Daniel S Nettleton

List of Publications by Year
in descending order

173	13,402	31974	24978
papers	citations	53	109
		h-index	g-index

178	178	178	15869
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The B73 Maize Genome: Complexity, Diversity, and Dynamics. Science, 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. PLoS Genetics, 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. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6805-6810.	7.1	399
4	Gene Mapping via Bulked Segregant RNA-Seq (BSR-Seq). PLoS ONE, 2012, 7, e36406.	2.5	297
5	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
6	Developmental Transcript Profiling of Cyst Nematode Feeding Cells in Soybean Roots. Molecular Plant-Microbe Interactions, 2007, 20, 510-525.	2.6	240
7	Duplicate gene expression in allopolyploid Gossypiumreveals two temporally distinct phases of expression evolution. BMC Biology, 2008, 6, 16.	3.8	235
8	Gene Expression Programs during Shoot, Root, and Callus Development in Arabidopsis Tissue Culture. Plant Physiology, 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 Â Â. Plant Physiology, 2012, 159, 321-335.	4.8	214
10	Interaction-Dependent Gene Expression in Mla-Specified Response to Barley Powdery Mildew[W]. Plant Cell, 2004, 16, 2514-2528.	6.6	204
11	Parallel Genome-Wide Expression Profiling of Host and Pathogen During Soybean Cyst Nematode Infection of Soybean. Molecular Plant-Microbe Interactions, 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. PLoS Genetics, 2009, 5, e1000733.	3.5	196
13	Transcriptional responses of *Pseudomonas syringae* to growth in epiphytic versus apoplastic leaf sites. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E425-34.	7.1	190
14	Host-Induced Gene Silencing in Barley Powdery Mildew Reveals a Class of Ribonuclease-Like Effectors. Molecular Plant-Microbe Interactions, 2013, 26, 633-642.	2.6	190
15	Arabidopsisgene expression changes during cyst nematode parasitism revealed by statistical analyses of microarray expression profiles. Plant Journal, 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. Plant Physiology, 2005, 139, 1255-1267.	4.8	179
17	Complementation contributes to transcriptome complexity in maize (*Zea mays* L.) hybrids relative to their inbred parents. Genome Research, 2012, 22, 2445-2454.	5.5	154
18	Transcriptomic and Proteomic Analyses of Pericycle Cells of the Maize Primary Root. Plant Physiology, 2007, 145, 575-588.	4.8	144

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19	Paternal Dominance of Trans-eQTL Influences Gene Expression Patterns in Maize Hybrids. Science, 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. PLoS Pathogens, 2014, 10, e1003972.	4.7	137
21	Genetic Regulation of Gene Expression During Shoot Development in Arabidopsis. Genetics, 2006, 172, 1155-1164.	2.9	131
22	Soybean Homologs of MPK4 Negatively Regulate Defense Responses and Positively Regulate Growth and Development Â Â. Plant Physiology, 2011, 157, 1363-1378.	4.8	130
23	Spatial Analysis of Arabidopsis thaliana Gene Expression in Response to Turnip mosaic virus Infection. Molecular Plant-Microbe Interactions, 2007, 20, 358-370.	2.6	129
24	Global gene expression analysis of the shoot apical meristem of maize (*Zea mays* L.). Plant Journal, 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. Plant Journal, 2009, 58, 485-498.	5.7	118
26	Transcriptional profiling of myostatinâ€knockout mice implicates Wnt signaling in postnatal skeletal muscle growth and hypertrophy. FASEB Journal, 2006, 20, 580-582.	0.5	115
27	Distinct Biphasic mRNA Changes in Response to Asian Soybean Rust Infection. Molecular Plant-Microbe Interactions, 2007, 20, 887-899.	2.6	112
28	*QQS* orphan gene regulates carbon and nitrogen partitioning across species via NF-YC interactions. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14734-14739.	7.1	109
