Klaus Wimmers

List of Publications by Year
in descending order

325 papers	6,273 citations	108046 37 h-index	175968 55 g-index
330 all docs	330 docs citations	330 times ranked	6298 citing authors

#	Article	IF	Citations
1	Brain Transcriptome Responses to Dexamethasone Depending on Dose and Sex Reveal Factors Contributing to Sex-Specific Vulnerability to Stress-Induced Disorders. Neuroendocrinology, 2022, 112, 235-251.	1.2	6
2	Soil and Plant Responses to Phosphorus Inputs from Different Phytase-Associated Animal Diets. Agronomy, 2022, 12, 130.	1.3	0
3	Multi-Omics Reveals Different Strategies in the Immune and Metabolic Systems of High-Yielding Strains of Laying Hens. Frontiers in Genetics, 2022, 13, 858232.	1.1	3
4	Genetic regulation and variation of expression of miRNA and mRNA transcripts in fetal muscle tissue in the context of sex, dam and variable fetal weight. Biology of Sex Differences, 2022, 13, 24.	1.8	5
5	tiRNAs: Insights into Their Biogenesis, Functions, and Future Applications in Livestock Research. Non-coding RNA, 2022, 8, 37.	1.3	1
6	The Growth Performance, Nutrient Digestibility, Gut Bacteria and Bone Strength of Broilers Offered Alternative, Sustainable Diets Varying in Nutrient Specification and Phytase Dose. Animals, 2022, 12, 1669.	1.0	2
7	Effects of excessive or restricted phosphorus and calcium intake during early life on markers of bone architecture and composition in pigs. Journal of Animal Physiology and Animal Nutrition, 2021, 105, 52-62.	1.0	13
8	Differences between Holstein dairy cows in renal clearance rate of urea affect milk urea concentration and the relationship between milk urea and urinary nitrogen excretion. Science of the Total Environment, 2021, 755, 143198.	3.9	23
9	PUFA Treatment Affects C2C12 Myocyte Differentiation, Myogenesis Related Genes and Energy Metabolism. Genes, 2021, 12, 192.	1.0	8
10	Transcriptome analysis of porcine PBMCs reveals lipopolysaccharide-induced immunomodulatory responses and crosstalk of immune and glucocorticoid receptor signaling. Virulence, 2021, 12, 1808-1824.	1.8	8
11	rePROBE: Workflow for Revised Probe Assignment and Updated Probe-set Annotation in Microarrays. Genomics, Proteomics and Bioinformatics, 2021, 19, 1043-1049.	3.0	4
12	Genetic regulation and heritability of miRNA and mRNA expression link to phosphorus utilization and gut microbiome. Open Biology, 2021, 11, 200182.	1.5	4
13	Control of Protein and Energy Metabolism in the Pituitary Gland in Response to Three-Week Running Training in Adult Male Mice. Cells, 2021, 10, 736.	1.8	4
14	mRNA Profiles of Porcine Parathyroid Glands Following Variable Phosphorus Supplies throughout Fetal and Postnatal Life. Biomedicines, 2021, 9, 454.	1.4	8
15	Prenatal Skeletal Muscle Transcriptome Analysis Reveals Novel MicroRNA-mRNA Networks Associated with Intrauterine Growth Restriction in Pigs. Cells, 2021, 10, 1007.	1.8	15
16	Shifted excitation Raman difference spectroscopy as enabling technique for the analysis of animal feedstuff. Journal of Raman Spectroscopy, 2021, 52, 1418-1427.	1.2	7
17	SINE jumping contributes to large-scale polymorphisms in the pig genomes. Mobile DNA, 2021, 12, 17.	1.3	21
18	Transcriptional responses in jejunum of two layer chicken strains following variations in dietary calcium and phosphorus levels. BMC Genomics, 2021, 22, 485.	1.2	11

#	Article	IF	Citations
19	Wnt signaling related transcripts and their relationship to energy metabolism in C2C12 myoblasts under temperature stress. PeerJ, 2021, 9, e11625.	0.9	8
20	Genome-Wide SNP Analysis for Milk Performance Traits in Indigenous Sheep: A Case Study in the Egyptian Barki Sheep. Animals, 2021, 11, 1671.	1.0	5
21	Mineral Phosphorus Supply in Piglets Impacts the Microbial Composition and Phytate Utilization in the Large Intestine. Microorganisms, 2021, 9, 1197.	1.6	6
22	Genomeâ€wide SNP analysis clearly distinguished the Belarusian Red cattle from other European cattle breeds. Animal Genetics, 2021, 52, 720-724.	0.6	8
23	SINE Insertion in the Intron of Pig GHR May Decrease Its Expression by Acting as a Repressor. Animals, 2021, 11, 1871.	1.0	6
24	Dietary phosphorus and calcium in feed affects miRNA profiles and their mRNA targets in jejunum of two strains of laying hens. Scientific Reports, 2021, 11, 13534.	1.6	5
25	Genetic background and production periods shape the microRNA profiles of the gut in laying hens. Genomics, 2021, 113, 1790-1801.	1.3	6
26	SNP-Based Genotyping Provides Insight Into the West Asian Origin of Russian Local Goats. Frontiers in Genetics, 2021, 12, 708740.	1.1	12
27	Does chronic dietary exposure to the mycotoxin deoxynivalenol affect the porcine hepatic transcriptome when an acute-phase response is initiated through first or second-pass LPS challenge of the liver?. Innate Immunity, 2021, 27, 388-408.	1.1	0
28	Identification of Genomic Regions Influencing N-Metabolism and N-Excretion in Lactating Holstein-Friesians. Frontiers in Genetics, 2021, 12, 699550.	1.1	8
29	In Utero Fetal Weight in Pigs Is Regulated by microRNAs and Their Target Genes. Genes, 2021, 12, 1264.	1.0	8
30	Multi-Transcript Level Profiling Revealed Distinct mRNA, miRNA, and tRNA-Derived Fragment Bio-Signatures for Coping Behavior Linked Haplotypes in HPA Axis and Limbic System. Frontiers in Genetics, 2021, 12, 635794.	1.1	5
31	A 192Âbp ERV fragment insertion in the first intron of porcine TLR6 may act as an enhancer associated with the increased expressions of TLR6 and TLR1. Mobile DNA, 2021, 12, 20.	1.3	7
32	Genome-Wide Analysis for Early Growth-Related Traits of the Locally Adapted Egyptian Barki Sheep. Genes, 2021, 12, 1243.	1.0	8
33	Comfrey (Symphytum spp.) as a feed supplement in pig nutrition contributes to regional resource cycles. Science of the Total Environment, 2021, 796, 148988.	3.9	4
34	Jejunal transcriptomic profiling of two layer strains throughout the entire production period. Scientific Reports, 2021, 11, 20086.	1.6	6
35	PSXI-6 Genome-wide SNP analysis of three Azerbaijani sheep breeds. Journal of Animal Science, 2021, 99, 245-245.	0.2	0
36	Pig genome functional annotation enhances the biological interpretation of complex traits and human disease. Nature Communications, 2021, 12, 5848.	5.8	70

