

Zhihua Jiang

List of Publications by Year in descending order

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154
papers

4,196
citations

126907

33
h-index

138484

58
g-index

158
all docs

158
docs citations

158
times ranked

5086
citing authors

#	ARTICLE	IF	CITATIONS
1	Maternal exercise intergenerationally drives muscle-based thermogenesis via activation of apelin-AMPK signaling. <i>EBioMedicine</i> , 2022, 76, 103842.	6.1	19
2	A novel quantitative real-time PCR method for the detection of mammalian and poultry species based on a shared single-copy nuclear DNA sequence. <i>Food Chemistry</i> , 2021, 341, 128170.	8.2	7
3	Genome-to-phenome research in rats: progress and perspectives. <i>International Journal of Biological Sciences</i> , 2021, 17, 119-133.	6.4	2
4	Alternative transcriptome analysis to build the genome-phenome bridges in animals. , 2021, , 49-59.		0
5	Long-term trends of microplastics in seawater and farmed oysters in the Maowei Sea, China. <i>Environmental Pollution</i> , 2021, 273, 116450.	7.5	35
6	Positive selection of skeleton-related genes during duck domestication revealed by whole genome sequencing. <i>Bmc Ecology and Evolution</i> , 2021, 21, 165.	1.6	6
7	Genome-wide association study shows that microtia in Altay sheep is caused by a 76 bp duplication of <i>HMX1</i> . <i>Animal Genetics</i> , 2020, 51, 132-136.	1.7	11
8	A joint analysis strategy reveals genetic changes associated with artificial selection between egg-type and meat-type ducks. <i>Animal Genetics</i> , 2020, 51, 890-898.	1.7	5
9	Maternal Inactivity Programs Skeletal Muscle Dysfunction in Offspring Mice by Attenuating Apelin Signaling and Mitochondrial Biogenesis. <i>Cell Reports</i> , 2020, 33, 108461.	6.4	27
10	RNA-seq analysis on <i>ets1</i> mutant embryos of <i>Xenopus tropicalis</i> identifies <i>microseminoprotein beta gene 3</i> as an essential regulator of neural crest migration. <i>FASEB Journal</i> , 2020, 34, 12726-12738.	0.5	6
11	Effect of RNF4-Sac II gene polymorphism on reproductive traits of Landrace × Large White crossbred sows. <i>Reproduction in Domestic Animals</i> , 2020, 55, 1286-1293.	1.4	1
12	Maternal exercise via exerkine apelin enhances brown adipogenesis and prevents metabolic dysfunction in offspring mice. <i>Science Advances</i> , 2020, 6, eaaz0359.	10.3	51
13	Modeling of Genome-Wide Polyadenylation Signals in <i>Xenopus tropicalis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 647.	2.3	4
14	Inheritance patterns of the transcriptome in hybrid chickens and their parents revealed by expression analysis. <i>Scientific Reports</i> , 2019, 9, 5750.	3.3	31
15	Deep Genome Resequencing Reveals Artificial and Natural Selection for Visual Deterioration, Plateau Adaptability and High Prolificacy in Chinese Domestic Sheep. <i>Frontiers in Genetics</i> , 2019, 10, 300.	2.3	33
16	Alternative polyadenylation coordinates embryonic development, sexual dimorphism and longitudinal growth in <i>Xenopus tropicalis</i> . <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 2185-2198.	5.4	16
17	341 Up-regulation of wound healing pathway may trigger adipogenic potentials of intramuscular progenitor cells in Wagyu as compared to Angus cattle. <i>Journal of Animal Science</i> , 2019, 97, 95-96.	0.5	0
18	Vapor Cannabis Exposure Promotes Genetic Plasticity in the Rat Hypothalamus. <i>Scientific Reports</i> , 2019, 9, 16866.	3.3	12

