

# Daniel S Nettleton

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/5288965/daniel-s-nettleton-publications-by-citations.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

171  
papers

10,472  
citations

51  
h-index

100  
g-index

178  
ext. papers

12,300  
ext. citations

5  
avg, IF

5.8  
L-index

#	Paper	IF	Citations
171	The B73 maize genome: complexity, diversity, and dynamics. <i>Science</i> , <b>2009</b> , 326, 1112-5	33.3	2949
170	Maize inbreds exhibit high levels of copy number variation (CNV) and presence/absence variation (PAV) in genome content. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000734	6	389
169	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> , <b>2006</b> , 103, 6805-10	11.5	314
168	Gene mapping via bulked segregant RNA-Seq (BSR-Seq). <i>PLoS ONE</i> , <b>2012</b> , 7, e36406	3.7	212
167	Developmental transcript profiling of cyst nematode feeding cells in soybean roots. <i>Molecular Plant-Microbe Interactions</i> , <b>2007</b> , 20, 510-25	3.6	201
166	Duplicate gene expression in allopolyploid <i>Gossypium</i> reveals two temporally distinct phases of expression evolution. <i>BMC Biology</i> , <b>2008</b> , 6, 16	7.3	194
165	Gene expression programs during shoot, root, and callus development in <i>Arabidopsis</i> tissue culture. <i>Plant Physiology</i> , <b>2006</b> , 141, 620-37	6.6	194
164	Detecting differential expression in RNA-sequence data using quasi-likelihood with shrunken dispersion estimates. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2012</b> , 11,	1.2	191
163	Parallel genome-wide expression profiling of host and pathogen during soybean cyst nematode infection of soybean. <i>Molecular Plant-Microbe Interactions</i> , <b>2007</b> , 20, 293-305	3.6	176
162	Interaction-dependent gene expression in Mla-specified response to barley powdery mildew. <i>Plant Cell</i> , <b>2004</b> , 16, 2514-28	11.6	174
161	The <i>Arabidopsis</i> microRNA396-GRF1/GRF3 regulatory module acts as a developmental regulator in the reprogramming of root cells during cyst nematode infection. <i>Plant Physiology</i> , <b>2012</b> , 159, 321-35	6.6	168
160	<i>Arabidopsis</i> gene expression changes during cyst nematode parasitism revealed by statistical analyses of microarray expression profiles. <i>Plant Journal</i> , <b>2003</b> , 33, 911-21	6.9	163
159	Mu transposon insertion sites and meiotic recombination events co-localize with epigenetic marks for open chromatin across the maize genome. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000733	6	154
158	Isolation, characterization, and pericycle-specific transcriptome analyses of the novel maize lateral and seminal root initiation mutant rum1. <i>Plant Physiology</i> , <b>2005</b> , 139, 1255-67	6.6	148
157	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> , <b>2013</b> , 110, E425-34	11.5	141
156	Host-induced gene silencing in barley powdery mildew reveals a class of ribonuclease-like effectors. <i>Molecular Plant-Microbe Interactions</i> , <b>2013</b> , 26, 633-42	3.6	136
155	Spatial analysis of <i>Arabidopsis thaliana</i> gene expression in response to Turnip mosaic virus infection. <i>Molecular Plant-Microbe Interactions</i> , <b>2007</b> , 20, 358-70	3.6	120

