

Jiuzhou Song

List of Publications by Year in descending order

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Version: 2024-02-01

138
papers

5,360
citations

125106

35
h-index

107981

68
g-index

150
all docs

150
docs citations

150
times ranked

6730
citing authors

#	ARTICLE	IF	CITATIONS
1	Pan-RNA editing analysis of the bovine genome. <i>RNA Biology</i> , 2021, 18, 368-381.	1.5	4
2	Narrow H3K4me2 is required for chicken PGC formation. <i>Journal of Cellular Physiology</i> , 2021, 236, 1391-1400.	2.0	14
3	Taxonomic and functional adaption of the gastrointestinal microbiome of goats kept at high altitude (4800Âm) under intensive or extensive rearing conditions. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	12
4	Long Noncoding RNA LncPGCR Mediated by TCF7L2 Regulates Primordial Germ Cell Formation in Chickens. <i>Animals</i> , 2021, 11, 292.	1.0	4
5	Glycolysis Combined with Core Pluripotency Factors to Promote the Formation of Chicken Induced Pluripotent Stem Cells. <i>Animals</i> , 2021, 11, 425.	1.0	1
6	Metabolic Regulations by lncRNA, miRNA, and ceRNA Under Grass-Fed and Grain-Fed Regimens in Angus Beef Cattle. <i>Frontiers in Genetics</i> , 2021, 12, 579393.	1.1	6
7	Genotype by environment interactions for body weight in Mediterranean buffaloes using reaction norm models. <i>Revista Colombiana De Ciencias Pecuarias</i> , 2021, 34, 166-176.	0.4	0
8	Characterization of Alternative Splicing (AS) Events during Chicken (<i>Gallus gallus</i>) Male Germ-Line Stem Cell Differentiation with Single-Cell RNA-seq. <i>Animals</i> , 2021, 11, 1469.	1.0	4
9	Role and function of the Hintw in early sex differentiation in chicken (<i>Gallus gallus</i>) embryo. <i>Animal Biotechnology</i> , 2021, , 1-11.	0.7	6
10	Integration of selection signatures and multi-trait GWAS reveals polygenic genetic architecture of carcass traits in beef cattle. <i>Genomics</i> , 2021, 113, 3325-3336.	1.3	19
11	Identification of a novel differentially methylated region adjacent to ATG16L2 in lung cancer cells using methyl-CpG binding domain protein-enriched genome sequencing. <i>Genome</i> , 2021, 64, 1-14.	0.9	4
12	Integrated Small RNA Sequencing, Transcriptome and GWAS Data Reveal microRNA Regulation in Response to Milk Protein Traits in Chinese Holstein Cattle. <i>Frontiers in Genetics</i> , 2021, 12, 726706.	1.1	6
13	105 The Epigenetics and Plasticity of CD4+ T Cells in Poultry Health. <i>Journal of Animal Science</i> , 2021, 99, 55-55.	0.2	0
14	Growth curve, blood parameters and carcass traits of grass-fed Angus steers. <i>Animal</i> , 2021, 15, 100381.	1.3	3
15	Tributyryn, a Butyrate Pro-Drug, Primes Satellite Cells for Differentiation by Altering the Epigenetic Landscape. <i>Cells</i> , 2021, 10, 3475.	1.8	4
16	The Profiling of DNA Methylation and Its Regulation on Divergent Tenderness in Angus Beef Cattle. <i>Frontiers in Genetics</i> , 2020, 11, 939.	1.1	13
17	Adiponectin and its receptor genes' expression in response to Marek's disease virus infection of White Leghorns. <i>Poultry Science</i> , 2020, 99, 4249-4258.	1.5	1
18	Diet induced the change of mtDNA copy number and metabolism in Angus cattle. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 84.	2.1	4