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19	Evolution of cis- and trans-regulatory divergence in the chicken genome between two contrasting breeds analyzed using three tissue types at one-day-old. <i>BMC Genomics</i> , 2019, 20, 933.	2.8	12
20	Alternative polyadenylation drives genome-to-phenome information detours in the AMPK $\hat{\pm}$ 1 and AMPK $\hat{\pm}$ 2 knockout mice. <i>Scientific Reports</i> , 2018, 8, 6462.	3.3	10
21	Whole-genome resequencing reveals signatures of selection and timing of duck domestication. <i>GigaScience</i> , 2018, 7, .	6.4	86
22	Mapping diet-induced alternative polyadenylation of hypothalamic transcripts in the obese rat. <i>Physiology and Behavior</i> , 2018, 188, 173-180.	2.1	16
23	The role of ppar $\hat{\gamma}$ 3 in embryonic development of <i>Xenopus tropicalis</i> under triphenyltin-induced teratogenicity. <i>Science of the Total Environment</i> , 2018, 633, 1245-1252.	8.0	13
24	Alternative polyadenylation analysis in animals and plants: newly developed strategies for profiling, processing and validation. <i>International Journal of Biological Sciences</i> , 2018, 14, 1709-1714.	6.4	6
25	Investigating the effect of GDF9 , BMP15 , BMP6 and BMPR1B polymorphisms on Egyptian sheep fecundity and their transcripts expression in ovarian cells. <i>Small Ruminant Research</i> , 2018, 165, 34-40.	1.2	10
26	MicroRNA expression profiling in alveolar macrophages of indigenous Chinese Tongcheng pigs infected with PRRSV in vivo. <i>Journal of Applied Genetics</i> , 2017, 58, 539-544.	1.9	9
27	A single nucleotide polymorphism possibly associated with fat deposition is methylated in the bovine TFAM promoter. <i>Acta Agriculturae Slovenica</i> , 2017, 108, 65.	0.3	0
28	Genome Wide Sampling Sequencing for SNP Genotyping: Methods, Challenges and Future Development. <i>International Journal of Biological Sciences</i> , 2016, 12, 100-108.	6.4	77
29	P1044 Whole transcriptome termini site sequencing: A next generation sequencing method to accurately profile gene expression and alternative polyadenylation with 1 pipeline. <i>Journal of Animal Science</i> , 2016, 94, 36-36.	0.5	0
30	Genome-wide screening of candidate genes for improving fertility in Egyptian native Rahmani sheep. <i>Animal Genetics</i> , 2016, 47, 513-513.	1.7	5
31	Review: Animal model and the current understanding of molecule dynamics of adipogenesis. <i>Animal</i> , 2016, 10, 927-932.	3.3	25
32	Accurate Profiling of Gene Expression and Alternative Polyadenylation with Whole Transcriptome Termini Site Sequencing (WTTS-Seq). <i>Genetics</i> , 2016, 203, 683-697.	2.9	31
33	Myostatin inhibits porcine intramuscular preadipocyte differentiation in vitro. <i>Domestic Animal Endocrinology</i> , 2016, 55, 25-31.	1.6	18
34	Long noncoding RNAs in regulating adipogenesis: new RNAs shed lights on obesity. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 2079-2087.	5.4	92
35	INVITED REVIEW: Evolution of meat animal growth research during the past 50 years: Adipose and muscle stem cells. <i>Journal of Animal Science</i> , 2015, 93, 457-481.	0.5	26
36	Mining Next Generation Sequencing Data: How to Avoid ?Treasure in, Error Out?. <i>Journal of Data Mining in Genomics & Proteomics</i> , 2015, 06, .	0.5	1