154	Transcriptomic and proteomic analyses of pericycle cells of the maize primary root. <i>Plant Physiology</i> , <b>2007</b> , 145, 575-88	6.6	120
153	Soybean homologs of MPK4 negatively regulate defense responses and positively regulate growth and development. <i>Plant Physiology</i> , <b>2011</b> , 157, 1363-78	6.6	109
152	Global gene expression analysis of the shoot apical meristem of maize ( <i>Zea mays</i> L.). <i>Plant Journal</i> , <b>2007</b> , 52, 391-404	6.9	108
151	Genetic regulation of gene expression during shoot development in Arabidopsis. <i>Genetics</i> , <b>2006</b> , 172, 1155-64	4	107
150	Transcriptional profiling of myostatin-knockout mice implicates Wnt signaling in postnatal skeletal muscle growth and hypertrophy. <i>FASEB Journal</i> , <b>2006</b> , 20, 580-2	0.9	103
149	Paternal dominance of trans-eQTL influences gene expression patterns in maize hybrids. <i>Science</i> , <b>2009</b> , 326, 1118-20	33.3	98
148	Complementation contributes to transcriptome complexity in maize ( <i>Zea mays</i> L.) hybrids relative to their inbred parents. <i>Genome Research</i> , <b>2012</b> , 22, 2445-54	9.7	97
147	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> , <b>2014</b> , 10, e1003972	7.6	94
146	Distinct biphasic mRNA changes in response to Asian soybean rust infection. <i>Molecular Plant-Microbe Interactions</i> , <b>2007</b> , 20, 887-99	3.6	94
145	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> , <b>2009</b> , 5, e1000737	6	92
144	Identification of the novel protein QQS as a component of the starch metabolic network in Arabidopsis leaves. <i>Plant Journal</i> , <b>2009</b> , 58, 485-98	6.9	88
143	Estimating the number of true null hypotheses from a histogram of p values. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , <b>2006</b> , 11, 337-356	1.9	81
142	Differential gene expression in the rat soleus muscle during early work overload-induced hypertrophy. <i>FASEB Journal</i> , <b>2002</b> , 16, 207-9	0.9	80
141	The Soybean Rhg1 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> , <b>2011</b> , 155, 1960-75	6.6	74
140	BarleyBase--an expression profiling database for plant genomics. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D614-D617	20.1	74
139	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> , <b>2006</b> , 19, 939-47	3.6	71
138	A novel approach for characterizing expression levels of genes duplicated by polyploidy. <i>Genetics</i> , <b>2006</b> , 173, 1823-7	4	70
137	The maize brown midrib2 (bm2) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. <i>Plant Journal</i> , <b>2014</b> , 77, 380-92	6.9	67

136	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> , <b>2010</b> , 298, R494-507	3.2	67
135	Microdissection of shoot meristem functional domains. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000476	6	64
134	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> , <b>2015</b> , 112, 14734-9	11.5	63
133	Accounting for variability in the use of permutation testing to detect quantitative trait loci. <i>Biometrics</i> , <b>2000</b> , 56, 52-8	1.8	62
132	Genomics, prior probability, and statistical tests of multiple hypotheses. <i>Genome Research</i> , <b>2004</b> , 14, 997-1001	9.7	61
131	Ontogeny of the maize shoot apical meristem. <i>Plant Cell</i> , <b>2012</b> , 24, 3219-34	11.6	60
130	Copy number variation detection using next generation sequencing read counts. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 109	3.6	59
129	Laser microdissection of narrow sheath mutant maize uncovers novel gene expression in the shoot apical meristem. <i>PLoS Genetics</i> , <b>2007</b> , 3, e101	6	58
128	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> , <b>2015</b> , 84, 587-96	6.9	57
127	Validation of a first-generation long-oligonucleotide microarray for transcriptional profiling in the pig. <i>Genomics</i> , <b>2005</b> , 86, 618-25	4.3	57
126	Unique genome-wide transcriptome profiles of chicken macrophages exposed to Salmonella-derived endotoxin. <i>BMC Genomics</i> , <b>2010</b> , 11, 545	4.5	55
125	CmeR functions as a pleiotropic regulator and is required for optimal colonization of <i>Campylobacter jejuni</i> in vivo. <i>Journal of Bacteriology</i> , <b>2008</b> , 190, 1879-90	3.5	54
124	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> , <b>2016</b> , 67, 1123-35	7	53
123	A discussion of statistical methods for design and analysis of microarray experiments for plant scientists. <i>Plant Cell</i> , <b>2006</b> , 18, 2112-21	11.6	52
122	Transcriptional profiling of <i>Mycoplasma hyopneumoniae</i> during heat shock using microarrays. <i>Infection and Immunity</i> , <b>2006</b> , 74, 160-6	3.7	52
121	Extensive tissue-specific transcriptomic plasticity in maize primary roots upon water deficit. <i>Journal of Experimental Botany</i> , <b>2016</b> , 67, 1095-107	7	51
120	Identification of differentially expressed gene categories in microarray studies using nonparametric multivariate analysis. <i>Bioinformatics</i> , <b>2008</b> , 24, 192-201	7.2	47
119	Distinct genetic architectures for phenotype means and plasticities in <i>Zea mays</i> . <i>Nature Plants</i> , <b>2017</b> , 3, 715-723	11.5	46

