Analyses of pig genomes provide insight into porcine de

Nature 491, 393-398 DOI: 10.1038/nature11622

Citation Report

#	Article	IF	CITATIONS
1	Regions of Homozygosity in the Porcine Genome: Consequence of Demography and the Recombination Landscape. PLoS Genetics, 2012, 8, e1003100.	1.5	266
2	Strong signatures of selection in the domestic pig genome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19529-19536.	3.3	548
3	Pig geneticists go the whole hog. Nature, 2012, 491, 315-316.	13.7	5
4	A high density recombination map of the pig reveals a correlation between sex-specific recombination and GC content. BMC Genomics, 2012, 13, 586.	1.2	150
5	A gene expression atlas of the domestic pig. BMC Biology, 2012, 10, 90.	1.7	199
6	Pairwise comparisons of ten porcine tissues identify differential transcriptional regulation at the gene, isoform, promoter and transcription start site level. Biochemical and Biophysical Research Communications, 2013, 438, 346-352.	1.0	29
7	3D organization of telomeres in porcine neutrophils and analysis of LPS-activation effect. BMC Cell Biology, 2013, 14, 30.	3.0	9
8	Regions of XY homology in the pig X chromosome and the boundary of the pseudoautosomal region. BMC Genetics, 2013, 14, 3.	2.7	30
9	Evolutionary dynamics of copy number variation in pig genomes in the context of adaptation and domestication. BMC Genomics, 2013, 14, 449.	1.2	118
10	Detection of selective sweeps in cattle using genome-wide SNP data. BMC Genomics, 2013, 14, 382.	1.2	102
11	Structural and functional annotation of the porcine immunome. BMC Genomics, 2013, 14, 332.	1.2	203
12	High throughput transcriptome analysis of lipid metabolism in Syrian hamster liver in absence of an annotated genome. BMC Genomics, 2013, 14, 237.	1.2	8
13	Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. BMC Genomics, 2013, 14, 148.	1.2	45
14	How immunogenetically different are domestic pigs from wild boars: a perspective from single-nucleotide polymorphisms of 19 immunity-related candidate genes. Immunogenetics, 2013, 65, 737-748.	1.2	7
15	The new pig on the block: modelling cancer in pigs. Transgenic Research, 2013, 22, 673-680.	1.3	50
16	Complicated Relationships: A Review of Biological Interaction Networks and Pathways in Animal Science. Springer Science Reviews, 2013, 1, 73-83.	1.3	3
17	Role of DNA Methylation in Expression and Transmission of Porcine Endogenous Retroviruses. Journal of Virology, 2013, 87, 12110-12120.	1.5	11
18	Broad-scale phylogenomics provides insights into retrovirus–host evolution. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20146- <u>20151</u> .	3.3	91

ARTICLE IF CITATIONS # Expression variation of the porcine ADRB2 has a complex genetic background. Molecular Genetics and 19 1.0 6 Genomics, 2013, 288, 615-625. Web Apollo: a web-based genomic annotation editing platform. Genome Biology, 2013, 14, R93. 329 The impact of breed and tissue compartment on the response of pig macrophages to 21 1.2 83 lipopolysaccharide. BMC Genomics, 2013, 14, 581. Correlated mRNAs and miRNAs from co-expression and regulatory networks affect porcine muscle 54 and finally meat properties. BMC Genomics, 2013, 14, 533. Galaxy tools to study genome diversity. GigaScience, 2013, 2, 17. 23 3.3 19 The peripheral blood transcriptome reflects variations in immunity traits in swine: towards the 1.2 37 identification of biomarkers. BMC Genomics, 2013, 14, 894. Kinotypes: stable species- and individual-specific profiles of cellular kinase activity. BMC Genomics, 25 1.2 17 2013, 14, 854. Genome-wide and local pattern of linkage disequilibrium and persistence of phase for 3 Danish pig 2.7 26 breeds. BMC Genetics, 2013, 14, 115. Allelic frequencies of <scp>PRKAG</scp>3 in several pig breeds and its technological consequences on 27 a <scp>D</scp>urocÂ×Â<scp>L</scp>andraceâ€<scp>L</scp>arge <scp>W<∫scp>hite cross. Journal of 0.8 10 Animal Breeding and Genetics, 2013, 130, 382-393. Porcine synapsin 1: <i>SYN1</i>Âgene analysis and functional characterization of the promoter. FEBS 1.0 14 Open Bio, 2013, 3, 411-420. Genomic analyses identify distinct patterns of selection in domesticated pigs and Tibetan wild boars. 29 472 9.4 Nature Genetics, 2013, 45, 1431-1438. Potentializing the Research Piglet in Experimental Neonatal Research. Current Anthropology, 2013, 54, 0.8 S118-S128. The Anthropology of Potentiality in Biomedicine. Current Anthropology, 2013, 54, S3-S14. $\mathbf{31}$ 0.8 142 Porcine colonization of the Americas: a 60k SNP story. Heredity, 2013, 110, 321-330. 1.2 33 A population genetics view of animal domestication. Trends in Genetics, 2013, 29, 197-205. 2.9 233 Molecular advances in QTL discovery and application in pig breeding. Trends in Genetics, 2013, 29, 215-224. A detailed method for preparation of a functional and flexible bloodâ€"brain barrier model using 35 1.1 93 porcine brain endothelial cells. Brain Research, 2013, 1521, 16-30. Minipig and beagle animal model genomes aid species selection in pharmaceutical discovery and 1.3 development. Toxicology and Applied Pharmacology, 2013, 270, 149-157.

	CITATION R	EPORT	
#	Article	IF	Citations
37	Pig genomics for biomedicine. Nature Biotechnology, 2013, 31, 122-123.	9.4	49
38	Oligodeoxyribonucleotides derived from salmon sperm DNA: An alternative to defibrotide. Biologicals, 2013, 41, 190-196.	0.5	3
39	Advances in biotechnology and informatics to link variation in the genome to phenotypes in plants and animals. Functional and Integrative Genomics, 2013, 13, 1-9.	1.4	12
41	Haplotype-based prediction of gene alleles using pedigrees and SNP genotypes. , 2013, , .		6
42	Protein composition of bronchoalveolar lavage fluid and airway surface liquid from newborn pigs. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2013, 305, L256-L266.	1.3	33
43	Association Analysis between Single Nucleotide Polymorphisms in the Promoter Region of <i>LEP, MYF6, MYOD1, OPN, SCD</i> Genes and Carcass Traits in Heavy Pigs. Italian Journal of Animal Science, 2013, 12, e13.	0.8	5
44	Signatures of Diversifying Selection in European Pig Breeds. PLoS Genetics, 2013, 9, e1003453.	1.5	228
45	Systems Biology Approach to the Dissection of the Complexity of Regulatory Networks in the S. scrofa Cardiocirculatory System. International Journal of Molecular Sciences, 2013, 14, 23160-23187.	1.8	7
46	Linkage disequilibrium and haplotype block structure in six commercial pig lines. Journal of Animal Science, 2013, 91, 3493-3501.	0.2	56
47	The Expansion and Functional Diversification of the Mammalian Ribonuclease A Superfamily Epitomizes the Efficiency of Multigene Families at Generating Biological Novelty. Genome Biology and Evolution, 2013, 5, 2124-2140.	1.1	43
48	Comparative Organization and Gene Expression Profiles of the Porcine Pseudoautosomal Region. Cytogenetic and Genome Research, 2013, 141, 26-36.	0.6	10
49	Genome sequencing reveals fine scale diversification and reticulation history during speciation in Sus. Genome Biology, 2013, 14, R107.	13.9	137
50	SUS-BAR: a database of pig proteins with statistically validated structural and functional annotation. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat065-bat065.	1.4	4
51	Livestock and the promise of genomics. Genome, 2013, 56, 556-566.	0.9	6
52	Socio-economic, industrial and cultural parameters of pig-borne infections. Clinical Microbiology and Infection, 2013, 19, 605-610.	2.8	19
53	Use of pigs as a potential model for research into dietary modulation of the human gut microbiota. Nutrition Research Reviews, 2013, 26, 191-209.	2.1	275
54	Genome-Wide Patterns of Genetic Variation in Two Domestic Chickens. Genome Biology and Evolution, 2013, 5, 1376-1392.	1.1	65
55	ãf−ā,¿ã®ãf¬ã,·ãf"ã,'åºfã•a,‹æ¥µä,Šã,²ãfŽãfæf…å±. Nature Digest, 2013, 10, 22-23.	0.0	0

