Daniel S Nettleton

List of Publications by Year in Descending Order

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	A residual-based approach for robust random forest regression. *Statistics and Its Interface*, **2021**, 14, 389-402	0.4	0
170	KAT4IA: -Means Assisted Training for Image Analysis of Field-Grown Plant Phenotypes. *Plant Phenomics*, **2021**, 2021, 9805489	7	3
169	Variable importance assessments and backward variable selection for multi-sample problems. *Journal of Multivariate Analysis*, **2021**, 186, 104807	1.4	
168	rmRNAseq: differential expression analysis for repeated-measures RNA-seq data. *Bioinformatics*, **2020**, 36, 4432-4439	7.2	5
167	Metabolomic Profiling of Spp. Nectars Indicate That Pollinator Feeding Preference Is a Stronger Determinant Than Plant Phylogenetics in Shaping Nectar Diversity. *Metabolites*, **2020**, 10,	5.6	3
166	Adjusting for Spatial Effects in Genomic Prediction. *Journal of Agricultural, Biological, and Environmental Statistics*, **2020**, 25, 699-718	1.9	6
165	Tree aggregation for random forest class probability estimation. *Statistical Analysis and Data Mining*, **2020**, 13, 134-150	1.4	11
164	Random Forest Prediction Intervals. *American Statistician*, **2020**, 74, 392-406	5	18
163	Stress response to CO2 deprivation by Arabidopsis thaliana in plant cultures. *PLoS ONE*, **2019**, 14, e0212462	3.7	8
162	Sparse model identification and learning for ultra-high-dimensional additive partially linear models. *Journal of Multivariate Analysis*, **2019**, 173, 204-228	1.4	1
161	Additive partially linear models for ultra-high-dimensional regression. *Stat*, **2019**, 8, e223	0.7	3
160	QQS orphan gene and its interactor NF-YC4 reduce susceptibility to pathogens and pests. *Plant Biotechnology Journal*, **2019**, 17, 252-263	11.6	19
159	Fully Bayesian analysis of RNA-seq counts for the detection of gene expression heterosis. *Journal of the American Statistical Association*, **2019**, 114, 610-621	2.8	6
158	Small RNA discovery in the interaction between barley and the powdery mildew pathogen. *BMC Genomics*, **2019**, 20, 610	4.5	17
157	Assessing plant performance in the Enviratron. *Plant Methods*, **2019**, 15, 117	5.8	11
156	Detecting rare and faint signals via thresholding maximum likelihood estimators. *Annals of Statistics*, **2018**, 46,	3.2	1
155	Single-Parent Expression Is a General Mechanism Driving Extensive Complementation of Non-syntenic Genes in Maize Hybrids. *Current Biology*, **2018**, 28, 431-437.e4	6.3	21

154 A hidden Markov tree model for testing multiple hypotheses corresponding to Gene Ontology gene sets. *BMC Bioinformatics*, **2018**, 19, 107 — 3.6 — 2

153 Nested Hierarchical Functional Data Modeling and Inference for the Analysis of Functional Plant Phenotypes. *Journal of the American Statistical Association*, **2018**, 113, 593-606 — 2.8 — 12

152 From Arabidopsis to Crops: The Arabidopsis QQS Orphan Gene Modulates Nitrogen Allocation Across Species **2018**, 95-117 — 3

151 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 — 3.2 — 9

150 Crowdsourcing image analysis for plant phenomics to generate ground truth data for machine learning. *PLoS Computational Biology*, **2018**, 14, e1006337 — 5 — 27

149 Discovery and Characterization of the 3-Hydroxyacyl-ACP Dehydratase Component of the Plant Mitochondrial Fatty Acid Synthase System. *Plant Physiology*, **2017**, 173, 2010-2028 — 6.6 — 12

148 Stability of Single-Parent Gene Expression Complementation in Maize Hybrids upon Water Deficit Stress. *Plant Physiology*, **2017**, 173, 1247-1257 — 6.6 — 15

147 Substantial contribution of genetic variation in the expression of transcription factors to phenotypic variation revealed by eRD-GWAS. *Genome Biology*, **2017**, 18, 192 — 18.3 — 29

