

# Lauren M McIntyre

## List of Publications by Year in descending order

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114  
papers

8,165  
citations

66343

42  
h-index

49909

87  
g-index

126  
all docs

126  
docs citations

126  
times ranked

12233  
citing authors

#	ARTICLE	IF	CITATIONS
1	In Search of a Good Death: Observations of Patients, Families, and Providers. <i>Annals of Internal Medicine</i> , 2000, 132, 825.	3.9	898
2	Implementing false discovery rate control: increasing your power. <i>Oikos</i> , 2005, 108, 643-647.	2.7	807
3	Persistent Bacteremia Due to Methicillin-Resistant <i>Staphylococcus aureus</i> Infection Is Associated with <i>agr</i> Dysfunction and Low Level In Vitro Resistance to Thrombin-Induced Platelet Microbicidal Protein. <i>Journal of Infectious Diseases</i> , 2004, 190, 1140-1149.	4.0	327
4	The Chemical Interactions Underlying Tomato Flavor Preferences. <i>Current Biology</i> , 2012, 22, 1035-1039.	3.9	289
5	Neuropathological and Neuropsychological Changes in "Normal" Aging. <i>Journal of Neuropathology and Experimental Neurology</i> , 1998, 57, 1168-1174.	1.7	283
6	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.	7.1	273
7	RNA-seq: technical variability and sampling. <i>BMC Genomics</i> , 2011, 12, 293.	2.8	250
8	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.	4.8	247
9	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.	8.9	246
10	Successful range-expanding plants experience less above-ground and below-ground enemy impact. <i>Nature</i> , 2008, 456, 946-948.	27.8	238
11	High-Throughput Phenotyping of Maize Leaf Physiological and Biochemical Traits Using Hyperspectral Reflectance. <i>Plant Physiology</i> , 2017, 173, 614-626.	4.8	215
12	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.	7.1	202
13	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.	2.2	178
14	Ago HITS-CLIP Expands Understanding of Kaposi's Sarcoma-associated Herpesvirus miRNA Function in Primary Effusion Lymphomas. <i>PLoS Pathogens</i> , 2012, 8, e1002884.	4.7	167
15	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.	4.8	166
16	Potential Associations between Hematogenous Complications and Bacterial Genotype in <i>Staphylococcus aureus</i> Infection. <i>Journal of Infectious Diseases</i> , 2007, 196, 738-747.	4.0	148
17	Nematode-Induced Changes of Transporter Gene Expression in <i>Arabidopsis</i> Roots. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 1247-1257.	2.6	121
18	Incidence of Stroke and Season of the Year: Evidence of an Association. <i>American Journal of Epidemiology</i> , 2000, 152, 558-564.	3.4	103

