

Lauren M McIntyre

List of Publications by Year in descending order

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114
papers

8,165
citations

66315

42
h-index

49868

87
g-index

126
all docs

126
docs citations

126
times ranked

12233
citing authors

#	ARTICLE	IF	CITATIONS
1	The metabolome as a biomarker of aging in <i>Drosophila melanogaster</i> . <i>Aging Cell</i> , 2022, 21, e13548.	3.0	22
2	GAIT-GM integrative cross-omics analyses reveal cholinergic defects in a <i>C. elegans</i> model of Parkinson's disease. <i>Scientific Reports</i> , 2022, 12, 3268.	1.6	2
3	Variation in leaf transcriptome responses to elevated ozone corresponds with physiological sensitivity to ozone across maize inbred lines. <i>Genetics</i> , 2022, 221, .	1.2	1
4	Risk Factors for Recurrent <i>Staphylococcus aureus</i> Bacteremia. <i>Clinical Infectious Diseases</i> , 2021, 72, 1891-1899.	2.9	23
5	Testcrosses are an efficient strategy for identifying cis-regulatory variation: Bayesian analysis of allele-specific expression (BayesASE). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
6	Long-Term Metabolomics Reference Material. <i>Analytical Chemistry</i> , 2021, 93, 9193-9199.	3.2	11
7	Power calculator for detecting allelic imbalance using hierarchical Bayesian model. <i>BMC Research Notes</i> , 2021, 14, 436.	0.6	1
8	tappAS: a comprehensive computational framework for the analysis of the functional impact of differential splicing. <i>Genome Biology</i> , 2020, 21, 119.	3.8	40
9	Fibrinogen binding is affected by amino acid substitutions in C-terminal repeat region of fibronectin binding protein A. <i>Scientific Reports</i> , 2019, 9, 11619.	1.6	10
10	Uncovering hidden genetic variation in photosynthesis of field-grown maize under ozone pollution. <i>Global Change Biology</i> , 2019, 25, 4327-4338.	4.2	39
11	Kinetic Analysis of Hepatic Metabolism Using Hyperpolarized Dihydroxyacetone. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 605-614.	2.5	6
12	SECIMTools: a suite of metabolomics data analysis tools. <i>BMC Bioinformatics</i> , 2018, 19, 151.	1.2	34
13	Intergenerational environmental effects: functional signals in offspring transcriptomes and metabolomes after parental jasmonic acid treatment in apomictic dandelion. <i>New Phytologist</i> , 2018, 217, 871-882.	3.5	36
14	Direct Testing for Allele-Specific Expression Differences Between Conditions. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 447-460.	0.8	13
15	A Robust Methodology for Assessing Differential Homeolog Contributions to the Transcriptomes of Allopolyploids. <i>Genetics</i> , 2018, 210, 883-894.	1.2	21
16	Variable selection in omics data: A practical evaluation of small sample sizes. <i>PLoS ONE</i> , 2018, 13, e0197910.	1.1	44
17	Analysis of Gene Expression Variance in Schizophrenia Using Structural Equation Modeling. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 192.	1.4	20
18	Event Analysis: Using Transcript Events To Improve Estimates of Abundance in RNA-seq Data. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2923-2940.	0.8	11