#	Article	IF	Citations
37	PSVIII-1 Genetic characteristics of Karachaev sheep inferred from genome-wide SNP analysis. Journal of Animal Science, 2021, 99, 243-243.	0.2	0
38	PSXVI-17 Estimation of inbreeding in local sheep breeds of west Asian and central Asian origin based on high-density SNP-genotypes. Journal of Animal Science, 2021, 99, 222-223.	0.2	1
39	Insights into molecular pathways and fatty acid membrane composition during the temperature stress response in the murine C2C12 cell model. Science of the Total Environment, 2021, 807, 151019.	3.9	2
40	Central Suppression of the GH/IGF Axis and Abrogation of Exercise-Related mTORC1/2 Activation in the Muscle of Phenotype-Selected Male Marathon Mice (DUhTP). Cells, 2021, 10, 3418.	1.8	3
41	Reduced phosphorus intake throughout gestation and lactation of sows is mitigated by transcriptional adaptations in kidney and intestine. BMC Genomics, 2020, 21, 626.	1.2	7
42	Phytate Degradation, Transcellular Mineral Transporters, and Mineral Utilization by Two Strains of Laying Hens as Affected by Dietary Phosphorus and Calcium. Animals, 2020, 10, 1736.	1.0	16
43	A natural Ala610Val substitution causing glucocorticoid receptor hypersensitivity aggravates consequences of endotoxemia. Brain, Behavior, and Immunity, 2020, 90, 174-183.	2.0	6
44	Morphological and Molecular Features of Porcine Mesenchymal Stem Cells Derived From Different Types of Synovial Membrane, and Genetic Background of Cell Donors. Frontiers in Cell and Developmental Biology, 2020, 8, 601212.	1.8	2
45	Phytate degradation, myo-inositol release, and utilization of phosphorus and calcium by two strains of laying hens in five production periods. Poultry Science, 2020, 99, 6797-6808.	1.5	15
46	Insight into the Current Genetic Diversity and Population Structure of Domestic Reindeer (Rangifer) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	9
47	Comfrey (Symphytum spp.) as an alternative field crop contributing to closed agricultural cycles in chicken feeding. Science of the Total Environment, 2020, 742, 140490.	3.9	6
48	Analysis of Candidate Genes for Growth and Milk Performance Traits in the Egyptian Barki Sheep. Animals, 2020, 10, 197.	1.0	32
49	Ileal Transcriptome Profiles of Japanese Quail Divergent in Phosphorus Utilization. International Journal of Molecular Sciences, 2020, 21, 2762.	1.8	8
50	Host-Microbiota Interactions in Ileum and Caecum of Pigs Divergent in Feed Efficiency Contribute to Nutrient Utilization. Microorganisms, 2020, 8, 563.	1.6	15
51	Identification of the Key Molecular Drivers of Phosphorus Utilization Based on Host miRNA-mRNA and Gut Microbiome Interactions. International Journal of Molecular Sciences, 2020, 21, 2818.	1.8	14
52	Genetic Diversity of Bubalus bubalis in Germany and Global Relations of Its Genetic Background. Frontiers in Genetics, 2020, 11, 610353.	1.1	7
53	Two new SINE insertion polymorphisms in pig Vertnin (VRTN) gene revealed by comparative genomic alignment. Journal of Integrative Agriculture, 2020, 19, 2514-2522.	1.7	9
54	PSX-17 Genome-wide diversity and demographic history of Russian native goat breeds. Journal of Animal Science, 2020, 98, 450-450.	0.2	1

#	Article	IF	Citations
55	Selection signatures in two oldest Russian native cattle breeds revealed using high-density single nucleotide polymorphism analysis. PLoS ONE, 2020, 15, e0242200.	1.1	22
56	Profiling of circulating microRNA and pathway analysis in normal- versus over-conditioned dairy cows during the dry period and early lactation. Journal of Dairy Science, 2020, 103, 9534-9547.	1.4	7
57	Seasonal variations in quantitative and qualitative sperm characteristics in fertile and subfertile stallions. Archives Animal Breeding, 2020, 63, 145-154.	0.5	5
58	PSX-25 The distribution of runs of homozygosity in nine native Russian sheep breeds. Journal of Animal Science, 2020, 98, 456-457.	0.2	1
59	PSXII-32 Testing of low-density SNP panel in wild and domestic reindeer populations (Rangifer) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.2	0
60	PSX-16 Genome-wide association studies for growth and carcass traits in Russian sheep. Journal of Animal Science, 2020, 98, 449-450.	0.2	0
61	PSX-18 High-density genomic description of Russian native sheep breed of the Republic of Tyva. Journal of Animal Science, 2020, 98, 453-454.	0.2	1
62	PSXII-21 Genome-wide search for genomic regions under putative selection in two Russian native cattle breeds using high-density SNP Bead Chip. Journal of Animal Science, 2020, 98, 242-243.	0.2	1
63	PSIII-13 Genetic assessment of isolated reindeer (Rangifer Tarandus) population from Tuva, Russia. Journal of Animal Science, 2020, 98, 238-239.	0.2	0
64	Deep sequencing of small non-coding RNA highlights brain-specific expression patterns and RNA cleavage. RNA Biology, 2019, 16, 1764-1774.	1.5	6
65	DNA methylation analysis of porcine mammary epithelial cells reveals differentially methylated loci associated with immune response against Escherichia coli challenge. BMC Genomics, 2019, 20, 623.	1.2	17
66	Genetic Contribution to Variation in Blood Calcium, Phosphorus, and Alkaline Phosphatase Activity in Pigs. Frontiers in Genetics, 2019, 10, 590.	1.1	25
67	Transcriptome Responses to Dexamethasone Depending on Dose and Glucocorticoid Receptor Sensitivity in the Liver. Frontiers in Genetics, 2019, 10, 559.	1.1	14
68	Cross-talk between energy metabolism and epigenetics during temperature stress response in C2C12 myoblasts. International Journal of Hyperthermia, 2019, 36, 775-783.	1.1	14
69	Breed, Diet, and Interaction Effects on Adipose Tissue Transcriptome in Iberian and Duroc Pigs Fed Different Energy Sources. Genes, 2019, 10, 589.	1.0	27
70	Transcriptome profiles of hypothalamus and adrenal gland linked to haplotype related to coping behavior in pigs. Scientific Reports, 2019, 9, 13038.	1.6	7
71	Haplotypes of coping behavior associated QTL regions reveal distinct transcript profiles in amygdala and hippocampus. Behavioural Brain Research, 2019, 372, 112038.	1.2	5
72	Epigenome-wide skeletal muscle DNA methylation profiles at the background of distinct metabolic types and ryanodine receptor variation in pigs. BMC Genomics, 2019, 20, 492.	1.2	29

