Klaus Wimmers

List of Publications by Year
in descending order

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325	6,273	94381	155592
papers	citations	37 h-index	55 g-index

330	330	330	5883
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Empirical Evaluation of Genetic Clustering Methods Using Multilocus Genotypes From 20 Chicken Breeds. Genetics, 2001, 159, 699-713.	1.2	306
2	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
3	Genetic distinctness of African, Asian and South American local chickens. Animal Genetics, 2000, 31, 159-165.	0.6	105
4	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
5	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
6	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
7	Population structure and genetic diversity of 25 Russian sheep breeds based on whole-genome genotyping. Genetics Selection Evolution, 2018, 50, 29.	1.2	76
8	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
9	QTL for microstructural and biophysical muscle properties and body composition in pigs. BMC Genetics, 2006, 7, 15.	2.7	74
10	Association of HPA axis-related genetic variation with stress reactivity and aggressive behaviour in pigs. BMC Genetics, 2010, 11, 74.	2.7	74
11	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
12	Pig genome functional annotation enhances the biological interpretation of complex traits and human disease. Nature Communications, 2021, 12, 5848.	5.8	70
13	Pigsâ€™ aggressive temperament affects pre-slaughter mixing aggression, stress and meat quality. Animal, 2010, 4, 604-616.	1.3	69
14	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
15	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
16	Combined line-cross and half-sib QTL analysis in Durocâ€“Pietrain population. Mammalian Genome, 2008, 19, 429-438.	1.0	63
17	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
18	The genetics of feed conversion efficiency traits in a commercial broiler line. Scientific Reports, 2015, 5, 16387.	1.6	60

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19	Genomic selection using low density marker panels with application to a sire line in pigs. Genetics Selection Evolution, 2013, 45, 28.	1.2	58
20	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
21	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
22	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
23	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
24	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
25	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
26	Candidate gene markers for sperm quality and fertility of boar. Animal Reproduction Science, 2006, 92, 349-363.	0.5	48
27	Comparing Two Intestinal Porcine Epithelial Cell Lines (IPECs): Morphological Differentiation, Function and Metabolism. PLoS ONE, 2015, 10, e0132323.	1.1	48
28	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
29	MicroRNAs Regulate Cellular ATP Levels by Targeting Mitochondrial Energy Metabolism Genes during C2C12 Myoblast Differentiation. PLoS ONE, 2015, 10, e0127850.	1.1	44
30	Microarray-based transcriptional profiling ofEimeria bovis-infected bovine endothelial host cells. Veterinary Research, 2010, 41, 70.	1.1	44
31	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
32	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
33	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
34	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
35	Whole genome population genetics analysis of Sudanese goats identifies regions harboring genes associated with major traits. BMC Genetics, 2017, 18, 92.	2.7	42
36	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

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37	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
38	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
39	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
40	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
41	Identification of Common Regulators of Genes in Co-Expression Networks Affecting Muscle and Meat Properties. PLoS ONE, 2015, 10, e0123678.	1.1	39
42	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
43	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
44	Polymorphisms in candidate genes as markers for sperm quality and boar fertility. Animal Genetics, 2005, 36, 152-155.	0.6	35
45	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
46	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
47	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
48	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
49	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
50	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
51	Population Structure and Genetic Diversity of Sheep Breeds in the Kyrgyzstan. Frontiers in Genetics, 2019, 10, 1311.	1.1	34
52	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
53	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
54	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

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55	Pre- and post-natal muscle microRNA expression profiles of two pig breeds differing in muscularity. Gene, 2015, 561, 190-198.	1.0	33
56	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
57	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
58	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
59	Analysis of Candidate Genes for Growth and Milk Performance Traits in the Egyptian Barki Sheep. Animals, 2020, 10, 197.	1.0	32
60	Peptidylarginine deiminase gene is differentially expressed in freshwater and brackish water rainbow trout. Molecular Biology Reports, 2010, 37, 2333-2339.	1.0	31
61	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
62	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
63	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
64	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
65	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
66	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
67	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
68	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
69	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
70	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
71	Lower dietary phosphorus supply in pigs match both animal welfare aspects and resource efficiency. Ambio, 2018, 47, 20-29.	2.8	28
72	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

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73	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
74	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
75	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
76	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
77	Mapping of 93 porcine ESTs preferentially expressed in liver. Mammalian Genome, 2001, 12, 869-872.	1.0	26
78	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
79	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
80	Mapping quantitative trait loci for innate immune response in the pig. International Journal of Immunogenetics, 2011, 38, 121-131.	0.8	26
81	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
82	Genetic Contribution to Variation in Blood Calcium, Phosphorus, and Alkaline Phosphatase Activity in Pigs. Frontiers in Genetics, 2019, 10, 590.	1.1	25
83	Detection of quantitative trait loci for carcass traits in the pig by using AFLP. Mammalian Genome, 2002, 13, 206-210.	1.0	24
84	Intrafallopian transfer of gametes and early stage embryos for in vivo culture in cattle. Theriogenology, 2005, 64, 30-40.	0.9	24
85	QTL for the heritable inverted teat defect in pigs. Mammalian Genome, 2008, 19, 127-138.	1.0	24
86	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
87	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
88	Association of PPARGC1A and CAPNS1 gene polymorphisms and expression with meat quality traits in pigs. Meat Science, 2011, 89, 478-485.	2.7	23
89	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
90	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