#	Article	IF	CITATIONS
56	SNPs detection in DHPS-WDR83 overlapping genes mapping on porcine chromosome 2 in a QTL region for meat pH. BMC Genetics, 2013, 14, 99.	2.7	7
57	Conservation genomic analysis of domestic and wild pig populations from the Iberian Peninsula. BMC Genetics, 2013, 14, 106.	2.7	87
58	RNA Profiles of Porcine Embryos during Genome Activation Reveal Complex Metabolic Switch Sensitive to In Vitro Conditions. PLoS ONE, 2013, 8, e61547.	1.1	21
59	Genome-Wide Association Analyses for Fatty Acid Composition in Porcine Muscle and Abdominal Fat Tissues. PLoS ONE, 2013, 8, e65554.	1.1	40
60	Plasma Proteome Profiles Associated with Diet-Induced Metabolic Syndrome and the Early Onset of Metabolic Syndrome in a Pig Model. PLoS ONE, 2013, 8, e73087.	1.1	27
61	Development of Transgenic Minipigs with Expression of Antimorphic Human Cryptochrome 1. PLoS ONE, 2013, 8, e76098.	1.1	9
62	Molecular Cloning and Characterization of Porcine Na+/K+·ATPase Isoforms α1, α2, α3 and the ATP1A3 Promoter. PLoS ONE, 2013, 8, e79127.	1.1	25
63	An F2 Pig Resource Population as a Model for Genetic Studies of Obesity and Obesity-Related Diseases in Humans: Design and Genetic Parameters. Frontiers in Genetics, 2013, 4, 29.	1.1	42
64	Genomic and Epigenomic Insights into Nutrition and Brain Disorders. Nutrients, 2013, 5, 887-914.	1.7	68
65	Extensive Expression Differences along Porcine Small Intestine Evidenced by Transcriptome Sequencing. PLoS ONE, 2014, 9, e88515.	1.1	44
66	Molecular Evolution of the Porcine Type I Interferon Family: Subtype-Specific Expression and Antiviral Activity. PLoS ONE, 2014, 9, e112378.	1.1	41
67	Characterization of Sus scrofa Small Non-Coding RNAs Present in Both Female and Male Gonads. PLoS ONE, 2014, 9, e113249.	1.1	10
68	Impact of sensory feed additives on feed intake, feed preferences, and growth of female piglets during the early postweaning period1. Journal of Animal Science, 2014, 92, 2133-2140.	0.2	29
69	Genetic anchoring of whole-genome shotgun assemblies. Frontiers in Genetics, 2014, 5, 208.	1.1	48
70	Systems genetics of obesity in an F2 pig model by genome-wide association, genetic network, and pathway analyses. Frontiers in Genetics, 2014, 5, 214.	1.1	25
71	Identification of selection signatures in livestock species. Genetics and Molecular Biology, 2014, 37, 330-342.	0.6	103
72	A genomeâ€wide scan for selection signatures in Yorkshire and Landrace pigs based on sequencing data. Animal Genetics, 2014, 45, 808-816.	0.6	19
73	Is there a single porcine protegrin gene?. FEBS Journal, 2014, 281, 5418-5419.	2.2	0

#	Article	IF	CITATIONS
74	Genome sequencing and analysis of Mangalica, a fatty local pig of Hungary. BMC Genomics, 2014, 15, 761.	1.2	40
75	Changes in renal medulla gene expression in a pre-clinical model of post cardiopulmonary bypass acute kidney injury. BMC Genomics, 2014, 15, 916.	1.2	12
76	Dysregulation of genome-wide gene expression and DNA methylation in abnormal cloned piglets. BMC Genomics, 2014, 15, 811.	1.2	45
77	Population history and genomic signatures for high-altitude adaptation in Tibetan pigs. BMC Genomics, 2014, 15, 834.	1.2	140
78	Defining the genetic relationship of protegrinâ€related sequences and the <i>inÂvivo</i> expression of protegrins. FEBS Journal, 2014, 281, 5420-5431.	2.2	11
79	Classic Selective Sweeps Revealed by Massive Sequencing in Cattle. PLoS Genetics, 2014, 10, e1004148.	1.5	254
80	Porcine Endogenous Retroviruses in Xenotransplantation—Molecular Aspects. Viruses, 2014, 6, 2062-2083.	1.5	42
81	A Splice Mutation in the PHKG1 Gene Causes High Glycogen Content and Low Meat Quality in Pig Skeletal Muscle. PLoS Genetics, 2014, 10, e1004710.	1.5	101
82	The study of biodiversity in the era of massive sequencing. Revista Mexicana De Biodiversidad, 2014, 85, 1249-1264.	0.4	8
83	Identification of genes regulating growth and fatness traits in pig through hypothalamic transcriptome analysis. Physiological Genomics, 2014, 46, 195-206.	1.0	56
84	Linkage disequilibrium patterns and persistence of phase in purebred and crossbred pig (Sus scrofa) populations. BMC Genetics, 2014, 15, 126.	2.7	33
85	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. Proceedings of the United States of America, 2014, 111, E5661-9.	3.3	260
87	Dystrophin insufficiency causes selective muscle histopathology and loss of dystrophinâ€glycoprotein complex assembly in pig skeletal muscle. FASEB Journal, 2014, 28, 1600-1609.	0.2	25
88	Snapshot of Structural Variations in the Tibetan Wild Boar Genome at Single-Nucleotide Resolution. Journal of Genetics and Genomics, 2014, 41, 653-657.	1.7	6
89	Variation in the coding and 3′ untranslated regions of the porcine prolactin receptor short form modifies protein expression and function. Animal Genetics, 2014, 45, 74-86.	0.6	10
90	Mutation discovery for <scp>M</scp> endelian traits in nonâ€laboratory animals: a review of achievements up to 2012. Animal Genetics, 2014, 45, 157-170.	0.6	33
91	Proteomics in farm animals models of human diseases. Proteomics - Clinical Applications, 2014, 8, 677-688.	0.8	14
92	A genome-wide association study reveals a novel candidate gene for sperm motility in pigs. Animal Reproduction Science, 2014, 151, 201-207.	0.5	28

#	Article	IF	CITATIONS
93	Genomic relationships computed from either nextâ€generation sequence or array <scp>SNP</scp> data. Journal of Animal Breeding and Genetics, 2014, 131, 85-96.	0.8	24
94	A genomeâ€wide linkage analysis for reproductive traits in F 2 L arge W hite × M eishan cross gilts. Animal Genetics, 2014, 45, 191-197.	0.6	39
95	Comparative genomics reveals insights into avian genome evolution and adaptation. Science, 2014, 346, 1311-1320.	6.0	895
96	Genome-Wide Identification of Long Intergenic Noncoding RNA Genes and Their Potential Association with Domestication in Pigs. Genome Biology and Evolution, 2014, 6, 1387-1392.	1.1	121
97	Identification of speciesâ€ s pecific novel transcripts in pig reproductive tissues using <scp>RNA</scp> â€seq. Animal Genetics, 2014, 45, 198-204.	0.6	22
98	Pig models of neurodegenerative disorders: Utilization in cell replacementâ€based preclinical safety and efficacy studies. Journal of Comparative Neurology, 2014, 522, 2784-2801.	0.9	43
99	Taste and odorant receptors of the coelacanth—A gene repertoire in transition. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2014, 322, 403-414.	0.6	31
100	Morphology and chronology of diphyodont dentition in miniature pigs, Sus Scrofa. Oral Diseases, 2014, 20, 367-379.	1.5	36
101	Identifying genetic loci controlling neonatal passive transfer of immunity using a hybrid genotyping strategy. Animal Genetics, 2014, 45, 340-349.	0.6	13
102	The pig as an animal model for human pathologies: A proteomics perspective. Proteomics - Clinical Applications, 2014, 8, 715-731.	0.8	213
103	Characterization of the porcine nutrient and taste receptor gene repertoire in domestic and wild populations across the globe. BMC Genomics, 2014, 15, 1057.	1.2	30
104	Reconstruction of gross avian genome structure, organization and evolution suggests that the chicken lineage most closely resembles the dinosaur avian ancestor. BMC Genomics, 2014, 15, 1060.	1.2	71
105	Increasing gene discovery and coverage using RNA-seq of globin RNA reduced porcine blood samples. BMC Genomics, 2014, 15, 954.	1.2	43
106	Cytokines from the pig conceptus: roles in conceptus development in pigs. Journal of Animal Science and Biotechnology, 2014, 5, 51.	2.1	64
107	Recombination of the porcine X chromosome: a high density linkage map. BMC Genetics, 2014, 15, 148.	2.7	13
108	Genomic and Phenotypic Characterization of a Wild Medaka Population: Towards the Establishment of an Isogenic Population Genetic Resource in Fish. G3: Genes, Genomes, Genetics, 2014, 4, 433-445.	0.8	54
109	Genome-wide association and pathway analysis of feed efficiency in pigs reveal candidate genes and pathways for residual feed intake. Frontiers in Genetics, 2014, 5, 307.	1.1	84
110	Testing models of speciation from genome sequences: divergence and asymmetric admixture in <scp>l</scp> sland <scp>S</scp> outhâ€ <scp>E</scp> ast <scp>A</scp> sian <i><scp>S</scp>us</i> species during the <scp>P</scp> lioâ€ <scp>P</scp> leistocene climatic fluctuations. Molecular Ecology, 2014, 23, 5566.5574	2.0	32