29	Estimating the number of true null hypotheses from a histogram of p values. Journal of Agricultural, Biological, and Environmental Statistics, 2006, 11, 337-356.	1.4	107
30	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. PLoS Genetics, 2009, 5, e1000737.	3.5	106
31	The Soybean *Rhg1* Locus for Resistance to the Soybean Cyst Nematode *Heterodera glycines* Regulates the Expression of a Large Number of Stress- and Defense-Related Genes in Degenerating Feeding Cells Â Â Â. Plant Physiology, 2011, 155, 1960-1975.	4.8	102
32	Distinct genetic architectures for phenotype means and plasticities in Zea mays. Nature Plants, 2017, 3, 715-723.	9.3	98
33	The maize *brown midrib2* (*bm2*) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. Plant Journal, 2014, 77, 380-392.	5.7	94
34	Extremeâ€phenotype genomeâ€wide association study (XP‑GWAS): a method for identifying traitâ€associated variants by sequencing pools of individuals selected from a diversity panel. Plant Journal, 2015, 84, 587-596.	5.7	93
35	Differential gene expression in the rat soleus muscle during early work overloadâ€induced hypertrophy. FASEB Journal, 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. Molecular Plant-Microbe Interactions, 2006, 19, 939-947.	2.6	88

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37	BarleyBase--an expression profiling database for plant genomics. Nucleic Acids Research, 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. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2010, 298, R494-R507.	1.8	83
39	Nonsyntenic Genes Drive Highly Dynamic Complementation of Gene Expression in Maize Hybrids. Plant Cell, 2014, 26, 3939-3948.	6.6	80
40	Extensive tissue-specific transcriptomic plasticity in maize primary roots upon water deficit. Journal of Experimental Botany, 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.). Journal of Experimental Botany, 2016, 67, 1123-1135.	4.8	76
42	Copy number variation detection using next generation sequencing read counts. BMC Bioinformatics, 2014, 15, 109.	2.6	75
43	A Novel Approach for Characterizing Expression Levels of Genes Duplicated by Polyploidy. Genetics, 2006, 173, 1823-1827.	2.9	74
44	Laser Microdissection of Narrow Sheath Mutant Maize Uncovers Novel Gene Expression in the Shoot Apical Meristem. PLoS Genetics, 2007, 3, e101.	3.5	73
45	Microdissection of Shoot Meristem Functional Domains. PLoS Genetics, 2009, 5, e1000476.	3.5	73
46	Ontogeny of the Maize Shoot Apical Meristem. Plant Cell, 2012, 24, 3219-3234.	6.6	72
47	Accounting for Variability in the Use of Permutation Testing to Detect Quantitative Trait Loci. Biometrics, 2000, 56, 52-58.	1.4	69
48	Genomics, Prior Probability, and Statistical Tests of Multiple Hypotheses. Genome Research, 2004, 14, 997-1001.	5.5	68
49	Validation of a first-generation long-oligonucleotide microarray for transcriptional profiling in the pig. Genomics, 2005, 86, 618-625.	2.9	64
50	Unique genome-wide transcriptome profiles of chicken macrophages exposed to Salmonella-derived endotoxin. BMC Genomics, 2010, 11, 545.	2.8	64
51	A Discussion of Statistical Methods for Design and Analysis of Microarray Experiments for Plant Scientists. Plant Cell, 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. Journal of Bacteriology, 2008, 190, 1879-1890.	2.2	60
53	Identification of differentially expressed gene categories in microarray studies using nonparametric multivariate analysis. Bioinformatics, 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 Â Â. Plant Physiology, 2011, 157, 355-371.	4.8	59

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55	Transcriptional Profiling of Mycoplasma hyopneumoniae during Heat Shock Using Microarrays. Infection and Immunity, 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. Functional Plant Biology, 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. Genome Biology, 2017, 18, 192.	8.8	56