#	Article	IF	Citations
73	Retrotransposons evolution and impact on lncRNA and protein coding genes in pigs. Mobile DNA, 2019, 10, 19.	1.3	22
74	Genetic Regulation of Liver Metabolites and Transcripts Linking to Biochemical-Clinical Parameters. Frontiers in Genetics, 2019, 10, 348.	1.1	8
75	High-density genotyping reveals signatures of selection related to acclimation and economically important traits in 15 local sheep breeds from Russia. BMC Genomics, 2019, 20, 294.	1.2	57
76	Kinetics of Physiological and Behavioural Responses in Endotoxemic Pigs with or without Dexamethasone Treatment. International Journal of Molecular Sciences, 2019, 20, 1393.	1.8	2
77	Physiological and Transcriptional Responses in Weaned Piglets Fed Diets with Varying Phosphorus and Calcium Levels. Nutrients, 2019, 11, 436.	1.7	16
78	Genome wide association study of body weight and feed efficiency traits in a commercial broiler chicken population, a re-visitation. Scientific Reports, 2019, 9, 922.	1.6	28
79	RNA-Seq of Liver From Pigs Divergent in Feed Efficiency Highlights Shifts in Macronutrient Metabolism, Hepatic Growth and Immune Response. Frontiers in Genetics, 2019, 10, 117.	1.1	43
80	Tissue-Wide Gene Expression Analysis of Sodium/Phosphate Co-Transporters in Pigs. International Journal of Molecular Sciences, 2019, 20, 5576.	1.8	14
81	Population Structure and Genetic Diversity of Sheep Breeds in the Kyrgyzstan. Frontiers in Genetics, 2019, 10, 1311.	1.1	34
82	Elevated haplotypes frequencies reveal similarities for selection signatures in Western and Russian Simmental populations. Journal of Central European Agriculture, 2019, 20, 1-11.	0.3	7
83	Methane prediction based on individual or groups of milk fatty acids for dairy cows fed rations with or without linseed. Journal of Dairy Science, 2019, 102, 1788-1802.	1.4	14
84	Transcriptome analysis of adipose tissue from pigs divergent in feed efficiency reveals alteration in gene networks related to adipose growth, lipid metabolism, extracellular matrix, and immune response. Molecular Genetics and Genomics, 2019, 294, 395-408.	1.0	21
85	Genomic assessment and phenotypic characteristics of F2 resource sheep population. Agricultural Science Euro-North-East, 2019, 20, 498-507.	0.2	0
86	Analysis of meat quality traits and gene expression profiling of pigs divergent in residual feed intake. Meat Science, 2018, 137, 265-274.	2.7	32
87	Lower dietary phosphorus supply in pigs match both animal welfare aspects and resource efficiency. Ambio, 2018, 47, 20-29.	2.8	28
88	Integrative approach using liver and duodenum RNA-Seq data identifies candidate genes and pathways associated with feed efficiency in pigs. Scientific Reports, 2018, 8, 558.	1.6	68
89	Intravenous lipid infusion affects dry matter intake, methane yield, and rumen bacteria structure in late-lactating Holstein cows. Journal of Dairy Science, 2018, 101, 6032-6046.	1.4	5
90	Implication of transcriptome profiling of spermatozoa for stallion fertility. Reproduction, Fertility and Development, 2018, 30, 1087.	0.1	14

#	Article	IF	Citations
91	Temperature alterations during embryogenesis have a sex-dependent influence on growth properties and muscle metabolism of day-old chicks and 35-day-old broilers. Animal, 2018, 12, 1224-1231.	1.3	3
92	Deoxynivalenol Affects Cell Metabolism and Increases Protein Biosynthesis in Intestinal Porcine Epithelial Cells (IPEC-J2): DON Increases Protein Biosynthesis. Toxins, 2018, 10, 464.	1.5	9
93	Genetic diversity and population structure of domestic and wild reindeer (Rangifer tarandus L. 1758): A novel approach using BovineHD BeadChip. PLoS ONE, 2018, 13, e0207944.	1.1	11
94	PSVI-23 Genetic characteristics and differentiation of four valid subspecies of snow sheep (Ovis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	0.2	7
95	RNA-seq of muscle from pigs divergent in feed efficiency and product quality identifies differences in immune response, growth, and macronutrient and connective tissue metabolism. BMC Genomics, 2018, 19, 791.	1.2	56
96	Transcriptional shifts account for divergent resource allocation in feed efficient broiler chickens. Scientific Reports, 2018, 8, 12903.	1.6	12
97	Fast and reliable dissection of porcine parathyroid glands â€" A protocol for molecular and histological analyses. Annals of Anatomy, 2018, 219, 76-81.	1.0	2
98	Genetic variants of major genes contributing to phosphate and calcium homeostasis and their association with serum parameters in pigs. Journal of Applied Genetics, 2018, 59, 325-333.	1.0	7
99	miRNAs regulate acute transcriptional changes in broiler embryos in response to modification of incubation temperature. Scientific Reports, 2018, 8, 11371.	1.6	13
100	Population structure and genetic diversity of 25 Russian sheep breeds based on whole-genome genotyping. Genetics Selection Evolution, 2018, 50, 29.	1.2	76
101	Whole-genome SNP analysis elucidates the genetic structure of Russian cattle and its relationship with Eurasian taurine breeds. Genetics Selection Evolution, 2018, 50, 37.	1.2	34
102	Bridging Gaps in the Agricultural Phosphorus Cycle from an Animal Husbandry Perspectiveâ€"The Case of Pigs and Poultry. Sustainability, 2018, 10, 1825.	1.6	22
103	Lowered dietary phosphorus affects intestinal and renal gene expression to maintain mineral homeostasis with immunomodulatory implications in weaned piglets. BMC Genomics, 2018, 19, 207.	1.2	15
104	Genomeâ€wide association study of body morphological traits in Sudanese goats. Animal Genetics, 2018, 49, 478-482.	0.6	11
105	Feed-efficient pigs exhibit molecular patterns allowing a timely circulation of hormones and nutrients. Physiological Genomics, 2018, 50, 726-734.	1.0	9
106	Genomeâ€wide <scp>SNP</scp> analysis unveils genetic structure and phylogeographic history of snow sheep (Ovis nivicola) populations inhabiting the Verkhoyansk Mountains and Momsky Ridge (northeastern Siberia). Ecology and Evolution, 2018, 8, 8000-8010.	0.8	9
107	Genetic diversity of Nubian ibex in comparison to other ibex and domesticated goat species. European Journal of Wildlife Research, 2018, 64, 1.	0.7	3
108	Evaluation of current geneÂpool of Kholmogor andÂBlack-and-white cattle breeds based on whole genome SNP analysis. Vavilovskii Zhurnal Genetiki I Selektsii, 2018, 22, 742-747.	0.4	8

#	Article	IF	Citations
109	Airâ€“liquid interface enhances oxidative phosphorylation in intestinal epithelial cell line IPEC-J2. Cell Death Discovery, 2017, 3, 17001.	2.0	19
110	Exploring the genetics of feed efficiency and feeding behaviour traits in a pig line highly selected for performance characteristics. Molecular Genetics and Genomics, 2017, 292, 1001-1011.	1.0	56
111	Detection of the important chromosomal regions determining production traits in meat-type chicken using entropy analysis. British Poultry Science, 2017, 58, 358-365.	0.8	8
112	Genetic aspects of feed efficiency and reduction of environmental footprint in broilers: a review. Journal of Applied Genetics, 2017, 58, 487-498.	1.0	43
113	Detection of pig genome regions determining production traits using an information theory approach. Livestock Science, 2017, 205, 31-35.	0.6	15
114	Genetics of body fat mass and related traits in a pig population selected for leanness. Scientific Reports, 2017, 7, 9118.	1.6	17
115	Possible Molecular Mechanisms by Which an Essential Oil Blend from Star Anise, Rosemary, Thyme, and Oregano and Saponins Increase the Performance and Ileal Protein Digestibility of Growing Broilers. Journal of Agricultural and Food Chemistry, 2017, 65, 6821-6830.	2.4	43
116	Genetic architecture and regulatory impact on hepatic microRNA expression linked to immune and metabolic traits. Open Biology, 2017, 7, 170101.	1.5	14
117	Mitochondrial-nuclear crosstalk, haplotype and copy number variation distinct in muscle fiber type, mitochondrial respiratory and metabolic enzyme activities. Scientific Reports, 2017, 7, 14024.	1.6	16
118	Genetic characteristics of Kodar snow sheep using SNP markers. Contemporary Problems of Ecology, 2017, 10, 591-598.	0.3	2
119	TRIENNIAL GROWTH AND DEVELOPMENT SYMPOSIUM: Factors influencing bovine intramuscular adipose tissue development and cellularity1. Journal of Animal Science, 2017, 95, 2244-2254.	0.2	13
120	MicroRNA expression profiling of porcine mammary epithelial cells after challenge with Escherichia coli in vitro. BMC Genomics, 2017, 18, 660.	1.2	13
121	Sex-Specific Muscular Maturation Responses Following Prenatal Exposure to Methylation-Related Micronutrients in Pigs. Nutrients, 2017, 9, 74.	1.7	8
122	Strategies towards Improved Feed Efficiency in Pigs Comprise Molecular Shifts in Hepatic Lipid and Carbohydrate Metabolism. International Journal of Molecular Sciences, 2017, 18, 1674.	1.8	34
123	Genome-wide association analysis and functional annotation of positional candidate genes for feed conversion efficiency and growth rate in pigs. PLoS ONE, 2017, 12, e0173482.	1.1	32
124	Whole genome population genetics analysis of Sudanese goats identifies regions harboring genes associated with major traits. BMC Genetics, 2017, 18, 92.	2.7	42
125	POPULATION-GENETIC CHARACTERISTICS OF DOMESTIC REINDEER OF YAKUTIA BASED ON WHOLE-GENOME SNP ANALYSIS. Sel'skokhozyaistvennaya Biologiya, 2017, 52, 669-678.	0.1	3
126	TRIENNIAL GROWTH AND DEVELOPMENT SYMPOSIUM: Factors influencing bovine intramuscular adipose tissue development and cellularity. Journal of Animal Science, 2017, 95, 2244.	0.2	10