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19	Transcriptome Sequencing and Comparative Analysis of Amphoteric ESCs and PGCs in Chicken (<i>Gallus</i>) Tj ETQq1 1 0,784314,rgBT /Oyer	1.0	2
20	Genome-wide characterization of copy number variations in the host genome in genetic resistance to Marek's disease using next generation sequencing. <i>BMC Genetics</i> , 2020, 21, 77.	2.7	2
21	C1EIP Functions as an Activator of ENO1 to Promote Chicken PGCs Formation via Inhibition of the Notch Signaling Pathway. <i>Frontiers in Genetics</i> , 2020, 11, 751.	1.1	1
22	Diet-induced changes in bacterial communities in the jejunum and their associations with bile acids in Angus beef cattle. <i>Animal Microbiome</i> , 2020, 2, 33.	1.5	14
23	P53 and H3K4me2 activate N6-methylated lncPGCAT to regulate primordial germ cell formation via MAPK signaling. <i>Journal of Cellular Physiology</i> , 2020, 235, 9895-9909.	2.0	7
24	CYP19A1 (aromatase) dominates female gonadal differentiation in chicken (<i>Gallus gallus</i>) embryos sexual differentiation. <i>Bioscience Reports</i> , 2020, 40, .	1.1	10
25	Marek's Disease Virus Infection Induced Mitochondria Changes in Chickens. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3150.	1.8	5
26	DNA methylation, microRNA expression profiles and their relationships with transcriptome in grass-fed and grain-fed Angus cattle rumen tissue. <i>PLoS ONE</i> , 2019, 14, e0214559.	1.1	10
27	Allele-Specific Expression of CD4+ T Cells in Response to Marek's Disease Virus Infection. <i>Genes</i> , 2019, 10, 718.	1.0	5
28	Parent-of-origin has no detectable effect on survival days of Marek's disease virus infected White Leghorns. <i>Poultry Science</i> , 2019, 98, 4498-4503.	1.5	1
29	The different effects of viral and bacterial mimics maternal stimuli on ethology of hens and reproduction of their offspring. <i>Poultry Science</i> , 2019, 98, 4153-4160.	1.5	1
30	Integrated analysis of lncRNA and mRNA repertoires in Marek's disease infected spleens identifies genes relevant to resistance. <i>BMC Genomics</i> , 2019, 20, 245.	1.2	46
31	Distinct roles of retinoic acid and BMP4 pathways in the formation of chicken primordial germ cells and spermatogonial stem cells. <i>Food and Function</i> , 2019, 10, 7152-7163.	2.1	14
32	Linc-GALMD1 Regulates Viral Gene Expression in the Chicken. <i>Frontiers in Genetics</i> , 2019, 10, 1122.	1.1	8
33	Study on immortal conditions of chicken embryonic stem cells. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 1376-1385.	1.2	2
34	Functional characterization of the Sox2, c-Myc, and Oct4 promoters. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 332-342.	1.2	9
35	DNA Methylation and Regulatory Elements during Chicken Germline Stem Cell Differentiation. <i>Stem Cell Reports</i> , 2018, 10, 1793-1806.	2.3	19
36	Increased carotid intima-media thickness in African American pediatric kidney transplant recipients. <i>Pediatric Transplantation</i> , 2018, 22, e13163.	0.5	2