#	Article	IF	CITATIONS
111	Living on a volcano's edge: genetic isolation of an extremophile terrestrial metazoan. Heredity, 2014, 112, 132-142.	1.2	16
112	Sulforaphane pretreatment prevents systemic inflammation and renal injury in response to cardiopulmonary bypass. Journal of Thoracic and Cardiovascular Surgery, 2014, 148, 690-697.e3.	0.4	25
113	Genomics to systems biology in animal and veterinary sciences: Progress, lessons and opportunities. Livestock Science, 2014, 166, 232-248.	0.6	69
114	The evolution of porcine embryo inÂvitro production. Theriogenology, 2014, 81, 24-37.	0.9	115
115	On the relationship between an Asian haplotype on chromosome 6 that reduces androstenone levels in boars and the differential expression of SULT2A1 in the testis. BMC Genetics, 2014, 15, 4.	2.7	7
116	Stage-specific differential gene expression profiling and functional network analysis during morphogenesis of diphyodont dentition in miniature pigs, Sus Scrofa. BMC Genomics, 2014, 15, 103.	1.2	21
117	A genome-wide scan for signatures of selection in Chinese indigenous and commercial pig breeds. BMC Genetics, 2014, 15, 7.	2.7	96
118	Climate rather than geography separates two <scp>E</scp> uropean honeybee subspecies. Molecular Ecology, 2014, 23, 2353-2361.	2.0	29
119	Discovery of a novel long terminal repeat (<scp>LTR</scp> 2i_ <scp>SS</scp>) in <i><scp>S</scp>us <scp>S</scp>crofa</i> . Animal Genetics, 2014, 45, 367-372.	0.6	1
120	Domestication Genomics: Evidence from Animals. Annual Review of Animal Biosciences, 2014, 2, 65-84.	3.6	98
121	Genome sequencing and population genomics in non-model organisms. Trends in Ecology and Evolution, 2014, 29, 51-63.	4.2	570
122	Applied Animal Genomics: Results from the Field. Annual Review of Animal Biosciences, 2014, 2, 105-139.	3.6	102
123	A Paleogenomic Perspective on Evolution and Gene Function: New Insights from Ancient DNA. Science, 2014, 343, 1236573.	6.0	197
124	The impact of whole-genome sequencing on the reconstruction of human population history. Nature Reviews Genetics, 2014, 15, 149-162.	7.7	147
125	Pathways and genes involved in steroid hormone metabolism in male pigs: A review and update. Journal of Steroid Biochemistry and Molecular Biology, 2014, 140, 44-55.	1.2	37
126	Genetically modified pigs to model human diseases. Journal of Applied Genetics, 2014, 55, 53-64.	1.0	56
127	Copy number variants in a highly inbred <scp>I</scp> berian porcine strain. Animal Genetics, 2014, 45, 357-366.	0.6	20
129	Pig Skin Includes Dendritic Cell Subsets Transcriptomically Related to Human CD1a and CD14 Dendritic Cells Presenting Different Migrating Behaviors and T Cell Activation Capacities. Journal of Immunology, 2014, 193, 5883-5893.	0.4	50

	Сітатіо	CITATION REPORT	
#		IF	CITATIONS
130	Porcine SLITRK1: Molecular cloning and characterization. FEBS Open Bio, 2014, 4, 872-878.	1.0	7
131	Mixed signals from hybrid genomes. Molecular Ecology, 2014, 23, 3941-3943.	2.0	10
132	A new approach to predict human intestinal absorption using porcine intestinal tissue and biorelevant matrices. European Journal of Pharmaceutical Sciences, 2014, 63, 167-177.	1.9	106
133	Mining the pig genome to investigate the domestication process. Heredity, 2014, 113, 471-484.	1.2	30
134	Structured RNAs and synteny regions in the pig genome. BMC Genomics, 2014, 15, 459.	1.2	20
135	Unraveling the effect of genomic structural changes in the rhesus macaque - implications for the adaptive role of inversions. BMC Genomics, 2014, 15, 530.	1.2	24
136	Design and development of exome capture sequencing for the domestic pig (Sus scrofa). BMC Genomics, 2014, 15, 550.	1.2	24
137	Global copy number analyses by next generation sequencing provide insight into pig genome variation. BMC Genomics, 2014, 15, 593.	1.2	44
138	Whole-genome sequence analysis reveals differences in population management and selection of European low-input pig breeds. BMC Genomics, 2014, 15, 601.	1.2	44
139	An update of the goat genome assembly using dense radiation hybrid maps allows detailed analysis of evolutionary rearrangements in Bovidae. BMC Genomics, 2014, 15, 625.	1.2	19
140	Genome-wide DNA methylation changes in skeletal muscle between young and middle-aged pigs. BMC Genomics, 2014, 15, 653.	1.2	73
141	Demographic history and gene flow during silkworm domestication. BMC Evolutionary Biology, 2014, 14, 185.	3.2	33
142	SeqControl: process control for DNA sequencing. Nature Methods, 2014, 11, 1071-1075.	9.0	10
144	The porcine innate immune system: An update. Developmental and Comparative Immunology, 2014, 45, 321-343.	1.0	235
145	Drastic population fluctuations explain the rapid extinction of the passenger pigeon. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10636-10641.	3.3	142
146	Imprinted loci in domestic livestock species as epigenomic targets for artificial selection of complex traits. Animal Genetics, 2014, 45, 25-39.	0.6	21
147	A Dysfunctional Sense of Smell: The Irreversibility of Olfactory Evolution in Free-Living Pigs. Evolutionary Biology, 2014, 41, 229-239.	0.5	17
148	A genome-wide association study of production traits in a commercial population of Large White pigs: evidence of haplotypes affecting meat quality. Genetics Selection Evolution, 2014, 46, 12.	1.2	71

#	Article	IF	CITATIONS
149	From SNP co-association to RNA co-expression: Novel insights into gene networks for intramuscular fatty acid composition in porcine. BMC Genomics, 2014, 15, 232.	1.2	44
150	Analysis of the genetics of boar taint reveals both single SNPs and regional effects. BMC Genomics, 2014, 15, 424.	1.2	30
151	Gene co-expression network analysis identifies porcine genes associated with variation in Salmonella shedding. BMC Genomics, 2014, 15, 452.	1.2	65
152	Genomic variation in macrophage-cultured European porcine reproductive and respiratory syndrome virus Olot/91 revealed using ultra-deep next generation sequencing. Virology Journal, 2014, 11, 42.	1.4	15
153	Untangling the hybrid nature of modern pig genomes: a mosaic derived from biogeographically distinct and highly divergent <i>Sus scrofa</i> populations. Molecular Ecology, 2014, 23, 4089-4102.	2.0	52
154	Development and characterisation of monoclonal antibodies reactive with porcine CSF1R (CD115). Developmental and Comparative Immunology, 2014, 47, 123-128.	1.0	6
155	Role of stem cells in large animal genetic engineering in the TALENs–CRISPR era. Reproduction, Fertility and Development, 2014, 26, 65.	0.1	14
156	Genomic analysis reveals selection for Asian genes in European pigs following human-mediated introgression. Nature Communications, 2014, 5, 4392.	5.8	137
157	Toxicokinetics of Seven Perfluoroalkyl Sulfonic and Carboxylic Acids in Pigs Fed a Contaminated Diet. Journal of Agricultural and Food Chemistry, 2014, 62, 6861-6870.	2.4	55
158	Transcriptome Profiling Identifies Differentially Expressed Genes in Postnatal Developing Pituitary Gland of Miniature Pig. DNA Research, 2014, 21, 207-216.	1.5	36
159	The sheep genome illuminates biology of the rumen and lipid metabolism. Science, 2014, 344, 1168-1173.	6.0	436
160	Characterization of the liver-macrophages isolated from a mixed primary culture of neonatal swine hepatocytes. Results in Immunology, 2014, 4, 1-7.	2.2	15
161	Development of gut immunoglobulin A production in piglet in response to innate and environmental factors. Developmental and Comparative Immunology, 2014, 44, 235-244.	1.0	35
162	Association and expression analysis of porcine ACLY gene related to growth and carcass quality traits in Italian Large White and Italian Duroc breeds. Livestock Science, 2014, 165, 1-7.	0.6	6
163	Genomic profiling to improve embryogenesis in the pig. Animal Reproduction Science, 2014, 149, 39-45.	0.5	7
164	DNA analyses of wild boar remains from archaeological sites in Guangxi, China. Quaternary International, 2014, 354, 147-153.	0.7	4
165	Switching on sex: transcriptional regulation of the testis-determining gene <i>Sry</i> . Development (Cambridge), 2014, 141, 2195-2205.	1.2	113
166	Effects of chronic intake of starch-, glucose- and fructose-containing diets on eating behaviour in adult minipigs. Applied Animal Behaviour Science, 2014, 157, 61-71.	0.8	11

