Jiuzhou Song

List of Publications by Year
in descending order

138

papers

5,360

citations

109137

35

h-index

95083

68

g-index

150

all docs

150

docs citations

150

times ranked

6213

citing authors

#	Article	IF	Citations
1	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	6.0	1,038
2	KEGG-PATH: Kyoto encyclopedia of genes and genomes-based pathway analysis using a path analysis model. Molecular BioSystems, 2014, 10, 2441-2447.	2.9	330
3	Analysis of copy number variations among diverse cattle breeds. Genome Research, 2010, 20, 693-703.	2.4	280
4	Copy number variation of individual cattle genomes using next-generation sequencing. Genome Research, 2012, 22, 778-790.	2.4	259
5	Genomic characteristics of cattle copy number variations. BMC Genomics, 2011, 12, 127.	1.2	201
6	Genomic Signatures Reveal New Evidences for Selection of Important Traits in Domestic Cattle. Molecular Biology and Evolution, 2015, 32, 711-725.	3.5	173
7	Whole-genome sequencing of eight goat populations for the detection of selection signatures underlying production and adaptive traits. Scientific Reports, 2016, 6, 38932.	1.6	132
8	Male fertility status is associated with DNA methylation signatures in sperm and transcriptomic profiles of bovine preimplantation embryos. BMC Genomics, 2017, 18, 280.	1.2	110
9	Genetic Architecture and Selection of Chinese Cattle Revealed by Whole Genome Resequencing. Molecular Biology and Evolution, 2018, 35, 688-699.	3.5	97
10	Population-genetic properties of differentiated copy number variations in cattle. Scientific Reports, 2016, 6, 23161.	1.6	91
11	Fine mapping of copy number variations on two cattle genome assemblies using high density SNP array. BMC Genomics, 2012, 13, 376.	1.2	90
12	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. BMC Genomics, 2014, 15, 683.	1.2	89
13	Genomic regions showing copy number variations associate with resistance or susceptibility to gastrointestinal nematodes in Angus cattle. Functional and Integrative Genomics, 2012, 12, 81-92.	1.4	87
14	Analysis of recent segmental duplications in the bovine genome. BMC Genomics, 2009, 10, 571.	1.2	86
15	Trac-looping measures genome structure and chromatin accessibility. Nature Methods, 2018, 15, 741-747.	9.0	74
16	The conservation and signatures of lincRNAs in Marekâ€™s disease of chicken. Scientific Reports, 2015, 5, 15184.	1.6	69
17	<scp>GO</scp>â€‹<scp>FAANG</scp> meeting: a Gathering On Functional Annotation of <scp>An</scp>imal Genomes. Animal Genetics, 2016, 47, 528-533.	0.6	65
18	MLL4 prepares the enhancer landscape for Foxp3 induction via chromatin looping. Nature Immunology, 2017, 18, 1035-1045.	7.0	63