118	Nonsyntenic genes drive highly dynamic complementation of gene expression in maize hybrids. <i>Plant Cell</i> , <b>2014</b> , 26, 3939-48	11.6	43
117	Comparative gene expression profiles between heterotic and non-heterotic hybrids of tetraploid <i>Medicago sativa</i> . <i>BMC Plant Biology</i> , <b>2009</b> , 9, 107	5.3	42
116	Transcriptional analysis of the global regulatory networks active in <i>Pseudomonas syringae</i> during leaf colonization. <i>MBio</i> , <b>2014</b> , 5, e01683-14	7.8	41
115	Pooling mRNA in microarray experiments and its effect on power. <i>Bioinformatics</i> , <b>2007</b> , 23, 1217-24	7.2	41
114	Root Type-Specific Reprogramming of Maize Pericycle Transcriptomes by Local High Nitrate Results in Disparate Lateral Root Branching Patterns. <i>Plant Physiology</i> , <b>2016</b> , 170, 1783-98	6.6	39
113	Distinct peripheral blood RNA responses to <i>Salmonella</i> in pigs differing in <i>Salmonella</i> shedding levels: intersection of IFNG, TLR and miRNA pathways. <i>PLoS ONE</i> , <b>2011</b> , 6, e28768	3.7	38
112	Biphasic gene expression changes elicited by <i>Phakopsora pachyrhizi</i> in soybean correlate with fungal penetration and haustoria formation. <i>Plant Physiology</i> , <b>2011</b> , 157, 355-71	6.6	38
111	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> , <b>2008</b> , 9, 437	4.5	38
110	Transcriptional profiling of <i>Mycoplasma hyopneumoniae</i> during iron depletion using microarrays. <i>Microbiology (United Kingdom)</i> , <b>2006</b> , 152, 937-944	2.9	38
109	Transcriptome analyses and virus induced gene silencing identify genes in the Rpp4-mediated Asian soybean rust resistance pathway. <i>Functional Plant Biology</i> , <b>2013</b> , 40, 1029-1047	2.7	37
108	SimSeq: a nonparametric approach to simulation of RNA-sequence datasets. <i>Bioinformatics</i> , <b>2015</b> , 31, 2131-40	7.2	37
107	Spotted cotton oligonucleotide microarrays for gene expression analysis. <i>BMC Genomics</i> , <b>2007</b> , 8, 81	4.5	37
106	Gene expression profiling in <i>Salmonella Choleraesuis</i> -infected porcine lung using a long oligonucleotide microarray. <i>Mammalian Genome</i> , <b>2006</b> , 17, 777-89	3.2	37
105	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> , <b>2007</b> , 8, R211	18.3	36
104	Adaptive and dynamic adaptive procedures for false discovery rate control and estimation. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , <b>2012</b> , 74, 163-182	3.9	35
103	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> , <b>2009</b> , 38, 98-111	3.6	34
102	Sequence mining and transcript profiling to explore cyst nematode parasitism. <i>BMC Genomics</i> , <b>2009</b> , 10, 58	4.5	34
101	Multiple Marginal Independence Testing for Pick Any/C Variables. <i>Communications in Statistics Part B: Simulation and Computation</i> , <b>2000</b> , 29, 1285-1316	0.6	33