#	Article	IF	CITATIONS
167	Evolutionary characterization of pig interferon-inducible transmembrane gene family and member expression dynamics in tracheobronchial lymph nodes of pigs infected with swine respiratory disease viruses. Veterinary Immunology and Immunopathology, 2014, 159, 180-191.	0.5	19
168	A detailed three-step protocol for live imaging of intracellular traffic in polarized primary porcine RPE monolayers. Experimental Eye Research, 2014, 124, 74-85.	1.2	49
169	Advances in swine immunology help move vaccine technology forward. Veterinary Immunology and Immunopathology, 2014, 159, 202-207.	0.5	17
170	The novel porcine gene early growth response 4 (Egr4) is differentially expressed in the ovaries of Erhualian and Pietrain pigs. Reproduction, Fertility and Development, 2014, 26, 587.	0.1	6
171	The challenges and importance of structural variation detection in livestock. Frontiers in Genetics, 2014, 5, 37.	1.1	104
172	Genetically identical co-housed pigs as models for dietary studies of gut microbiomes. Microbiome Science and Medicine, 2014, 1, .	0.3	3
173	Functional study of a genetic marker allele associated with resistance to <i>Ascaris suum</i> in pigs. Parasitology, 2014, 141, 777-787.	0.7	9
174	Genomic selection in a pig population including information from slaughtered full sibs of boars within a sib-testing program. Animal, 2015, 9, 750-759.	1.3	4
175	Novel and disruptive biological strategies for resolving gut health challenges in monogastric food animal production. Animal Nutrition, 2015, 1, 138-143.	2.1	8
176	Software solutions for the livestock genomics SNP array revolution. Animal Genetics, 2015, 46, 343-353.	0.6	22
177	Animal Models of Barrett's Esophagus and Esophageal Adenocarcinoma–Past, Present, and Future. Clinical and Translational Science, 2015, 8, 841-847.	1.5	45
178	Genetic diversity and population structure of six Chinese indigenous pig breeds in the Taihu Lake region revealed by sequencing data. Animal Genetics, 2015, 46, 697-701.	0.6	41
179	Hyperinsulinemia shifted energy supply from glucose to ketone bodies in early nonalcoholic steatohepatitis from high-fat high-sucrose diet induced Bama minipigs. Scientific Reports, 2015, 5, 13980.	1.6	29
180	Donkey genome and insight into the imprinting of fast karyotype evolution. Scientific Reports, 2015, 5, 14106.	1.6	29
181	Genome-wide whole blood microRNAome and transcriptome analyses reveal miRNA-mRNA regulated host response to foodborne pathogen Salmonella infection in swine. Scientific Reports, 2015, 5, 12620.	1.6	33
182	Transcriptome Analysis in Domesticated Species: Challenges and Strategies. Bioinformatics and Biology Insights, 2015, 9S4, BBI.S29334.	1.0	17
183	Transposons, Genome Size, and Evolutionary Insights in Animals. Cytogenetic and Genome Research, 2015, 147, 217-239.	0.6	119
184	Adult porcine genome-wide DNA methylation patterns support pigs as a biomedical model. BMC Genomics, 2015, 16, 743.	1.2	96

#	Article	IF	CITATIONS
185	Functional analysis and transcriptional output of the Göttingen minipig genome. BMC Genomics, 2015, 16, 932.	1.2	15
186	Genome-wide analysis of DNA methylation in pigs using reduced representation bisulfite sequencing. DNA Research, 2015, 22, 343-355.	1.5	72
187	Selective Reproduction: Social and Temporal Imaginaries for Negotiating the Value of Life in Human and Animal Neonates. Medical Anthropology Quarterly, 2015, 29, 178-195.	0.7	14
188	Imputation of genotypes in Danish purebred and two-way crossbred pigs using low-density panels. Genetics Selection Evolution, 2015, 47, 54.	1.2	13
189	Conservation analysis of sequences flanking the testis-determining gene Sry in 17 mammalian species. BMC Developmental Biology, 2015, 15, 34.	2.1	5
190	Identification and annotation of conserved promoters and macrophage-expressed genes in the pig genome. BMC Genomics, 2015, 16, 970.	1.2	22
191	Accuracy of Predicted Genomic Breeding Values in Purebred and Crossbred Pigs. G3: Genes, Genomes, Genetics, 2015, 5, 1575-1583.	0.8	41
192	Estimation of Additive, Dominance, and Imprinting Genetic Variance Using Genomic Data. G3: Genes, Genomes, Genetics, 2015, 5, 2629-2637.	0.8	35
193	Experimental infection with the Toxoplasma gondii ME-49 strain in the Brazilian BR-1 mini pig is a suitable animal model for human toxoplasmosis. Memorias Do Instituto Oswaldo Cruz, 2015, 110, 95-100.	0.8	15
194	<i>PKD1</i> Mono-Allelic Knockout Is Sufficient to Trigger Renal Cystogenesis in a Mini-Pig Model. International Journal of Biological Sciences, 2015, 11, 361-369.	2.6	25
195	Quality Assessment of Domesticated Animal Genome Assemblies. Bioinformatics and Biology Insights, 2015, 9S4, BBI.S29333.	1.0	11
196	Alternatives to Antibiotics in Animal Agriculture: An Ecoimmunological View. Pathogens, 2015, 4, 1-19.	1.2	21
197	Epigenetic marks: regulators of livestock phenotypes and conceivable sources of missing variation in livestock improvement programs. Frontiers in Genetics, 2015, 6, 302.	1.1	125
198	Identification of Low-Confidence Regions in the Pig Reference Genome (Sscrofa10.2). Frontiers in Genetics, 2015, 6, 338.	1.1	28
199	Alternatives to the Use of Nonhuman Primates in Regulatory Toxicology. , 2015, , 337-355.		5
200	Adaptive Evolution of Toll-Like Receptors (TLRs) in the Family Suidae. PLoS ONE, 2015, 10, e0124069.	1.1	22
201	Effects of the Sequence of Isocaloric Meals with Different Protein Contents on Plasma Biochemical Indexes in Pigs. PLoS ONE, 2015, 10, e0125640.	1.1	17
202	A Genetic Porcine Model of Cancer. PLoS ONE, 2015, 10, e0128864.	1.1	128

#	Article	IF	Citations
203	Accuracy of genomic prediction using deregressed breeding values estimated from purebred and crossbred offspring phenotypes in pigs1. Journal of Animal Science, 2015, 93, 3313-3321.	0.2	10
204	Genome Wide Distributions and Functional Characterization of Copy Number Variations between Chinese and Western Pigs. PLoS ONE, 2015, 10, e0131522.	1.1	47
205	Gender and Obesity Specific MicroRNA Expression in Adipose Tissue from Lean and Obese Pigs. PLoS ONE, 2015, 10, e0131650.	1.1	45
206	Size Reduction in Early European Domestic Cattle Relates to Intensification of Neolithic Herding Strategies. PLoS ONE, 2015, 10, e0141873.	1.1	28
207	Reduced Representation Libraries from DNA Pools Analysed with Next Generation Semiconductor Based-Sequencing to Identify SNPs in Extreme and Divergent Pigs for Back Fat Thickness. International Journal of Genomics, 2015, 2015, 1-8.	0.8	12
208	Genetic engineering of pigs for the creation of translational models of human pathologies. Animal Frontiers, 2015, 5, 50-56.	0.8	6
209	Analysis of horse genomes provides insight into the diversification and adaptive evolution of karyotype. Scientific Reports, 2014, 4, 4958.	1.6	108
210	Considerations on pig models for appetite, metabolic syndrome and obese type 2 diabetes: From food intake to metabolic disease. European Journal of Pharmacology, 2015, 759, 231-239.	1.7	80
211	Group Behavior: Social Context Modulates Behavioral Responses to Sensory Stimuli. Current Biology, 2015, 25, R467-R469.	1.8	1
212	Evolution: A Genomic Guide to Bird Population History. Current Biology, 2015, 25, R465-R467.	1.8	2
213	Copy number variation in the speciation of pigs: a possible prominent role for olfactory receptors. BMC Genomics, 2015, 16, 330.	1.2	85
214	Ancient DNA sheds light on the ancestry of pre-hispanic Canarian pigs. Genetics Selection Evolution, 2015, 47, 40.	1.2	13
215	Distribution of miRNA genes in the pig genome. BMC Genetics, 2015, 16, 6.	2.7	15
216	Copy number variations in high and low fertility breeding boars. BMC Genomics, 2015, 16, 280.	1.2	34
217	Integrative structural annotation of de novo RNA-Seq provides an accurate reference gene set of the enormous genome of the onion (Allium cepa L.). DNA Research, 2015, 22, 19-27.	1.5	59
218	The Impact of Food Bioactives on Health. , 2015, , .		208
219	Using genome-wide measures of coancestry to maintain diversity and fitness in endangered and domestic pig populations. Genome Research, 2015, 25, 970-981.	2.4	77
220	Swine as a Model for Influenza A Virus Infection and Immunity. ILAR Journal, 2015, 56, 44-52.	1.8	89