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19	SHH Protein Variance in the Limb Bud Is Constrained by Feedback Regulation and Correlates with Altered Digit Patterning. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 851-858.	0.8	7
20	A comprehensive analysis of myocardial substrate preference emphasizes the need for a synchronized fluxomic/metabolomic research design. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2017, 312, H1215-H1223.	1.5	9
21	Back to the Future: Multiparent Populations Provide the Key to Unlocking the Genetic Basis of Complex Traits. <i>Genetics</i> , 2017, 206, 527-529.	1.2	24
22	UBASH3A Mediates Risk for Type 1 Diabetes Through Inhibition of T-Cell Receptor-Induced NF- κ B Signaling. <i>Diabetes</i> , 2017, 66, 2033-2043.	0.3	54
23	Disease-specific biases in alternative splicing and tissue-specific dysregulation revealed by multitissue profiling of lymphocyte gene expression in type 1 diabetes. <i>Genome Research</i> , 2017, 27, 1807-1815.	2.4	29
24	Elevated ozone reduces photosynthetic carbon gain by accelerating leaf senescence of inbred and hybrid maize in a genotype-specific manner. <i>Plant, Cell and Environment</i> , 2017, 40, 3088-3100.	2.8	40
25	High-Throughput Phenotyping of Maize Leaf Physiological and Biochemical Traits Using Hyperspectral Reflectance. <i>Plant Physiology</i> , 2017, 173, 614-626.	2.3	215
26	Reliable Detection of Herpes Simplex Virus Sequence Variation by High-Throughput Resequencing. <i>Viruses</i> , 2017, 9, 226.	1.5	9
27	Back to the Future: Multiparent Populations Provide the Key to Unlocking the Genetic Basis of Complex Traits. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1617-1618.	0.8	13
28	Buffering of Genetic Regulatory Networks in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2016, 203, 1177-1190.	1.2	43
29	Using Genotyping by Sequencing to Map Two Novel Anthracnose Resistance Loci in <i>Sorghum bicolor</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1935-1946.	0.8	29
30	Neurons That Underlie <i>Drosophila melanogaster</i> Reproductive Behaviors: Detection of a Large Male-Bias in Gene Expression in fruitless-Expressing Neurons. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2455-2465.	0.8	20
31	Presence of arachidonoyl-carnitine is associated with adverse cardiometabolic responses in hypertensive patients treated with atenolol. <i>Metabolomics</i> , 2016, 12, 1.	1.4	14
32	RNA-seq analysis of impact of PNN on gene expression and alternative splicing in corneal epithelial cells. <i>Molecular Vision</i> , 2016, 22, 40-60.	1.1	9
33	The wright stuff: reimagining path analysis reveals novel components of the sex determination hierarchy in <i>drosophila melanogaster</i> . <i>BMC Systems Biology</i> , 2015, 9, 53.	3.0	14
34	GENETICS and G3: Community-Driven Science, Community-Driven Journals. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1567-1568.	0.8	0
35	LANA Binds to Multiple Active Viral and Cellular Promoters and Associates with the H3K4Methyltransferase hSET1 Complex. <i>PLoS Pathogens</i> , 2014, 10, e1004240.	2.1	68
36	GENETICS and G3: Community-Driven Science, Community-Driven Journals. <i>Genetics</i> , 2014, 198, 1-2.	1.2	6