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37	Effects of obesity and metabolic syndrome on cardiovascular outcomes in pediatric kidney transplant recipients: a longitudinal study. <i>Pediatric Nephrology</i> , 2018, 33, 1419-1428.	0.9	14
38	Genetic Architecture and Selection of Chinese Cattle Revealed by Whole Genome Resequencing. <i>Molecular Biology and Evolution</i> , 2018, 35, 688-699.	3.5	97
39	DNA methylation profiles correlated to striped bass sperm fertility. <i>BMC Genomics</i> , 2018, 19, 244.	1.2	18
40	Interaction of the primordial germ cell-specific protein C2EIP with PTCH2 directs differentiation of embryonic stem cells via HH signaling activation. <i>Cell Death and Disease</i> , 2018, 9, 497.	2.7	18
41	<i>Hsd3b2</i> associated in modulating steroid hormone synthesis pathway regulates the differentiation of chicken embryonic stem cells into spermatogonial stem cells. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 1111-1121.	1.2	3
42	Cloning, expression pattern analysis, and subcellular localization of <i>Capra hircus</i> SCD1 gene with production of transgenic mice. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 2240-2247.	1.2	0
43	Transgenerational transmission of maternal stimulatory experience in domesticated birds. <i>FASEB Journal</i> , 2018, 32, 7002-7017.	0.2	10
44	Genetic assessment of inbred chicken lines indicates genomic signatures of resistance to Marek's disease. <i>Journal of Animal Science and Biotechnology</i> , 2018, 9, 65.	2.1	9
45	Gga-miR-130b-3p inhibits MSB1 cell proliferation, migration, invasion, and its downregulation in MD tumor is attributed to hypermethylation. <i>Oncotarget</i> , 2018, 9, 24187-24198.	0.8	10
46	Whole-genome bisulfite sequencing of goat skins identifies signatures associated with hair cycling. <i>BMC Genomics</i> , 2018, 19, 638.	1.2	37
47	NICD-mediated notch transduction regulates the different fate of chicken primordial germ cells and spermatogonial stem cells. <i>Cell and Bioscience</i> , 2018, 8, 40.	2.1	23
48	RXR α associated in PPAR signal regulated the differentiation of primordial germ cell. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 6926-6934.	1.2	18
49	Genome Wide Identification of Novel Long Non-coding RNAs and Their Potential Associations With Milk Proteins in Chinese Holstein Cows. <i>Frontiers in Genetics</i> , 2018, 9, 281.	1.1	30
50	Trac-looping measures genome structure and chromatin accessibility. <i>Nature Methods</i> , 2018, 15, 741-747.	9.0	74
51	CRISPR/Cas9-Mediated Deletion of <i>C1EIS</i> Inhibits Chicken Embryonic Stem Cell Differentiation Into Male Germ Cells (<i>Gallus gallus</i>). <i>Journal of Cellular Biochemistry</i> , 2017, 118, 2380-2386.	1.2	6
52	Inducing goat pluripotent stem cells with four transcription factor mRNAs that activate endogenous promoters. <i>BMC Biotechnology</i> , 2017, 17, 11.	1.7	24
53	Male fertility status is associated with DNA methylation signatures in sperm and transcriptomic profiles of bovine preimplantation embryos. <i>BMC Genomics</i> , 2017, 18, 280.	1.2	110
54	Dynamic expression and regulatory mechanism of TGF- β 2 signaling in chicken embryonic stem cells differentiating into spermatogonial stem cells. <i>Bioscience Reports</i> , 2017, 37, .	1.1	11

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55	Genome-wide mapping of DNase I hypersensitive sites in rare cell populations using single-cell DNase sequencing. <i>Nature Protocols</i> , 2017, 12, 2342-2354.	5.5	41
56	Long intergenic non-coding RNA GALMD3 in chicken Marek's disease. <i>Scientific Reports</i> , 2017, 7, 10294.	1.6	23
57	MLL4 prepares the enhancer landscape for Foxp3 induction via chromatin looping. <i>Nature Immunology</i> , 2017, 18, 1035-1045.	7.0	63
58	Gga-miR-219b targeting BCL11B suppresses proliferation, migration and invasion of Marek's disease tumor cell MSB1. <i>Scientific Reports</i> , 2017, 7, 4247.	1.6	20
59	Regulation of crucial lncRNAs in differentiation of chicken embryonic stem cells to spermatogonia stem cells. <i>Animal Genetics</i> , 2017, 48, 191-204.	0.6	10
60	Regulation of Hedgehog Signaling in Chicken Embryonic Stem Cells Differentiation Into Male Germ Cells (<i>Gallus</i>). <i>Journal of Cellular Biochemistry</i> , 2017, 118, 1379-1386.	1.2	10
61	Characterization of Copy Number Variation's Potential Role in Marek's Disease. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1020.	1.8	9
62	Genomic Variation between Genetic Lines of White Leghorns Differed in Resistance to Marek's Disease. <i>Journal of Clinical Epigenetics</i> , 2017, 03, .	0.3	6
63	Detection of threshold points for gene expressions under multiple biological conditions. <i>Statistics and Its Interface</i> , 2017, 10, 643-655.	0.2	1
64	Diversity and population-genetic properties of copy number variations and multicopy genes in cattle. <i>DNA Research</i> , 2016, 23, 253-262.	1.5	59
65	Whole-genome regulation analysis of histone H3 lysin 27 trimethylation in subclinical mastitis cows infected by <i>Staphylococcus aureus</i> . <i>BMC Genomics</i> , 2016, 17, 565.	1.2	29
66	A decision analysis model for KEGG pathway analysis. <i>BMC Bioinformatics</i> , 2016, 17, 407.	1.2	46
67	Chicken gga-miR-103-3p Targets CCNE1 and TFDP2 and Inhibits MDCC-MSB1 Cell Migration. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1277-1285.	0.8	19
68	Whole-genome sequencing of eight goat populations for the detection of selection signatures underlying production and adaptive traits. <i>Scientific Reports</i> , 2016, 6, 38932.	1.6	132
69	Chicken gga-miR-130a targets HOXA3 and MDFIC and inhibits Marek's disease lymphoma cell proliferation and migration. <i>Molecular Biology Reports</i> , 2016, 43, 667-676.	1.0	19
70	Abomasal mucosal immune responses of cattle with limited or continuous exposure to pasture-borne gastrointestinal nematode parasite infection. <i>Veterinary Parasitology</i> , 2016, 229, 118-125.	0.7	8
71	GOFAANG meeting: a Gathering On Functional Annotation of Animal Genomes. <i>Animal Genetics</i> , 2016, 47, 528-533.	0.6	65
72	Systematic profiling of short tandem repeats in the cattle genome. <i>Genome Biology and Evolution</i> , 2016, 9, evw256.	1.1	20