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37	Enhanced mitogenesis in stromal vascular cells derived from subcutaneous adipose tissue of Wagyu compared with those of Angus cattle. <i>Journal of Animal Science</i> , 2015, 93, 1015.	0.5	14
38	Genome Wide Distributions and Functional Characterization of Copy Number Variations between Chinese and Western Pigs. <i>PLoS ONE</i> , 2015, 10, e0131522.	2.5	47
39	Whole transcriptome analysis with sequencing: methods, challenges and potential solutions. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 3425-3439.	5.4	141
40	Molecular characterization of the porcine S100A6 gene and analysis of its expression in pigs infected with highly pathogenic porcine reproductive and respiratory syndrome virus (HP-PRRSV). <i>Journal of Applied Genetics</i> , 2015, 56, 355-363.	1.9	9
41	Genome Wide Screening of Candidate Genes for Improving Piglet Birth Weight Using High and Low Estimated Breeding Value Populations. <i>International Journal of Biological Sciences</i> , 2014, 10, 236-244.	6.4	31
42	Porcine glucocorticoid receptor (NR3C1) gene: Tissue-specificity of transcriptional strength and glucocorticoid responsiveness of alternative promoters. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2014, 141, 87-93.	2.5	12
43	Evolutionary characterization of pig interferon-inducible transmembrane gene family and member expression dynamics in tracheobronchial lymph nodes of pigs infected with swine respiratory disease viruses. <i>Veterinary Immunology and Immunopathology</i> , 2014, 159, 180-191.	1.2	19
44	Adipose Cell Precursors: Stem Cells in Medicine, Tissue Engineering, and Reconstructive Surgery. , 2014, , 19-22.		1
45	Emerging roles of zinc finger proteins in regulating adipogenesis. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 4569-4584.	5.4	71
46	Two completely linked polymorphisms in the <i>PPARG</i> transcriptional regulatory region significantly affect gene expression and intramuscular fat deposition in the longissimus dorsi muscle of Erhualian pigs. <i>Animal Genetics</i> , 2013, 44, 458-462.	1.7	14
47	Hsp70 positively regulates porcine circovirus type 2 replication in vitro. <i>Virology</i> , 2013, 447, 52-62.	2.4	40
48	Two-dimensional liquid chromatography-tandem mass spectrometry coupled with isobaric tags for relative and absolute quantification (iTRAQ) labeling approach revealed first proteome profiles of pulmonary alveolar macrophages infected with porcine circovirus type 2. <i>Journal of Proteomics</i> , 2013, 79, 72-86.	2.4	44
49	Molecular characterization of porcine SARM1 and its role in regulating TLRs signaling during highly pathogenic porcine reproductive and respiratory syndrome virus infection in vivo. <i>Developmental and Comparative Immunology</i> , 2013, 39, 117-126.	2.3	13
50	Bovine dedifferentiated adipose tissue (DFAT) cells. <i>Adipocyte</i> , 2013, 2, 148-159.	2.8	19
51	Interferon Induced <i>IFIT</i> Family Genes in Host Antiviral Defense. <i>International Journal of Biological Sciences</i> , 2013, 9, 200-208.	6.4	197
52	Cell Supermarket: Adipose Tissue as a Source of Stem Cells. <i>Journal of Genomics</i> , 2013, 1, 39-44.	0.9	21
53	Adipogenesis: It Is Not Just Lipid That Comprises Adipose Tissue. <i>Journal of Genomics</i> , 2013, 1, 1-4.	0.9	10
54	Adenovirus-mediated interference of FABP4 regulates mRNA expression of ADIPOQ, LEP and LEPR in bovine adipocytes. <i>Genetics and Molecular Research</i> , 2013, 12, 494-505.	0.2	21