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37	A flexible Bayesian method for detecting allelic imbalance in RNA-seq data. BMC Genomics, 2014, 15, 920.	1.2	41
38	What the X Has to Do with It: Differences in Regulatory Variability between the Sexes in <i>Drosophila simulans</i> . Genome Biology and Evolution, 2014, 6, 818-829.	1.1	17
39	LEVERAGING BIOLOGICAL REPLICATES TO IMPROVE ANALYSIS IN CHIP-SEQ EXPERIMENTS. Computational and Structural Biotechnology Journal, 2014, 9, e201401002.	1.9	57
40	A systems biology approach identified different regulatory networks targeted by KSHV miR-K12-11 in B cells and endothelial cells. BMC Genomics, 2014, 15, 668.	1.2	12
41	Male-specific Fruitless isoforms have different regulatory roles conferred by distinct zinc finger DNA binding domains. BMC Genomics, 2013, 14, 659.	1.2	57
42	Consistent Errors in First Strand cDNA Due to Random Hexamer Mispriming. PLoS ONE, 2013, 8, e85583.	1.1	38
43	Purification of Transcripts and Metabolites from <i>Drosophila</i> Heads. Journal of Visualized Experiments, 2013, , e50245.	0.2	10
44	Plants Know Where It Hurts: Root and Shoot Jasmonic Acid Induction Elicit Differential Responses in <i>Brassica oleracea</i> . PLoS ONE, 2013, 8, e65502.	1.1	63
45	Ago HITS-CLIP Expands Understanding of Kaposi's Sarcoma-associated Herpesvirus miRNA Function in Primary Effusion Lymphomas. PLoS Pathogens, 2012, 8, e1002884.	2.1	167
46	Facilitating Discovery: The Role of Society Journals in Collaborative Science. G3: Genes, Genomes, Genetics, 2012, 2, 151-152.	0.8	1
47	Facilitating Discovery: The Role of Society Journals in Collaborative Science. Genetics, 2012, 190, 285-286.	1.2	2
48	Setting the Standard: A Special Focus on Genomic Selection in GENETICS and G3. Genetics, 2012, 190, 1151-1152.	1.2	7
49	Transcriptional Network Structure Has Little Effect on the Rate of Regulatory Evolution in Yeast. Molecular Biology and Evolution, 2012, 29, 1899-1905.	3.5	9
50	Genotype-phenotype mapping in a post-GWAS world. Trends in Genetics, 2012, 28, 421-426.	2.9	61
51	Genetic variation in the Yolk protein expression network of <i>Drosophila melanogaster</i> : sex-biased negative correlations with longevity. Heredity, 2012, 109, 226-234.	1.2	28
52	Allelic Imbalance in <i>Drosophila</i> Hybrid Heads: Exons, Isoforms, and Evolution. Molecular Biology and Evolution, 2012, 29, 1521-1532.	3.5	92
53	The Chemical Interactions Underlying Tomato Flavor Preferences. Current Biology, 2012, 22, 1035-1039.	1.8	289
54	EXPRESSION OF DEFENSE GENES IN <i>DROSOPHILA</i> EVOLVES UNDER A DIFFERENT SELECTIVE REGIME FROM EXPRESSION OF OTHER GENES. Evolution; International Journal of Organic Evolution, 2011, 65, 1068-1078.	1.1	6

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55	Transcriptome Profiling of Embryonic Development Rate in Rainbow Trout Advanced Backcross Introgression Lines. <i>Marine Biotechnology</i> , 2011, 13, 215-231.	1.1	28
56	Generalized shrinkage F-like statistics for testing an interaction term in gene expression analysis in the presence of heteroscedasticity. <i>BMC Bioinformatics</i> , 2011, 12, 427.	1.2	1
57	RNA-seq: technical variability and sampling. <i>BMC Genomics</i> , 2011, 12, 293.	1.2	250
58	Partitioning Transcript Variation in <i>Drosophila</i> : Abundance, Isoforms, and Alleles. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 427-436.	0.8	7
59	Polymorphisms in fibronectin binding protein A of <i>Staphylococcus aureus</i> are associated with infection of cardiovascular devices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18372-18377.	3.3	69
60	Potential Associations between Severity of Infection and the Presence of Virulence-Associated Genes in Clinical Strains of <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2011, 6, e18673.	1.1	38
61	SOLiD sequencing of four <i>Vibrio vulnificus</i> genomes enables comparative genomic analysis and identification of candidate clade-specific virulence genes. <i>BMC Genomics</i> , 2010, 11, 512.	1.2	48
62	Maize grain yield responses to plant height variability resulting from crop rotation and tillage system in a long-term experiment. <i>Soil and Tillage Research</i> , 2010, 106, 227-240.	2.6	81
63	Direct mapping of density response in a population of B73 \times Mo17 recombinant inbred lines of maize (<i>Zea Mays</i> L.). <i>Heredity</i> , 2010, 104, 583-599.	1.2	32
64	Epistasis: Obstacle or Advantage for Mapping Complex Traits?. <i>PLoS ONE</i> , 2010, 5, e12264.	1.1	13
65	Data: The Foundation of Science. <i>Genetics</i> , 2010, 184, 1-1.	1.2	3
66	Phenotypic plasticity in cell walls of maize brown midrib mutants is limited by lignin composition. <i>Journal of Experimental Botany</i> , 2010, 61, 2479-2490.	2.4	60
67	Comparison between NuGEN's WT-Ovation Pico and one-direct amplification systems. <i>Journal of Biomolecular Techniques</i> , 2010, 21, 141-7.	0.8	11
68	Regulatory Divergence in <i>Drosophila melanogaster</i> and <i>D. simulans</i> , a Genomewide Analysis of Allele-Specific Expression. <i>Genetics</i> , 2009, 183, 547-561.	1.2	87
69	Sex-Specific Splicing in <i>Drosophila</i> : Widespread Occurrence, Tissue Specificity and Evolutionary Conservation. <i>Genetics</i> , 2009, 181, 421-434.	1.2	79
70	Defining gene and QTL networks. <i>Current Opinion in Plant Biology</i> , 2009, 12, 241-246.	3.5	46
71	Natural genetic variation in transcriptome reflects network structure inferred with major effect mutations: insulin/TOR and associated phenotypes in <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2009, 10, 124.	1.2	19
72	Allele-specific expression assays using Solexa. <i>BMC Genomics</i> , 2009, 10, 422.	1.2	37

