## List of Publications by Year in descending order

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RANG LUL

#	Article	IF	CITATIONS
1	LongSAGE analysis of skeletal muscle at three prenatal stages in Tongcheng and Landrace pigs. Genome Biology, 2007, 8, R115.	9.6	123
2	Genome Wide Sampling Sequencing for SNP Genotyping: Methods, Challenges and Future Development. International Journal of Biological Sciences, 2016, 12, 100-108.	6.4	77
3	Genomeâ€wide analysis reveals artificial selection on coat colour and reproductive traits in <scp>C</scp> hinese domestic pigs. Molecular Ecology Resources, 2015, 15, 414-424.	4.8	74
4	Molecular Characterization of Transcriptome-wide Interactions between Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus and Porcine Alveolar Macrophages in vivo. International Journal of Biological Sciences, 2011, 7, 947-959.	6.4	65
5	Genomeâ€wide scans to detect positive selection in Large White and Tongcheng pigs. Animal Genetics, 2014, 45, 329-339.	1.7	51
6	Genome Wide Distributions and Functional Characterization of Copy Number Variations between Chinese and Western Pigs. PLoS ONE, 2015, 10, e0131522.	2.5	47
7	Identification of Differentially Expressed Genes in the Longissimus Dorsi Muscle Tissue between Duroc and Erhualian Pigs by mRNA Differential Display. Asian-Australasian Journal of Animal Sciences, 2003, 16, 1066-1070.	2.4	46
8	TEAD1-dependent expression of the FoxO3a gene in mouse skeletal muscle. BMC Molecular Biology, 2011, 12, 1.	3.0	39
9	The genetic polymorphisms of TGFÎ <sup>2</sup> superfamily genes are associated with litter size in a Chinese indigenous sheep breed (Hu sheep). Animal Reproduction Science, 2018, 189, 19-29.	1.5	35
10	Reactomes of Porcine Alveolar Macrophages Infected with Porcine Reproductive and Respiratory Syndrome Virus. PLoS ONE, 2013, 8, e59229.	2.5	33
11	Deep Genome Resequencing Reveals Artificial and Natural Selection for Visual Deterioration, Plateau Adaptability and High Prolificacy in Chinese Domestic Sheep. Frontiers in Genetics, 2019, 10, 300.	2.3	33
12	Porcine CSRP3: polymorphism and association analyses with meat quality traits and comparative analyses with CSRP1 and CSRP2. Molecular Biology Reports, 2010, 37, 451-459.	2.3	32
13	Investigation of Lpin1 as a candidate gene for fat deposition in pigs. Molecular Biology Reports, 2009, 36, 1175-1180.	2.3	31
14	Differences of immune responses between Tongcheng (Chinese local breed) and Large White pigs after artificial infection with highly pathogenic porcine reproductive and respiratory syndrome virus. Virus Research, 2016, 215, 84-93.	2.2	30
15	Transcriptome Differences in Porcine Alveolar Macrophages from Tongcheng and Large White Pigs in Response to Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) Infection. International Journal of Molecular Sciences, 2017, 18, 1475.	4.1	30
16	Multiplex PCR assay for identification and quantification of bovine and equine in minced meats using novel specific nuclear DNA sequences. Food Control, 2019, 105, 29-37.	5.5	30
17	Investigation of LDHA and COPB1 as candidate genes for muscle development in the MYOD1 region of pig chromosome 2. Molecular Biology Reports, 2010, 37, 629-636.	2.3	25
18	2′,5′-Oligoadenylate synthetase 1(OAS1) inhibits PRRSV replication in Marc-145Âcells. Antiviral Research, 2016, 132, 268-273.	4.1	24

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19	Regulation of iNOS-Derived ROS Generation by HSP90 and Cav-1 in Porcine Reproductive and Respiratory Syndrome Virus-Infected Swine Lung Injury. Inflammation, 2017, 40, 1236-1244.	3.8	23
20	lsolation, mapping, SNP detection and association with backfat traits of the porcine CTNNBL1 and DGAT2 genes. Molecular Biology Reports, 2012, 39, 4485-4490.	2.3	22