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19	Integrated metabolomic and transcriptome analyses reveal finishing forage affects metabolic pathways related to beef quality and animal welfare. Scientific Reports, 2016, 6, 25948.	1.6	61
20	MiRNA expression signatures induced by Marek's disease virus infection in chickens. Genomics, 2012, 99, 152-159.	1.3	60
21	Diversity and population-genetic properties of copy number variations and multicopy genes in cattle. DNA Research, 2016, 23, 253-262.	1.5	59
22	Encapsulation of selenium in chitosan nanoparticles improves selenium availability and protects cells from selenium-induced DNA damage response. Journal of Nutritional Biochemistry, 2011, 22, 1137-1142.	1.9	56
23	DNMT gene expression and methylome in Marekâ€™s disease resistant and susceptible chickens prior to and following infection by MDV. Epigenetics, 2013, 8, 431-444.	1.3	50
24	A decision analysis model for KEGG pathway analysis. BMC Bioinformatics, 2016, 17, 407.	1.2	46
25	Integrated analysis of lncRNA and mRNA repertoires in Marekâ€™s disease infected spleens identifies genes relevant to resistance. BMC Genomics, 2019, 20, 245.	1.2	46
26	Crucial Genes and Pathways in Chicken Germ Stem Cell Differentiation. Journal of Biological Chemistry, 2015, 290, 13605-13621.	1.6	43
27	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
28	Genome-wide mapping of DNase I hypersensitive sites in rare cell populations using single-cell DNase sequencing. Nature Protocols, 2017, 12, 2342-2354.	5.5	41
29	Muscle transcriptomic analyses in Angus cattle with divergent tenderness. Molecular Biology Reports, 2012, 39, 4185-4193.	1.0	40
30	Genome-Wide H3K4me3 Analysis in Angus Cattle with Divergent Tenderness. PLoS ONE, 2015, 10, e0115358.	1.1	40
31	Wavelet to predict bacterial ori and ter: a tendency towards a physical balance. BMC Genomics, 2003, 4, 17.	1.2	38
32	Functional Genomic Analysis of Variation on Beef Tenderness Induced by Acute Stress in Angus Cattle. Comparative and Functional Genomics, 2012, 2012, 1-11.	2.0	38
33	Comparative Analysis of CNV Calling Algorithms: Literature Survey and a Case Study Using Bovine High-Density SNP Data. Microarrays (Basel, Switzerland), 2013, 2, 171-185.	1.4	37
34	Site-Directed Genome Knockout in Chicken Cell Line and Embryos Can Use CRISPR/Cas Gene Editing Technology. G3: Genes, Genomes, Genetics, 2016, 6, 1787-1792.	0.8	37
35	Whole-genome bisulfite sequencing of goat skins identifies signatures associated with hair cycling. BMC Genomics, 2018, 19, 638.	1.2	37
36	Genome-Wide Copy Number Variant Analysis in Inbred Chickens Lines With Different Susceptibility to Marekâ€™s Disease. G3: Genes, Genomes, Genetics, 2013, 3, 217-223.	0.8	36

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37	Functional proteomic and interactome analysis of proteins associated with beef tenderness in Angus cattle. Livestock Science, 2014, 161, 201-209.	0.6	35
38	Genome-wide identification of copy number variations between two chicken lines that differ in genetic resistance to Marekâ€™s disease. BMC Genomics, 2015, 16, 843.	1.2	35
39	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
40	Temporal transcriptome changes induced by MDV in marek's disease-resistant and -susceptible inbred chickens. BMC Genomics, 2011, 12, 501.	1.2	33
41	Genome Wide Identification of Novel Long Non-coding RNAs and Their Potential Associations With Milk Proteins in Chinese Holstein Cows. Frontiers in Genetics, 2018, 9, 281.	1.1	30
42	Down-regulation of promoter methylation level of CD4 gene after MDV infection in MD-susceptible chicken line. BMC Proceedings, 2011, 5, S7.	1.8	29
43	Whole-genome regulation analysis of histone H3 lysin 27 trimethylation in subclinical mastitis cows infected by Staphylococcus aureus. BMC Genomics, 2016, 17, 565.	1.2	29
44	Differential Gene Expression by RamA in Ciprofloxacin-Resistant Salmonella Typhimurium. PLoS ONE, 2011, 6, e22161.	1.1	27
45	DNA Methylation Fluctuation Induced by Virus Infection Differs between MD-resistant and -susceptible Chickens. Frontiers in Genetics, 2012, 3, 20.	1.1	27
46	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
47	Chicken gga-miR-181a targets MYBL1 and shows an inhibitory effect on proliferation of Marek's disease virus-transformed lymphoid cell line. Poultry Science, 2015, 94, 2616-2621.	1.5	26
48	A genome-wide survey reveals a deletion polymorphism associated with resistance to gastrointestinal nematodes in Angus cattle. Functional and Integrative Genomics, 2014, 14, 333-339.	1.4	24
49	Inducing goat pluripotent stem cells with four transcription factor mRNAs that activate endogenous promoters. BMC Biotechnology, 2017, 17, 11.	1.7	24
50	Long intergenic non-coding RNA GALMD3 in chicken Marekâ€™s disease. Scientific Reports, 2017, 7, 10294.	1.6	23
51	NICD-mediated notch transduction regulates the different fate of chicken primordial germ cells and spermatogonial stem cells. Cell and Bioscience, 2018, 8, 40.	2.1	23
52	Genome-wide mapping of DNase I hypersensitive sites and association analysis with gene expression in MSB1 cells. Frontiers in Genetics, 2014, 5, 308.	1.1	21
53	Histone Methylation Analysis and Pathway Predictions in Chickens after MDV Infection. PLoS ONE, 2012, 7, e41849.	1.1	21
54	Systematic profiling of short tandem repeats in the cattle genome. Genome Biology and Evolution, 2016, 9, evw256.	1.1	20