100	Convergence properties of the EM algorithm in constrained parameter spaces. <i>Canadian Journal of Statistics</i> , <b>1999</b> , 27, 639-648	0.4	33
99	Broadly Conserved Fungal Effector BEC1019 Suppresses Host Cell Death and Enhances Pathogen Virulence in Powdery Mildew of Barley ( <i>Hordeum vulgare</i> L.). <i>Molecular Plant-Microbe Interactions</i> , <b>2015</b> , 28, 968-83	3.6	32
98	A systems biology approach toward understanding seed composition in soybean. <i>BMC Genomics</i> , <b>2015</b> , 16 Suppl 3, S9	4.5	31
97	Microarray analysis of vegetative phase change in maize. <i>Plant Journal</i> , <b>2008</b> , 56, 1045-57	6.9	31
96	Global transcriptional response of porcine mesenteric lymph nodes to <i>Salmonella enterica</i> serovar Typhimurium. <i>Genomics</i> , <b>2007</b> , 90, 72-84	4.3	31
95	Exploring the information in p-values for the analysis and planning of multiple-test experiments. <i>Biometrics</i> , <b>2007</b> , 63, 483-95	1.8	30
94	Substantial contribution of genetic variation in the expression of transcription factors to phenotypic variation revealed by eRD-GWAS. <i>Genome Biology</i> , <b>2017</b> , 18, 192	18.3	29
93	Quantitative trait loci associated with adventitious shoot formation in tissue culture and the program of shoot development in <i>Arabidopsis</i> . <i>Genetics</i> , <b>2004</b> , 167, 1883-92	4	29
92	Using Random Forests to distinguish gahnite compositions as an exploration guide to Broken Hill-type Pb <sub>2</sub> SnAg deposits in the Broken Hill domain, Australia. <i>Journal of Geochemical Exploration</i> , <b>2015</b> , 149, 74-86	3.8	28
91	Reverse engineering and analysis of large genome-scale gene networks. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, e24	20.1	28
90	<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> , <b>2015</b> , 21, 227-41	2.7	27
89	The maize brown midrib4 ( <i>bm4</i> ) gene encodes a functional folylpolyglutamate synthase. <i>Plant Journal</i> , <b>2015</b> , 81, 493-504	6.9	27
88	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> , <b>2005</b> , 3, 225-35	11.6	27
87	Crowdsourcing image analysis for plant phenomics to generate ground truth data for machine learning. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1006337	5	27
86	Endometrial gene expression profiling in pregnant Meishan and Yorkshire pigs on day 12 of gestation. <i>BMC Genomics</i> , <b>2014</b> , 15, 156	4.5	22
85	Quantitative and temporal definition of the <i>Mla</i> transcriptional regulon during barley-powdery mildew interactions. <i>Molecular Plant-Microbe Interactions</i> , <b>2011</b> , 24, 694-705	3.6	22
84	Scanning microarrays at multiple intensities enhances discovery of differentially expressed genes. <i>Bioinformatics</i> , <b>2006</b> , 22, 1863-70	7.2	22
83	Single-Parent Expression Is a General Mechanism Driving Extensive Complementation of Non-syntenic Genes in Maize Hybrids. <i>Current Biology</i> , <b>2018</b> , 28, 431-437.e4	6.3	21