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55	Cellular and Molecular Implications of Mature Adipocyte Dedifferentiation. <i>Journal of Genomics</i> , 2013, 1, 5-12.	0.9	27
56	Reactomes of Porcine Alveolar Macrophages Infected with Porcine Reproductive and Respiratory Syndrome Virus. <i>PLoS ONE</i> , 2013, 8, e59229.	2.5	33
57	Obesity Gene Atlas in Mammals. <i>Journal of Genomics</i> , 2013, 1, 45-55.	0.9	55
58	Genome-Wide Genetic Diversity and Differentially Selected Regions among Suffolk, Rambouillet, Columbia, Polypay, and Targhee Sheep. <i>PLoS ONE</i> , 2013, 8, e65942.	2.5	58
59	Like pigs, and unlike other breeds of cattle examined, mature Angus-derived adipocytes may extrude lipid prior to proliferation in vitro. <i>Adipocyte</i> , 2012, 1, 237-241.	2.8	6
60	Two-Dimensional Liquid Chromatography-Tandem Mass Spectrometry Coupled with Isobaric Tags for Relative and Absolute Quantification (iTRAQ) Labeling Approach Revealed First Proteome Profiles of Pulmonary Alveolar Macrophages Infected with Porcine Reproductive and Respiratory Syndrome Virus. <i>Journal of Proteome Research</i> , 2012, 11, 2890-2903.	3.7	50
61	Bovine mature adipocytes readily return to a proliferative state. <i>Tissue and Cell</i> , 2012, 44, 385-390.	2.2	9
62	Coordinated miRNA/mRNA Expression Profiles for Understanding Breed-Specific Metabolic Characters of Liver between Erhualian and Large White Pigs. <i>PLoS ONE</i> , 2012, 7, e38716.	2.5	21
63	Catalog of MicroRNA Seed Polymorphisms in Vertebrates. <i>PLoS ONE</i> , 2012, 7, e30737.	2.5	61
64	Quantitative Genomics of 30 Complex Phenotypes in Wagyu x Angus F ₁ Progeny. <i>International Journal of Biological Sciences</i> , 2012, 8, 838-858.	6.4	13
65	Expression Profiles of the Insulin-like Growth Factor System Components in Liver Tissue during Embryonic and Postnatal Growth of Erhualian and Yorkshire Reciprocal Cross F1 Pigs. <i>Asian-Australasian Journal of Animal Sciences</i> , 2012, 25, 903-912.	2.4	15
66	A Global View of 54,001 Single Nucleotide Polymorphisms (SNPs) on the Illumina BovineSNP50 BeadChip and Their Transferability to Water Buffalo. <i>International Journal of Biological Sciences</i> , 2011, 7, 18-27.	6.4	37
67	Development and Initial Characterization of A HAPPY Panel for Mapping the X. <i>Tropicalis</i> Genome. <i>International Journal of Biological Sciences</i> , 2011, 7, 1037-1044.	6.4	4
68	The Heparan and Heparin Metabolism Pathway is Involved in Regulation of Fatty Acid Composition. <i>International Journal of Biological Sciences</i> , 2011, 7, 659-663.	6.4	20
69	Obesity, Metabolic Syndrome, and Adipocytes. <i>Journal of Lipids</i> , 2011, 2011, 1-5.	4.8	32
70	Potential Impact of Mature Adipocyte Dedifferentiation in Terms of Cell Numbers. <i>International Journal of Stem Cells</i> , 2011, 4, 76-77.	1.8	13
71	Reproductive Genomics: Genome, Transcriptome, and Proteome Resources. , 2010, , 3-22.		0
72	Genomics of Reproductive Diseases in Cattle and Swine. , 2010, , 99-127.		0

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73	Physiological Genomics of Conceptus-Endometrial Interactions Mediating Corpus Luteum Rescue. , 2010, , 231-249.		0
74	Biotechnology and Fertility Regulation. , 2010, , 317-338.		0
75	Comparative Genomics of the Y Chromosome and Male Fertility. , 2010, , 129-155.		4
76	Quantitative Genomics of Male Reproduction. , 2010, , 53-66.		0
77	Genetics and Genomics of Reproductive Disorders. , 2010, , 67-97.		1
78	Nutrigenomics for Improved Reproduction. , 2010, , 413-438.		0
79	Quantitative Genomics of Female Reproduction. , 2010, , 23-51.		1
80	Functional Genomics Studies of Ovarian Function in Livestock: Physiological Insight Gained and Perspective for the Future. , 2010, , 181-203.		0
81	Physiological Genomics of Placental Growth and Development. , 2010, , 251-268.		0
82	Cellular, Molecular, and Genomic Mechanisms Regulating Testis Function in Livestock. , 2010, , 269-290.		0
83	The Epigenome and Its Relevance to Somatic Cell Nuclear Transfer and Nuclear Reprogramming. , 2010, , 291-316.		0
84	Proteomics of Male Seminal Plasma. , 2010, , 339-366.		4
85	Toxicogenomics of Reproductive Endocrine Disruption. , 2010, , 397-412.		2
86	Mitochondriomics of Reproduction and Fertility. , 2010, , 157-179.		0
87	Physiological Genomics of Preimplantation Embryo Development in Production Animals. , 2010, , 205-229.		0
88	Allied Industry Approaches to Alter Intramuscular Fat Content and Composition in Beef Animals. Journal of Food Science, 2010, 75, R1-8.	3.1	59
89	Water Buffalo Genome Science Comes of Age. International Journal of Biological Sciences, 2010, 6, 333-349.	6.4	100
90	Skeletal Muscle Stem Cells from Animals I. Basic Cell Biology. International Journal of Biological Sciences, 2010, 6, 465-474.	6.4	53