#	Article	IF	CITATIONS
221	Spatio-temporal regulation of circular RNA expression during porcine embryonic brain development. Genome Biology, 2015, 16, 245.	3.8	422
222	Epitope Recognition in the Human–Pig Comparison Model on Fixed and Embedded Material. Journal of Histochemistry and Cytochemistry, 2015, 63, 805-822.	1.3	14
223	Engineering of a Secretory Active Three-Dimensional Lacrimal Gland Construct on the Basis of Decellularized Lacrimal Gland Tissue. Tissue Engineering - Part A, 2015, 21, 2605-2617.	1.6	27
224	Role of Toll-like receptors in diabetic renal lesions in a miniature pig model. Science Advances, 2015, 1, e1400183.	4.7	33
225	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.	1.3	17
226	Artificial selection on introduced Asian haplotypes shaped the genetic architecture in European commercial pigs. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20152019.	1.2	25
227	Comparison of minipig, dog, monkey and human drug metabolism and disposition. Journal of Pharmacological and Toxicological Methods, 2015, 74, 80-92.	0.3	93
228	Toward sophisticated basal ganglia neuromodulation: Review on basal ganglia deep brain stimulation. Neuroscience and Biobehavioral Reviews, 2015, 58, 186-210.	2.9	52
229	Unraveling the Swine Genome: Implications for Human Health. Annual Review of Animal Biosciences, 2015, 3, 219-244.	3.6	70
230	Pan-vertebrate comparative genomics unmasks retrovirus macroevolution. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 464-469.	3.3	136
231	Adaptation and possible ancient interspecies introgression in pigs identified by whole-genome sequencing. Nature Genetics, 2015, 47, 217-225.	9.4	288
233	Copy number variation detection using SNP genotyping arrays in three Chinese pig breeds. Animal Genetics, 2015, 46, 101-109.	0.6	17
234	Evaluation of the Use of Göttingen Minipigs to Predict Food Effects on the Oral Absorption of Drugs in Humans. Journal of Pharmaceutical Sciences, 2015, 104, 135-143.	1.6	18
235	Genome data from a sixteenth century pig illuminate modern breed relationships. Heredity, 2015, 114, 175-184.	1.2	39
236	On genetic differentiation between domestic pigs and Tibetan wild boars. Nature Genetics, 2015, 47, 190-192.	9.4	4
237	Reply to 'Evolution of Tibetan wild boars'. Nature Genetics, 2015, 47, 189-190.	9.4	0
238	Genome-wide identification, classification and functional analyses of the bHLH transcription factor family in the pig, Sus scrofa. Molecular Genetics and Genomics, 2015, 290, 1415-1433.	1.0	4
239	Reply to 'On genetic differentiation between domestic pigs and Tibetan wild boars'. Nature Genetics, 2015, 47, 192-192.	9.4	0

#	Article	IF	CITATIONS
240	Repeated range expansions and inter-/postglacial recolonization routes of Sargentodoxa cuneata (Oliv.) Rehd. et Wils. (Lardizabalaceae) in subtropical China revealed by chloroplast phylogeography. Molecular Phylogenetics and Evolution, 2015, 85, 238-246.	1.2	47
241	Gene coexpression networks reveal key drivers of phenotypic divergence in porcine muscle. BMC Genomics, 2015, 16, 50.	1.2	11
242	A systems genetics study of swine illustrates mechanisms underlying human phenotypic traits. BMC Genomics, 2015, 16, 88.	1.2	28
243	The Genome 10K Project: A Way Forward. Annual Review of Animal Biosciences, 2015, 3, 57-111.	3.6	294
244	Single nucleotide polymorphism analysis of Korean native chickens using next generation sequencing data. Molecular Biology Reports, 2015, 42, 471-477.	1.0	9
245	Evolution of Tibetan wild boars. Nature Genetics, 2015, 47, 188-189.	9.4	10
246	Review on porcine endogenous retrovirus detection assays—impact on quality and safety of xenotransplants. Xenotransplantation, 2015, 22, 95-101.	1.6	23
247	Porcine EEF1A1 and EEF1A2 genes: genomic structure, polymorphism, mapping and expression. Molecular Biology Reports, 2015, 42, 1257-1264.	1.0	5
248	New cryptic karyotypic differences between cattle (Bos taurus) and goat (Capra hircus). Chromosome Research, 2015, 23, 225-235.	1.0	8
249	An Integrative Breakage Model of genome architecture, reshuffling and evolution. BioEssays, 2015, 37, 479-488.	1.2	54
250	Splicing variants of porcine synphilin-1. Meta Gene, 2015, 5, 32-42.	0.3	3
251	A genome survey sequencing of the Java mouse deer (Tragulus javanicus) adds new aspects to the evolution of lineage specific retrotransposons in Ruminantia (Cetartiodactyla). Gene, 2015, 571, 271-278.	1.0	8
252	Detection of a quantitative trait locus associated with resistance to infection with Trichuris suis in pigs. Veterinary Parasitology, 2015, 210, 264-269.	0.7	5
253	Hybrid origin of European commercial pigs examined by an in-depth haplotype analysis on chromosome 1. Frontiers in Genetics, 2014, 5, 442.	1.1	19
254	Genomic selection needs to be carefully assessed to meet specific requirements in livestock breeding programs. Frontiers in Genetics, 2015, 6, 49.	1.1	57
255	Whole-genome resequencing analyses of five pig breeds, including Korean wild and native, and three European origin breeds. DNA Research, 2015, 22, 259-267.	1.5	54
256	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	0.6	97
257	Wild boars from Sweden, Austria, the Czech Republic and Japan possess intact mannoseâ€binding lectin 2 (<scp>MBL</scp> 2) genes. International Journal of Immunogenetics, 2015, 42, 204-207.	0.8	0

#	Article	IF	CITATIONS
258	The chimerical genome of <scp>I</scp> sla del <scp>C</scp> oco feral pigs (<scp>C</scp> osta) Tj ETQq0 0 0 rgBT Ecology, 2015, 24, 2364-2378.	/Overlock 2.0	10 Tf 50 74 15
259	Activation of the Transcription Factor Nuclear Factor-Kappa B in Uterine Luminal Epithelial Cells by Interleukin 1 Beta 2: A Novel Interleukin 1 Expressed by the Elongating Pig Conceptus1. Biology of Reproduction, 2015, 92, 107.	1.2	40
260	Development of a simultaneous high resolution typing method for three SLA class II genes, SLA-DQA, SLA-DQB1, and SLA-DRB1 and the analysis of SLA class II haplotypes. Gene, 2015, 564, 228-232.	1.0	23
261	Embryo and gamete cryopreservation for genetic resources conservation of laboratory animals. Russian Journal of Developmental Biology, 2015, 46, 47-59.	0.1	9
262	Genome-wide association study using deregressed breeding values for cryptorchidism and scrotal/inguinal hernia in two pig lines. Genetics Selection Evolution, 2015, 47, 18.	1.2	26
263	Phenotype and animal domestication: A study of dental variation between domestic, wild, captive, hybrid and insular Sus scrofa. BMC Evolutionary Biology, 2015, 15, 6.	3.2	65
264	A genome-wide scan for signatures of directional selection in domesticated pigs. BMC Genomics, 2015, 16, 130.	1.2	67
265	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. Genome Biology, 2015, 16, 57.	3.8	331
266	Haplotypic diversity of porcine LEP and LEPR genes involved in growth and fatness regulation. Journal of Applied Genetics, 2015, 56, 525-533.	1.0	8
267	Understanding the molecular mechanisms of human microtia via a pig model of <i>HOXA1</i> syndrome. DMM Disease Models and Mechanisms, 2015, 8, 611-622.	1.2	17
268	Whole-genome sequencing of Berkshire (European native pig) provides insights into its origin and domestication. Scientific Reports, 2015, 4, 4678.	1.6	81
269	Respiratory nanoparticle-based vaccines and challenges associated with animal models and translation. Journal of Controlled Release, 2015, 219, 622-631.	4.8	25
270	Hemodynamics and right-ventricle functional characteristics of a swine carotid artery-jugular vein shunt model of pulmonary arterial hypertension: An 18-month experimental study. Experimental Biology and Medicine, 2015, 240, 1362-1372.	1.1	5
271	Dynamic Pluripotent Stem Cell States and Their Applications. Cell Stem Cell, 2015, 17, 509-525.	5.2	133
272	Population structure and history of the Welsh sheep breeds determined by whole genome genotyping. BMC Genetics, 2015, 16, 65.	2.7	69
273	Expansion of the HSFY gene family in pig lineages. BMC Genomics, 2015, 16, 442.	1.2	10
274	Bioinformatics Annotation of Human Y Chromosome-Encoded Protein Pathways and Interactions. Journal of Proteome Research, 2015, 14, 3503-3518.	1.8	9
275	Evidence of long-term gene flow and selection during domestication from analyses of Eurasian wild and domestic pig genomes. Nature Genetics, 2015, 47, 1141-1148.	9.4	263