82	Changes in genome content generated via segregation of non-allelic homologs. <i>Plant Journal</i> , <b>2012</b> , 72, 390-9	6.9	21
81	<i>Helicobacter bilis</i> colonization enhances susceptibility to Typhlocolitis following an inflammatory trigger. <i>Digestive Diseases and Sciences</i> , <b>2011</b> , 56, 2838-48	4	21
80	Transcript-based cloning of RRP46, a regulator of rRNA processing and R gene-independent cell death in barley-powdery mildew interactions. <i>Plant Cell</i> , <b>2009</b> , 21, 3280-95	11.6	21
79	Principal Components Regression With Data Chosen Components and Related Methods. <i>Technometrics</i> , <b>2003</b> , 45, 70-79	1.4	21
78	ArcA Controls Metabolism, Chemotaxis, and Motility Contributing to the Pathogenicity of Avian Pathogenic <i>Escherichia coli</i> . <i>Infection and Immunity</i> , <b>2015</b> , 83, 3545-54	3.7	20
77	A Hidden Markov Model Approach to Testing Multiple Hypotheses on a Tree-Transformed Gene Ontology Graph. <i>Journal of the American Statistical Association</i> , <b>2010</b> , 105, 1444-1454	2.8	20
76	QQS orphan gene and its interactor NF-YC4 reduce susceptibility to pathogens and pests. <i>Plant Biotechnology Journal</i> , <b>2019</b> , 17, 252-263	11.6	19
75	Case-Specific Random Forests. <i>Journal of Computational and Graphical Statistics</i> , <b>2016</b> , 25, 49-65	1.4	18
74	Post-weaning blood transcriptomic differences between Yorkshire pigs divergently selected for residual feed intake. <i>BMC Genomics</i> , <b>2016</b> , 17, 73	4.5	18
73	Random Forest Prediction Intervals. <i>American Statistician</i> , <b>2020</b> , 74, 392-406	5	18
72	Small RNA discovery in the interaction between barley and the powdery mildew pathogen. <i>BMC Genomics</i> , <b>2019</b> , 20, 610	4.5	17
71	Using random forests to estimate win probability before each play of an NFL game. <i>Journal of Quantitative Analysis in Sports</i> , <b>2014</b> , 10,	1.2	17
70	Testing the equality of distributions of random vectors with categorical components. <i>Computational Statistics and Data Analysis</i> , <b>2001</b> , 37, 195-208	1.6	17
69	Transcriptional profiling using a novel cDNA array identifies differential gene expression during porcine embryo elongation. <i>Molecular Reproduction and Development</i> , <b>2005</b> , 71, 129-39	2.6	16
68	Stability of Single-Parent Gene Expression Complementation in Maize Hybrids upon Water Deficit Stress. <i>Plant Physiology</i> , <b>2017</b> , 173, 1247-1257	6.6	15
67	Gene expression in intestinal mucosal biopsy specimens obtained from dogs with chronic enteropathy. <i>American Journal of Veterinary Research</i> , <b>2012</b> , 73, 1219-29	1.1	14
66	A Clade-Specific Arabidopsis Gene Connects Primary Metabolism and Senescence. <i>Frontiers in Plant Science</i> , <b>2016</b> , 7, 983	6.2	13
65	Discovery and Characterization of the 3-Hydroxyacyl-ACP Dehydratase Component of the Plant Mitochondrial Fatty Acid Synthase System. <i>Plant Physiology</i> , <b>2017</b> , 173, 2010-2028	6.6	12



64	Complexity and specificity of the maize ( <i>Zea mays</i> L.) root hair transcriptome. <i>Journal of Experimental Botany</i> , <b>2017</b> , 68, 2175-2185	7	12
63	Nested Hierarchical Functional Data Modeling and Inference for the Analysis of Functional Plant Phenotypes. <i>Journal of the American Statistical Association</i> , <b>2018</b> , 113, 593-606	2.8	12
62	Microbial community sequencing analysis of the calf eye microbiota and relationship to infectious bovine keratoconjunctivitis. <i>Veterinary Microbiology</i> , <b>2017</b> , 207, 267-279	3.3	12
61	Estimation of false discovery rate using sequential permutation p-values. <i>Biometrics</i> , <b>2013</b> , 69, 1-7	1.8	12
60	Comparison of Transcript Profiles in Wild-Type and o2 Maize Endosperm in Different Genetic Backgrounds. <i>Crop Science</i> , <b>2007</b> , 47, S-45	2.4	12
59	Array-based genomic comparative hybridization analysis of field strains of <i>Mycoplasma hyopneumoniae</i> . <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 7977-82	3.5	12
58	Assessing plant performance in the Enviratron. <i>Plant Methods</i> , <b>2019</b> , 15, 117	5.8	11
57	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> , <b>2009</b> , 11, 374-83	9.3	11
56	Tree aggregation for random forest class probability estimation. <i>Statistical Analysis and Data Mining</i> , <b>2020</b> , 13, 134-150	1.4	11
55	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> , <b>2008</b> , 35, 603-16	4	10
54	Identifying genes associated with a quantitative trait or quantitative trait locus via selective transcriptional profiling. <i>Biometrics</i> , <b>2006</b> , 62, 504-14	1.8	10
53	High-resolution genotyping via whole genome hybridizations to microarrays containing long oligonucleotide probes. <i>PLoS ONE</i> , <b>2010</b> , 5, e14178	3.7	10
52	Proteomics-based, multivariate random forest method for prediction of protein separation behavior during cation-exchange chromatography. <i>Journal of Chromatography A</i> , <b>2012</b> , 1249, 103-14	4.5	9
51	Testing for the Supremacy of a Multinomial Cell Probability. <i>Journal of the American Statistical Association</i> , <b>2009</b> , 104, 1052-1059	2.8	9
50	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> , <b>2018</b> , 8, 3567-3575	3.2	9
49	Stress response to CO2 deprivation by <i>Arabidopsis thaliana</i> in plant cultures. <i>PLoS ONE</i> , <b>2019</b> , 14, e0212462	3.62	8
48	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> , <b>2017</b> , 68, 403-414	7	8
47	Genes and Small RNA Transcripts Exhibit Dosage-Dependent Expression Pattern in Maize Copy-Number Alterations. <i>Genetics</i> , <b>2016</b> , 203, 1133-47	4	8



