

Daniel S Nettleton

List of Publications by Year in descending order

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Version: 2024-02-01

173
papers

13,402
citations

36691

53
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28425

109
g-index

178
all docs

178
docs citations

178
times ranked

17681
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Single-parent expression complementation contributes to phenotypic heterosis in maize hybrids. <i>Plant Physiology</i> , 2022, , . | 2.3 | 6 |
| 2 | A residual-based approach for robust random forest regression. <i>Statistics and Its Interface</i> , 2021, 14, 389-402. | 0.2 | 2 |
| 3 | KAT4IA: K-Means Assisted Training for Image Analysis of Field-Grown Plant Phenotypes. <i>Plant Phenomics</i> , 2021, 2021, 9805489. | 2.5 | 5 |
| 4 | Variable importance assessments and backward variable selection for multi-sample problems. <i>Journal of Multivariate Analysis</i> , 2021, 186, 104807. | 0.5 | 0 |
| 5 | Random Forest Prediction Intervals. <i>American Statistician</i> , 2020, 74, 392-406. | 0.9 | 46 |
| 6 | Tree aggregation for random forest class probability estimation. <i>Statistical Analysis and Data Mining</i> , 2020, 13, 134-150. | 1.4 | 19 |
| 7 | rmRNAseq: differential expression analysis for repeated-measures RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 4432-4439. | 1.8 | 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. | 1.3 | 8 |
| 9 | Adjusting for Spatial Effects in Genomic Prediction. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2020, 25, 699-718. | 0.7 | 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. | 4.1 | 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. | 1.8 | 7 |
| 12 | Small RNA discovery in the interaction between barley and the powdery mildew pathogen. <i>BMC Genomics</i> , 2019, 20, 610. | 1.2 | 37 |
| 13 | Assessing plant performance in the Envirotron. <i>Plant Methods</i> , 2019, 15, 117. | 1.9 | 13 |
| 14 | Stress response to CO2 deprivation by <i>Arabidopsis thaliana</i> in plant cultures. <i>PLoS ONE</i> , 2019, 14, e0212462. | 1.1 | 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. | 0.5 | 2 |
| 16 | Additive partially linear models for ultra-high-dimensional regression. <i>Stat</i> , 2019, 8, e223. | 0.3 | 4 |
| 17 | Detecting rare and faint signals via thresholding maximum likelihood estimators. <i>Annals of Statistics</i> , 2018, 46, . | 1.4 | 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. | 1.8 | 50 |