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19	Circumventing multiple testing: A multilocus Monte Carlo approach to testing for association. <i>Genetic Epidemiology</i> , 2000, 19, 18-29.	1.3	96
20	Sex-specific expression of alternative transcripts in <i>Drosophila</i> . <i>Genome Biology</i> , 2006, 7, R79.	9.6	93
21	Allelic Imbalance in <i>Drosophila</i> Hybrid Heads: Exons, Isoforms, and Evolution. <i>Molecular Biology and Evolution</i> , 2012, 29, 1521-1532.	8.9	92
22	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.	2.9	87
23	Using mating designs to uncover QTL and the genetic architecture of complex traits. <i>Heredity</i> , 2006, 96, 139-149.	2.6	83
24	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.	5.6	81
25	Sex-Specific Splicing in <i>Drosophila</i> : Widespread Occurrence, Tissue Specificity and Evolutionary Conservation. <i>Genetics</i> , 2009, 181, 421-434.	2.9	79
26	Validation of a trauma questionnaire in veteran women. <i>Journal of General Internal Medicine</i> , 1999, 14, 186-189.	2.6	78
27	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.	7.1	69
28	LANA Binds to Multiple Active Viral and Cellular Promoters and Associates with the H3K4Methyltransferase hSET1 Complex. <i>PLoS Pathogens</i> , 2014, 10, e1004240.	4.7	68
29	Evolution of Gene Expression in the <i>Drosophila</i> Olfactory System. <i>Molecular Biology and Evolution</i> , 2008, 25, 1081-1092.	8.9	67
30	Plants Know Where It Hurts: Root and Shoot Jasmonic Acid Induction Elicit Differential Responses in <i>Brassica oleracea</i> . <i>PLoS ONE</i> , 2013, 8, e65502.	2.5	63
31	Genotype-phenotype mapping in a post-GWAS world. <i>Trends in Genetics</i> , 2012, 28, 421-426.	6.7	61
32	Additivity and trans-acting Effects on Gene Expression in Male <i>Drosophila simulans</i> . <i>Genetics</i> , 2004, 168, 1413-1420.	2.9	60
33	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.	4.8	60
34	Male-specific Fruitless isoforms have different regulatory roles conferred by distinct zinc finger DNA binding domains. <i>BMC Genomics</i> , 2013, 14, 659.	2.8	57
35	LEVERAGING BIOLOGICAL REPLICATES TO IMPROVE ANALYSIS IN CHIP-SEQ EXPERIMENTS. <i>Computational and Structural Biotechnology Journal</i> , 2014, 9, e201401002.	4.1	57
36	Changes in skeletal muscle gene expression following clenbuterol administration. <i>BMC Genomics</i> , 2006, 7, 320.	2.8	56

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37	UBASH3A Mediates Risk for Type 1 Diabetes Through Inhibition of T-Cell Receptor-Induced NF- $\kappa$ B Signaling. <i>Diabetes</i> , 2017, 66, 2033-2043.	0.6	54
38	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.	2.8	48
39	Measuring Patient Expectations. <i>Medical Care</i> , 2001, 39, 100-108.	2.4	46
40	Defining gene and QTL networks. <i>Current Opinion in Plant Biology</i> , 2009, 12, 241-246.	7.1	46
41	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.	7.1	45
42	Differential Expression of Genes Important for Adaptation in <i>Capsella bursa-pastoris</i> (Brassicaceae). <i>Plant Physiology</i> , 2007, 145, 160-173.	4.8	45
43	Variable selection in omics data: A practical evaluation of small sample sizes. <i>PLoS ONE</i> , 2018, 13, e0197910.	2.5	44
44	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.	8.9	43
45	Buffering of Genetic Regulatory Networks in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2016, 203, 1177-1190.	2.9	43
46	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.	1.6	42
47	A flexible Bayesian method for detecting allelic imbalance in RNA-seq data. <i>BMC Genomics</i> , 2014, 15, 920.	2.8	41
48	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.	5.7	40
49	tappAS: a comprehensive computational framework for the analysis of the functional impact of differential splicing. <i>Genome Biology</i> , 2020, 21, 119.	8.8	40
50	Uncovering hidden genetic variation in photosynthesis of field-grown maize under ozone pollution. <i>Global Change Biology</i> , 2019, 25, 4327-4338.	9.5	39
51	Dementia with Lewy bodies and Alzheimer's disease. <i>Acta Neuropathologica</i> , 2001, 102, 621-626.	7.7	38
52	Consistent Errors in First Strand cDNA Due to Random Hexamer Mispriming. <i>PLoS ONE</i> , 2013, 8, e85583.	2.5	38
53	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.	2.5	38
54	Allele-specific expression assays using Solexa. <i>BMC Genomics</i> , 2009, 10, 422.	2.8	37