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55	Gga-miR-219b targeting BCL11B suppresses proliferation, migration and invasion of Marekâ€™s disease tumor cell MSB1. Scientific Reports, 2017, 7, 4247.	1.6	20
56	Ruminal Transcriptomic Analysis of Grass-Fed and Grain-Fed Angus Beef Cattle. PLoS ONE, 2015, 10, e0116437.	1.1	20
57	miRNA-dysregulation associated with tenderness variation induced by acute stress in Angus cattle. Journal of Animal Science and Biotechnology, 2012, 3, 12.	2.1	19
58	Chicken gga-miR-103-3p Targets CCNE1 and TFDP2 and Inhibits MDCC-MSB1 Cell Migration. G3: Genes, Genomes, Genetics, 2016, 6, 1277-1285.	0.8	19
59	Chicken gga-miR-130a targets HOXA3 and MDFIC and inhibits Marekâ€™s disease lymphoma cell proliferation and migration. Molecular Biology Reports, 2016, 43, 667-676.	1.0	19
60	DNA Methylation and Regulatory Elements during Chicken Germline Stem Cell Differentiation. Stem Cell Reports, 2018, 10, 1793-1806.	2.3	19
61	Integration of selection signatures and multi-trait GWAS reveals polygenic genetic architecture of carcass traits in beef cattle. Genomics, 2021, 113, 3325-3336.	1.3	19
62	DNA methylation profiles correlated to striped bass sperm fertility. BMC Genomics, 2018, 19, 244.	1.2	18
63	Interaction of the primordial germ cell-specific protein C2EIP with PTCH2 directs differentiation of embryonic stem cells via HH signaling activation. Cell Death and Disease, 2018, 9, 497.	2.7	18
64	RXRG associated in PPAR signal regulated the differentiation of primordial germ cell. Journal of Cellular Biochemistry, 2018, 119, 6926-6934.	1.2	18
65	Alternative splicing variants and DNA methylation status of BDNF in inbred chicken lines. Brain Research, 2009, 1269, 1-10.	1.1	17
66	A Comparative Evaluation of the Protective Efficacy of rMd5Î”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. Avian Diseases, 2011, 55, 384-390.	0.4	17
67	Marekâ€™s disease virus infection induces widespread differential chromatin marks in inbred chicken lines. BMC Genomics, 2012, 13, 557.	1.2	17
68	Genome-Wide Bovine H3K27me3 Modifications and the Regulatory Effects on Genes Expressions in Peripheral Blood Lymphocytes. PLoS ONE, 2012, 7, e39094.	1.1	16
69	Isolation of chicken embryonic stem cell and preparation of chicken chimeric model. Molecular Biology Reports, 2013, 40, 2149-2156.	1.0	14
70	Effects of obesity and metabolic syndrome on cardiovascular outcomes in pediatric kidney transplant recipients: a longitudinal study. Pediatric Nephrology, 2018, 33, 1419-1428.	0.9	14
71	Distinct roles of retinoic acid and BMP4 pathways in the formation of chicken primordial germ cells and spermatogonial stem cells. Food and Function, 2019, 10, 7152-7163.	2.1	14
72	Diet-induced changes in bacterial communities in the jejunum and their associations with bile acids in Angus beef cattle. Animal Microbiome, 2020, 2, 33.	1.5	14