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|----|---|-----|-----------|
| 19 | A hidden Markov tree model for testing multiple hypotheses corresponding to Gene Ontology gene sets. <i>BMC Bioinformatics</i> , 2018, 19, 107. | 1.2 | 2 |
| 20 | Nested Hierarchical Functional Data Modeling and Inference for the Analysis of Functional Plant Phenotypes. <i>Journal of the American Statistical Association</i> , 2018, 113, 593-606. | 1.8 | 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. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3567-3575. | 0.8 | 19 |
| 22 | Crowdsourcing image analysis for plant phenomics to generate ground truth data for machine learning. <i>PLoS Computational Biology</i> , 2018, 14, e1006337. | 1.5 | 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.). <i>Journal of Experimental Botany</i> , 2017, 68, erw422. | 2.4 | 11 |
| 25 | Discovery and Characterization of the 3-Hydroxyacyl-ACP Dehydratase Component of the Plant Mitochondrial Fatty Acid Synthase System. <i>Plant Physiology</i> , 2017, 173, 2010-2028. | 2.3 | 21 |
| 26 | Stability of Single-Parent Gene Expression Complementation in Maize Hybrids upon Water Deficit Stress. <i>Plant Physiology</i> , 2017, 173, 1247-1257. | 2.3 | 36 |
| 27 | Interchromosomal Transfer of Immune Regulation During Infection of Barley with the Powdery Mildew Pathogen. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3317-3329. | 0.8 | 6 |
| 28 | Microbial community sequencing analysis of the calf eye microbiota and relationship to infectious bovine keratoconjunctivitis. <i>Veterinary Microbiology</i> , 2017, 207, 267-279. | 0.8 | 17 |
| 29 | Substantial contribution of genetic variation in the expression of transcription factors to phenotypic variation revealed by eRD-GWAS. <i>Genome Biology</i> , 2017, 18, 192. | 3.8 | 56 |
| 30 | Complexity and specificity of the maize (<i>Zea mays</i> L.) root hair transcriptome. <i>Journal of Experimental Botany</i> , 2017, 68, 2175-2185. | 2.4 | 19 |
| 31 | Distinct genetic architectures for phenotype means and plasticities in <i>Zea mays</i> . <i>Nature Plants</i> , 2017, 3, 715-723. | 4.7 | 98 |
| 32 | A Clade-Specific Arabidopsis Gene Connects Primary Metabolism and Senescence. <i>Frontiers in Plant Science</i> , 2016, 7, 983. | 1.7 | 24 |
| 33 | Post-weaning blood transcriptomic differences between Yorkshire pigs divergently selected for residual feed intake. <i>BMC Genomics</i> , 2016, 17, 73. | 1.2 | 53 |
| 34 | Accounting for host cell protein behavior in anion-exchange chromatography. <i>Biotechnology Progress</i> , 2016, 32, 1453-1463. | 1.3 | 2 |
| 35 | Genes and Small RNA Transcripts Exhibit Dosage-Dependent Expression Pattern in Maize Copy-Number Alterations. <i>Genetics</i> , 2016, 203, 1133-1147. | 1.2 | 12 |
| 36 | Root Type-Specific Reprogramming of Maize Pericycle Transcriptomes by Local High Nitrate Results in Disparate Lateral Root Branching Patterns. <i>Plant Physiology</i> , 2016, 170, 1783-1798. | 2.3 | 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. | 2.4 | 76 |
| 38 | Case-Specific Random Forests. <i>Journal of Computational and Graphical Statistics</i> , 2016, 25, 49-65. | 0.9 | 25 |
| 39 | Extensive tissue-specific transcriptomic plasticity in maize primary roots upon water deficit. <i>Journal of Experimental Botany</i> , 2016, 67, 1095-1107. | 2.4 | 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. | 0.7 | 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. | 2.8 | 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. | 0.7 | 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. | 0.7 | 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. | 0.7 | 0 |
| 45 | A systems biology approach toward understanding seed composition in soybean. <i>BMC Genomics</i> , 2015, 16, S9. | 1.2 | 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. | 1.7 | 14 |
| 47 | SimSeq: a nonparametric approach to simulation of RNA-sequence datasets. <i>Bioinformatics</i> , 2015, 31, 2131-2140. | 1.8 | 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. | 1.4 | 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. | 1.5 | 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. | 1.1 | 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. | 2.8 | 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. | 1.0 | 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. | 3.3 | 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. | 2.1 | 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. | 1.8 | 55 |
| 56 | Nonsyntenic Genes Drive Highly Dynamic Complementation of Gene Expression in Maize Hybrids. <i>Plant Cell</i> , 2014, 26, 3939-3948. | 3.1 | 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, . | 0.5 | 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. | 1.7 | 1 |