#	Article	IF	Citations
127	1711 Genomic evaluation and population structure of eleven Russian sheep breeds. Journal of Animal Science, 2016, 94, 834-834.	0.2	1
128	Transient Shifts of Incubation Temperature Reveal Immediate and Long-Term Transcriptional Response in Chicken Breast Muscle Underpinning Resilience and Phenotypic Plasticity. PLoS ONE, 2016, 11, e0162485.	1.1	8
129	Gene expression profile of Musculus longissimus dorsi in bulls of a Charolais Ã— Holstein F 2 -cross with divergent intramuscular fat content. Genomics Data, 2016, 7, 131-133.	1.3	19
130	Altered incubation temperatures between embryonic Days 7 and 13 influence the weights and the mitochondrial respiratory and enzyme activities in breast and leg muscles of broiler embryos. Molecular Reproduction and Development, 2016, 83, 71-78.	1.0	15
131	A naturally hypersensitive glucocorticoid receptor elicits a compensatory reduction of hypothalamusâ€“pituitaryâ€“adrenal axis activity early in ontogeny. Open Biology, 2016, 6, 150193.	1.5	29
132	Genetically regulated hepatic transcripts and pathways orchestrate haematological, biochemical and body composition traits. Scientific Reports, 2016, 6, 39614.	1.6	13
133	MicroRNA-mRNA regulatory networking fine-tunes the porcine muscle fiber type, muscular mitochondrial respiratory and metabolic enzyme activities. BMC Genomics, 2016, 17, 531.	1.2	23
134	Toward improved phosphorus efficiency in monogastricsâ€”interplay of serum, minerals, bone, and immune system after divergent dietary phosphorus supply in swine. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2016, 310, R917-R925.	0.9	28
135	Transcriptome profiling of Musculus longissimus dorsi in two cattle breeds with different intramuscular fat deposition. Genomics Data, 2016, 7, 109-111.	1.3	15
136	Immediate and long-term transcriptional response of hind muscle tissue to transient variation of incubation temperature in broilers. BMC Genomics, 2016, 17, 323.	1.2	7
137	Molecular changes in mitochondrial respiratory activity and metabolic enzyme activity in muscle of four pig breeds with distinct metabolic types. Journal of Bioenergetics and Biomembranes, 2016, 48, 55-65.	1.0	6
138	Methylating micronutrient supplementation during pregnancy influences foetal hepatic gene expression and IGF signalling and increases foetal weight. European Journal of Nutrition, 2016, 55, 1717-1727.	1.8	29
139	Genetic variation of the porcine NR5A1 is associated with meat color. Journal of Applied Genetics, 2016, 57, 81-89.	1.0	2
140	Single- and Bayesian Multi-Marker Genome-Wide Association for Haematological Parameters in Pigs. PLoS ONE, 2016, 11, e0159212.	1.1	22
141	A Natural Mutation in Helix 5 of the Ligand Binding Domain of Glucocorticoid Receptor Enhances Receptor-Ligand Interaction. PLoS ONE, 2016, 11, e0164628.	1.1	15
142	STUDY OF GENETIC DIVERSITY AND POPULATION STRUCTURE OF FIVE RUSSIAN CATTLE BREEDS USING WHOLE-GENOME SNP ANALYSIS. Sel'skokhozyaistvennaya Biologiya, 2016, 51, 788-800.	0.1	9
143	PBMC transcriptomic responses to primary and secondary vaccination differ due to divergent lean growth and antibody titers in a pig model. Physiological Genomics, 2015, 47, 470-478.	1.0	5
144	Integrated Genome-wide association and hypothalamus eQTL studies indicate a link between the circadian rhythm-related gene PER1 and coping behavior. Scientific Reports, 2015, 5, 16264.	1.6	29

#	Article	IF	Citations
145	The genetics of feed conversion efficiency traits in a commercial broiler line. Scientific Reports, 2015, 5, 16387.	1.6	60
146	Gene expression profiling of porcine mammary epithelial cells after challenge with Escherichia coli and Staphylococcus aureus in vitro. Veterinary Research, 2015, 46, 50.	1.1	21
147	Analysis of non-synonymous SNPs of the porcineSERPINA6gene as potential causal variants for a QTL affecting plasma cortisol levels on SSC7. Animal Genetics, 2015, 46, 239-246.	0.6	7
148	Identification and Functional Characterization of Cis-Regulatory Elements Controlling Expression of the Porcine ADRB2 Gene. International Journal of Biological Sciences, 2015, 11, 1006-1015.	2.6	6
149	Muscle Transcriptional Profile Based on Muscle Fiber, Mitochondrial Respiratory Activity, and Metabolic Enzymes. International Journal of Biological Sciences, 2015, 11, 1348-1362.	2.6	27
150	Identification of Common Regulators of Genes in Co-Expression Networks Affecting Muscle and Meat Properties. PLoS ONE, 2015, 10, e0123678.	1.1	39
151	MicroRNAs Regulate Cellular ATP Levels by Targeting Mitochondrial Energy Metabolism Genes during C2C12 Myoblast Differentiation. PLoS ONE, 2015, 10, e0127850.	1.1	44
152	Comparing Two Intestinal Porcine Epithelial Cell Lines (IPECs): Morphological Differentiation, Function and Metabolism. PLoS ONE, 2015, 10, e0132323.	1.1	48
153	Genome-wide identification of allele-specific expression in response to Streptococcus suis 2 infection in two differentially susceptible pig breeds. Journal of Applied Genetics, 2015, 56, 481-491.	1.0	10
154	Pre- and post-natal muscle microRNA expression profiles of two pig breeds differing in muscularity. Gene, 2015, 561, 190-198.	1.0	33
155	Deoxynivalenol, but not E. coli lipopolysaccharide, changes the response pattern of intestinal porcine epithelial cells (IPEC-J2) according to its route of application. Toxicology Letters, 2015, 239, 161-171.	0.4	4
156	Identification of novel putative adipomyokines by a cross-species annotation of secretomes and expression profiles. Archives of Physiology and Biochemistry, 2015, 121, 194-205.	1.0	14
157	Bioanalytical validation for simultaneous quantification of non-aromatic steroids in follicular fluid from cattle via ESI-LCâ€“MS/MS. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2015, 1007, 132-139.	1.2	11
158	The Fight-Or-Flight Response Is Associated with PBMC Expression Profiles Related to Immune Defence and Recovery in Swine. PLoS ONE, 2015, 10, e0120153.	1.1	21
159	Genetic Association of the Porcine C9 Complement Component with Hemolytic Complement Activity. Asian-Australasian Journal of Animal Sciences, 2015, 28, 1354-1361.	2.4	3
160	Discovery of Candidate Genes for Muscle Traits Based on GWAS Supported by eQTL-analysis. International Journal of Biological Sciences, 2014, 10, 327-337.	2.6	41
161	Breed-specific transcriptome response of spleen from six to eight week old piglet after infection with Streptococcus suis type 2. Molecular Biology Reports, 2014, 41, 7865-7873.	1.0	13
162	Transcriptional responses of PBMC in psychosocially stressed animals indicate an alerting of the immune system in female but not in castrated male pigs. BMC Genomics, 2014, 15, 967.	1.2	10