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91	Cellular and molecular comparison of redifferentiation of intramuscular- and visceral-adipocyte derived progeny cells. <i>International Journal of Biological Sciences</i> , 2010, 6, 80-88.	6.4	38
92	Lipid metabolism, adipocyte depot physiology and utilization of meat animals as experimental models for metabolic research. <i>International Journal of Biological Sciences</i> , 2010, 6, 691-699.	6.4	89
93	Evolutionary Genomics of Sex Determination in Domestic Animals. , 2010, , 367-395.		0
94	Perspectives on the formation of an interdisciplinary research team. <i>Biochemical and Biophysical Research Communications</i> , 2010, 391, 1155-1157.	2.1	13
95	Examination of adipose depot-specific PPAR moieties. <i>Biochemical and Biophysical Research Communications</i> , 2010, 394, 241-242.	2.1	4
96	The Reverse Cholesterol Transport Pathway Improves Understanding of Genetic Networks for Fat Deposition and Muscle Growth in Beef Cattle. <i>PLoS ONE</i> , 2010, 5, e15203.	2.5	11
97	The <i>Glypican</i> 3-Hosted Murine <i>Mir717</i> Gene: Sequence Conservation, Seed Region Polymorphisms and Putative Targets. <i>International Journal of Biological Sciences</i> , 2010, 6, 769-772.	6.4	19
98	Differential display of expressed genes reveals a novel function of <i>SFRS18</i> in regulation of intramuscular fat deposition. <i>International Journal of Biological Sciences</i> , 2009, 5, 28-33.	6.4	24
99	Discovery of novel genetic networks associated with 19 economically important traits in beef cattle. <i>International Journal of Biological Sciences</i> , 2009, 5, 528-542.	6.4	66
100	Porcine skeletal muscle differentially expressed gene <i>CMYA1</i> : isolation, characterization, mapping, expression and association analysis with carcass traits. <i>Animal Genetics</i> , 2009, 40, 255-261.	1.7	5
101	BOARD-INVITED REVIEW: The biology and regulation of preadipocytes and adipocytes in meat animals ^{1,2} . <i>Journal of Animal Science</i> , 2009, 87, 1218-1246.	0.5	279
102	Clonal Mature Adipocyte Production of Proliferative-competent Daughter Cells Requires Lipid Export Prior to Cell Division. <i>International Journal of Stem Cells</i> , 2009, 2, 76-79.	1.8	13
103	Old can be new again: HAPPY whole genome sequencing, mapping and assembly. <i>International Journal of Biological Sciences</i> , 2009, 5, 298-303.	6.4	14
104	Lipoproteins, cholesterol homeostasis and cardiac health. <i>International Journal of Biological Sciences</i> , 2009, 5, 474-488.	6.4	130
105	The Porcine Mitochondrial Transcription Factor <i>a</i> Gene: Molecular Characterization, Radiation Hybrid Mapping and Genetic Diversity among 12 Pig Breeds. <i>American Journal of Animal and Veterinary Sciences</i> , 2009, 4, 129-135.	0.5	2
106	The pig p160 co-activator family: Full length cDNA cloning, expression and effects on intramuscular fat content in Longissimus Dorsi muscle. <i>Domestic Animal Endocrinology</i> , 2008, 35, 208-216.	1.6	13
107	The Complementary Neighborhood Patterns and Methylation-to-Mutation Likelihood Structures of 15,110 Single-Nucleotide Polymorphisms in the Bovine Genome. <i>Genetics</i> , 2008, 180, 639-647.	2.9	9
108	Comparative understanding of <i>UTS2</i> and <i>UTS2R</i> genes for their involvement in type 2 diabetes mellitus. <i>International Journal of Biological Sciences</i> , 2008, 4, 96-102.	6.4	23