58	Transcriptional Analysis of the Global Regulatory Networks Active in Pseudomonas syringae during Leaf Colonization. MBio, 2014, 5, e01683-14.	4.1	55
59	SimSeq: a nonparametric approach to simulation of RNA-sequence datasets. Bioinformatics, 2015, 31, 2131-2140.	4.1	55
60	Post-weaning blood transcriptomic differences between Yorkshire pigs divergently selected for residual feed intake. BMC Genomics, 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. Plant Physiology, 2016, 170, 1783-1798.	4.8	53
62	Comparative gene expression profiles between heterotic and non-heterotic hybrids of tetraploid Medicago sativa. BMC Plant Biology, 2009, 9, 107.	3.6	51
63	<i><scp>QQS</scp></i> orphan gene and its interactor <i><scp>NF</scp>â€<scp>YC</scp>4</i> reduce susceptibility to pathogens and pests. Plant Biotechnology Journal, 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. Current Biology, 2018, 28, 431-437.e4.	3.9	50
65	Crowdsourcing image analysis for plant phenomics to generate ground truth data for machine learning. PLoS Computational Biology, 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. PLoS ONE, 2011, 6, e28768.	2.5	47
67	Random Forest Prediction Intervals. American Statistician, 2020, 74, 392-406.	1.6	46
68	Pooling mRNA in microarray experiments and its effect on power. Bioinformatics, 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. Physiological Genomics, 2009, 38, 98-111.	2.3	44
70	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
71	Spotted cotton oligonucleotide microarrays for gene expression analysis. BMC Genomics, 2007, 8, 81.	2.8	43
72	Sequence mining and transcript profiling to explore cyst nematode parasitism. BMC Genomics, 2009, 10, 58.	2.8	43

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73	The maize *brown midrib4* (*bm4*) gene encodes a functional folylpolyglutamate synthase. Plant Journal, 2015, 81, 493-504.	5.7	42
74	Gene expression profiling in Salmonella Choleraesuis-infected porcine lung using a long oligonucleotide microarray. Mammalian Genome, 2006, 17, 777-789.	2.2	41
75	Analysis of Porcine Transcriptional Response to Salmonella enterica serovar Choleraesuis suggests novel targets of NFkappaB are activated in the Mesenteric Lymph Node. BMC Genomics, 2008, 9, 437.	2.8	41
76	ArcA Controls Metabolism, Chemotaxis, and Motility Contributing to the Pathogenicity of Avian Pathogenic Escherichia coli. Infection and Immunity, 2015, 83, 3545-3554.	2.2	41
77	Multiple Marginal Independence Testing for Pick Any/C Variables. Communications in Statistics Part B: Simulation and Computation, 2000, 29, 1285-1316.	1.2	40
78	Transcriptional profiling of Mycoplasma hyopneumoniae during iron depletion using microarrays. Microbiology (United Kingdom), 2006, 152, 937-944.	1.8	40
79	Divergent evolution of arrested development in the dauer stage of Caenorhabditis elegans and the infective stage of Heterodera glycines. Genome Biology, 2007, 8, R211.	9.6	40
80	Endometrial gene expression profiling in pregnant Meishan and Yorkshire pigs on day 12 of gestation. BMC Genomics, 2014, 15, 156.	2.8	40
81	A systems biology approach toward understanding seed composition in soybean. BMC Genomics, 2015, 16, S9.	2.8	39
82	Convergence properties of the EM algorithm in constrained parameter spaces. Canadian Journal of Statistics, 1999, 27, 639-648.	0.9	38
83	Microarray analysis of vegetative phase change in maize. Plant Journal, 2008, 56, 1045-1057.	5.7	37
84	Salmonella enterica serovar Typhimurium-infected pigs with different shedding levels exhibit distinct clinical, peripheral cytokine and transcriptomic immune response phenotypes. Innate Immunity, 2015, 21, 227-241.	2.4	37
85	Small RNA discovery in the interaction between barley and the powdery mildew pathogen. BMC Genomics, 2019, 20, 610.	2.8	37