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55	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.	7.3	36
56	The maize Brown midrib1 locus affects cell wall composition and plant development in a dose-dependent manner. <i>Heredity</i> , 2002, 88, 450-457.	2.6	34
57	SECIMTools: a suite of metabolomics data analysis tools. <i>BMC Bioinformatics</i> , 2018, 19, 151.	2.6	34
58	Direct mapping of density response in a population of B73 × Mo17 recombinant inbred lines of maize ( <i>Zea Mays</i> L.). <i>Heredity</i> , 2010, 104, 583-599.	2.6	32
59	Expression profile analysis of wild-type and fcc1 mutant strains of <i>Fusarium verticillioides</i> during fumonisin biosynthesis. <i>Fungal Genetics and Biology</i> , 2004, 41, 647-656.	2.1	31
60	Sex- and segment-specific modulation of gene expression profiles in <i>Drosophila</i> . <i>Developmental Biology</i> , 2005, 288, 528-544.	2.0	30
61	The Validity in Persons With Spinal Cord Injury of a Self-Reported Functional Measure Derived From the Functional Independence Measure. <i>Spine</i> , 1999, 24, 539-543.	2.0	29
62	Detection and localization of a single binary trait locus in experimental populations. <i>Genetical Research</i> , 2001, 78, 79-92.	0.9	29
63	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.	1.8	29
64	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.	5.5	29
65	Transcriptome Profiling of Embryonic Development Rate in Rainbow Trout Advanced Backcross Introgression Lines. <i>Marine Biotechnology</i> , 2011, 13, 215-231.	2.4	28
66	Genetic variation in the Yolk protein expression network of <i>Drosophila melanogaster</i> : sex-biased negative correlations with longevity. <i>Heredity</i> , 2012, 109, 226-234.	2.6	28
67	Time to flowering in brown midrib mutants of maize: an alternative approach to the analysis of developmental traits. <i>Heredity</i> , 1999, 83, 171-178.	2.6	25
68	Back to the Future: Multiparent Populations Provide the Key to Unlocking the Genetic Basis of Complex Traits. <i>Genetics</i> , 2017, 206, 527-529.	2.9	24
69	Risk Factors for Recurrent <i>Staphylococcus aureus</i> Bacteremia. <i>Clinical Infectious Diseases</i> , 2021, 72, 1891-1899.	5.8	23
70	Mapping Density Response in Maize: A Direct Approach for Testing Genotype and Treatment Interactions. <i>Genetics</i> , 2006, 173, 331-348.	2.9	22
71	The metabolome as a biomarker of aging in <i>Drosophila melanogaster</i> . <i>Aging Cell</i> , 2022, 21, e13548.	6.7	22
72	Identification of co-regulated transcripts affecting male body size in <i>Drosophila</i> . <i>Genome Biology</i> , 2005, 6, R53.	9.6	21

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73	A Robust Methodology for Assessing Differential Homeolog Contributions to the Transcriptomes of Allopolyploids. <i>Genetics</i> , 2018, 210, 883-894.	2.9	21
74	Mapping reciprocal effects and interactions with plant density stress in <i>Zea mays</i> L. <i>Heredity</i> , 2007, 99, 14-30.	2.6	20
75	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.	1.8	20
76	Analysis of Gene Expression Variance in Schizophrenia Using Structural Equation Modeling. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 192.	2.9	20
77	Model Selection in Binary Trait Locus Mapping. <i>Genetics</i> , 2005, 170, 1281-1297.	2.9	19
78	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.	2.8	19
79	Genetic Architecture of Two Fitness-related Traits in <i>Drosophila melanogaster</i> : Ovariole Number and Thorax Length. <i>Genetica</i> , 2005, 125, 211-222.	1.1	17
80	What the X Has to Do with It: Differences in Regulatory Variability between the Sexes in <i>Drosophila simulans</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 818-829.	2.5	17
81	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
82	Presence of arachidonoyl-carnitine is associated with adverse cardiometabolic responses in hypertensive patients treated with atenolol. <i>Metabolomics</i> , 2016, 12, 1.	3.0	14
83	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
84	Epistasis: Obstacle or Advantage for Mapping Complex Traits?. <i>PLoS ONE</i> , 2010, 5, e12264.	2.5	13
85	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.	1.8	13
86	Direct Testing for Allele-Specific Expression Differences Between Conditions. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 447-460.	1.8	13
87	A systems biology approach identified different regulatory networks targeted by KSHV miR-K12-11 in B cells and endothelial cells. <i>BMC Genomics</i> , 2014, 15, 668.	2.8	12
88	Event Analysis: Using Transcript Events To Improve Estimates of Abundance in RNA-seq Data. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2923-2940.	1.8	11
89	Long-Term Metabolomics Reference Material. <i>Analytical Chemistry</i> , 2021, 93, 9193-9199.	6.5	11
90	Comparison between NuGEN's WT-Ovation Pico and one-direct amplification systems. <i>Journal of Biomolecular Techniques</i> , 2010, 21, 141-7.	1.5	11