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73	Successful range-expanding plants experience less above-ground and below-ground enemy impact. <i>Nature</i> , 2008, 456, 946-948.	13.7	238
74	Powdery Mildew Induces Defense-Oriented Reprogramming of the Transcriptome in a Susceptible But Not in a Resistant Grapevine. <i>Plant Physiology</i> , 2008, 146, 236-249.	2.3	247
75	Evolution of Gene Expression in the <i>Drosophila</i> Olfactory System. <i>Molecular Biology and Evolution</i> , 2008, 25, 1081-1092.	3.5	67
76	Cis and Trans Regulatory Effects Contribute to Natural Variation in Transcriptome of <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2007, 25, 101-110.	3.5	43
77	Simpler mode of inheritance of transcriptional variation in male <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18577-18582.	3.3	45
78	Potential Associations between Hematogenous Complications and Bacterial Genotype in <i>Staphylococcus aureus</i> Infection. <i>Journal of Infectious Diseases</i> , 2007, 196, 738-747.	1.9	148
79	Differential Expression of Genes Important for Adaptation in <i>Capsella bursa-pastoris</i> (Brassicaceae). <i>Plant Physiology</i> , 2007, 145, 160-173.	2.3	45
80	Mapping reciprocal effects and interactions with plant density stress in <i>Zea mays</i> L. <i>Heredity</i> , 2007, 99, 14-30.	1.2	20
81	Sex-specific expression of alternative transcripts in <i>Drosophila</i> . <i>Genome Biology</i> , 2006, 7, R79.	13.9	93
82	Mapping Density Response in Maize: A Direct Approach for Testing Genotype and Treatment Interactions. <i>Genetics</i> , 2006, 173, 331-348.	1.2	22
83	Using mating designs to uncover QTL and the genetic architecture of complex traits. <i>Heredity</i> , 2006, 96, 139-149.	1.2	83
84	Changes in skeletal muscle gene expression following clenbuterol administration. <i>BMC Genomics</i> , 2006, 7, 320.	1.2	56
85	Nematode-Induced Changes of Transporter Gene Expression in <i>Arabidopsis</i> Roots. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 1247-1257.	1.4	121
86	Implementing false discovery rate control: increasing your power. <i>Oikos</i> , 2005, 108, 643-647.	1.2	807
87	Genetic Architecture of Two Fitness-related Traits in <i>Drosophila melanogaster</i> : Ovariole Number and Thorax Length. <i>Genetica</i> , 2005, 125, 211-222.	0.5	17
88	Model Selection in Binary Trait Locus Mapping. <i>Genetics</i> , 2005, 170, 1281-1297.	1.2	19
89	Sex- and segment-specific modulation of gene expression profiles in <i>Drosophila</i> . <i>Developmental Biology</i> , 2005, 288, 528-544.	0.9	30
90	Identification of co-regulated transcripts affecting male body size in <i>Drosophila</i> . <i>Genome Biology</i> , 2005, 6, R53.	13.9	21