86	Global transcriptional response of porcine mesenteric lymph nodes to Salmonella enterica serovar Typhimurium. Genomics, 2007, 90, 72-84.	2.9	36
87	Exploring the Information in p-Values for the Analysis and Planning of Multiple-Test Experiments. Biometrics, 2007, 63, 483-495.	1.4	36
88	Stability of Single-Parent Gene Expression Complementation in Maize Hybrids upon Water Deficit Stress. Plant Physiology, 2017, 173, 1247-1257.	4.8	36
89	Reverse engineering and analysis of large genome-scale gene networks. Nucleic Acids Research, 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. Journal of Geochemical Exploration, 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. Genetics, 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). Molecular Plant-Microbe Interactions, 2015, 28, 968-983.	2.6	33
93	Principal Components Regression With Data Chosen Components and Related Methods. Technometrics, 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. Plant Biotechnology Journal, 2005, 3, 225-235.	8.3	28
95	Scanning microarrays at multiple intensities enhances discovery of differentially expressed genes. Bioinformatics, 2006, 22, 1863-1870.	4.1	28
96	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. Plant Cell, 2009, 21, 3280-3295.	6.6	26
97	Helicobacter bilis Colonization Enhances Susceptibility to Typhlocolitis Following an Inflammatory Trigger. Digestive Diseases and Sciences, 2011, 56, 2838-2848.	2.3	26
98	Using random forests to estimate win probability before each play of an NFL game. Journal of Quantitative Analysis in Sports, 2014, 10, .	1.0	25
99	Case-Specific Random Forests. Journal of Computational and Graphical Statistics, 2016, 25, 49-65.	1.7	25
100	Quantitative and Temporal Definition of the <i>Mla</i> Transcriptional Regulon During Barleyâ€"Powdery Mildew Interactions. Molecular Plant-Microbe Interactions, 2011, 24, 694-705.	2.6	24
101	Changes in genome content generated via segregation of nonâ€allelic homologs. Plant Journal, 2012, 72, 390-399.	5.7	24
102	A Clade-Specific Arabidopsis Gene Connects Primary Metabolism and Senescence. Frontiers in Plant Science, 2016, 7, 983.	3.6	24
103	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
104	Testing the equality of distributions of random vectors with categorical components. Computational Statistics and Data Analysis, 2001, 37, 195-208.	1.2	21
105	A Hidden Markov Model Approach to Testing Multiple Hypotheses on a Tree-Transformed Gene Ontology Graph. Journal of the American Statistical Association, 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. Plant Physiology, 2017, 173, 2010-2028.	4.8	21
107	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
108	Transcriptional profiling using a novel cDNA array identifies differential gene expression during porcine embryo elongation. Molecular Reproduction and Development, 2005, 71, 129-139.	2.0	19

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109	Complexity and specificity of the maize (Zea mays L.) root hair transcriptome. Journal of Experimental Botany, 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. G3: Genes, Genomes, Genetics, 2018, 8, 3567-3575.	1.8	19
111	Tree aggregation for random forest class probability estimation. Statistical Analysis and Data Mining, 2020, 13, 134-150.	2.8	19
112	Microbial community sequencing analysis of the calf eye microbiota and relationship to infectious bovine keratoconjunctivitis. Veterinary Microbiology, 2017, 207, 267-279.	1.9	17
113	Mucosal gene expression profiles following the colonization of immunocompetent defined-flora C3H mice with Helicobacter bilis: a prelude to typhlocolitis. Microbes and Infection, 2009, 11, 374-383.	1.9	15
114	Identifying Genes Associated with a Quantitative Trait or Quantitative Trait Locus via Selective Transcriptional Profiling. Biometrics, 2006, 62, 504-514.	1.4	14