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91	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
92	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
93	Polymorphism and expression of the porcine Tenascin C gene associated with meat and carcass quality. Meat Science, 2011, 89, 76-83.	2.7	22
94	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
95	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
96	Retrotransposons evolution and impact on lncRNA and protein coding genes in pigs. Mobile DNA, 2019, 10, 19.	1.3	22
97	Single- and Bayesian Multi-Marker Genome-Wide Association for Haematological Parameters in Pigs. PLoS ONE, 2016, 11, e0159212.	1.1	22
98	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
99	Molecular characterization of the pig C3 gene and its association with complement activity. Immunogenetics, 2003, 54, 714-724.	1.2	21
100	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
101	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
102	SINE jumping contributes to large-scale polymorphisms in the pig genomes. Mobile DNA, 2021, 12, 17.	1.3	21
103	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
104	Annotation and <i>in silico</i> localization of the Affymetrix GeneChip Porcine Genome Array. Archives Animal Breeding, 2010, 53, 230-238.	0.5	20
105	A source for expression profiling in single preimplantation bovine embryos. Theriogenology, 2002, 57, 1611-1624.	0.9	19
106	Identification of differentially expressed protective genes in liver of two rainbow trout strains. Veterinary Immunology and Immunopathology, 2012, 145, 305-315.	0.5	19
107	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
108	Airâ€"liquid interface enhances oxidative phosphorylation in intestinal epithelial cell line IPEC-J2. Cell Death Discovery, 2017, 3, 17001.	2.0	19

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109	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
110	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
111	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
112	Characterization of Dehydrodolichyl diphosphate synthase gene in rainbow trout (Oncorhynchus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 260-265.	0.7	18
113	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
114	Application of differential display RT-PCR to identify porcine liver ESTs. Gene, 2001, 280, 75-85.	1.0	17
115	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
116	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
117	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
118	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
119	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
120	Genetics of body fat mass and related traits in a pig population selected for leanness. Scientific Reports, 2017, 7, 9118.	1.6	17
121	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
122	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
123	Brief communication. Comparison of multilocus DNA fingerprints and microsatellites in an estimate of genetic distance in chicken. , 1999, 90, 656-659.		16
124	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
125	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
126	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

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127	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
128	Transcript variants of the porcine glucocorticoid receptor gene (NR3C1). General and Comparative Endocrinology, 2013, 189, 127-133.	0.8	16
129	Transcriptomic Response of Porcine PBMCs to Vaccination with Tetanus Toxoid as a Model Antigen. PLoS ONE, 2013, 8, e58306.	1.1	16
130	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
131	Physiological and Transcriptional Responses in Weaned Piglets Fed Diets with Varying Phosphorus and Calcium Levels. Nutrients, 2019, 11, 436.	1.7	16
132	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
133	Molecular cloning and sequencing of porcine C5 gene and its association with immunological traits. Immunogenetics, 2004, 55, 811-817.	1.2	15
134	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
135	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
136	Genomeâ€wide association analysis for growth, muscularity and meat quality in PiÃ©train pigs. Animal Genetics, 2014, 45, 350-356.	0.6	15
137	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
138	Transcriptome profiling of Musculus longissimus dorsi in two cattle breeds with different intramuscular fat deposition. Genomics Data, 2016, 7, 109-111.	1.3	15
139	Detection of pig genome regions determining production traits using an information theory approach. Livestock Science, 2017, 205, 31-35.	0.6	15
140	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
141	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
142	Host-Microbiota Interactions in Ileum and Caecum of Pigs Divergent in Feed Efficiency Contribute to Nutrient Utilization. Microorganisms, 2020, 8, 563.	1.6	15
143	Prenatal Skeletal Muscle Transcriptome Analysis Reveals Novel MicroRNA-mRNA Networks Associated with Intrauterine Growth Restriction in Pigs. Cells, 2021, 10, 1007.	1.8	15
144	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

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145	Maternal influences on litter size and growth in reciprocal crossed Miniature Pigs and Durocs. Archives Animal Breeding, 1999, 42, 83-92.	0.5	15
146	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
147	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
148	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
149	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
150	Genetic architecture and regulatory impact on hepatic microRNA expression linked to immune and metabolic traits. Open Biology, 2017, 7, 170101.	1.5	14
151	Implication of transcriptome profiling of spermatozoa for stallion fertility. Reproduction, Fertility and Development, 2018, 30, 1087.	0.1	14
152	Transcriptome Responses to Dexamethasone Depending on Dose and Glucocorticoid Receptor Sensitivity in the Liver. Frontiers in Genetics, 2019, 10, 559.	1.1	14
153	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
154	Tissue-Wide Gene Expression Analysis of Sodium/Phosphate Co-Transporters in Pigs. International Journal of Molecular Sciences, 2019, 20, 5576.	1.8	14
155	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
156	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
157	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
158	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
159	KRT8, FAF1 and PTH1R gene polymorphisms are associated with leg weakness traits in pigs. Molecular Biology Reports, 2013, 40, 2859-2866.	1.0	13
160	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
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	Genetically regulated hepatic transcripts and pathways orchestrate haematological, biochemical and body composition traits. Scientific Reports, 2016, 6, 39614.	1.6	13

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163	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
164	MicroRNA expression profiling of porcine mammary epithelial cells after challenge with Escherichia coli in vitro. BMC Genomics, 2017, 18, 660.	1.2	13
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