146 Complexity and specificity of the maize (Zea mays L.) root hair transcriptome. *Journal of Experimental Botany*, **2017**, 68, 2175-2185 — 7 — 12

145 Non-syntenic genes drive RTCS-dependent regulation of the embryo transcriptome during formation of seminal root primordia in maize (Zea mays L.). *Journal of Experimental Botany*, **2017**, 68, 403-414 — 7 — 8

144 Interchromosomal Transfer of Immune Regulation During Infection of Barley with the Powdery Mildew Pathogen. *G3: Genes, Genomes, Genetics*, **2017**, 7, 3317-3329 — 3.2 — 2

143 Microbial community sequencing analysis of the calf eye microbiota and relationship to infectious bovine keratoconjunctivitis. *Veterinary Microbiology*, **2017**, 207, 267-279 — 3.3 — 12

142 Distinct genetic architectures for phenotype means and plasticities in Zea mays. *Nature Plants*, **2017**, 3, 715-723 — 11.5 — 46

141 Extensive tissue-specific transcriptomic plasticity in maize primary roots upon water deficit. *Journal of Experimental Botany*, **2016**, 67, 1095-107 — 7 — 51

140 Genes and Small RNA Transcripts Exhibit Dosage-Dependent Expression Pattern in Maize Copy-Number Alterations. *Genetics*, **2016**, 203, 1133-47 — 4 — 8

139 Root Type-Specific Reprogramming of Maize Pericycle Transcriptomes by Local High Nitrate Results in Disparate Lateral Root Branching Patterns. *Plant Physiology*, **2016**, 170, 1783-98 — 6.6 — 39

138 Transcriptomic and anatomical complexity of primary, seminal, and crown roots highlight root type-specific functional diversity in maize (Zea mays L.). *Journal of Experimental Botany*, **2016**, 67, 1123-35 — 7 — 53

137 Case-Specific Random Forests. *Journal of Computational and Graphical Statistics*, **2016**, 25, 49-65 — 1.4 — 18

136	A Clade-Specific Arabidopsis Gene Connects Primary Metabolism and Senescence. *Frontiers in Plant Science*, **2016**, 7, 983	6.2	13
135	Post-weaning blood transcriptomic differences between Yorkshire pigs divergently selected for residual feed intake. *BMC Genomics*, **2016**, 17, 73	4.5	18
134	Accounting for host cell protein behavior in anion-exchange chromatography. *Biotechnology Progress*, **2016**, 32, 1453-1463	2.8	2
133	Salmonella enterica serovar Typhimurium-infected pigs with different shedding levels exhibit distinct clinical, peripheral cytokine and transcriptomic immune response phenotypes. *Innate Immunity*, **2015**, 21, 227-41	2.7	27
132	The maize brown midrib4 (bm4) gene encodes a functional folylpolyglutamate synthase. *Plant Journal*, **2015**, 81, 493-504	6.9	27
131	ArcA Controls Metabolism, Chemotaxis, and Motility Contributing to the Pathogenicity of Avian Pathogenic Escherichia coli. *Infection and Immunity*, **2015**, 83, 3545-54	3.7	20
130	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, 14734-9	11.5	63
129	Empirical Bayes analysis of RNA-seq data for detection of gene expression heterosis. *Journal of Agricultural, Biological, and Environmental Statistics*, **2015**, 20, 614-628	1.9	7
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. *Plant Journal*, **2015**, 84, 587-96	6.9	57
127	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	1.9	6
126	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	1.9	2
125	A systems biology approach toward understanding seed composition in soybean. *BMC Genomics*, **2015**, 16 Suppl 3, S9	4.5	31
124	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	6.2	6
123	SimSeq: a nonparametric approach to simulation of RNA-sequence datasets. *Bioinformatics*, **2015**, 31, 2131-40	7.2	37
122	Broadly Conserved Fungal Effector BEC1019 Suppresses Host Cell Death and Enhances Pathogen Virulence in Powdery Mildew of Barley (Hordeum vulgare L.). *Molecular Plant-Microbe Interactions*, **2015**, 28, 968-83	3.6	32
121	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	3.8	28
120	The maize brown midrib2 (bm2) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. *Plant Journal*, **2014**, 77, 380-92	6.9	67
119	An improved method for computing q-values when the distribution of effect sizes is asymmetric. *Bioinformatics*, **2014**, 30, 3044-53	7.2	2