#	Article	IF	Citations
163	biomvRhsmm:Genomic Segmentation with Hidden Semi-Markov Model. BioMed Research International, 2014, 2014, 1-11.	0.9	4
164	Genomeâ€wide association analysis for growth, muscularity and meat quality in PiÃ©train pigs. Animal Genetics, 2014, 45, 350-356.	0.6	15
165	Differential Expression of miRNAs and Their Target mRNAs in Endometria Prior to Maternal Recognition of Pregnancy Associates with Endometrial Receptivity for In Vivo- and In Vitro-Produced Bovine Embryos1. Biology of Reproduction, 2014, 91, 135.	1.2	43
166	Investigations on the pattern of linkage disequilibrium and selection signatures in the genomes of German PiÃ©train pigs. Journal of Animal Breeding and Genetics, 2014, 131, 473-482.	0.8	10
167	Association of Nâ€terminal domain polymorphisms of the porcine glucocorticoid receptor with carcass composition and meat quality traits. Animal Genetics, 2014, 45, 125-129.	0.6	8
168	A study based on records taken at time of hoof trimming reveals a strong association between the IQ motif-containing GTPase-activating protein 1 (IQGAP1) gene and sole hemorrhage in Holstein cattle. Journal of Dairy Science, 2014, 97, 507-519.	1.4	17
169	UBXN1 polymorphism and its expression in porcine M. longissimus dorsi are associated with water holding capacity. Molecular Biology Reports, 2014, 41, 1411-1418.	1.0	3
170	Hepatic expression patterns in psychosocially high-stressed pigs suggest mechanisms following allostatic principles. Physiology and Behavior, 2014, 128, 159-165.	1.0	8
171	Highâ€and lowâ€protein gestation diets do not provoke common transcriptional responses representing universal targetâ€pathways in muscle and liver of porcine progeny. Acta Physiologica, 2014, 210, 202-214.	1.8	7
172	Molecular Heterogeneities of Adipose Depots - Potential Effects on Adipose-Muscle Cross-Talk in Humans, Mice and Farm Animals. Journal of Genomics, 2014, 2, 31-44.	0.6	41
173	<scp>QTL</scp> regionâ€“specific microarrays reveal differential expression of positional candidate genes of signaling pathways associated with the liability for the inverted teat defect. Animal Genetics, 2013, 44, 139-148.	0.6	5
174	KRT8, FAF1 and PTH1R gene polymorphisms are associated with leg weakness traits in pigs. Molecular Biology Reports, 2013, 40, 2859-2866.	1.0	13
175	Transcriptome Profiling of Gill Tissue in Regionally Bred and Globally Farmed Rainbow Trout Strains Reveals Different Strategies for Coping with Thermal Stress. Marine Biotechnology, 2013, 15, 445-460.	1.1	75
176	UBE3B and ZRANB1 polymorphisms and transcript abundance are associated with water holding capacity of porcine M. longissimus dorsi. Meat Science, 2013, 95, 166-172.	2.7	8
177	Deoxynivalenol affects the composition of the basement membrane proteins and influences en route the migration of CD16+ cells into the intestinal epithelium. Mycotoxin Research, 2013, 29, 245-254.	1.3	15
178	A genetical genomics approach reveals new candidates and confirms known candidate genes for drip loss in a porcine resource population. Mammalian Genome, 2013, 24, 416-426.	1.0	22
179	Expression variation of the porcine ADRB2 has a complex genetic background. Molecular Genetics and Genomics, 2013, 288, 615-625.	1.0	6
180	Genomic selection using low density marker panels with application to a sire line in pigs. Genetics Selection Evolution, 2013, 45, 28.	1.2	58

#	Article	IF	Citations
181	Correlated mRNAs and miRNAs from co-expression and regulatory networks affect porcine muscle and finally meat properties. BMC Genomics, 2013, 14, 533.	1.2	54
182	Gene expression profiling of articular cartilage reveals functional pathways and networks of candidate genes for osteochondrosis in pigs. Physiological Genomics, 2013, 45, 856-865.	1.0	9
183	Association of TLR5 sequence variants and mRNA level with cytokine transcription in pigs. Immunogenetics, 2013, 65, 125-132.	1.2	5
184	Dietary protein restriction and excess of pregnant German Landrace sows induce changes in hepatic gene expression and promoter methylation of key metabolic genes in the offspring. Journal of Nutritional Biochemistry, 2013, 24, 484-495.	1.9	37
185	Transcript variants of the porcine glucocorticoid receptor gene (NR3C1). General and Comparative Endocrinology, 2013, 189, 127-133.	0.8	16
186	Transcriptional profiling and miRNA-dependent regulatory network analysis of longissimus dorsi muscle during prenatal and adult stages in two distinct pig breeds. Animal Genetics, 2013, 44, 398-407.	0.6	17
187	Ironâ€“sulfur cluster scaffold (ISCU) gene is duplicated in salmonid fish and tissue and temperature dependent expressed in rainbow trout. Gene, 2013, 512, 251-258.	1.0	3
188	Transcriptomic Response of Porcine PBMCs to Vaccination with Tetanus Toxoid as a Model Antigen. PLoS ONE, 2013, 8, e58306.	1.1	16
189	PBMC Transcription Profiles of Pigs with Divergent Humoral Immune Responses and Lean Growth Performance. International Journal of Biological Sciences, 2013, 9, 907-916.	2.6	13
190	Genome-Wide Association Identifies TBX5 as Candidate Gene for Osteochondrosis Providing a Functional Link to Cartilage Perfusion as Initial Factor. Frontiers in Genetics, 2013, 4, 78.	1.1	17
191	Identification of predicted genes expressed differentially in pituitary gland tissue of young growing bulls revealed by cDNA-AFLP technique. Czech Journal of Animal Science, 2013, 58, 147-158.	0.5	4
192	A Genome-Wide Association Study to Detect QTL for Commercially Important Traits in Swiss Large White Boars. PLoS ONE, 2013, 8, e55951.	1.1	35
193	Novel SNPs of the porcine TRIP12 are associated with water holding capacity of meat. Czech Journal of Animal Science, 2013, 58, 525-533.	0.5	0
194	Transcriptional response of skeletal muscle to a low-protein gestation diet in porcine offspring accumulates in growth- and cell cycle-regulating pathways. Physiological Genomics, 2012, 44, 811-818.	1.0	14
195	Elucidating Molecular Networks That Either Affect or Respond to Plasma Cortisol Concentration in Target Tissues of Liver and Muscle. Genetics, 2012, 192, 1109-1122.	1.2	35
196	Somatic cytochrome c (CYCS) gene expression and promoter-specific DNA methylation in a porcine model of prenatal exposure to maternal dietary protein excess and restriction. British Journal of Nutrition, 2012, 107, 791-799.	1.2	24
197	Maternal dietary protein restriction and excess affects offspring gene expression and methylation of non-SMC subunits of condensin I in liver and skeletal muscle. Epigenetics, 2012, 7, 239-252.	1.3	63
198	Identification of differentially expressed protective genes in liver of two rainbow trout strains. Veterinary Immunology and Immunopathology, 2012, 145, 305-315.	0.5	19

