematode Feeding Cells in Soybean Roots. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 510-525.	2.6	240
129	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
130	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
131	Spatial Analysis of <i>Arabidopsis thaliana</i> Gene Expression in Response to Turnip mosaic virus Infection. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 358-370.	2.6	129
132	Distinct Biphasic mRNA Changes in Response to Asian Soybean Rust Infection. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 887-899.	2.6	112
133	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
134	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
135	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
136	Spotted cotton oligonucleotide microarrays for gene expression analysis. <i>BMC Genomics</i> , 2007, 8, 81.	2.8	43
137	Gene Expression Programs during Shoot, Root, and Callus Development in <i>Arabidopsis</i> Tissue Culture. <i>Plant Physiology</i> , 2006, 141, 620-637.	4.8	225
138	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
139	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
140	Selective transcriptional profiling for trait-based eQTL mapping. <i>Animal Genetics</i> , 2006, 37, 13-17.	1.7	10
141	Identifying differentially expressed genes in unreplicated multiple-treatment microarray timecourse experiments. <i>Computational Statistics and Data Analysis</i> , 2006, 50, 518-532.	1.2	4
142	A Novel Approach for Characterizing Expression Levels of Genes Duplicated by Polyploidy. <i>Genetics</i> , 2006, 173, 1823-1827.	2.9	74
143	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
144	Gene expression profiling in <i>Salmonella Choleraesuis</i> -infected porcine lung using a long oligonucleotide microarray. <i>Mammalian Genome</i> , 2006, 17, 777-789.	2.2	41

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145	Scanning microarrays at multiple intensities enhances discovery of differentially expressed genes. <i>Bioinformatics</i> , 2006, 22, 1863-1870.	4.1	28
146	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
147	Genetic Regulation of Gene Expression During Shoot Development in Arabidopsis. <i>Genetics</i> , 2006, 172, 1155-1164.	2.9	131
148	Transcriptional profiling of <i>Mycoplasma hyopneumoniae</i> during iron depletion using microarrays. <i>Microbiology (United Kingdom)</i> , 2006, 152, 937-944.	1.8	40
149	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
150	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
151	Transcriptional Profiling of <i>Mycoplasma hyopneumoniae</i> during Heat Shock Using Microarrays. <i>Infection and Immunity</i> , 2006, 74, 160-166.	2.2	57
152	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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