21	Analysis of Genome-Wide Copy Number Variations in Chinese Indigenous and Western Pig Breeds by 60 K SNP Genotyping Arrays. PLoS ONE, 2014, 9, e106780.	2.5	22
22	Dual-output toehold-mediated strand displacement amplification for sensitive homogeneous electrochemical detection of specie-specific DNA sequences for species identification. Biosensors and Bioelectronics, 2020, 161, 112256.	10.1	22
23	Assignment and expression patterns of porcine muscle-specific isoform of phosphoglycerate mutase gene. Journal of Genetics and Genomics, 2008, 35, 257-260.	3.9	21
24	Investigation of four porcine candidate genes (H-FABP, MYOD1, UCP3 and MASTR) for meat quality traits in Large White pigs. Molecular Biology Reports, 2012, 39, 6599-6605.	2.3	21
25	Species Identification of Fox-, Mink-, Dog-, and Rabbit-Derived Ingredients by Multiplex PCR and Real-Time PCR Assay. Applied Biochemistry and Biotechnology, 2018, 185, 1-12.	2.9	21
26	Identification of Differentially Expressed Non-coding RNA in Porcine Alveolar Macrophages from Tongcheng and Large White Pigs Responded to PRRSV. Scientific Reports, 2018, 8, 15621.	3.3	20
27	Association of two porcine reproductive and respiratory syndrome virus (PRRSV) receptor genes, CD163 and SN with immune traits. Molecular Biology Reports, 2012, 39, 3971-3976.	2.3	17
28	TEAD1 controls C2C12 cell proliferation and differentiation and regulates three novel target genes. Cellular Signalling, 2013, 25, 674-681.	3.6	17
29	ICAM-1-dependent and ICAM-1-independent neutrophil lung infiltration by porcine reproductive and respiratory syndrome virus infection. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2015, 309, L226-L236.	2.9	17
30	Recombinase Polymerase Amplification Based Multiplex Lateral Flow Dipstick for Fast Identification of Duck Ingredient in Adulterated Beef. Animals, 2020, 10, 1765.	2.3	17
31	Effect of breed, sex and birth parity on growth, carcass and meat quality in pigs. Frontiers of Agriculture in China, 2008, 2, 331-337.	0.2	16
32	Molecular characterization, chromosomal localization and association analysis with back-fat thickness of porcine LPIN2 and LPIN3. Molecular Biology Reports, 2009, 36, 1819-1824.	2.3	15
33	Association of polymorphisms in <i><scp>NR</scp>6A1</i> , <i><scp>PLAG</scp>1</i> and <i><scp>VRTN</scp></i> with the number of vertebrae in Chinese TongchengÂA—ÂLarge White crossbred pigs. Animal Genetics, 2018, 49, 353-354.	1.7	15
34	Porcine TEF1 and RTEF1: Molecular characterization and association analyses with growth traits. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2008, 150, 447-453.	1.6	14
35	Molecular characterization, chromosomal location, alternative splicing and polymorphism of porcine GFAT1 gene. Molecular Biology Reports, 2010, 37, 2711-2717.	2.3	14
36	Molecular characterization of porcine SARM1 and its role in regulating TLRs signaling during highly pathogenic porcine reproductive and respiratory syndrome virus infection in vivo. Developmental and Comparative Immunology, 2013, 39, 117-126.	2.3	13

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37	A multiplex PCR method for detection of five animal species in processed meat products using novel species-specific nuclear DNA sequences. European Food Research and Technology, 2020, 246, 1351-1360.	3.3	13
38	The molecular characterization and associations of porcine cardiomyopathy asssociated 5 (CMYA5) gene with carcass trait and meat quality. Molecular Biology Reports, 2011, 38, 2085-2090.	2.3	12
39	LSM14A inhibits porcine reproductive and respiratory syndrome virus (PRRSV) replication by activating IFN-β signaling pathway in Marc-145. Molecular and Cellular Biochemistry, 2015, 399, 247-256.	3.1	12
40	Molecular Characterization and Expression Pattern of the Porcine STARS, a Striated Muscle-Specific Expressed Gene. Biochemical Genetics, 2008, 46, 644-651.	1.7	11