#	Article	IF	CITATIONS
276	Cartilage Repair Using Composites of Human Umbilical Cord Blood-Derived Mesenchymal Stem Cells and Hyaluronic Acid Hydrogel in a Minipig Model. Stem Cells Translational Medicine, 2015, 4, 1044-1051.	1.6	87
277	Inferring Bottlenecks from Genome-Wide Samples of Short Sequence Blocks. Genetics, 2015, 201, 1157-1169.	1.2	40
278	Resequencing diverse Chinese indigenous breeds to enrich the map of genomic variations in swine. Genomics, 2015, 106, 286-294.	1.3	8
279	Genome sequencing of the extinct Eurasian wild aurochs, Bos primigenius, illuminates the phylogeography and evolution of cattle. Genome Biology, 2015, 16, 234.	3.8	178
280	Current transcriptomics in pig immunity research. Mammalian Genome, 2015, 26, 1-20.	1.0	34
281	Uterine Responses to the Preattachment Embryo in Domestic Ungulates: Recognition of Pregnancy and Preparation for Implantation. Annual Review of Animal Biosciences, 2015, 3, 489-511.	3.6	36
282	Association of eight EST-derived SNPs with carcass and meat quality traits in pigs. Journal of Applied Genetics, 2015, 56, 85-95.	1.0	0
283	Dangerous Viral Pathogens of Animal Origin: Risk and Biosecurity. , 2015, , 1015-1062.		1
284	Porcine NOD1 polymorphisms with impaired ligand recognition and their distribution in pig populations. Molecular Immunology, 2015, 63, 305-311.	1.0	7
285	A 2.5-Kilobase Deletion Containing a Cluster of Nine MicroRNAs in the Latency-Associated-Transcript Locus of the Pseudorabies Virus Affects the Host Response of Porcine Trigeminal Ganglia during Established Latency. Journal of Virology, 2015, 89, 428-442.	1.5	24
286	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.	2.2	74
287	Mitochondrial DNA Sequence and Phylogenetic Evaluation of Geographically DisparateSus scrofaBreeds. Animal Biotechnology, 2015, 26, 17-28.	0.7	13
288	Cloning and characterization of the porcine DBC1 gene encoding deleted in bladder cancer. Molecular Biology Reports, 2015, 42, 383-391.	1.0	2
289	Detecting mitochondrial signatures of selection in wild Tibetan pigs and domesticated pigs. Mitochondrial DNA, 2016, 27, 747-752.	0.6	20
290	A Porcine Anterior Segment Perfusion and Transduction Model With Direct Visualization of the Trabecular Meshwork. , 2016, 57, 1338.		31
291	Quantification of Focal Outflow Enhancement Using Differential Canalograms. , 2016, 57, 2831.		43
292	Gnotobiotic Neonatal Pig ModelÂof Rotavirus Infection andÂDisease. , 2016, , 219-241.		3
293	Identification of protein-damaging mutations in 10 swine taste receptors and 191 appetite-reward genes. BMC Genomics, 2016, 17, 685.	1.2	5

#	Article	IF	CITATIONS
294	The use of genomic information can enhance the efficiency of conservation programs. Animal Frontiers, 2016, 6, 59-64.	0.8	8
295	Epithelial, metabolic and innate immunity transcriptomic signatures differentiating the rumen from other sheep and mammalian gastrointestinal tract tissues. PeerJ, 2016, 4, e1762.	0.9	87

The Use of Genomics in Conservation Management of the Endangered Visayan Warty Pig (<i>Sus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50

297	Altered Methylation Profile of Lymphocytes Is Concordant with Perturbation of Lipids Metabolism and Inflammatory Response in Obesity. Journal of Diabetes Research, 2016, 2016, 1-11.	1.0	31
298	Generative Power and Closure Properties of Watson-Crick Grammars. Applied Computational Intelligence and Soft Computing, 2016, 2016, 1-12.	1.6	4
299	Tissue-based in vitro and exÂvivoÂmodels for intestinal permeability studies. , 2016, , 203-236.		12
300	How Active Are Porcine Endogenous Retroviruses (PERVs)?. Viruses, 2016, 8, 215.	1.5	64
301	Historical Perspectives of Livestock Handling. , 2016, , 1-11.		0
302	Engineered Swine Models of Cancer. Frontiers in Genetics, 2016, 7, 78.	1.1	56
303	Inferring Population Size History from Large Samples of Genome-Wide Molecular Data - An Approximate Bayesian Computation Approach. PLoS Genetics, 2016, 12, e1005877.	1.5	144
304	Molecular and Cellular Biology of Wound Healing and Skin Regeneration. , 2016, , 19-47.		11
305	Discovery of Gene Sources for Economic Traits in Hanwoo by Whole-genome Resequencing. Asian-Australasian Journal of Animal Sciences, 2016, 29, 1353-1362.	2.4	7
306	The Pig PeptideAtlas: A resource for systems biology in animal production and biomedicine. Proteomics, 2016, 16, 634-644.	1.3	47
307	Genomeâ€wide association study reveals regions associated with gestation length in two pig populations. Animal Genetics, 2016, 47, 223-226.	0.6	9
308	Genomic prediction of growth in pigs based on a model including additive and dominance effects. Journal of Animal Breeding and Genetics, 2016, 133, 180-186.	0.8	15
309	Accuracy of genomic prediction of purebreds for cross bred performance in pigs. Journal of Animal Breeding and Genetics, 2016, 133, 443-451.	0.8	24
310	The Ensembl gene annotation system. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw093.	1.4	912
311	Impact of neonatal iron deficiency on hippocampal DNA methylation and gene transcription in a porcine biomedical model of cognitive development. BMC Genomics, 2016, 17, 856.	1.2	44

#	Article	IF	CITATIONS
312	Effects of Linked Selective Sweeps on Demographic Inference and Model Selection. Genetics, 2016, 204, 1207-1223.	1.2	144
314	CD14 in the TLRs signaling pathway is associated with the resistance to E. coli F18 in Chinese domestic weaned piglets. Scientific Reports, 2016, 6, 24611.	1.6	22
315	Genomic selection in pigs: state of the art and perspectives. Italian Journal of Animal Science, 2016, 15, 211-232.	0.8	56
316	Transcriptome analysis revealed chimeric RNAs, single nucleotide polymorphisms and allele-specific expression in porcine prenatal skeletal muscle. Scientific Reports, 2016, 6, 29039.	1.6	8
317	A genome-wide association study of fetal response to type 2 porcine reproductive and respiratory syndrome virus challenge. Scientific Reports, 2016, 6, 20305.	1.6	19
318	After genome-wide association studies: Gene networks elucidating candidate genes divergences for number of teats across two pig populations1. Journal of Animal Science, 2016, 94, 1446-1458.	0.2	11
319	A genome-wide association analysis for susceptibility of pigs to enterotoxigenic Escherichia coli F41. Animal, 2016, 10, 1602-1608.	1.3	7
320	The genomes and history of domestic animals. Molecular Genetics, Microbiology and Virology, 2016, 31, 197-202.	0.0	11
321	Local and global patterns of admixture and population structure in Iranian native cattle. BMC Genetics, 2016, 17, 108.	2.7	42
322	Interleukins, interferons, and establishment of pregnancy in pigs. Reproduction, 2016, 151, R111-R122.	1.1	39
323	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. Plant Biotechnology Journal, 2016, 14, 1511-1522.	4.1	20
324	Identification of the Q969R gain-of-function polymorphism in the gene encoding porcine NLRP3 and its distribution in pigs of Asian and European origin. Immunogenetics, 2016, 68, 693-701.	1.2	6
325	Critical review evaluating the pig as a model for human nutritional physiology. Nutrition Research Reviews, 2016, 29, 60-90.	2.1	204
326	The evolution of the molecular response to stress and its relevance to trauma and stressor-related disorders. Neuroscience and Biobehavioral Reviews, 2016, 68, 134-147.	2.9	11
327	The Pig Olfactory Brain: A Primer. Chemical Senses, 2016, 41, 415-425.	1.1	22
328	<scp>PSMC</scp> analysis of effective population sizes in molecular ecology and its application to blackâ€andâ€white <i>Ficedula</i> flycatchers. Molecular Ecology, 2016, 25, 1058-1072.	2.0	225
329	Pigs in Toxicology. Toxicologic Pathology, 2016, 44, 575-590.	0.9	37
330	Lack of polymorphism at the MC1R wild-type allele and evidence of domestic allele introgression across European wild boar populations. Mammalian Biology, 2016, 81, 477-479.	0.8	17