118	Estimation and Testing of Gene Expression Heterosis. *Journal of Agricultural, Biological, and Environmental Statistics*, **2014**, 19, 319-337	1.9	4
117	Copy number variation detection using next generation sequencing read counts. *BMC Bioinformatics*, **2014**, 15, 109	3.6	59
116	Endometrial gene expression profiling in pregnant Meishan and Yorkshire pigs on day 12 of gestation. *BMC Genomics*, **2014**, 15, 156	4.5	22
115	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	7.6	94
114	Transcriptional analysis of the global regulatory networks active in Pseudomonas syringae during leaf colonization. *MBio*, **2014**, 5, e01683-14	7.8	41
113	Nonsyntenic genes drive highly dynamic complementation of gene expression in maize hybrids. *Plant Cell*, **2014**, 26, 3939-48	11.6	43
112	Using random forests to estimate win probability before each play of an NFL game. *Journal of Quantitative Analysis in Sports*, **2014**, 10,	1.2	17
111	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	3.2	0
110	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	3.1	6
109	Design of RNA Sequencing Experiments **2014**, 93-113		1
108	Predictor augmentation in random forests. *Statistics and Its Interface*, **2014**, 7, 177-186	0.4	0
107	Transcriptome analyses and virus induced gene silencing identify genes in the Rpp4-mediated Asian soybean rust resistance pathway. *Functional Plant Biology*, **2013**, 40, 1029-1047	2.7	37
106	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	11.5	141
105	Host-induced gene silencing in barley powdery mildew reveals a class of ribonuclease-like effectors. *Molecular Plant-Microbe Interactions*, **2013**, 26, 633-42	3.6	136
104	Reverse engineering and analysis of large genome-scale gene networks. *Nucleic Acids Research*, **2013**, 41, e24	20.1	28
103	Estimation of false discovery rate using sequential permutation p-values. *Biometrics*, **2013**, 69, 1-7	1.8	12
102	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	1
101	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, 1178-87	1.8	3

100	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,	2.1	2
99	A hierarchical semiparametric model for incorporating intergene information for analysis of genomic data. *Biometrics*, **2012**, 68, 1168-77	1.8	1
98	Changes in genome content generated via segregation of non-allelic homologs. *Plant Journal*, **2012**, 72, 390-9	6.9	21
97	Detecting differential expression in RNA-sequence data using quasi-likelihood with shrunken dispersion estimates. *Statistical Applications in Genetics and Molecular Biology*, **2012**, 11,	1.2	191
96	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	1.9	
95	Proteomics-based, multivariate random forest method for prediction of protein separation behavior during cation-exchange chromatography. *Journal of Chromatography A*, **2012**, 1249, 103-14	4.5	9
94	Design of Gene Expression Microarray Experiments. *Wiley Series in Probability and Statistics*, **2012**, 73-108	1.3	2
93	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	3.9	35
92	Gene expression in intestinal mucosal biopsy specimens obtained from dogs with chronic enteropathy. *American Journal of Veterinary Research*, **2012**, 73, 1219-29	1.1	14
91	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, 321-35	6.6	168
90	Complementation contributes to transcriptome complexity in maize (Zea mays L.) hybrids relative to their inbred parents. *Genome Research*, **2012**, 22, 2445-54	9.7	97
89	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	1.2	5
88	Ontogeny of the maize shoot apical meristem. *Plant Cell*, **2012**, 24, 3219-34	11.6	60
87	Gene mapping via bulked segregant RNA-Seq (BSR-Seq). *PLoS ONE*, **2012**, 7, e36406	3.7	212
86	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	3.7	38
85	Quantitative and temporal definition of the Mla transcriptional regulon during barley-powdery mildew interactions. *Molecular Plant-Microbe Interactions*, **2011**, 24, 694-705	3.6	22
84	Helicobacter bilis colonization enhances susceptibility to Typhlocolitis following an inflammatory trigger. *Digestive Diseases and Sciences*, **2011**, 56, 2838-48	4	21
83	Accounting for spot matching uncertainty in the analysis of proteomics data from two-dimensional gel electrophoresis. *Sankhya B*, **2011**, 73, 123-143	0.4	3