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73	Integrated metabolomic and transcriptome analyses reveal finishing forage affects metabolic pathways related to beef quality and animal welfare. <i>Scientific Reports</i> , 2016, 6, 25948.	1.6	61
74	Population-genetic properties of differentiated copy number variations in cattle. <i>Scientific Reports</i> , 2016, 6, 23161.	1.6	91
75	Site-Directed Genome Knockout in Chicken Cell Line and Embryos Can Use CRISPR/Cas Gene Editing Technology. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1787-1792.	0.8	37
76	0306 Exploring the feasibility of using copy number variants as genetic markers through large-scale whole genome sequencing experiments. <i>Journal of Animal Science</i> , 2016, 94, 146-146.	0.2	1
77	The conservation and signatures of lincRNAs in Marek's disease of chicken. <i>Scientific Reports</i> , 2015, 5, 15184.	1.6	69
78	DNMT3B4-del Contributes to Aberrant DNA Methylation Patterns in Lung Tumorigenesis. <i>EBioMedicine</i> , 2015, 2, 1340-1350.	2.7	7
79	Genome-wide identification of copy number variations between two chicken lines that differ in genetic resistance to Marek's disease. <i>BMC Genomics</i> , 2015, 16, 843.	1.2	35
80	Transcriptomic Profiling of Spleen in Grass-Fed and Grain-Fed Angus Cattle. <i>PLoS ONE</i> , 2015, 10, e0135670.	1.1	9
81	Epigenetics and animal virus infections. <i>Frontiers in Genetics</i> , 2015, 6, 48.	1.1	7
82	Histone modifications induced by MDV infection at early cytolytic and latency phases. <i>BMC Genomics</i> , 2015, 16, 311.	1.2	13
83	Crucial Genes and Pathways in Chicken Germ Stem Cell Differentiation. <i>Journal of Biological Chemistry</i> , 2015, 290, 13605-13621.	1.6	43
84	Chicken gga-miR-181a targets MYBL1 and shows an inhibitory effect on proliferation of Marek's disease virus-transformed lymphoid cell line. <i>Poultry Science</i> , 2015, 94, 2616-2621.	1.5	26
85	Genomic Signatures Reveal New Evidences for Selection of Important Traits in Domestic Cattle. <i>Molecular Biology and Evolution</i> , 2015, 32, 711-725.	3.5	173
86	Methylome Analysis in Chickens Immunized with Infectious Laryngotracheitis Vaccine. <i>PLoS ONE</i> , 2015, 10, e0100476.	1.1	10
87	Genome-Wide H3K4me3 Analysis in Angus Cattle with Divergent Tenderness. <i>PLoS ONE</i> , 2015, 10, e0115358.	1.1	40
88	Ruminal Transcriptomic Analysis of Grass-Fed and Grain-Fed Angus Beef Cattle. <i>PLoS ONE</i> , 2015, 10, e0116437.	1.1	20
89	Co-Expression Analysis of Fetal Weight-Related Genes in Ovine Skeletal Muscle during Mid and Late Fetal Development Stages. <i>International Journal of Biological Sciences</i> , 2014, 10, 1039-1050.	2.6	13
90	Genome-wide mapping of DNase I hypersensitive sites and association analysis with gene expression in MSB1 cells. <i>Frontiers in Genetics</i> , 2014, 5, 308.	1.1	21