115	Array-Based Genomic Comparative Hybridization Analysis of Field Strains of<i>Mycoplasma hyopneumoniae</i>. Journal of Bacteriology, 2007, 189, 7977-7982.	2.2	14
116	Floret-specific differences in gene expression and support for the hypothesis that tapetal degeneration of Zea mays L. occurs via programmed cell death. Journal of Genetics and Genomics, 2008, 35, 603-616.	3.9	14
117	Estimation of False Discovery Rate Using Sequential Permutation <i>p</i>€Values. Biometrics, 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. Frontiers in Plant Science, 2015, 6, 409.	3.6	14
119	Stress response to CO2 deprivation by Arabidopsis thaliana in plant cultures. PLoS ONE, 2019, 14, e0212462.	2.5	14
120	From Arabidopsis to Crops: The Arabidopsis QQS Orphan Gene Modulates Nitrogen Allocation Across Species. , 2018, , 95-117.		13
121	Assessing plant performance in the Enviratron. Plant Methods, 2019, 15, 117.	4.3	13
122	Comparison of Transcript Profiles in Wild€Type and o2 Maize Endosperm in Different Genetic Backgrounds. Crop Science, 2007, 47, S-45.	1.8	12
123	Genes and Small RNA Transcripts Exhibit Dosage-Dependent Expression Pattern in Maize Copy-Number Alterations. Genetics, 2016, 203, 1133-1147.	2.9	12
124	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
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.). Journal of Experimental Botany, 2017, 68, erw422.	4.8	11
126	High-Resolution Genotyping via Whole Genome Hybridizations to Microarrays Containing Long Oligonucleotide Probes. PLoS ONE, 2010, 5, e14178.	2.5	11

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127	Selective transcriptional profiling for trait-based eQTL mapping. Animal Genetics, 2006, 37, 13-17.	1.7	10
128	Testing for the Supremacy of a Multinomial Cell Probability. Journal of the American Statistical Association, 2009, 104, 1052-1059.	3.1	10
129	rmRNAseq: differential expression analysis for repeated-measures RNA-seq data. Bioinformatics, 2020, 36, 4432-4439.	4.1	10
130	Adjusting for Spatial Effects in Genomic Prediction. Journal of Agricultural, Biological, and Environmental Statistics, 2020, 25, 699-718.	1.4	10
131	Empirical Bayes Analysis of RNA-seq Data for Detection of Gene Expression Heterosis. Journal of Agricultural, Biological, and Environmental Statistics, 2015, 20, 614-628.	1.4	9
132	Metabolomic Profiling of Nicotiana Spp. Nectars Indicate That Pollinator Feeding Preference Is a Stronger Determinant Than Plant Phylogenetics in Shaping Nectar Diversity. Metabolites, 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. Bioenergy Research, 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. Journal of Agricultural, Biological, and Environmental Statistics, 2015, 20, 577-597.	1.4	7
135	Fully Bayesian Analysis of RNA-seq Counts for the Detection of Gene Expression Heterosis. Journal of the American Statistical Association, 2019, 114, 610-621.	3.1	7
136	Linear Mixed Model Selection for False Discovery Rate Control in Microarray Data Analysis. Biometrics, 2010, 66, 621-629.	1.4	6
137	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
138	Single-parent expression complementation contributes to phenotypic heterosis in maize hybrids. Plant Physiology, 2022, , .	4.8	6
139	Interval Mapping of Quantitative Trait Loci through Order-Restricted Inference. Biometrics, 1998, 54, 74.	1.4	5
140	Order-restricted hypothesis testing in a variation of the normal mixture model. Canadian Journal of Statistics, 1999, 27, 383-394.	0.9	5
141	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
142	Estimation and Testing of Gene Expression Heterosis. Journal of Agricultural, Biological, and Environmental Statistics, 2014, 19, 319-337.	1.4	5
143	Detecting rare and faint signals via thresholding maximum likelihood estimators. Annals of Statistics, 2018, 46, .	2.6	5
144	KAT4IA: K-Means Assisted Training for Image Analysis of Field-Grown Plant Phenotypes. Plant Phenomics, 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