#	Article	IF	CITATIONS
331	Pigs as models of human cancers. Theriogenology, 2016, 86, 433-437.	0.9	49
332	Application of whole genome shotgun sequencing for detection and characterization of genetically modified organisms and derived products. Analytical and Bioanalytical Chemistry, 2016, 408, 4595-4614.	1.9	43
333	Revealing new candidate genes for reproductive traits in pigs: combining Bayesian GWAS and functional pathways. Genetics Selection Evolution, 2016, 48, 9.	1.2	68
334	Genomic variation in the porcine immunoglobulin lambda variable region. Immunogenetics, 2016, 68, 285-293.	1.2	12
335	Structural and Biochemical Analyses of Swine Major Histocompatibility Complex Class I Complexes and Prediction of the Epitope Map of Important Influenza A Virus Strains. Journal of Virology, 2016, 90, 6625-6641.	1.5	33
336	Genetics of Adiposity in Large Animal Models for Human Obesity—Studies on Pigs and Dogs. Progress in Molecular Biology and Translational Science, 2016, 140, 233-270.	0.9	32
337	Molecular characterization and analysis of the porcine NURR1 gene. Biochimie Open, 2016, 3, 26-39.	3.2	2
338	The devil is in the details: the effect of population structure on demographic inference. Heredity, 2016, 116, 349-350.	1.2	28
339	A GWA study reveals genetic loci for body conformation traits in Chinese Laiwu pigs and its implications for human BMI. Mammalian Genome, 2016, 27, 610-621.	1.0	26
340	A regulatory gene network related to the porcine umami taste receptor (<i><scp>TAS</scp>1R1</i> <scp>TAS</scp> 1R3). Animal Genetics, 2016, 47, 114-119.	0.6	5
341	Olfactory genes in Tibetan wild boar. Nature Genetics, 2016, 48, 972-973.	9.4	6
342	Reply to 'Olfactory genes in Tibetan wild boar (NG-CR42819)'. Nature Genetics, 2016, 48, 973-974.	9.4	Ο
343	Detection of selection signatures of populationâ€specific genomic regions selected during domestication process in Jinhua pigs. Animal Genetics, 2016, 47, 672-681.	0.6	17
344	Novel Yâ€chromosome short tandem repeats in <i>Sus scrofa</i> and their variation in European wild boar and domestic pig populations. Animal Genetics, 2016, 47, 682-690.	0.6	6
345	Genetic variations associated with six-white-point coat pigmentation in Diannan small-ear pigs. Scientific Reports, 2016, 6, 27534.	1.6	22
346	Novel Insights into Chromosome Evolution in Birds, Archosaurs, and Reptiles. Genome Biology and Evolution, 2016, 8, 2442-2451.	1.1	66
347	NGS-based reverse genetic screen for common embryonic lethal mutations compromising fertility in livestock. Genome Research, 2016, 26, 1333-1341.	2.4	71
348	A reference gene catalogue of the pig gut microbiome. Nature Microbiology, 2016, 1, 16161.	5.9	416

#	Article	IF	CITATIONS
349	Efficient production of multi-modified pigs for xenotransplantation by â€~combineering', gene stacking and gene editing. Scientific Reports, 2016, 6, 29081.	1.6	129
350	Mammalian comparative genomics reveals genetic and epigenetic features associated with genome reshuffling in Rodentia. Genome Biology and Evolution, 2016, 8, evw276.	1.1	21
351	Profiling the genome-wide DNA methylation pattern of porcine ovaries using reduced representation bisulfite sequencing. Scientific Reports, 2016, 6, 22138.	1.6	39
352	Applications of Systems Genetics and Biology for Obesity Using Pig Models. , 2016, , 25-42.		7
353	Endonuclease mediated genome editing in drug discovery and development: promises and challenges. Drug Discovery Today: Technologies, 2016, 21-22, 17-25.	4.0	2
354	Possible introgression of the VRTN mutation increasing vertebral number, carcass length and teat number from Chinese pigs into European pigs. Scientific Reports, 2016, 6, 19240.	1.6	58
355	Genomic analysis reveals selection in Chinese native black pig. Scientific Reports, 2016, 6, 36354.	1.6	32
356	Structural Variant Detection by Large-scale Sequencing Reveals New Evolutionary Evidence on Breed Divergence between Chinese and European Pigs. Scientific Reports, 2016, 6, 18501.	1.6	26
357	Generation of human organs in pigs via interspecies blastocyst complementation. Reproduction in Domestic Animals, 2016, 51, 18-24.	0.6	21
358	Genome-wide analysis of DNA methylation in obese, lean and miniature pig breeds. Scientific Reports, 2016, 6, 30160.	1.6	29
359	Stress-induced transposon reactivation: a mediator or an estimator of allostatic load?. Environmental Epigenetics, 2016, 2, dvw015.	0.9	23
360	Genomic prediction using models with dominance and imprinting effects for backfat thickness and average daily gain in Danish Duroc pigs. Genetics Selection Evolution, 2016, 48, 67.	1.2	21
361	Evidence for adaptation of porcine Toll-like receptors. Immunogenetics, 2016, 68, 179-189.	1.2	7
362	gEVAL — a web-based browser for evaluating genome assemblies. Bioinformatics, 2016, 32, 2508-251	0.1.8	319
363	Validation of a Preclinical Model of Diethylnitrosamine-Induced Hepatic Neoplasia in Yucatan Miniature Pigs. Oncology, 2016, 91, 90-100.	0.9	25
364	A decade of pig genome sequencing: a window on pig domestication and evolution. Genetics Selection Evolution, 2016, 48, 23.	1.2	102
365	Identification of genetic variation in the swine toll-like receptors and development of a porcine TLR genotyping array. Genetics Selection Evolution, 2016, 48, 28.	1.2	7
366	Evolutionary patterns of Toll-like receptor signaling pathway genes in the Suidae. BMC Evolutionary Biology, 2016, 16, 33.	3.2	8

		KLFOKT	
#	Article	IF	CITATIONS
367	Increased prediction accuracy using a genomic feature model including prior information on quantitative trait locus regions in purebred Danish Duroc pigs. BMC Genetics, 2016, 17, 11.	2.7	60
368	Genome-wide analysis of long non-coding RNAs at early stage of skin pigmentation in goats (Capra) Tj ETQq1	1 0.784314 1.2	rgBT/Overlo
369	Whipworms in humans and pigs: origins and demography. Parasites and Vectors, 2016, 9, 37.	1.0	21
370	The contribution of transposable elements to size variations between four teleost genomes. Mobile DNA, 2016, 7, 4.	1.3	71
371	First update of the International Xenotransplantation Association consensus statement on conditions for undertaking clinical trials of porcine islet products in type 1 diabetes—Chapter 5: recipient monitoring and response plan for preventing disease transmission. Xenotransplantation, 2016, 23, 53-59.	1.6	38
372	Pilot study on in vitro silver nanoparticles permeation through meningeal membrane. Colloids and Surfaces B: Biointerfaces, 2016, 146, 245-249.	2.5	9
373	A new tactile device using magneto-rheological sponge cells for medical applications: Experimental investigation. Sensors and Actuators A: Physical, 2016, 239, 61-69.	2.0	34
374	Tailored Pig Models for Preclinical Efficacy and Safety Testing of Targeted Therapies. Toxicologic Pathology, 2016, 44, 346-357.	0.9	45
375	Comparative genomic analysis of eutherian tumor necrosis factor ligand genes. Immunogenetics, 2016, 68, 125-132.	1.2	9
376	Experimental Approaches to Study Endothelial Responses to Shear Stress. Antioxidants and Redox Signaling, 2016, 25, 389-400.	2.5	12
377	Worldwide patterns of genomic variation and admixture in gray wolves. Genome Research, 2016, 26, 163-173.	2.4	160
378	The pig X and Y Chromosomes: structure, sequence, and evolution. Genome Research, 2016, 26, 130-139.	2.4	69
379	On the importance of being structured: instantaneous coalescence rates and human evolution—lessons for ancestral population size inference?. Heredity, 2016, 116, 362-371.	1.2	233
380	Porcine Reproductive and Respiratory Syndrome Virus (PRRSV): Pathogenesis and Interaction with the Immune System. Annual Review of Animal Biosciences, 2016, 4, 129-154.	3.6	471
381	Anatomical features for an adequate choice of experimental animal model in biomedicine: II. Small laboratory rodents, rabbit, and pig. Annals of Anatomy, 2016, 204, 11-28.	1.0	61
382	The Use of Minipig in Drug Discovery and Development. Toxicologic Pathology, 2016, 44, 467-473.	0.9	25
383	Domestic animals as models for biomedical research. Upsala Journal of Medical Sciences, 2016, 121, 1-11.	0.4	38
384	Miniature Swine for Preclinical Modeling of Complexities of Human Disease for Translational Scientific Discovery and Accelerated Development of Therapies and Medical Devices. Toxicologic Pathology, 2016, 44, 299-314.	0.9	73