| 59 | Significant Variation for Bio-oil Compounds After Pyrolysis/Gas Chromatography-Mass Spectrometry of Cobs and Stover Among Five Near-Isogenic Brown Midrib Hybrids in Maize. <i>Bioenergy Research</i> , 2014, 7, 693-701. | 2.2 | 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. | 2.8 | 94 |
| 61 | An improved method for computing q-values when the distribution of effect sizes is asymmetric. <i>Bioinformatics</i> , 2014, 30, 3044-3053. | 1.8 | 3 |
| 62 | Estimation and Testing of Gene Expression Heterosis. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2014, 19, 319-337. | 0.7 | 5 |
| 63 | Copy number variation detection using next generation sequencing read counts. <i>BMC Bioinformatics</i> , 2014, 15, 109. | 1.2 | 75 |
| 64 | Endometrial gene expression profiling in pregnant Meishan and Yorkshire pigs on day 12 of gestation. <i>BMC Genomics</i> , 2014, 15, 156. | 1.2 | 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. | 0.2 | 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. | 1.1 | 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. | 3.3 | 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. | 1.4 | 190 |
| 70 | Reverse engineering and analysis of large genome-scale gene networks. <i>Nucleic Acids Research</i> , 2013, 41, e24-e24. | 6.5 | 34 |
| 71 | Estimation of False Discovery Rate Using Sequential Permutation p -Values. <i>Biometrics</i> , 2013, 69, 1-7. | 0.8 | 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. <i>American Journal of Veterinary Research</i> , 2012, 73, 1219-1229. | 0.3 | 22 |
| 74 | The Arabidopsis MicroRNA396-GRF1/GRF3 Regulatory Module Acts as a Developmental Regulator in the Reprogramming of Root Cells during Cyst Nematode Infection. <i>Plant Physiology</i> , 2012, 159, 321-335. | 2.3 | 214 |
| 75 | Complementation contributes to transcriptome complexity in maize (<i>Zea mays</i> L.) hybrids relative to their inbred parents. <i>Genome Research</i> , 2012, 22, 2445-2454. | 2.4 | 154 |
| 76 | Borrowing Information Across Genes and Experiments for Improved Error Variance Estimation in Microarray Data Analysis. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, Article 12. | 0.2 | 5 |
| 77 | Ontogeny of the Maize Shoot Apical Meristem. <i>Plant Cell</i> , 2012, 24, 3219-3234. | 3.1 | 72 |
| 78 | 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> , 2012, 6, . | 0.5 | 2 |
| 79 | A Hierarchical Semiparametric Model for Incorporating Intergene Information for Analysis of Genomic Data. <i>Biometrics</i> , 2012, 68, 1168-1177. | 0.8 | 2 |
| 80 | Changes in genome content generated via segregation of non-allelic homologs. <i>Plant Journal</i> , 2012, 72, 390-399. | 2.8 | 24 |
| 81 | Detecting Differential Expression in RNA-sequence Data Using Quasi-likelihood with Shrunken Dispersion Estimates. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, . | 0.2 | 282 |
| 82 | Estimating the Number of Genes That Are Differentially Expressed in Both of Two Independent Experiments. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2012, 17, 583-600. | 0.7 | 1 |
| 83 | Proteomics-based, multivariate random forest method for prediction of protein separation behavior during cation-exchange chromatography. <i>Journal of Chromatography A</i> , 2012, 1249, 103-114. | 1.8 | 11 |
| 84 | Adaptive and Dynamic Adaptive Procedures for False Discovery Rate Control and Estimation. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2012, 74, 163-182. | 1.1 | 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. <i>Biometrics</i> , 2012, 68, 1178-1187. | 0.8 | 4 |
| 86 | Gene Mapping via Bulk Segregant RNA-Seq (BSR-Seq). <i>PLoS ONE</i> , 2012, 7, e36406. | 1.1 | 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. <i>PLoS ONE</i> , 2011, 6, e28768. | 1.1 | 47 |
| 89 | Quantitative and Temporal Definition of the Mla Transcriptional Regulon During Barley-Powdery Mildew Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 694-705. | 1.4 | 24 |
| 90 | Helicobacter bilis Colonization Enhances Susceptibility to Typhlocolitis Following an Inflammatory Trigger. <i>Digestive Diseases and Sciences</i> , 2011, 56, 2838-2848. | 1.1 | 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. | 0.4 | 4 |
| 92 | Soybean Homologs of MPK4 Negatively Regulate Defense Responses and Positively Regulate Growth and Development. <i>Plant Physiology</i> , 2011, 157, 1363-1378. | 2.3 | 130 |
| 93 | Biphasic Gene Expression Changes Elicited by <i>Phakopsora pachyrhizi</i> in Soybean Correlate with Fungal Penetration and Haustoria Formation. <i>Plant Physiology</i> , 2011, 157, 355-371. | 2.3 | 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. <i>Plant Physiology</i> , 2011, 155, 1960-1975. | 2.3 | 102 |
| 95 | Unique genome-wide transcriptome profiles of chicken macrophages exposed to Salmonella-derived endotoxin. <i>BMC Genomics</i> , 2010, 11, 545. | 1.2 | 64 |
| 96 | Linear Mixed Model Selection for False Discovery Rate Control in Microarray Data Analysis. <i>Biometrics</i> , 2010, 66, 621-629. | 0.8 | 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. | 0.9 | 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. | 1.8 | 21 |