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73	Narrow H3K4me2 is required for chicken PGC formation. Journal of Cellular Physiology, 2021, 236, 1391-1400.	2.0	14
74	Co-Expression Analysis of Fetal Weight-Related Genes in Ovine Skeletal Muscle during Mid and Late Fetal Development Stages. International Journal of Biological Sciences, 2014, 10, 1039-1050.	2.6	13
75	Transcriptome analysis reveals an activation of major histocompatibility complex 1 and 2 pathways in chicken trachea immunized with infectious laryngotracheitis virus vaccine. Poultry Science, 2014, 93, 848-855.	1.5	13
76	Host genetic resistance to Marek's disease sustains protective efficacy of herpesvirus of turkey in both experimental and commercial lines of chickens. Vaccine, 2014, 32, 1820-1827.	1.7	13
77	Histone modifications induced by MDV infection at early cytolytic and latency phases. BMC Genomics, 2015, 16, 311.	1.2	13
78	The Profiling of DNA Methylation and Its Regulation on Divergent Tenderness in Angus Beef Cattle. Frontiers in Genetics, 2020, 11, 939.	1.1	13
79	Taxonomic and functional adaption of the gastrointestinal microbiome of goats kept at high altitude (4800Âm) under intensive or extensive rearing conditions. FEMS Microbiology Ecology, 2021, 97, .	1.3	12
80	Dynamic expression and regulatory mechanism of TGF-Î² signaling in chicken embryonic stem cells differentiating into spermatogonial stem cells. Bioscience Reports, 2017, 37, .	1.1	11
81	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
82	Targeting Werner syndrome protein sensitizes U-2 OS osteosarcoma cells to selenium-induced DNA damage response and necrotic death. Biochemical and Biophysical Research Communications, 2012, 420, 24-28.	1.0	10
83	Regulation of crucial lnc<scp>RNA</scp>s in differentiation of chicken embryonic stem cells to spermatogonia stem cells. Animal Genetics, 2017, 48, 191-204.	0.6	10
84	Regulation of Hedgehog Signaling in Chicken Embryonic Stem Cells Differentiation Into Male Germ Cells (Gallus). Journal of Cellular Biochemistry, 2017, 118, 1379-1386.	1.2	10
85	Transgenerational transmission of maternal stimulatory experience in domesticated birds. FASEB Journal, 2018, 32, 7002-7017.	0.2	10
86	Gga-miR-130b-3p inhibits MSB1 cell proliferation, migration, invasion, and its downregulation in MD tumor is attributed to hypermethylation. Oncotarget, 2018, 9, 24187-24198.	0.8	10
87	DNA methylation, microRNA expression profiles and their relationships with transcriptome in grass-fed and grain-fed Angus cattle rumen tissue. PLoS ONE, 2019, 14, e0214559.	1.1	10
88	CYP19A1 (aromatase) dominates female gonadal differentiation in chicken (<i>Gallus gallus</i>) embryos sexual differentiation. Bioscience Reports, 2020, 40, .	1.1	10
89	Methylome Analysis in Chickens Immunized with Infectious Laryngotracheitis Vaccine. PLoS ONE, 2015, 10, e0100476.	1.1	10
90	Transcriptomic Profiling of Spleen in Grass-Fed and Grain-Fed Angus Cattle. PLoS ONE, 2015, 10, e0135670.	1.1	9