41	Cloning, chromosomal localization, expression profile and association analysis of the porcine WNT10B gene with backfat thickness. Molecular Biology Reports, 2011, 38, 3095-3099.	2.3	11
42	Development of a colloidal gold immunochromatographic strip assay for simple and fast detection of human α-lactalbumin in genetically modified cow milk. Journal of Dairy Science, 2016, 99, 1773-1779.	3.4	11
43	Investigation of the porcine PA28 activator gamma-subunit (PSME3) gene: isolation, polymorphism and its chromosomal localization. Journal of Animal Breeding and Genetics, 2004, 121, 142-148.	2.0	10
44	Detection of two exogenous genes in transgenic cattle by loop-mediated isothermal amplification. Transgenic Research, 2012, 21, 1367-1373.	2.4	10
45	Sequencing, tissue distribution and physical mapping of the porcine homologue of cardiomyopathy associated 3 (CMYA3 ). Animal Genetics, 2003, 34, 473-474.	1.7	9
46	Mapping and expression analyses during porcine foetal muscle development of 12 genes involved in histone modifications. Animal Genetics, 2009, 40, 242-246.	1.7	9
47	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). Journal of Applied Genetics, 2015, 56, 355-363.	1.9	9
48	Genome-Wide Analysis and Functional Characterization of the Polyadenylation Site in Pigs Using RNAseq Data. Scientific Reports, 2016, 6, 36388.	3.3	9
49	MicroRNA expression profiling in alveolar macrophages of indigenous Chinese Tongcheng pigs infected with PRRSV in vivo. Journal of Applied Genetics, 2017, 58, 539-544.	1.9	9
50	Porcine Interferon Stimulated Gene 12a Restricts Porcine Reproductive and Respiratory Syndrome Virus Replication in MARC-145 Cells. International Journal of Molecular Sciences, 2017, 18, 1613.	4.1	9
51	Radiation hybrid mapping of porcine <b><i>CMYA2</i></b> and <b><i>CMYA4</i></b> . Animal Genetics, 2005, 36, 511-511.	1.7	8
52	Molecular characterization, expression profiles, and association analysis with hematologic parameters of the porcine HPSE and HPSE2 genes. Journal of Applied Genetics, 2013, 54, 71-78.	1.9	8
53	Germplasm characteristics and conservation of Tongcheng pig: A case study for preservation and utilization of Chinese indigenous pig breeds. Animal Genetic Resources Information, 2006, 39, 51-63.	0.1	7
54	Molecular characterization, chromosomal localization, expression profile and association analysis with carcass traits of the porcine dickkopf homolog1 gene. Molecular Biology Reports, 2011, 38, 1929-1934.	2.3	7

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55	Identification of positive selection signatures in pigs by comparing linkage disequilibrium variances. Animal Genetics, 2017, 48, 600-605.	1.7	7
56	Wholeâ€genome sequencing reveals breedâ€differential CNVs between Tongcheng and Large White pigs. Animal Genetics, 2020, 51, 940-944.	1.7	7
57	A novel quantitative real-time PCR method for the detection of mammalian and poultry species based on a shared single-copy nuclear DNA sequence. Food Chemistry, 2021, 341, 128170.	8.2	7
58	A multiplex real-time PCR approach for identification and quantification of sheep/goat, fox and murine fractions in meats using nuclear DNA sequences. Food Control, 2021, 126, 108035.	5.5	7
59	Molecular characterization of the porcine JHDM1A gene associated with average daily gain: evaluation its role in skeletal muscle development and growth. Molecular Biology Reports, 2011, 38, 4697-4704.	2.3	6
60	Molecular characterization, expression profiles of the porcine SDC2 and HSPG2 genes and their association with hematologic parameters. Molecular Biology Reports, 2013, 40, 2549-2556.	2.3	6
61	Global Analysis of Alternative Splicing Difference in Peripheral Immune Organs between Tongcheng Pigs and Large White Pigs Artificially Infected with PRRSV <i>In Vivo</i> . BioMed Research International, 2020, 2020, 1-14.	1.9	6