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91	Transcriptome analysis reveals an activation of major histocompatibility complex 1 and 2 pathways in chicken trachea immunized with infectious laryngotracheitis virus vaccine. <i>Poultry Science</i> , 2014, 93, 848-855.	1.5	13
92	Host genetic resistance to Marek's disease sustains protective efficacy of herpesvirus of turkey in both experimental and commercial lines of chickens. <i>Vaccine</i> , 2014, 32, 1820-1827.	1.7	13
93	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. <i>BMC Genomics</i> , 2014, 15, 683.	1.2	89
94	A genome-wide survey reveals a deletion polymorphism associated with resistance to gastrointestinal nematodes in Angus cattle. <i>Functional and Integrative Genomics</i> , 2014, 14, 333-339.	1.4	24
95	KEGG-PATH: Kyoto encyclopedia of genes and genomes-based pathway analysis using a path analysis model. <i>Molecular BioSystems</i> , 2014, 10, 2441-2447.	2.9	330
96	Functional proteomic and interactome analysis of proteins associated with beef tenderness in Angus cattle. <i>Livestock Science</i> , 2014, 161, 201-209.	0.6	35
97	Down-Regulation of Promoter Methylation Level of CD4 Gene After MDV Infection in MD-Susceptible Chicken Line. , 2014, , 51-62.		0
98	Isolation of chicken embryonic stem cell and preparation of chicken chimeric model. <i>Molecular Biology Reports</i> , 2013, 40, 2149-2156.	1.0	14
99	Cloning of the Xuhuai Goat PPAR β Gene and the Preparation of Transgenic Sheep. <i>Biochemical Genetics</i> , 2013, 51, 543-553.	0.8	6
100	DNA Methylation Down-Regulates EGFR Expression in Chickens. <i>Avian Diseases</i> , 2013, 57, 366-371.	0.4	4
101	Comparative Analysis of CNV Calling Algorithms: Literature Survey and a Case Study Using Bovine High-Density SNP Data. <i>Microarrays (Basel, Switzerland)</i> , 2013, 2, 171-185.	1.4	37
102	DNMT gene expression and methylome in Marek's disease resistant and susceptible chickens prior to and following infection by MDV. <i>Epigenetics</i> , 2013, 8, 431-444.	1.3	50
103	Genome-Wide Copy Number Variant Analysis in Inbred Chickens Lines With Different Susceptibility to Marek's Disease. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 217-223.	0.8	36
104	Functional Genomic Analysis of Variation on Beef Tenderness Induced by Acute Stress in Angus Cattle. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-11.	2.0	38
105	MiRNA expression signatures induced by Marek's disease virus infection in chickens. <i>Genomics</i> , 2012, 99, 152-159.	1.3	60
106	Targeting Werner syndrome protein sensitizes U-2 OS osteosarcoma cells to selenium-induced DNA damage response and necrotic death. <i>Biochemical and Biophysical Research Communications</i> , 2012, 420, 24-28.	1.0	10
107	Marek's disease virus infection induces widespread differential chromatin marks in inbred chicken lines. <i>BMC Genomics</i> , 2012, 13, 557.	1.2	17
108	Analysis for temporal gene expressions under multiple biological conditions. <i>Statistics in Biosciences</i> , 2012, 4, 282-299.	0.6	2