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91	Characterization of Copy Number Variationâ€™s Potential Role in Marekâ€™s Disease. International Journal of Molecular Sciences, 2017, 18, 1020.	1.8	9
92	Genetic assessment of inbred chicken lines indicates genomic signatures of resistance to Marekâ€™s disease. Journal of Animal Science and Biotechnology, 2018, 9, 65.	2.1	9
93	Functional characterization of the Sox2 , câ€Myc , and Oct4 promoters. Journal of Cellular Biochemistry, 2019, 120, 332-342.	1.2	9
94	WaveSeq: A Novel Data-Driven Method of Detecting Histone Modification Enrichments Using Wavelets. PLoS ONE, 2012, 7, e45486.	1.1	9
95	Vaccine by Chicken Line Interaction Alters the Protective Efficacy against Challenge with a Very Virulent plus Strain of Marekâ€™s Disease Virus in White Leghorn Chickens. World Journal of Vaccines, 2012, 02, 1-11.	0.8	9
96	Calibration of Mutation Rates Reveals Diverse Subfamily Structure of Galliform CR1 Repeats. Genome Biology and Evolution, 2009, 1, 119-130.	1.1	8
97	Abomasal mucosal immune responses of cattle with limited or continuous exposure to pasture-borne gastrointestinal nematode parasite infection. Veterinary Parasitology, 2016, 229, 118-125.	0.7	8
98	Linc-GALMD1 Regulates Viral Gene Expression in the Chicken. Frontiers in Genetics, 2019, 10, 1122.	1.1	8
99	âˆ† DNMT3B4-del Contributes to Aberrant DNA Methylation Patterns in Lung Tumorigenesis. EBioMedicine, 2015, 2, 1340-1350.	2.7	7
100	Epigenetics and animal virus infections. Frontiers in Genetics, 2015, 6, 48.	1.1	7
101	P53 and H3K4me2 activate N6â€methylated <i>LncPGCATâ€1</i> to regulate primordial germ cell formation via MAPK signaling. Journal of Cellular Physiology, 2020, 235, 9895-9909.	2.0	7
102	Cloning of the Xuhuai Goat PPARÎ³ Gene and the Preparation of Transgenic Sheep. Biochemical Genetics, 2013, 51, 543-553.	0.8	6
103	CRISPR/Cas9-Mediated Deletion of <i>C1EIS</i> Inhibits Chicken Embryonic Stem Cell Differentiation Into Male Germ Cells (<i>Gallus gallus</i>). Journal of Cellular Biochemistry, 2017, 118, 2380-2386.	1.2	6
104	Genomic Variation between Genetic Lines of White Leghorns Differed in Resistance to Marekâ€™s Disease. Journal of Clinical Epigenetics, 2017, 03, .	0.3	6
105	Metabolic Regulations by lncRNA, miRNA, and ceRNA Under Grass-Fed and Grain-Fed Regimens in Angus Beef Cattle. Frontiers in Genetics, 2021, 12, 579393.	1.1	6
106	Role and function of the Hintw in early sex differentiation in chicken (Gallus gallus) embryo. Animal Biotechnology, 2021, , 1-11.	0.7	6
107	Integrated Small RNA Sequencing, Transcriptome and GWAS Data Reveal microRNA Regulation in Response to Milk Protein Traits in Chinese Holstein Cattle. Frontiers in Genetics, 2021, 12, 726706.	1.1	6
108	Principal component tests: applied to temporal gene expression data. BMC Bioinformatics, 2009, 10, S26.	1.2	5