#	Article	IF	Citations
199	Gene expression analysis of mammary tissue during fetal bud formation and growth in two pig breeds â€“ indications of prenatal initiation of postnatal phenotypic differences. BMC Developmental Biology, 2012, 12, 13.	2.1	5
200	A low protein diet during pregnancy provokes a lasting shift of hepatic expression of genes related to cell cycle throughout ontogenesis in a porcine model. BMC Genomics, 2012, 13, 93.	1.2	16
201	Flexible and efficient genome tiling design with penalized uniqueness score. BMC Bioinformatics, 2012, 13, 323.	1.2	2
202	Gene Regulation of Intestinal Porcine Epithelial Cells IPEC-J2 Is Dependent on the Site of Deoxynivalenol Toxicological Action. PLoS ONE, 2012, 7, e34136.	1.1	28
203	A Gestational High Protein Diet Affects the Abundance of Muscle Transcripts Related to Cell Cycle Regulation throughout Development in Porcine Progeny. PLoS ONE, 2012, 7, e34519.	1.1	11
204	Gene Expression and DNA-Methylation of Bovine Pretransfer Endometrium Depending on Its Receptivity after In Vitro-Produced Embryo Transfer. PLoS ONE, 2012, 7, e42402.	1.1	39
205	A Substitution in the Ligand Binding Domain of the Porcine Glucocorticoid Receptor Affects Activity of the Adrenal Gland. PLoS ONE, 2012, 7, e45518.	1.1	38
206	Microarray analysis reveals genes and functional networks relevant to the predisposition to inverted teats in pigs1. Journal of Animal Science, 2012, 90, 1-15.	0.2	27
207	Association of TLR4 polymorphism with cytokine expression level and pulmonary lesion score in pigs. Molecular Biology Reports, 2012, 39, 7003-7009.	1.0	10
208	Effect of gestational protein deficiency and excess on hepatic expression of genes related to cell cycle and proliferation in offspring from late gestation to finishing phase in pig. Molecular Biology Reports, 2012, 39, 7095-7104.	1.0	11
209	Genes with expression levels correlating to drip loss prove association of their polymorphism with water holding capacity of pork. Molecular Biology Reports, 2012, 39, 97-107.	1.0	6
210	Association and expression study of MMP3, TGFÎ²1 and COL10A1 as candidate genes for leg weakness-related traits in pigs. Molecular Biology Reports, 2012, 39, 3893-3901.	1.0	12
211	Comparative molecular characterization of the regucalcin (RGN) gene in rainbow trout (Oncorhynchus mykiss) and maraena whitefish (Coregonus marena). Molecular Biology Reports, 2012, 39, 4291-4300.	1.0	9
212	Association and expression quantitative trait loci (eQTL) analysis of porcine AMBP, GC and PPP1R3B genes with meat quality traits. Molecular Biology Reports, 2012, 39, 4809-4821.	1.0	28
213	Detection of a polymorphic site of the porcine <i>C8G</i> gene and evaluation of association with haemolytic complement activity. Archives Animal Breeding, 2012, 55, 255-262.	0.5	0
214	MARCH5 gene is duplicated in rainbow trout, but only fish-specific gene copy is up-regulated after VHSV infection. Fish and Shellfish Immunology, 2011, 31, 1041-1050.	1.6	18
215	Investigation on interferon alpha-inducible protein 6 (IFI6) gene as a candidate for meat and carcass quality in pig. Meat Science, 2011, 88, 755-760.	2.7	12
216	Polymorphism and expression of the porcine Tenascin C gene associated with meat and carcass quality. Meat Science, 2011, 89, 76-83.	2.7	22

#	Article	IF	Citations
217	Association of PPARGC1A and CAPNS1 gene polymorphisms and expression with meat quality traits in pigs. Meat Science, 2011, 89, 478-485.	2.7	23
218	Advances in research on the prenatal development of skeletal muscle in animals in relation to the quality of muscle-based food. I. Regulation of myogenesis and environmental impact. Animal, 2011, 5, 703-717.	1.3	55
219	Advances in research on the prenatal development of skeletal muscle in animals in relation to the quality of muscle-based food. II â€“ Genetic factors related to animal performance and advances in methodology. Animal, 2011, 5, 718-730.	1.3	33
220	Mapping quantitative trait loci for innate immune response in the pig. International Journal of Immunogenetics, 2011, 38, 121-131.	0.8	26
221	The three-way relationship of polymorphisms of porcine genes encoding terminal complement components, their differential expression, and health-related phenotypes. BMC Proceedings, 2011, 5, S19.	1.8	4
222	Quantitative trait loci analysis for leg weakness-related traits in a Duroc Ã— Pietrain crossbred population. Genetics Selection Evolution, 2011, 43, 13.	1.2	23
223	Integrating expression profiling and whole-genome association for dissection of fat traits in a porcine model. Journal of Lipid Research, 2011, 52, 668-678.	2.0	46
224	Differential mRNA expression of genes in the porcine adrenal gland associated with psychosocial stress. Journal of Molecular Endocrinology, 2011, 46, 165-174.	1.1	16
225	A High Protein Diet during Pregnancy Affects Hepatic Gene Expression of Energy Sensing Pathways along Ontogenesis in a Porcine Model. PLoS ONE, 2011, 6, e21691.	1.1	17
226	Polymorphic sites in the 5Â´-region of the porcine <i>C8A</i> gene. Archives Animal Breeding, 2011, 54, 430-438.	0.5	2
227	Pigsâ€™ aggressive temperament affects pre-slaughter mixing aggression, stress and meat quality. Animal, 2010, 4, 604-616.	1.3	69
228	Mapping of quantitative trait loci for mycoplasma and tetanus antibodies and interferon-gamma in a porcine F2 DurocÂÃ—ÂPietrain resource population. Mammalian Genome, 2010, 21, 409-418.	1.0	16
229	Peptidylarginine deiminase gene is differentially expressed in freshwater and brackish water rainbow trout. Molecular Biology Reports, 2010, 37, 2333-2339.	1.0	31
230	Four loci differentially expressed in muscle tissue depending on water-holding capacity are associated with meat quality in commercial pig herds. Molecular Biology Reports, 2010, 37, 595-601.	1.0	22
231	Molecular characterization of PRR13 and its tissue-specific expression in rainbow trout (Oncorhynchus mykiss). Fish Physiology and Biochemistry, 2010, 36, 1271-1276.	0.9	6
232	Identification of expression QTL (eQTL) of genes expressed in porcine M. longissimus dorsi and associated with meat quality traits. BMC Genomics, 2010, 11, 572.	1.2	32
233	Association of HPA axis-related genetic variation with stress reactivity and aggressive behaviour in pigs. BMC Genetics, 2010, 11, 74.	2.7	74
234	Exclusion of sequence polymorphisms in the porcine ITGA5 and MIR148B loci as causal variation for congenital splay leg in piglets. Animal Genetics, 2010, 41, 447-448.	0.6	8