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109	miRNA-dysregulation associated with tenderness variation induced by acute stress in Angus cattle. <i>Journal of Animal Science and Biotechnology</i> , 2012, 3, 12.	2.1	19
110	Copy number variation of individual cattle genomes using next-generation sequencing. <i>Genome Research</i> , 2012, 22, 778-790.	2.4	259
111	Fine mapping of copy number variations on two cattle genome assemblies using high density SNP array. <i>BMC Genomics</i> , 2012, 13, 376.	1.2	90
112	Comprehensive Analysis of Gene-Environmental Interactions with Temporal Gene Expression Profiles in <i>Pseudomonas aeruginosa</i> . <i>PLoS ONE</i> , 2012, 7, e35993.	1.1	5
113	DNA Methylation Fluctuation Induced by Virus Infection Differs between MD-resistant and -susceptible Chickens. <i>Frontiers in Genetics</i> , 2012, 3, 20.	1.1	27
114	Genomic regions showing copy number variations associate with resistance or susceptibility to gastrointestinal nematodes in Angus cattle. <i>Functional and Integrative Genomics</i> , 2012, 12, 81-92.	1.4	87
115	Muscle transcriptomic analyses in Angus cattle with divergent tenderness. <i>Molecular Biology Reports</i> , 2012, 39, 4185-4193.	1.0	40
116	Genome-Wide Bovine H3K27me3 Modifications and the Regulatory Effects on Genes Expressions in Peripheral Blood Lymphocytes. <i>PLoS ONE</i> , 2012, 7, e39094.	1.1	16
117	Histone Methylation Analysis and Pathway Predictions in Chickens after MDV Infection. <i>PLoS ONE</i> , 2012, 7, e41849.	1.1	21
118	WaveSeq: A Novel Data-Driven Method of Detecting Histone Modification Enrichments Using Wavelets. <i>PLoS ONE</i> , 2012, 7, e45486.	1.1	9
119	Vaccine by Chicken Line Interaction Alters the Protective Efficacy against Challenge with a Very Virulent plus Strain of Marek's Disease Virus in White Leghorn Chickens. <i>World Journal of Vaccines</i> , 2012, 02, 1-11.	0.8	9
120	A Comparative Evaluation of the Protective Efficacy of rMd5 ⁺ Meq and CVI988/Rispens Against a vv+ Strain of Marek's Disease Virus Infection in a Series of Recombinant Congenic Strains of White Leghorn Chickens. <i>Avian Diseases</i> , 2011, 55, 384-390.	0.4	17
121	Differential Gene Expression by RamA in Ciprofloxacin-Resistant <i>Salmonella Typhimurium</i> . <i>PLoS ONE</i> , 2011, 6, e22161.	1.1	27
122	Encapsulation of selenium in chitosan nanoparticles improves selenium availability and protects cells from selenium-induced DNA damage response. <i>Journal of Nutritional Biochemistry</i> , 2011, 22, 1137-1142.	1.9	56
123	Down-regulation of promoter methylation level of CD4 gene after MDV infection in MD-susceptible chicken line. <i>BMC Proceedings</i> , 2011, 5, S7.	1.8	29
124	Genomic characteristics of cattle copy number variations. <i>BMC Genomics</i> , 2011, 12, 127.	1.2	201
125	Temporal transcriptome changes induced by MDV in marek's disease-resistant and -susceptible inbred chickens. <i>BMC Genomics</i> , 2011, 12, 501.	1.2	33
126	Analysis of copy number variations among diverse cattle breeds. <i>Genome Research</i> , 2010, 20, 693-703.	2.4	280

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127	A Genome-Wide Analysis of Array-Based Comparative Genomic Hybridization (CGH) Data to Detect Intra-Species Variations and Evolutionary Relationships. PLoS ONE, 2009, 4, e7978.	1.1	10
128	Calibration of Mutation Rates Reveals Diverse Subfamily Structure of Galliform CR1 Repeats. Genome Biology and Evolution, 2009, 1, 119-130.	1.1	8
129	Characterizing Gene Expressions Based on Their Temporal Observations. Journal of Biomedicine and Biotechnology, 2009, 2009, 1-5.	3.0	0
130	Principal component tests: applied to temporal gene expression data. BMC Bioinformatics, 2009, 10, S26.	1.2	5
131	Analysis of recent segmental duplications in the bovine genome. BMC Genomics, 2009, 10, 571.	1.2	86
132	Alternative splicing variants and DNA methylation status of BDNF in inbred chicken lines. Brain Research, 2009, 1269, 1-10.	1.1	17
133	Effect of Genotype, Environment, and Their Interaction on Chemical Composition and Antioxidant Properties of Low-Linolenic Soybeans Grown in Maryland. Journal of Agricultural and Food Chemistry, 2009, 57, 10163-10174.	2.4	41
134	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	6.0	1,038
135	An Integrated Epigenetic and Genetic Analysis of DNA Methyltransferase Genes (DNMTs) in Tumor Resistant and Susceptible Chicken Lines. PLoS ONE, 2008, 3, e2672.	1.1	34
136	Quantitative Evaluation of DNA Methylation Patterns for ALVE and TVB Genes in a Neoplastic Disease Susceptible and Resistant Chicken Model. PLoS ONE, 2008, 3, e1731.	1.1	27
137	The identification of functional motifs in temporal gene expression analysis. Evolutionary Bioinformatics, 2007, 1, 84-96.	0.6	1
138	Wavelet to predict bacterial ori and ter: a tendency towards a physical balance. BMC Genomics, 2003, 4, 17.	1.2	38