82	An Efficient and Scalable Implementation of SNP-Pair Interaction Testing for Genetic Association Studies **2011**,		3
81	Soybean homologs of MPK4 negatively regulate defense responses and positively regulate growth and development. *Plant Physiology*, **2011**, 157, 1363-78	6.6	109
80	Biphasic gene expression changes elicited by Phakopsora pachyrhizi in soybean correlate with fungal penetration and haustoria formation. *Plant Physiology*, **2011**, 157, 355-71	6.6	38
79	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. *Plant Physiology*, **2011**, 155, 1960-75	6.6	74
78	Linear mixed model selection for false discovery rate control in microarray data analysis. *Biometrics*, **2010**, 66, 621-9	1.8	5
77	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, R494-507	3.2	67
76	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	2.8	20
75	Unique genome-wide transcriptome profiles of chicken macrophages exposed to Salmonella-derived endotoxin. *BMC Genomics*, **2010**, 11, 545	4.5	55
74	High-resolution genotyping via whole genome hybridizations to microarrays containing long oligonucleotide probes. *PLoS ONE*, **2010**, 5, e14178	3.7	10
73	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	0.4	2
72	Differentially expressed microRNAs in dystrophin-deficient muscle.. *FASEB Journal*, **2010**, 24, 989.1	0.9	
71	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	3.6	34
70	Microdissection of shoot meristem functional domains. *PLoS Genetics*, **2009**, 5, e1000476	6	64
69	Maize inbreds exhibit high levels of copy number variation (CNV) and presence/absence variation (PAV) in genome content. *PLoS Genetics*, **2009**, 5, e1000734	6	389
68	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. *PLoS Genetics*, **2009**, 5, e1000737	6	92
67	Transcript-based cloning of RRP46, a regulator of rRNA processing and R gene-independent cell death in barley-powdery mildew interactions. *Plant Cell*, **2009**, 21, 3280-95	11.6	21
66	Paternal dominance of trans-eQTL influences gene expression patterns in maize hybrids. *Science*, **2009**, 326, 1118-20	33.3	98
65	Sequence mining and transcript profiling to explore cyst nematode parasitism. *BMC Genomics*, **2009**, 10, 58	4.5	34

64	Comparative gene expression profiles between heterotic and non-heterotic hybrids of tetraploid Medicago sativa. *BMC Plant Biology*, **2009**, 9, 107	5.3	42
63	Identification of the novel protein QQS as a component of the starch metabolic network in Arabidopsis leaves. *Plant Journal*, **2009**, 58, 485-98	6.9	88
62	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, 374-83	9.3	11
61	The B73 maize genome: complexity, diversity, and dynamics. *Science*, **2009**, 326, 1112-5	33.3	2949
60	Testing for the Supremacy of a Multinomial Cell Probability. *Journal of the American Statistical Association*, **2009**, 104, 1052-1059	2.8	9
59	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	6	154
58	Leptin mediates discriminate response to feed restriction in feed efficient pigs. *FASEB Journal*, **2009**, 23, 1022.3	0.9	
57	Microarray analysis of vegetative phase change in maize. *Plant Journal*, **2008**, 56, 1045-57	6.9	31
56	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	4.5	38
55	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, 603-16	4	10
54	CmeR functions as a pleiotropic regulator and is required for optimal colonization of Campylobacter jejuni in vivo. *Journal of Bacteriology*, **2008**, 190, 1879-90	3.5	54
53	Identification of differentially expressed gene categories in microarray studies using nonparametric multivariate analysis. *Bioinformatics*, **2008**, 24, 192-201	7.2	47
52	Combining classical trait and microarray data to dissect transcriptional regulation: a case study. *Theoretical and Applied Genetics*, **2008**, 116, 683-90	6	2
51	Duplicate gene expression in allopolyploid Gossypium reveals two temporally distinct phases of expression evolution. *BMC Biology*, **2008**, 6, 16	7.3	194
50	Spatial analysis of arabidopsis thaliana gene expression in response to Turnip mosaic virus infection. *Molecular Plant-Microbe Interactions*, **2007**, 20, 358-70	3.6	120
49	Distinct biphasic mRNA changes in response to Asian soybean rust infection. *Molecular Plant-Microbe Interactions*, **2007**, 20, 887-99	3.6	94
48	Comparison of Transcript Profiles in Wild-Type and o2 Maize Endosperm in Different Genetic Backgrounds. *Crop Science*, **2007**, 47, S-45	2.4	12
47	Global gene expression analysis of the shoot apical meristem of maize (Zea mays L.). *Plant Journal*, **2007**, 52, 391-404	6.9	108

