

Tieming Ji

List of Publications by Year in descending order

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42
papers

1,748
citations

471371

17
h-index

289141

40
g-index

43
all docs

43
docs citations

43
times ranked

2801
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Paternal Dominance of Trans-eQTL Influences Gene Expression Patterns in Maize Hybrids. <i>Science</i> , 2009, 326, 1118-1120.	6.0	137
4	Large offspring syndrome. <i>Epigenetics</i> , 2013, 8, 591-601.	1.3	125
5	Characterization of global loss of imprinting in fetal overgrowth syndrome induced by assisted reproduction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4618-4623.	3.3	114
6	Identification of micro RNA s and their mRNA targets during soybean nodule development: functional analysis of the role of miR393 in soybean nodulation. <i>New Phytologist</i> , 2015, 207, 748-759.	3.5	82
7	Global assessment of imprinted gene expression in the bovine conceptus by next generation sequencing. <i>Epigenetics</i> , 2016, 11, 501-516.	1.3	65
8	Global impacts of chromosomal imbalance on gene expression in <i>Arabidopsis</i> and other taxa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11321-E11330.	3.3	51
9	Expression of KCNQ10T1, CDKN1C, H19, and PLAGL1 and the methylation patterns at the KvDMR1 and H19/IGF2 imprinting control regions is conserved between human and bovine. <i>Journal of Biomedical Science</i> , 2012, 19, 95.	2.6	48
10	Glutamine supplementation enhances development of in vitro-produced porcine embryos and increases leucine consumption from the medium. <i>Biology of Reproduction</i> , 2018, 99, 938-948.	1.2	42
11	Identification and functional characterization of soybean root hair microRNA s expressed in response to <i>Rhizobium japonicum</i> infection. <i>Plant Biotechnology Journal</i> , 2016, 14, 332-341.	4.1	40
12	Production and Culture of the Bovine Embryo. <i>Methods in Molecular Biology</i> , 2019, 2006, 115-129.	0.4	39
13	Altered microRNA expression profiles in large offspring syndrome and Beckwith-Wiedemann syndrome. <i>Epigenetics</i> , 2019, 14, 850-876.	1.3	32
14	Global misregulation of genes largely uncoupled to DNA methylome epimutations characterizes a congenital overgrowth syndrome. <i>Scientific Reports</i> , 2017, 7, 12667.	1.6	30
15	Sequence of the supernumerary B chromosome of maize provides insight into its drive mechanism and evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	25
16	Genomic imbalance determines positive and negative modulation of gene expression in diploid maize. <i>Plant Cell</i> , 2021, 33, 917-939.	3.1	22
17	Predominantly inverse modulation of gene expression in genomically unbalanced disomic haploid maize. <i>Plant Cell</i> , 2021, 33, 901-916.	3.1	22
18	Maternal Hyperleptinemia Is Associated with Male Offspring's Altered Vascular Function and Structure in Mice. <i>PLoS ONE</i> , 2016, 11, e0155377.	1.1	15

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19	Magnitude of modulation of gene expression in aneuploid maize depends on the extent of genomic imbalance. <i>Journal of Genetics and Genomics</i> , 2020, 47, 93-103.	1.7	15
20	Consequences of assisted reproductive techniques on the embryonic epigenome in cattle. <i>Reproduction, Fertility and Development</i> , 2020, 32, 65.	0.1	14
21	The Gene Balance Hypothesis: Epigenetics and Dosage Effects in Plants. <i>Methods in Molecular Biology</i> , 2020, 2093, 161-171.	0.4	14
22	Lean maternal hyperglycemia alters offspring lipid metabolism and susceptibility to diet-induced obesity in mice. <i>Biology of Reproduction</i> , 2019, 100, 1356-1369.	1.2	13
23	Effects of the use of assisted reproduction and high-caloric diet consumption on body weight and cardiovascular health of juvenile mouse offspring. <i>Reproduction</i> , 2014, 147, 111-123.	1.1	12
24	Pharmacologic Reprogramming Designed to Induce a Warburg Effect in Porcine Fetal Fibroblasts Alters Gene Expression and Quantities of Metabolites from Conditioned Media Without Increased Cell Proliferation. <i>Cellular Reprogramming</i> , 2018, 20, 38-48.	0.5	12
25	Differential gene expression in response to eCry3.1Ab ingestion in an unselected and eCry3.1Ab-selected western corn rootworm (<i>Diabrotica virgifera virgifera</i> LeConte) population. <i>Scientific Reports</i> , 2019, 9, 4896.	1.6	12
26	Effects of the Use of Assisted Reproductive Technologies and an Obesogenic Environment on Resistance Artery Function and Diabetes Biomarkers in Mice Offspring. <i>PLoS ONE</i> , 2014, 9, e112651.	1.1	8
27	Effect of aneuploidy of a nonessential chromosome on gene expression in maize. <i>Plant Journal</i> , 2022, 110, 193-211.	2.8	8
28	Modeling allele-specific expression at the gene and SNP levels simultaneously by a Bayesian logistic mixed regression model. <i>BMC Bioinformatics</i> , 2019, 20, 530.	1.2	7
29	Hyper Nonlocal Priors for Variable Selection in Generalized Linear Models. <i>Sankhya A</i> , 2020, 82, 147-185.	0.4	7
30	Conditions of embryo culture from days 5 to 7 of development alter the DNA methylome of the bovine fetus at day 86 of gestation. <i>Journal of Assisted Reproduction and Genetics</i> , 2020, 37, 417-426.	1.2	7
31	Spontaneous and ART-induced large offspring syndrome: similarities and differences in DNA methylome. <i>Epigenetics</i> , 2022, 17, 1477-1496.	1.3	7
32	Modeling the next generation sequencing read count data for DNA copy number variant study. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 361-74.	0.2	6
33	A Bayesian Hidden Markov Model for Detecting Differentially Methylated Regions. <i>Biometrics</i> , 2019, 75, 663-673.	0.8	6
34	Allele-specific aberration of imprinted domain chromosome architecture associates with large offspring syndrome. <i>IScience</i> , 2022, 25, 104269.	1.9	6
35	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
36	Estimation and Testing of Gene Expression Heterosis. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2014, 19, 319-337.	0.7	5

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37	Porcine Fetal-Derived Fibroblasts Alter Gene Expression and Mitochondria to Compensate for Hypoxic Stress During Culture. Cellular Reprogramming, 2018, 20, 225-235.	0.5	4
38	Statistical models for DNA copy number variation detection using read-depth data from next generation sequencing experiments. Australian and New Zealand Journal of Statistics, 2016, 58, 473-491.	0.4	3
39	Transcriptome Changes in Response to Cold Acclimation in Perennial Ryegrass as Revealed by a Cross-Species Microarray Analysis. Crop Science, 2017, 57, S-179.	0.8	2
40	Detecting differentially expressed genes for syndromes by considering change in mean and dispersion simultaneously. BMC Bioinformatics, 2018, 19, 330.	1.2	2
41	Dosage-sensitive miRNAs trigger modulation of gene expression during genomic imbalance in maize. Nature Communications, 2022, 13, .	5.8	1
42	An empirical bayesian approach for testing gene expression fold change and its application in detecting global dosage effects. NAR Genomics and Bioinformatics, 2020, 2, lqaa072.	1.5	0