| 99 | High-Resolution Genotyping via Whole Genome Hybridizations to Microarrays Containing Long Oligonucleotide Probes. <i>PLoS ONE</i> , 2010, 5, e14178. | 1.1 | 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. | 0.2 | 4 |
| 101 | Differentially expressed microRNAs in dystrophin-deficient muscle. <i>FASEB Journal</i> , 2010, 24, 989.1. | 0.2 | 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. | 1.0 | 44 |
| 103 | Microdissection of Shoot Meristem Functional Domains. <i>PLoS Genetics</i> , 2009, 5, e1000476. | 1.5 | 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. | 1.5 | 484 |
| 105 | Loss of RNA-Dependent RNA Polymerase 2 (RDR2) Function Causes Widespread and Unexpected Changes in the Expression of Transposons, Genes, and 24-nt Small RNAs. <i>PLoS Genetics</i> , 2009, 5, e1000737. | 1.5 | 106 |
| 106 | Transcript-Based Cloning of <i>RRP46</i> , a Regulator of rRNA Processing and <i>RcGene</i> -Independent Cell Death in Barley-Powdery Mildew Interactions. <i>Plant Cell</i> , 2009, 21, 3280-3295. | 3.1 | 26 |
| 107 | Paternal Dominance of Trans-eQTL Influences Gene Expression Patterns in Maize Hybrids. <i>Science</i> , 2009, 326, 1118-1120. | 6.0 | 137 |
| 108 | Sequence mining and transcript profiling to explore cyst nematode parasitism. <i>BMC Genomics</i> , 2009, 10, 58. | 1.2 | 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. | 1.6 | 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. | 2.8 | 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. | 1.0 | 15 |
| 112 | The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115. | 6.0 | 3,612 |
| 113 | Testing for the Supremacy of a Multinomial Cell Probability. <i>Journal of the American Statistical Association</i> , 2009, 104, 1052-1059. | 1.8 | 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. | 1.5 | 196 |
| 115 | Leptin mediates discriminate response to feed restriction in feed efficient pigs. <i>FASEB Journal</i> , 2009, 23, 1022.3. | 0.2 | 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. | 1.8 | 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. | 1.7 | 235 |
| 118 | Microarray analysis of vegetative phase change in maize. <i>Plant Journal</i> , 2008, 56, 1045-1057. | 2.8 | 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. | 1.2 | 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. | 1.7 | 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. | 1.0 | 60 |
| 122 | Identification of differentially expressed gene categories in microarray studies using nonparametric multivariate analysis. <i>Bioinformatics</i> , 2008, 24, 192-201. | 1.8 | 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. | 1.5 | 73 |
| 124 | Pooling mRNA in microarray experiments and its effect on power. <i>Bioinformatics</i> , 2007, 23, 1217-1224. | 1.8 | 44 |
| 125 | Transcriptomic and Proteomic Analyses of Pericycle Cells of the Maize Primary Root. <i>Plant Physiology</i> , 2007, 145, 575-588. | 2.3 | 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. | 1.0 | 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. | 1.4 | 197 |
| 128 | Developmental Transcript Profiling of Cyst Nematode Feeding Cells in Soybean Roots. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 510-525. | 1.4 | 240 |
| 129 | Global transcriptional response of porcine mesenteric lymph nodes to <i>Salmonella enterica</i> serovar Typhimurium. <i>Genomics</i> , 2007, 90, 72-84. | 1.3 | 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. | 13.9 | 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. | 1.4 | 129 |
| 132 | Distinct Biphasic mRNA Changes in Response to Asian Soybean Rust Infection. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 887-899. | 1.4 | 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. | 0.8 | 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. | 2.8 | 123 |
| 135 | Exploring the Information in p-Values for the Analysis and Planning of Multiple-Test Experiments. <i>Biometrics</i> , 2007, 63, 483-495. | 0.8 | 36 |
| 136 | Spotted cotton oligonucleotide microarrays for gene expression analysis. <i>BMC Genomics</i> , 2007, 8, 81. | 1.2 | 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. | 2.3 | 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. | 1.4 | 88 |
| 139 | Identifying Genes Associated with a Quantitative Trait or Quantitative Trait Locus via Selective Transcriptional Profiling. <i>Biometrics</i> , 2006, 62, 504-514. | 0.8 | 14 |
| 140 | Selective transcriptional profiling for trait-based eQTL mapping. <i>Animal Genetics</i> , 2006, 37, 13-17. | 0.6 | 10 |
| 141 | Identifying differentially expressed genes in unreplicated multiple-treatment microarray timecourse experiments. <i>Computational Statistics and Data Analysis</i> , 2006, 50, 518-532. | 0.7 | 4 |
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