46	Exploring the information in p-values for the analysis and planning of multiple-test experiments. *Biometrics*, **2007**, 63, 483-95	1.8	30
45	Spotted cotton oligonucleotide microarrays for gene expression analysis. *BMC Genomics*, **2007**, 8, 81	4.5	37
44	Laser microdissection of narrow sheath mutant maize uncovers novel gene expression in the shoot apical meristem. *PLoS Genetics*, **2007**, 3, e101	6	58
43	Pooling mRNA in microarray experiments and its effect on power. *Bioinformatics*, **2007**, 23, 1217-24	7.2	41
42	Transcriptomic and proteomic analyses of pericycle cells of the maize primary root. *Plant Physiology*, **2007**, 145, 575-88	6.6	120
41	Array-based genomic comparative hybridization analysis of field strains of Mycoplasma hyopneumoniae. *Journal of Bacteriology*, **2007**, 189, 7977-82	3.5	12
40	Parallel genome-wide expression profiling of host and pathogen during soybean cyst nematode infection of soybean. *Molecular Plant-Microbe Interactions*, **2007**, 20, 293-305	3.6	176
39	Developmental transcript profiling of cyst nematode feeding cells in soybean roots. *Molecular Plant-Microbe Interactions*, **2007**, 20, 510-25	3.6	201
38	Global transcriptional response of porcine mesenteric lymph nodes to Salmonella enterica serovar Typhimurium. *Genomics*, **2007**, 90, 72-84	4.3	31
37	Divergent evolution of arrested development in the dauer stage of Caenorhabditis elegans and the infective stage of Heterodera glycines. *Genome Biology*, **2007**, 8, R211	18.3	36
36	Scanning microarrays at multiple intensities enhances discovery of differentially expressed genes. *Bioinformatics*, **2006**, 22, 1863-70	7.2	22
35	A discussion of statistical methods for design and analysis of microarray experiments for plant scientists. *Plant Cell*, **2006**, 18, 2112-21	11.6	52
34	Genetic regulation of gene expression during shoot development in Arabidopsis. *Genetics*, **2006**, 172, 1155-64	4	107
33	Transcriptional profiling of Mycoplasma hyopneumoniae during iron depletion using microarrays. *Microbiology (United Kingdom)*, **2006**, 152, 937-944	2.9	38
32	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, 6805-10	11.5	314
31	Transcriptional profiling of myostatin-knockout mice implicates Wnt signaling in postnatal skeletal muscle growth and hypertrophy. *FASEB Journal*, **2006**, 20, 580-2	0.9	103
30	Transcriptional profiling of Mycoplasma hyopneumoniae during heat shock using microarrays. *Infection and Immunity*, **2006**, 74, 160-6	3.7	52
29	Gene expression programs during shoot, root, and callus development in Arabidopsis tissue culture. *Plant Physiology*, **2006**, 141, 620-37	6.6	194