62	Change of Gut Microbiota in PRRSV-Resistant Pigs and PRRSV-Susceptible Pigs from Tongcheng Pigs and Large White Pigs Crossed Population upon PRRSV Infection. Animals, 2022, 12, 1504.	2.3	6
63	Expression patterns and subcellular localization of porcine (Sus Scrofa) lectin, galactose-binding, soluble 1 gene. Acta Biochimica Et Biophysica Sinica, 2008, 40, 85-90.	2.0	5
64	Porcine skeletal muscle differentially expressed gene <i>CMYA1</i> : isolation, characterization, mapping, expression and association analysis with carcass traits. Animal Genetics, 2009, 40, 255-261.	1.7	5
65	Molecular characterization of the porcine MTPAP gene associated with meat quality traits: chromosome localization, expression distribution, and transcriptional regulation. Molecular and Cellular Biochemistry, 2012, 364, 173-180.	3.1	5
66	NUDT6, the FGF-2's antisense gene, showed associations with fat deposition related traits in pigs. Molecular Biology Reports, 2012, 39, 4119-4126.	2.3	5
67	Detection of HbsAg and hATIII genetically modified goats (Caprahircus) by loop-mediated isothermal amplification. Molecular Biology Reports, 2013, 40, 6177-6182.	2.3	5
68	Genetic diversity analyses of 10 indigenous Chinese pig populations based on 20 microsatellites1. Journal of Animal Science, 2004, 82, 368-374.	0.5	5
69	MiR-142-5p/FAM134B Axis Manipulates ER-Phagy to Control PRRSV Replication. Frontiers in Immunology, 0, 13, .	4.8	5
70	Molecular characterization, expression and association analysis of the porcine <i>CMYA</i> 4 gene with carcass traits. Journal of Animal Breeding and Genetics, 2008, 125, 234-239.	2.0	4
71	Genome-Wide Characterization and Comparative Analyses of Simple Sequence Repeats among Four Miniature Pig Breeds. Animals, 2020, 10, 1792.	2.3	4
72	The Association of ANKRD2 with Loin Depth and Muscle Firmness in Pigs. Journal of Animal and Veterinary Advances, 2011, 10, 1462-1468.	0.1	4

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73	Integration of Transcriptome and Proteome in Lymph Nodes Reveal the Different Immune Responses to PRRSV Between PRRSV-Resistant Tongcheng Pigs and PRRSV-Susceptible Large White Pigs. Frontiers in Genetics, 2022, 13, 800178.	2.3	4
74	Preparation and analysis of spermatocyte meiotic pachytene bivalents of pigs for gene mapping. Cell Research, 2002, 12, 401-405.	12.0	3
75	Immunochromatrography Detection of Human Lactoferrin Protein in Milk from Transgenic Cattle. Journal of AOAC INTERNATIONAL, 2013, 96, 116-120.	1.5	3
76	Investigation of four candidate genes (IGF2, JHDM1A, COPB1 and TEF1) for growth rate and backfat thickness traits on SSC2q in Large White pigs. Molecular Biology Reports, 2014, 41, 309-315.	2.3	3
77	Two coupled mutations abolished the binding of CEBPB to the promoter of CXCL14 that displayed an antiviral effect on PRRSV by activating IFN signaling. FASEB Journal, 2020, 34, 11257-11271.	0.5	3
78	Alternative polyadenylation events differ dramatically between Tongcheng and Large White pigs in response to PRRSV infection. Animal Genetics, 2021, 52, 744-748.	1.7	2
79	Rapid visual genotyping method for germline mutants with small genomic fragment deletion by allele-specific PCR and lateral flow nucleic acid biosensor. Molecular Biology Reports, 2021, 48, 7325-7332.	2.3	1
80	A universal primer distinguishable PCR (UP-D-PCR) method for simultaneous identification and differentiation of bovine- and ovine/caprine-derived ingredients in ruminant feeds. European Food Research and Technology, 0, , 1.	3.3	0
81	Rapid Identification of HSA Genetically Modified Goats by Combining Recombinase Polymerase Amplification (RPA) with Lateral Flow Dipstick (LFD). Agriculture (Switzerland), 2022, 12, 927.	3.1	0