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109	Significant associations of stearoyl-CoA desaturase (<i>SCD1</i>) gene with fat deposition and composition in skeletal muscle. <i>International Journal of Biological Sciences</i> , 2008, 4, 345-351.	6.4	70
110	Genome Assembly Anchored QTL Map of Bovine Chromosome 14. <i>International Journal of Biological Sciences</i> , 2008, 4, 406-414.	6.4	38
111	A Novel Type of Sequence Variation: Multiple-Nucleotide Length Polymorphisms Discovered in the Bovine Genome. <i>Genetics</i> , 2007, 176, 403-407.	2.9	9
112	Advances in QTL Mapping in Pigs. <i>International Journal of Biological Sciences</i> , 2007, 3, 192-197.	6.4	114
113	A simplified QTL mapping approach for screening and mapping of novel AFLP markers associated with beef marbling. <i>Journal of Biotechnology</i> , 2007, 127, 177-187.	3.8	9
114	Corticotropin releasing hormone is a promising candidate gene for marbling and subcutaneous fat depth in beef cattle. <i>Genome</i> , 2007, 50, 939-945.	2.0	25
115	Swine Genome Science Comes of Age. <i>International Journal of Biological Sciences</i> , 2007, 3, 129-131.	6.4	17
116	Functional <i>UQCRC1</i> Polymorphisms Affect Promoter Activity and Body Lipid Accumulation. <i>Obesity</i> , 2007, 15, 2896-2901.	3.0	32
117	BRIEF NOTES: Development of a model for mapping cryptorchidism in sheep and initial evidence for association of <i>INSL3</i> with the defect. <i>Animal Genetics</i> , 2007, 38, 189-191.	1.7	3
118	Hitting the Jackpot Twice: Identifying and Patenting Gene Tests Related to Muscle Lipid Accumulation for Meat Quality in Animals and Type 2 Diabetes/Obesity in Humans. <i>Recent Patents on DNA & Gene Sequences</i> , 2007, 1, 100-111.	0.7	7
119	Significant association of the calpastatin gene with fertility and longevity in dairy cattle. <i>Animal Genetics</i> , 2006, 37, 304-305.	1.7	25
120	The bovine fatty acid binding protein 4 gene is significantly associated with marbling and subcutaneous fat depth in Wagyu x Limousin F2 crosses. <i>Animal Genetics</i> , 2006, 37, 400-402.	1.7	133
121	Cross Species Association Examination of <i>UCN3</i> and <i>CRHR2</i> as Potential Pharmacological Targets for Antiobesity Drugs. <i>PLoS ONE</i> , 2006, 1, e80.	2.5	19
122	A novel nuclear-encoded mitochondrial poly(A) polymerase <i>PAPD1</i> is a potential candidate gene for the extreme obesity related phenotypes in mammals. <i>International Journal of Biological Sciences</i> , 2006, 2, 171-178.	6.4	17
123	Frequency distribution of a Cys430Ser polymorphism in peroxisome proliferator-activated receptor-gamma coactivator-1 (<i>PPARGC1</i>) gene sequence in Chinese and Western pig breeds. <i>Journal of Animal Breeding and Genetics</i> , 2005, 122, 7-11.	2.0	19
124	An independent confirmation of a quantitative trait locus for milk yield and composition traits on bovine chromosome 26. <i>Journal of Animal Breeding and Genetics</i> , 2005, 122, 281-284.	2.0	7
125	Fine mapping of the bovine chromosome 22q24 region that harbours antimicrobial genes and a QTL for somatic cell score. <i>Animal Genetics</i> , 2005, 36, 448-450.	1.7	4
126	Pattern Profiling and Mapping of the Fat Body Transcriptome in <i>Drosophila melanogaster</i> . <i>Obesity</i> , 2005, 13, 1898-1904.	4.0	24