#	Article	IF	Citations
235	Expression quantitative trait loci analysis of genes in porcine muscle by quantitative real-time RT-PCR compared to microarray data. Heredity, 2010, 105, 309-317.	1.2	12
236	Functional genomics and genetical genomics approaches towards elucidating networks of genes affecting meat performance in pigs. Briefings in Functional Genomics, 2010, 9, 251-258.	1.3	28
237	Molecular Characterization of Five Porcine Candidate Genes for Drip Loss in Pork. Animal Biotechnology, 2010, 21, 114-121.	0.7	6
238	Expression of microRNAs is not related to increased expression of ZDHHC9 in hind leg muscles of splay leg piglets. Molecular and Cellular Probes, 2010, 24, 32-37.	0.9	11
239	Association of ZYX polymorphisms with carcass and meat quality traits in commercial pigs. Meat Science, 2010, 84, 159-164.	2.7	9
240	Microarray-based transcriptional profiling ofEimeria bovis-infected bovine endothelial host cells. Veterinary Research, 2010, 41, 70.	1.1	44
241	Annotation and <i>in silico</i> localization of the Affymetrix GeneChip Porcine Genome Array. Archives Animal Breeding, 2010, 53, 230-238.	0.5	20
242	Identification of candidate genes for congenital splay leg in piglets by alternative analysis of DNA microarray data. International Journal of Biological Sciences, 2009, 5, 331-337.	2.6	13
243	Differential expression of growth factors and their receptors indicates their involvement in the inverted teat defect in pigs1. Journal of Animal Science, 2009, 87, 3451-3457.	0.2	5
244	Evidence for association of lymphoid enhancer-binding factor-1 <i>(LEF1)</i> with the number of functional and inverted teats in pigs. Cytogenetic and Genome Research, 2009, 124, 139-146.	0.6	6
245	QTL for traits related to humoral immune response estimated from data of a porcine F2 resource population. International Journal of Immunogenetics, 2009, 36, 141-151.	0.8	33
246	Porcine muscle sensory attributes associate with major changes in gene networks involving CAPZB, ANKRD1, and CTBP2. Functional and Integrative Genomics, 2009, 9, 455-471.	1.4	39
247	Dual effect of a single nucleotide polymorphism in the first intron of the porcine Secreted phosphoprotein 1 gene: allele-specific binding of C/EBP beta and activation of aberrant splicing. BMC Molecular Biology, 2009, 10, 96.	3.0	26
248	Expression of the porcine adrenergic receptor beta 2 gene in longissimus dorsi muscle is affected by cisâ€regulatory DNA variation. Animal Genetics, 2009, 40, 80-89.	0.6	14
249	Association of parathyroid hormoneâ€like hormone (PTHLH) and its receptor (PTHR1) with the number of functional and inverted teats in pigs. Journal of Animal Breeding and Genetics, 2009, 126, 237-241.	0.8	9
250	Characterization of Dehydrodolichyl diphosphate synthase gene in rainbow trout (Oncorhynchus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 260-265.	0.7	18
251	Cloning and tissue-specific expression of a .DELTA.-COP homologue in a freshwater and a brackish water-adapted strain of rainbow trout (Oncorhynchus mykiss). Genes and Genetic Systems, 2009, 84, 239-243.	0.2	4
252	Regulatory Aspects of Fetal Growth and Muscle Development Relating to Postnatal Growth and Carcass Quality in Pigs. , 2009, , 203-241.		0

#	Article	IF	Citations
253	QTL for the heritable inverted teat defect in pigs. Mammalian Genome, 2008, 19, 127-138.	1.0	24
254	Combined line-cross and half-sib QTL analysis in Durocâ€“Pietrain population. Mammalian Genome, 2008, 19, 429-438.	1.0	63
255	Trait correlated expression combined with expression QTL analysis reveals biological pathways and candidate genes affecting water holding capacity of muscle. BMC Genomics, 2008, 9, 367.	1.2	80
256	Porcine IL12A and IL12B gene mapping, variation and evidence of association with lytic complement and blood leucocyte proliferation traits. International Journal of Immunogenetics, 2008, 35, 75-85.	0.8	3
257	Expression Profiling of Muscle Reveals Transcripts Differentially Expressed in Muscle That Affect Water-Holding Capacity of Pork. Journal of Agricultural and Food Chemistry, 2008, 56, 10311-10317.	2.4	40
258	Relationship between myosin heavy chain isoform expression and muscling in several diverse pig breeds1. Journal of Animal Science, 2008, 86, 795-803.	0.2	79
259	Verification of Chromosomal Regions Affecting the Innate Immunity in Pigs Using Linkage Mapping. Developments in Biologicals, 2008, 132, 279-286.	0.4	4
260	Porcine Genome-wide Gene Expression in Response to Tetanus Toxoid Vaccine. Developments in Biologicals, 2008, 132, 185-195.	0.4	7
261	Association of the FADS2 Gene withï‰-6 andï‰-3 PUFA Concentration in the Egg Yolk of Japanese Quail. Animal Biotechnology, 2007, 18, 189-201.	0.7	14
262	Pre- and postnatal hepatic gene expression profiles of two pig breeds differing in body composition: insight into pathways of metabolic regulation. Physiological Genomics, 2007, 29, 267-279.	1.0	35
263	Identification of genes differentially expressed during prenatal development of skeletal muscle in two pig breeds differing in muscularity. BMC Developmental Biology, 2007, 7, 109.	2.1	71
264	Structural and functional genomics to elucidate the genetic background of microstructural and biophysical muscle properties in the pig. Journal of Animal Breeding and Genetics, 2007, 124, 27-34.	0.8	13
265	A genome scan reveals QTL for growth, fatness, leanness and meat quality in a Duroc-Pietrain resource population. Animal Genetics, 2007, 38, 241-252.	0.6	136
266	Associations of functional candidate genes derived from geneâ€expression profiles of prenatal porcine muscle tissue with meat quality and muscle deposition. Animal Genetics, 2007, 38, 474-484.	0.6	66
267	Molecular genetic analysis of porcine mannose-binding lectin genes, MBL1 and MBL2, and their association with complement activity. International Journal of Immunogenetics, 2007, 34, 55-63.	0.8	30
268	Generation of an improved cytogenetic and comparative map of Bos taurus chromosome BTA27. Chromosome Research, 2007, 15, 203-213.	1.0	7
269	SNP analysis, genotyping and mapping of the porcine <i>PTHR1</i> gene to chromosome 13 (Brief report). Archives Animal Breeding, 2007, 50, 320-321.	0.5	1
270	Candidate gene markers for sperm quality and fertility of boar. Animal Reproduction Science, 2006, 92, 349-363.	0.5	48

#	Article	IF	Citations
271	Molecular characterization and evidencing of the porcine CRH gene as a functional-positional candidate for growth and body composition. Biochemical and Biophysical Research Communications, 2006, 342, 394-405.	1.0	17
272	Expression of the Prion Protein Gene (PRNP) and Cellular Prion Protein (PrPc) in Cattle and Sheep Fetuses and Maternal Tissues During Pregnancy. Gene Expression, 2006, 13, 283-297.	0.5	16
273	QTL for microstructural and biophysical muscle properties and body composition in pigs. BMC Genetics, 2006, 7, 15.	2.7	74
274	Haplotype analysis of ?-actin gene for its association with sperm quality and boar fertility. Journal of Animal Breeding and Genetics, 2006, 123, 384-388.	0.8	8
275	The Effect of Nitric Oxide Inhibition and Temporal Expression Patterns of the mRNA and Protein Products of Nitric Oxide Synthase Genes During In Vitro Development of Bovine Pre-implantation Embryos. Reproduction in Domestic Animals, 2006, 41, 501-509.	0.6	35
276	Transcript Profiles of Some Developmentally Important Genes Detected in Bovine Oocytes and In Vitro-produced Blastocysts Using RNA Amplification and cDNA Microarrays. Reproduction in Domestic Animals, 2006, 41, 527-534.	0.6	15
277	Evidence for Effects of Testis and Epididymis Expressed Genes on Sperm Quality and Boar Fertility Traits. Reproduction in Domestic Animals, 2006, 41, 538-543.	0.6	25
278	Association of corticotropin-releasing hormone gene variation with performance and meat quality traits in commercial pig lines. Animal Genetics, 2006, 37, 509-512.	0.6	10
279	Bovine NALP5, NALP8, and NALP9 Genes: Assignment to a QTL Region and the Expression in Adult Tissues, Oocytes, and Preimplantation Embryos. Biology of Reproduction, 2006, 74, 577-584.	1.2	33
280	Identification and characterization of an AFLP marker associated with carcass composition in the pig (Brief report). Archives Animal Breeding, 2006, 49, 413-414.	0.5	1
281	Expression of Retinoid X Receptor Transcripts and their Significance for Developmental Competence in In Vitro-produced Pre-implantation-stage Bovine Embryos. Reproduction in Domestic Animals, 2005, 40, 177-183.	0.6	17
282	Polymorphisms in candidate genes as markers for sperm quality and boar fertility. Animal Genetics, 2005, 36, 152-155.	0.6	35
283	SNP detection and genetic mapping of porcine genes encoding enzymes in hepatic metabolic pathways and evaluation of linkage with carcass traits. Animal Genetics, 2005, 36, 050912025950003-???.	0.6	26
284	Identification of functional candidate genes for body composition by expression analyses and evidencing impact by association analysis and mapping. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2005, 1730, 31-40.	2.4	23
285	Intrafallopian transfer of gametes and early stage embryos for in vivo culture in cattle. Theriogenology, 2005, 64, 30-40.	0.9	24
286	A Comparative Expression Analysis of Gene Transcripts in Post-fertilization Developmental Stages of Bovine Embryos Produced in Vitro or in Vivo. Reproduction in Domestic Animals, 2004, 39, 396-404.	0.6	53
287	Sequencing, SNP identification and mapping of the porcinePTHLHgene to chromosome 5. Animal Genetics, 2004, 35, 151-152.	0.6	5
288	Detection of SNPs and linkage and radiation hybrid mapping of the porcine C-reactive protein (CRPâ€Š) gene. Animal Genetics, 2004, 35, 469-470.	0.6	6