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91	Using Alpha Wisely: Improving Power to Detect Multiple QTL. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2004, 3, 1-24.	0.2	9
92	Differential Gene Expression in Response to Hydrogen Peroxide and the Putative PerR Regulon of <i>Synechocystis</i> sp. Strain PCC 6803. <i>Journal of Bacteriology</i> , 2004, 186, 3331-3345.	1.0	178
93	Persistent Bacteremia Due to Methicillin-Resistant <i>Staphylococcus aureus</i> Infection Is Associated with agr Dysfunction and Low-Level In Vitro Resistance to Thrombin-Induced Platelet Microbicidal Protein. <i>Journal of Infectious Diseases</i> , 2004, 190, 1140-1149.	1.9	327
94	Additivity and trans-acting Effects on Gene Expression in Male <i>Drosophila simulans</i> . <i>Genetics</i> , 2004, 168, 1413-1420.	1.2	60
95	Genome-wide transcription profile of field- and laboratory-selected dichlorodiphenyltrichloroethane (DDT)-resistant <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7034-7039.	3.3	202
96	Common Pattern of Evolution of Gene Expression Level and Protein Sequence in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2004, 21, 1308-1317.	3.5	246
97	Expression profile analysis of wild-type and <i>fcc1</i> mutant strains of <i>Fusarium verticillioides</i> during fumonisin biosynthesis. <i>Fungal Genetics and Biology</i> , 2004, 41, 647-656.	0.9	31
98	Intersection tests for single marker QTL analysis can be more powerful than two marker QTL analysis. <i>BMC Genetics</i> , 2003, 4, 10.	2.7	10
99	Microarray Analysis of the Genome-Wide Response to Iron Deficiency and Iron Reconstitution in the Cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Plant Physiology</i> , 2003, 132, 1825-1839.	2.3	166
100	Combining mapping and arraying: An approach to candidate gene identification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14903-14906.	3.3	273
101	Evidence for an evolutionarily conserved interaction between cell wall biosynthesis and flowering in maize and sorghum. <i>BMC Evolutionary Biology</i> , 2002, 2, 2.	3.2	13
102	The maize Brown midrib1 locus affects cell wall composition and plant development in a dose-dependent manner. <i>Heredity</i> , 2002, 88, 450-457.	1.2	34
103	Prognostic Significance of Molecular Genetic Aberrations on Chromosome Segment 11p15.5 in Non-Small-Cell Lung Cancer. <i>Journal of Clinical Oncology</i> , 2002, 20, 1353-1360.	0.8	42
104	Detection and localization of a single binary trait locus in experimental populations. <i>Genetical Research</i> , 2001, 78, 79-92.	0.3	29
105	Measuring Patient Expectations. <i>Medical Care</i> , 2001, 39, 100-108.	1.1	46
106	Dementia with Lewy bodies and Alzheimer's disease. <i>Acta Neuropathologica</i> , 2001, 102, 621-626.	3.9	38
107	In Search of a Good Death: Observations of Patients, Families, and Providers. <i>Annals of Internal Medicine</i> , 2000, 132, 825.	2.0	898
108	Circumventing multiple testing: A multilocus Monte Carlo approach to testing for association. <i>Genetic Epidemiology</i> , 2000, 19, 18-29.	0.6	96

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109	Incidence of Stroke and Season of the Year: Evidence of an Association. American Journal of Epidemiology, 2000, 152, 558-564.	1.6	103
110	Time to flowering in brown midrib mutants of maize: an alternative approach to the analysis of developmental traits. Heredity, 1999, 83, 171-178.	1.2	25
111	Validation of a trauma questionnaire in veteran women. Journal of General Internal Medicine, 1999, 14, 186-189.	1.3	78
112	The Validity in Persons With Spinal Cord Injury of a Self-Reported Functional Measure Derived From the Functional Independence Measure. Spine, 1999, 24, 539-543.	1.0	29
113	Neuropathological and Neuropsychological Changes in "Normal" Aging. Journal of Neuropathology and Experimental Neurology, 1998, 57, 1168-1174.	0.9	283
114	Hardy-Weinberg Testing for Continuous Data. Genetics, 1997, 147, 1965-1975.	1.2	4