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127	Evaluation of Candidate Gene Effects for Beef Backfat via Bayesian Model Selection. <i>Genetica</i> , 2005, 125, 103-113.	1.1	25
128	Multi-alignment of orthologous genome regions in five species provides new insights into the evolutionary make-up of mammalian genomes. <i>Chromosome Research</i> , 2005, 13, 707-715.	2.2	8
129	Significant associations of the mitochondrial transcription factor A promoter polymorphisms with marbling and subcutaneous fat depth in Wagyu x Limousin F2 crosses. <i>Biochemical and Biophysical Research Communications</i> , 2005, 334, 516-523.	2.1	48
130	In silico Discovery of Genes Expressed in Liver, Kidney, Spleen and Small Intestine of Pigs. <i>Asian-Australasian Journal of Animal Sciences</i> , 2005, 18, 170-178.	2.4	0
131	Comparative gene-based in silico analysis of transcriptomes in different bovine tissues and (or) organs. <i>Genome</i> , 2004, 47, 1164-1172.	2.0	3
132	A high-resolution radiation hybrid map of porcine chromosome 6. <i>Animal Genetics</i> , 2004, 35, 367-378.	1.7	10
133	Census of orthologous genes and self-organizing maps of biologically relevant transcriptional patterns in chickens (<i>Gallus gallus</i>). <i>Gene</i> , 2004, 340, 213-225.	2.2	12
134	The sequence of the bovine cysteine- and histidine-rich cytoplasmic gene: EST puzzle solving by comparative assembly and confirmation by genomic sequencing. <i>Journal of Animal Breeding and Genetics</i> , 2003, 120, 210-215.	2.0	2
135	Linking porcine microsatellite markers to known genome regions by identifying their human orthologs. <i>Genome</i> , 2003, 46, 798-808.	2.0	4
136	Census of Genes Expressed in Porcine Embryos and Reproductive Tissues by Mining an Expressed Sequence Tag Database Based on Human Genes. <i>Biology of Reproduction</i> , 2003, 69, 1177-1182.	2.7	12
137	Mapping Quantitative Trait Loci Affecting Female Reproductive Traits on Porcine Chromosome 81. <i>Biology of Reproduction</i> , 2003, 68, 2172-2179.	2.7	87
138	Measuring conservation of contiguous sets of autosomal markers on bovine and porcine genomes in relation to the map of the human genome. <i>Genome</i> , 2002, 45, 769-776.	2.0	9
139	Comparative mapping of Homo sapiens chromosome 4 (HSA4) and Sus scrofa chromosome 8 (SSC8) using orthologous genes representing different cytogenetic bands as landmarks. <i>Genome</i> , 2002, 45, 147-156.	2.0	25
140	No detectable association of the ESR Pvu II mutation with sow productivity in a Meishan x Large White F2 population. <i>Animal Genetics</i> , 2002, 33, 448-450.	1.7	27
141	A missense mutation in the follicle stimulating hormone receptor (FSHR) gene shows different allele effects on litter size in Chinese Erhualian and German Landrace pigs. <i>Journal of Animal Breeding and Genetics</i> , 2002, 119, 335-341.	2.0	5
142	The porcine gonadotropin-releasing hormone receptor gene (GNRHR): Genomic organization, polymorphisms, and association with the number of corpora lutea. <i>Genome</i> , 2001, 44, 7-12.	2.0	29
143	RH mapping of canine TOAST markers: a new strategy for species-specific primer design to prevent amplification of host orthologous gene products especially with similar sizes. <i>Mammalian Genome</i> , 2001, 12, 799-801.	2.2	2
144	Multi-primer target PCR for rapid identification of bovine DRB3 alleles. <i>Animal Genetics</i> , 2001, 32, 219-221.	1.7	30

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145	The porcine gonadotropin-releasing hormone receptor gene (<i>GNRHR</i>): Genomic organization, polymorphisms, and association with the number of corpora lutea. <i>Genome</i> , 2001, 44, 7-12.	2.0	28
146	Comparative mapping between humans and pigs: localization of 58 anchorage markers (TOASTs) by use of porcine somatic cell and radiation hybrid panels. <i>Mammalian Genome</i> , 2000, 11, 1098-1106.	2.2	35
147	Isolation and Genome Characterization of Porcine Reproductive and Respiratory Syndrome Virus in P. R. China. <i>Journal of Veterinary Diagnostic Investigation</i> , 2000, 12, 156-158.	1.1	25
148	Toward a dog radiation hybrid map. , 1999, 90, 62-67.		15
149	Bi-PASA genotyping of a new polymorphism in theAPOBgene shows no evidence for an association with fatness in pigs. <i>Animal Genetics</i> , 1999, 30, 54-57.	1.7	5
150	Genetic polymorphisms in the leptin gene and their association with fatness in four pig breeds. <i>Mammalian Genome</i> , 1999, 10, 191-193.	2.2	57
151	Characterization of 463 Type I markers suitable for dog genome mapping. <i>Mammalian Genome</i> , 1999, 10, 803-813.	2.2	20
152	Traced orthologous amplified sequence tags (TOASTs) and mammalian comparative maps. <i>Mammalian Genome</i> , 1998, 9, 577-587.	2.2	79
153	A Whole-Genome Radiation Hybrid Map of the Dog Genome. <i>Genomics</i> , 1998, 54, 361-378.	2.9	159
154	The porcine TTR locus maps to chromosome 6q. <i>Animal Genetics</i> , 1996, 27, 351-353.	1.7	4