#	Article	IF	Citations
289	Polymorphisms of the porcine androgen receptor gene affecting its amino acid sequence and expression level. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2004, 1678, 94-101.	2.4	8
290	Molecular cloning and sequencing of porcine C5 gene and its association with immunological traits. Immunogenetics, 2004, 55, 811-817.	1.2	15
291	Quantitative expression analysis of blastocyst-derived gene transcripts in preimplantation developmental stages of in vitro-produced bovine embryos using real-time polymerase chain reaction technology. Reproduction, Fertility and Development, 2004, 16, 753.	0.1	18
292	BF, HP, DQB and DRB are associated with haemolytic complement activity, acute phase protein reaction and antibody response in the pig. Veterinary Immunology and Immunopathology, 2004, 99, 215-228.	0.5	9
293	165RE-EXPANSION AND QUALITY OF SPLIT BOVINE EMBRYOS IN VITRO. Reproduction, Fertility and Development, 2004, 16, 205.	0.1	1
294	Identification and quantification of differentially expressed transcripts in in vitro-produced bovine preimplantation stage embryos. Molecular Reproduction and Development, 2003, 66, 105-114.	1.0	18
295	Molecular characterization of the pig C3 gene and its association with complement activity. Immunogenetics, 2003, 54, 714-724.	1.2	21
296	Isolation and characterization of 18 microsatellites in the Peking duck (Anas platyrhynchos) and their application in other waterfowl species. Molecular Ecology Notes, 2003, 3, 224-227.	1.7	81
297	Mapping of ESTs derived from pre-implantation stage cattle embryos to allocate 16 new additions to the ordered comparative map of cattle and human. Animal Genetics, 2003, 34, 449-452.	0.6	2
298	Effects of different laser-drilled openings in the zona pellucida on hatching of in vitroâ€“produced cattle blastocysts. Fertility and Sterility, 2003, 80, 714-719.	0.5	27
299	The GENETPIG database: a tool for comparative mapping in pig (Sus scrofa). Nucleic Acids Research, 2003, 31, 138-141.	6.5	7
300	A source for expression profiling in single preimplantation bovine embryos. Theriogenology, 2002, 57, 1611-1624.	0.9	19
301	Detection of quantitative trait loci for carcass traits in the pig by using AFLP. Mammalian Genome, 2002, 13, 206-210.	1.0	24
302	Chromosomal assignments for porcine genes encoding enzymes in hepatic metabolic pathways. Animal Genetics, 2002, 33, 255-263.	0.6	8
303	Isolation, polymorphism identification and linkage mapping of the porcine haptoglobin locus. Animal Genetics, 2002, 33, 324-325.	0.6	7
304	Molecular cloning and chromosome assignment of porcine vinculin gene (VCL). Animal Genetics, 2002, 33, 326-327.	0.6	1
305	SNP detection and linkage mapping of the porcine ferritin heavy-chain gene. Animal Genetics, 2002, 33, 325-326.	0.6	3
306	Sequence variation and linkage mapping of the porcine corticotropin releasing hormone (CRH) gene. Animal Genetics, 2002, 33, 233-234.	0.6	4

#	Article	IF	Citations
307	Polymorphism in the porcine transforming growth factor-Î²1 gene. Animal Genetics, 2002, 33, 234-235.	0.6	3
308	Linkage mapping of SNPs in the porcine relaxin gene. Animal Genetics, 2002, 33, 323-324.	0.6	3
309	Stage-specific expressed sequence tags obtained during preimplantation bovine development by differential display RT-PCR and suppression subtractive hybridization. Prenatal Diagnosis, 2002, 22, 1135-1142.	1.1	29
310	Application of differential display RT-PCR to identify porcine liver ESTs. Gene, 2001, 280, 75-85.	1.0	17
311	Mapping of 93 porcine ESTs preferentially expressed in liver. Mammalian Genome, 2001, 12, 869-872.	1.0	26
312	Polymorphic sites in exon 15 and 30 of the porcine C3 gene. Animal Genetics, 2001, 32, 46-47.	0.6	5
313	Expression of homeobox-containing genes in cDNA libraries derived from cattle oocytes and preimplantation stage embryo. Molecular Reproduction and Development, 2001, 60, 297-301.	1.0	18
314	Empirical Evaluation of Genetic Clustering Methods Using Multilocus Genotypes From 20 Chicken Breeds. Genetics, 2001, 159, 699-713.	1.2	306
315	Genetic distinctness of African, Asian and South American local chickens. Animal Genetics, 2000, 31, 159-165.	0.6	105
316	A highly polymorphic repetitive polypyrimidine/polypurine (CCTTT)n sequence in the 5â€² untranslated sequence of the porcine androgen receptor gene. Animal Genetics, 2000, 31, 288-289.	0.6	3
317	Porcine ESTs detected by differential display representing possible candidates for the trait 'eye muscle area'. Journal of Animal Breeding and Genetics, 2000, 117, 25-35.	0.8	11
318	Brief communication. Comparison of multilocus DNA fingerprints and microsatellites in an estimate of genetic distance in chicken. , 1999, 90, 656-659.		16
319	Maternal influences on litter size and growth in reciprocal crossed Miniature Pigs and Durocs. Archives Animal Breeding, 1999, 42, 83-92.	0.5	15
320	Evaluation of oligonucleotide probes for simple tandem repeats (STR) to produce informative DNA fingerprints of the chicken. British Poultry Science, 1998, 39, 62-69.	0.8	0
321	Evaluation of genetic variation within and between different chicken lines by DNA fingerprinting. , 1998, 89, 17-23.		12
322	Assessment of parental genomic proportions in crossbred chickens by DNA fingerprints. Journal of Animal Breeding and Genetics, 1997, 114, 55-68.	0.8	1
323	An assessment of applicability of Illumina GoatSNP50 BeadChip for genetic studies of Caucaian tur (Capra caucasica) â€. , 0, , .		0
324	A Study of Biodiversity of Russian Local Sheep Breeds Based on Pattern of Runs of Homozygosity ^{â€}. , 0, , .		3

#	Article	IF	Citations
325	Expression QTL and their applications in genetic improvement of farm animals.. CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources, 0, , 1-8.	0.6	1