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91	Intersection tests for single marker QTL analysis can be more powerful than two marker QTL analysis. BMC Genetics, 2003, 4, 10.	2.7	10
92	Purification of Transcripts and Metabolites from <i>Drosophila</i> Heads. Journal of Visualized Experiments, 2013, , e50245.	0.3	10
93	Fibrinogen binding is affected by amino acid substitutions in C-terminal repeat region of fibronectin binding protein A. Scientific Reports, 2019, 9, 11619.	3.3	10
94	Using Alpha Wisely: Improving Power to Detect Multiple QTL. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-24.	0.6	9
95	Transcriptional Network Structure Has Little Effect on the Rate of Regulatory Evolution in Yeast. Molecular Biology and Evolution, 2012, 29, 1899-1905.	8.9	9
96	A comprehensive analysis of myocardial substrate preference emphasizes the need for a synchronized fluxomic/metabolomic research design. American Journal of Physiology - Heart and Circulatory Physiology, 2017, 312, H1215-H1223.	3.2	9
97	Reliable Detection of Herpes Simplex Virus Sequence Variation by High-Throughput Resequencing. Viruses, 2017, 9, 226.	3.3	9
98	RNA-seq analysis of impact of PNN on gene expression and alternative splicing in corneal epithelial cells. Molecular Vision, 2016, 22, 40-60.	1.1	9
99	Partitioning Transcript Variation in <i>Drosophila</i>: Abundance, Isoforms, and Alleles. G3: Genes, Genomes, Genetics, 2011, 1, 427-436.	1.8	7
100	Setting the Standard: A Special Focus on Genomic Selection in GENETICS and G3. Genetics, 2012, 190, 1151-1152.	2.9	7
101	SHH Protein Variance in the Limb Bud Is Constrained by Feedback Regulation and Correlates with Altered Digit Patterning. G3: Genes, Genomes, Genetics, 2017, 7, 851-858.	1.8	7
102	EXPRESSION OF DEFENSE GENES IN DROSOPHILA EVOLVES UNDER A DIFFERENT SELECTIVE REGIME FROM EXPRESSION OF OTHER GENES. Evolution; International Journal of Organic Evolution, 2011, 65, 1068-1078.	2.3	6
103	GENETICS and G3: Community-Driven Science, Community-Driven Journals. Genetics, 2014, 198, 1-2.	2.9	6
104	Kinetic Analysis of Hepatic Metabolism Using Hyperpolarized Dihydroxyacetone. Journal of Chemical Information and Modeling, 2019, 59, 605-614.	5.4	6
105	Hardy-Weinberg Testing for Continuous Data. Genetics, 1997, 147, 1965-1975.	2.9	4
106	Data: The Foundation of Science. Genetics, 2010, 184, 1-1.	2.9	3
107	Testcrosses are an efficient strategy for identifying <i>cis</i>-regulatory variation: Bayesian analysis of allele-specific expression (BayesASE). G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	3
108	Facilitating Discovery: The Role of Society Journals in Collaborative Science. Genetics, 2012, 190, 285-286.	2.9	2

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109	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.	3.3	2
110	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.	2.6	1
111	Facilitating Discovery: The Role of Society Journals in Collaborative Science. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 151-152.	1.8	1
112	Power calculator for detecting allelic imbalance using hierarchical Bayesian model. <i>BMC Research Notes</i> , 2021, 14, 436.	1.4	1
113	Variation in leaf transcriptome responses to elevated ozone corresponds with physiological sensitivity to ozone across maize inbred lines. <i>Genetics</i> , 2022, 221, .	2.9	1
114	GENETICS and G3: Community-Driven Science, Community-Driven Journals. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1567-1568.	1.8	0