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109	Comprehensive Analysis of Gene-Environmental Interactions with Temporal Gene Expression Profiles in Pseudomonas aeruginosa. PLoS ONE, 2012, 7, e35993.	1.1	5
110	Marekâ€™s Disease Virus Infection Induced Mitochondria Changes in Chickens. International Journal of Molecular Sciences, 2019, 20, 3150.	1.8	5
111	Allele-Specific Expression of CD4+ T Cells in Response to Marekâ€™s Disease Virus Infection. Genes, 2019, 10, 718.	1.0	5
112	DNA Methylation Down-Regulates EGFR Expression in Chickens. Avian Diseases, 2013, 57, 366-371.	0.4	4
113	Diet induced the change of mtDNA copy number and metabolism in Angus cattle. Journal of Animal Science and Biotechnology, 2020, 11, 84.	2.1	4
114	Pan-RNA editing analysis of the bovine genome. RNA Biology, 2021, 18, 368-381.	1.5	4
115	Long Noncoding RNA LncPGCR Mediated by TCF7L2 Regulates Primordial Germ Cell Formation in Chickens. Animals, 2021, 11, 292.	1.0	4
116	Characterization of Alternative Splicing (AS) Events during Chicken (Gallus gallus) Male Germ-Line Stem Cell Differentiation with Single-Cell RNA-seq. Animals, 2021, 11, 1469.	1.0	4
117	Identification of a novel differentially methylated region adjacent to ATG16L2 in lung cancer cells using methyl-CpG binding domain protein-enriched genome sequencing. Genome, 2021, 64, 1-14.	0.9	4
118	Tributyrin, a Butyrate Pro-Drug, Primes Satellite Cells for Differentiation by Altering the Epigenetic Landscape. Cells, 2021, 10, 3475.	1.8	4
119	<i>Hsd3b2</i> associated in modulating steroid hormone synthesis pathway regulates the differentiation of chicken embryonic stem cells into spermatogonial stem cells. Journal of Cellular Biochemistry, 2018, 119, 1111-1121.	1.2	3
120	Growth curve, blood parameters and carcass traits of grass-fed Angus steers. Animal, 2021, 15, 100381.	1.3	3
121	Analysis for temporal gene expressions under multiple biological conditions. Statistics in Biosciences, 2012, 4, 282-299.	0.6	2
122	Increased carotid intimaâ€media thickness in African American pediatric kidney transplant recipients. Pediatric Transplantation, 2018, 22, e13163.	0.5	2
123	Study on immortal conditions of chicken embryonic stem cells. Journal of Cellular Biochemistry, 2019, 120, 1376-1385.	1.2	2
124	Transcriptome Sequencing and Comparative Analysis of Amphoteric ESCs and PGCs in Chicken (Gallus) Tj ETQq0 0 0 rgBT /Overlock 10	1.0	2
125	Genome-wide characterization of copy number variations in the host genome in genetic resistance to Marekâ€™s disease using next generation sequencing. BMC Genetics, 2020, 21, 77.	2.7	2
126	Parent-of-origin has no detectable effect on survival days of Marek's disease virus infected White Leghorns. Poultry Science, 2019, 98, 4498-4503.	1.5	1

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127	The different effects of viral and bacterial mimics maternal stimuli on ethology of hens and reproduction of their offspring. Poultry Science, 2019, 98, 4153-4160.	1.5	1
128	Adiponectin and its receptor genes' expression in response to Marek's disease virus infection of White Leghorns. Poultry Science, 2020, 99, 4249-4258.	1.5	1
129	C1EIP Functions as an Activator of ENO1 to Promote Chicken PGCs Formation via Inhibition of the Notch Signaling Pathway. Frontiers in Genetics, 2020, 11, 751.	1.1	1
130	Glycolysis Combined with Core Pluripotency Factors to Promote the Formation of Chicken Induced Pluripotent Stem Cells. Animals, 2021, 11, 425.	1.0	1
131	0306 Exploring the feasibility of using copy number variants as genetic markers through large-scale whole genome sequencing experiments. Journal of Animal Science, 2016, 94, 146-146.	0.2	1
132	Detection of threshold points for gene expressions under multiple biological conditions. Statistics and Its Interface, 2017, 10, 643-655.	0.2	1
133	The identification of functional motifs in temporal gene expression analysis. Evolutionary Bioinformatics, 2007, 1, 84-96.	0.6	1
134	Characterizing Gene Expressions Based on Their Temporal Observations. Journal of Biomedicine and Biotechnology, 2009, 2009, 1-5.	3.0	0
135	Cloning, expression pattern analysis, and subcellular localization of Capra hircus SCD1 gene with production of transgenic mice. Journal of Cellular Biochemistry, 2018, 119, 2240-2247.	1.2	0
136	Genotype by environment interactions for body weight in Mediterranean buffaloes using reaction norm models. Revista Colombiana De Ciencias Pecuarias, 2021, 34, 166-176.	0.4	0
137	105 The Epigenetics and Plasticity of CD4+ T Cells in Poultry Health. Journal of Animal Science, 2021, 99, 55-55.	0.2	0
138	Down-Regulation of Promoter Methylation Level of CD4 Gene After MDV Infection in MD-Susceptible Chicken Line. , 2014, , 51-62.		0