148	Improved Estimation of the Noncentrality Parameter Distribution from a Large Number of t-Statistics, with Applications to False Discovery Rate Estimation in Microarray Data Analysis. Biometrics, 2012, 68, 1178-1187.	1.4	4
149	Hierarchical Modeling and Differential Expression Analysis for RNA-seq Experiments with Inbred and Hybrid Genotypes. Journal of Agricultural, Biological, and Environmental Statistics, 2015, 20, 598-613.	1.4	4
150	Additive partially linear models for ultra‐high‐dimensional regression. Stat, 2019, 8, e223.	0.4	4
151	Variance model selection with application to joint analysis of multiple microarray datasets under false discovery rate control. Statistics and Its Interface, 2010, 3, 477-491.	0.3	4
152	Investigating the Probability of Sign Inconsistency in the Regression Coefficients of Markers Flanking Quantitative Trait Loci. Genetics, 2002, 160, 1697-1705.	2.9	4
153	An improved method for computing q-values when the distribution of effect sizes is asymmetric. Bioinformatics, 2014, 30, 3044-3053.	4.1	3
154	Investigating Home Court Advantage. Journal of Statistics Education, 1998, 6, .	1.4	2
155	Combining classical trait and microarray data to dissect transcriptional regulation: a case study. Theoretical and Applied Genetics, 2008, 116, 683-690.	3.6	2
156	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
157	A Hierarchical Semiparametric Model for Incorporating Intergene Information for Analysis of Genomic Data. Biometrics, 2012, 68, 1168-1177.	1.4	2
158	Accounting for host cell protein behavior in anion‐exchange chromatography. Biotechnology Progress, 2016, 32, 1453-1463.	2.6	2
159	A hidden Markov tree model for testing multiple hypotheses corresponding to Gene Ontology gene sets. BMC Bioinformatics, 2018, 19, 107.	2.6	2
160	Sparse model identification and learning for ultra-high-dimensional additive partially linear models. Journal of Multivariate Analysis, 2019, 173, 204-228.	1.0	2
161	A residual-based approach for robust random forest regression. Statistics and Its Interface, 2021, 14, 389-402.	0.3	2
162	Design of RNA Sequencing Experiments. , 2014, , 93-113.		2

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163	Testing for ordered means in a variation of the normal mixture model. Journal of Statistical Planning and Inference, 2002, 107, 143-153.	0.6	1
164	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
165	Does My Baby Really Look Like Me? Using Tests For Resemblance Between Parent and Child to Teach Topics in Categorical Data Analysis. Journal of Statistics Education, 2013, 21, .	1.4	1
166	Flor Revisited (Again): eQTL and Mutational Analysis of NB-LRR Mediated Immunity to Powdery Mildew in Barley. Journal of Integrative Agriculture, 2014, 13, 237-243.	3.5	1
167	Predictor augmentation in random forests. Statistics and Its Interface, 2014, 7, 177-186.	0.3	1
168	Expression pattern of yeast sporulation: a case study for regulatory changes after yeast genome duplication. Information Sciences, 2002, 145, 261-269.	6.9	0
169	Guest Editorsâ€™ Introduction to the Special Issue on â€œStatistical Genomics and Transcriptomics in Agricultureâ€. Journal of Agricultural, Biological, and Environmental Statistics, 2015, 20, 439-441.	1.4	0
170	Variable importance assessments and backward variable selection for multi-sample problems. Journal of Multivariate Analysis, 2021, 186, 104807.	1.0	0
171	Leptin mediates discriminate response to feed restriction in feed efficient pigs. FASEB Journal, 2009, 23, 1022.3.	0.5	0
172	Differentially expressed microRNAs in dystrophinâ€deficient muscle.. FASEB Journal, 2010, 24, 989.1.	0.5	0
173	A COMPUTATIONALLY EFFICIENT METHOD FOR DETERMINING SIGNIFICANCE IN INTERVAL MAPPING OF QUANTITATIVE TRAIT LOCI. Conference on Applied Statistics in Agriculture, 0, , .	0.0	0