46	Selective transcriptional profiling for trait-based eQTL mapping. <i>Animal Genetics</i> , <b>2006</b> , 37 Suppl 1, 13-7	2.5	8
45	Empirical Bayes analysis of RNA-seq data for detection of gene expression heterosis. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , <b>2015</b> , 20, 614-628	1.9	7
44	Adjusting for Spatial Effects in Genomic Prediction. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , <b>2020</b> , 25, 699-718	1.9	6
43	Fully Bayesian analysis of RNA-seq counts for the detection of gene expression heterosis. <i>Journal of the American Statistical Association</i> , <b>2019</b> , 114, 610-621	2.8	6
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> , <b>2015</b> , 20, 577-597	1.9	6
41	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> , <b>2015</b> , 6, 409	6.2	6
40	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> , <b>2014</b> , 7, 693-701	3.1	6
39	rmRNAseq: differential expression analysis for repeated-measures RNA-seq data. <i>Bioinformatics</i> , <b>2020</b> , 36, 4432-4439	7.2	5
38	Linear mixed model selection for false discovery rate control in microarray data analysis. <i>Biometrics</i> , <b>2010</b> , 66, 621-9	1.8	5
37	Borrowing information across genes and experiments for improved error variance estimation in microarray data analysis. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2012</b> , 11, Article 12	1.2	5
36	Estimation and Testing of Gene Expression Heterosis. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , <b>2014</b> , 19, 319-337	1.9	4
35	Additive partially linear models for ultra-high-dimensional regression. <i>Stat</i> , <b>2019</b> , 8, e223	0.7	3
34	Metabolomic Profiling of Spp. Nectars Indicate That Pollinator Feeding Preference Is a Stronger Determinant Than Plant Phylogenetics in Shaping Nectar Diversity. <i>Metabolites</i> , <b>2020</b> , 10,	5.6	3
33	From Arabidopsis to Crops: The Arabidopsis QQS Orphan Gene Modulates Nitrogen Allocation Across Species <b>2018</b> , 95-117		3
32	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. <i>Biometrics</i> , <b>2012</b> , 68, 1178-87	1.8	3
31	Accounting for spot matching uncertainty in the analysis of proteomics data from two-dimensional gel electrophoresis. <i>Sankhya B</i> , <b>2011</b> , 73, 123-143	0.4	3
30	An Efficient and Scalable Implementation of SNP-Pair Interaction Testing for Genetic Association Studies <b>2011</b> ,		3
29	Identifying differentially expressed genes in unreplicated multiple-treatment microarray timecourse experiments. <i>Computational Statistics and Data Analysis</i> , <b>2006</b> , 50, 518-532	1.6	3