28	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, 939-47	3.6	71
27	Identifying genes associated with a quantitative trait or quantitative trait locus via selective transcriptional profiling. *Biometrics*, **2006**, 62, 504-14	1.8	10
26	Selective transcriptional profiling for trait-based eQTL mapping. *Animal Genetics*, **2006**, 37 Suppl 1, 13-7	2.5	8
25	Identifying differentially expressed genes in unreplicated multiple-treatment microarray timecourse experiments. *Computational Statistics and Data Analysis*, **2006**, 50, 518-532	1.6	3
24	A novel approach for characterizing expression levels of genes duplicated by polyploidy. *Genetics*, **2006**, 173, 1823-7	4	70
23	Estimating the number of true null hypotheses from a histogram of p values. *Journal of Agricultural, Biological, and Environmental Statistics*, **2006**, 11, 337-356	1.9	81
22	Gene expression profiling in Salmonella Choleraesuis-infected porcine lung using a long oligonucleotide microarray. *Mammalian Genome*, **2006**, 17, 777-89	3.2	37
21	Validation of a first-generation long-oligonucleotide microarray for transcriptional profiling in the pig. *Genomics*, **2005**, 86, 618-25	4.3	57
20	BarleyBase--an expression profiling database for plant genomics. *Nucleic Acids Research*, **2005**, 33, D614-8	10.1	74
19	Transcriptional profiling using a novel cDNA array identifies differential gene expression during porcine embryo elongation. *Molecular Reproduction and Development*, **2005**, 71, 129-39	2.6	16
18	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, 225-35	11.6	27
17	Isolation, characterization, and pericycle-specific transcriptome analyses of the novel maize lateral and seminal root initiation mutant rum1. *Plant Physiology*, **2005**, 139, 1255-67	6.6	148
16	Interaction-dependent gene expression in Mla-specified response to barley powdery mildew. *Plant Cell*, **2004**, 16, 2514-28	11.6	174
15	Quantitative trait loci associated with adventitious shoot formation in tissue culture and the program of shoot development in Arabidopsis. *Genetics*, **2004**, 167, 1883-92	4	29
14	Genomics, prior probability, and statistical tests of multiple hypotheses. *Genome Research*, **2004**, 14, 997-1001	9.7	61
13	Principal Components Regression With Data Chosen Components and Related Methods. *Technometrics*, **2003**, 45, 70-79	1.4	21
12	Arabidopsis gene expression changes during cyst nematode parasitism revealed by statistical analyses of microarray expression profiles. *Plant Journal*, **2003**, 33, 911-21	6.9	163
11	Testing for ordered means in a variation of the normal mixture model. *Journal of Statistical Planning and Inference*, **2002**, 107, 143-153	0.8	

List of Publications

10	Expression pattern of yeast sporulation: a case study for regulatory changes after yeast genome duplication. *Information Sciences*, **2002**, 145, 261-269	7.7	
9	Differential gene expression in the rat soleus muscle during early work overload-induced hypertrophy. *FASEB Journal*, **2002**, 16, 207-9	0.9	80
8	Investigating the probability of sign inconsistency in the regression coefficients of markers flanking quantitative trait loci. *Genetics*, **2002**, 160, 1697-705	4	3
7	Testing the equality of distributions of random vectors with categorical components. *Computational Statistics and Data Analysis*, **2001**, 37, 195-208	1.6	17
6	Accounting for variability in the use of permutation testing to detect quantitative trait loci. *Biometrics*, **2000**, 56, 52-8	1.8	62
5	Multiple Marginal Independence Testing for Pick Any/C Variables. *Communications in Statistics Part B: Simulation and Computation*, **2000**, 29, 1285-1316	0.6	33
4	Order-restricted hypothesis testing in a variation of the normal mixture model. *Canadian Journal of Statistics*, **1999**, 27, 383-394	0.4	3
3	Convergence properties of the EM algorithm in constrained parameter spaces. *Canadian Journal of Statistics*, **1999**, 27, 639-648	0.4	33
2	Interval Mapping of Quantitative Trait Loci through Order-Restricted Inference. *Biometrics*, **1998**, 54, 74	1.8	3
1	Automatic Traits Extraction and Fitting for Field High-throughput Phenotyping Systems		2