28	Interval Mapping of Quantitative Trait Loci through Order-Restricted Inference. <i>Biometrics</i> , <b>1998</b> , 54, 74	1.8	3
27	Order-restricted hypothesis testing in a variation of the normal mixture model. <i>Canadian Journal of Statistics</i> , <b>1999</b> , 27, 383-394	0.4	3
26	Investigating the probability of sign inconsistency in the regression coefficients of markers flanking quantitative trait loci. <i>Genetics</i> , <b>2002</b> , 160, 1697-705	4	3
25	KAT4IA: -Means Assisted Training for Image Analysis of Field-Grown Plant Phenotypes. <i>Plant Phenomics</i> , <b>2021</b> , 2021, 9805489	7	3
24	A hidden Markov tree model for testing multiple hypotheses corresponding to Gene Ontology gene sets. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 107	3.6	2
23	An improved method for computing q-values when the distribution of effect sizes is asymmetric. <i>Bioinformatics</i> , <b>2014</b> , 30, 3044-53	7.2	2
22	Interchromosomal Transfer of Immune Regulation During Infection of Barley with the Powdery Mildew Pathogen. <i>G3: Genes, Genomes, Genetics</i> , <b>2017</b> , 7, 3317-3329	3.2	2
21	Hierarchical Modeling and Differential Expression Analysis for RNA-seq Experiments with Inbred and Hybrid Genotypes. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , <b>2015</b> , 20, 598-613 <sup>1.9</sup>	1.9	2
20	The importance of distinct modeling strategies for gene and gene-specific treatment effects in hierarchical models for microarray data. <i>Annals of Applied Statistics</i> , <b>2012</b> , 6,	2.1	2
19	Design of Gene Expression Microarray Experiments. <i>Wiley Series in Probability and Statistics</i> , <b>2012</b> , 73-108 <sup>3</sup>	3	2
18	Combining classical trait and microarray data to dissect transcriptional regulation: a case study. <i>Theoretical and Applied Genetics</i> , <b>2008</b> , 116, 683-90	6	2
17	Variance model selection with application to joint analysis of multiple microarray datasets under false discovery rate control. <i>Statistics and Its Interface</i> , <b>2010</b> , 3, 477-491	0.4	2
16	Automatic Traits Extraction and Fitting for Field High-throughput Phenotyping Systems		2
15	Accounting for host cell protein behavior in anion-exchange chromatography. <i>Biotechnology Progress</i> , <b>2016</b> , 32, 1453-1463	2.8	2
14	Sparse model identification and learning for ultra-high-dimensional additive partially linear models. <i>Journal of Multivariate Analysis</i> , <b>2019</b> , 173, 204-228	1.4	1
13	Detecting rare and faint signals via thresholding maximum likelihood estimators. <i>Annals of Statistics</i> , <b>2018</b> , 46,	3.2	1
12	A hierarchical semiparametric model for incorporating intergene information for analysis of genomic data. <i>Biometrics</i> , <b>2012</b> , 68, 1168-77	1.8	1
11	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> , <b>2013</b> , 21,	1	1

10	Design of RNA Sequencing Experiments <b>2014</b> , 93-113		1
9	Flor Revisited (Again): eQTL and Mutational Analysis of NB-LRR Mediated Immunity to Powdery Mildew in Barley. <i>Journal of Integrative Agriculture</i> , <b>2014</b> , 13, 237-243	3.2	○
8	Predictor augmentation in random forests. <i>Statistics and Its Interface</i> , <b>2014</b> , 7, 177-186	0.4	○
7	A residual-based approach for robust random forest regression. <i>Statistics and Its Interface</i> , <b>2021</b> , 14, 389-402	0.4	○
6	Estimating the Number of Genes That Are Differentially Expressed in Both of Two Independent Experiments. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , <b>2012</b> , 17, 583-600	1.9	
5	Testing for ordered means in a variation of the normal mixture model. <i>Journal of Statistical Planning and Inference</i> , <b>2002</b> , 107, 143-153	0.8	
4	Expression pattern of yeast sporulation: a case study for regulatory changes after yeast genome duplication. <i>Information Sciences</i> , <b>2002</b> , 145, 261-269	7.7	
3	Leptin mediates discriminate response to feed restriction in feed efficient pigs. <i>FASEB Journal</i> , <b>2009</b> , 23, 1022.3	0.9	
2	Differentially expressed microRNAs in dystrophin-deficient muscle.. <i>FASEB Journal</i> , <b>2010</b> , 24, 989.1	0.9	
1	Variable importance assessments and backward variable selection for multi-sample problems. <i>Journal of Multivariate Analysis</i> , <b>2021</b> , 186, 104807	1.4	