ARTICLE IF CITATIONS Differential A-to-I RNA editing of the serotonin-2C receptor G-protein-coupled, HTR2C, in porcine brain 385 1.3 4 tissues. Biochimie, 2016, 121, 189-196. Investigating the Metabolic Syndrome. Toxicologic Pathology, 2016, 44, 358-366. 387 The Evolution of Suidae. Annual Review of Animal Biosciences, 2016, 4, 61-85. 3.6 85 Detection of genetic diversity and selection at the coding region of the melanocortin receptor 1 () Tj ETQq1 1 0.784314 rgBT / Overlo An in-depth comparison of the porcine, murine and human inflammasomes; lessons from the porcine 389 0.8 102 genome and transcriptome. Veterinary Microbiology, 2017, 202, 2-15. Exploiting next-generation sequencing to solve the haplotyping puzzle in polyploids: a simulation study. Briefings in Bioinformatics, 2018, 19, bbw126. 390 3.2 391 Translational Safety Genetics. Toxicologic Pathology, 2017, 45, 119-126. 0.9 6 Comprehensive analysis of long non-coding RNAs highlights their spatio-temporal expression patterns 1.6 and evolutional conservation in Sus scrofa. Scientific Reports, 2017, 7, 43166. Hydrogel derived from decellularized porcine adipose tissue as a promising biomaterial for soft tissue 393 2.1 50 augmentation. Journal of Biomedical Materials Research - Part A, 2017, 105, 1756-1764. The evolution of the natural killer complex; a comparison between mammals using new high-quality 394 1.2 genome assemblies and targeted annotation. Immunogenetics, 2017, 69, 255-269. Genomeâ€editing technologies to improve research, reproduction, and production in pigs. Molecular 395 1.0 35 Reproduction and Development, 2017, 84, 1012-1017. Genetic architecture of gene expression underlying variation in host response to porcine 1.6 reproductive and respiratory syndrome virus infection. Scientific Reports, 2017, 7, 46203. Characterization and isolation of highly purified porcine satellite cells. Cell Death Discovery, 2017, 3, 397 2.0 62 17003. Characterization of genome-wide segmental duplications reveals a common genomic feature of 398 1.2 association with immunity among domestic animals. BMC Genomics, 2017, 18, 293. Sustainable ruminant production to help feed the planet. Italian Journal of Animal Science, 2017, 16, 399 0.8 56 140-171. A Pathway-Centered Analysis of Pig Domestication and Breeding in Eurasia. G3: Genes, Genomes, Genetics, 2017, 7, 2171-2184. The changes in glucose metabolism and cell proliferation in the kidneys of polycystic kidney disease 401 1.0 14 mini-pig models. Biochemical and Biophysical Research Communications, 2017, 488, 374-381. Structure, organization and tissue expression of the pig SLC13A1 and SLC13A4 sulfate transporter 402 genes. Biochemistry and Biophysics Reports, 2017, 10, 215-223.

#	ARTICLE	IF	CITATIONS
403	Association analysis of SNPs in the porcine CYP2E1 gene with skatole, indole, and androstenone levels in backfat of a crossbred pig population. Meat Science, 2017, 131, 68-73.	2.7	8
404	Gene co-expression network analysis identifies porcine genes associated with variation in metabolizing fenbendazole and flunixin meglumine in the liver. Scientific Reports, 2017, 7, 1357.	1.6	10
405	Transcriptome dynamics during proliferation and differentiation of porcine primary satellite cells. Gene Reports, 2017, 7, 169-175.	0.4	1
406	Transcriptomics of Meat Quality. , 2017, , 259-320.		11
407	Upgrading short-read animal genome assemblies to chromosome level using comparative genomics and a universal probe set. Genome Research, 2017, 27, 875-884.	2.4	97
408	Runs of homozygosity: current knowledge and applications in livestock. Animal Genetics, 2017, 48, 255-271.	0.6	242
409	Annotation of the Domestic Pig Genome by Quantitative Proteogenomics. Journal of Proteome Research, 2017, 16, 2887-2898.	1.8	25
410	A genomic landscape of mitochondrial DNA insertions in the pig nuclear genome provides evolutionary signatures of interspecies admixture. DNA Research, 2017, 24, 487-498.	1.5	17
411	Molecular approaches to the diagnosis and monitoring of production diseases in pigs. Research in Veterinary Science, 2017, 114, 266-272.	0.9	8
412	Reconstruction and evolutionary history of eutherian chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5379-E5388.	3.3	94
413	Genome-wide profiling of Sus scrofa circular RNAs across nine organs and three developmental stages. DNA Research, 2017, 24, 523-535.	1.5	135
414	Gene networks for total number born in pigs across divergent environments. Mammalian Genome, 2017, 28, 426-435.	1.0	3
415	The Mouse Lemur, a Genetic Model Organism for Primate Biology, Behavior, and Health. Genetics, 2017, 206, 651-664.	1.2	58
416	Novel effects of identified SNPs within the porcine Pregnancy-Associated Glycoprotein gene family () Tj ETQq1 1 Science, 2017, 114, 123-130.	0.784314 0.9	rgBT /Over 3
417	The viral innate immune antagonism and an alternative vaccine design for PRRS virus. Veterinary Microbiology, 2017, 209, 75-89.	0.8	34
418	Transcriptional immune response in mesenteric lymph nodes in pigs with different levels of resistance to Ascaris suum. Acta Parasitologica, 2017, 62, 141-153.	0.4	5
419	Evaluating Sequence-Based Genomic Prediction with an Efficient New Simulator. Genetics, 2017, 205, 939-953.	1.2	39
420	Comparative analysis of DNA methylome and transcriptome of skeletal muscle in lean-, obese-, and mini-type pigs. Scientific Reports, 2017, 7, 39883.	1.6	42

	CITATION	CITATION REPORT	
#	Article	IF	CITATIONS
421	Population admixture in Chinese and European Sus scrofa. Scientific Reports, 2017, 7, 13178.	1.6	5
422	<scp>PIWI</scp> s, pi <scp>RNA</scp> s and Retrotransposons: Complex battles during reprogramming in gametes and early embryos. Reproduction in Domestic Animals, 2017, 52, 28-38.	0.6	14
423	Draft genome of the gayal, Bos frontalis. GigaScience, 2017, 6, 1-7.	3.3	23
424	A genetically inducible porcine model of intestinal cancer. Molecular Oncology, 2017, 11, 1616-1629.	2.1	34
425	Genetic mapping using 1.4M SNP array refined loci for fatty acid composition traits in Chinese Erhualian and Bamaxiang pigs. Journal of Animal Breeding and Genetics, 2017, 134, 472-483.	0.8	10
426	Gene Location, Expression, and Function of FNDC5 in Meishan Pigs. Scientific Reports, 2017, 7, 7886.	1.6	10
427	A transcriptome atlas of rabbit revealed by PacBio single-molecule long-read sequencing. Scientific Reports, 2017, 7, 7648.	1.6	125
428	Convergent and divergent genetic changes in the genome of Chinese and European pigs. Scientific Reports, 2017, 7, 8662.	1.6	13
429	Pre-birth sense of smell in the wild boar: the ontogeny of the olfactory mucosa. Zoology, 2017, 123, 11-15.	0.6	11
430	Early intervention with Bifidobacterium lactis NCC2818 modulates the host-microbe interface independent of the sustained changes induced by the neonatal environment. Scientific Reports, 2017, 7, 5310.	1.6	10
431	Splice variants of porcine PPHLN1 encoding periphilin-1. Gene Reports, 2017, 7, 176-183.	0.4	2
432	Characterization of porcine simple sequence repeat variation on a population scale with genome resequencing data. Scientific Reports, 2017, 7, 2376.	1.6	14
433	Oncopig Soft-Tissue Sarcomas Recapitulate Key Transcriptional Features of Human Sarcomas. Scientific Reports, 2017, 7, 2624.	1.6	27
434	Isolation of subtelomeric sequences of porcine chromosomes for translocation screening reveals errors in the pig genome assembly. Animal Genetics, 2017, 48, 395-403.	0.6	25
435	A survey of single nucleotide polymorphisms identified from wholeâ€genome sequencing and their functional effect in the porcine genome [,] . Animal Genetics, 2017, 48, 404-411.	0.6	39
436	PigVar: a database of pig variations and positive selection signatures. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	11
437	Inactivation of porcine endogenous retrovirus in pigs using CRISPR-Cas9. Science, 2017, 357, 1303-1307.	6.0	570
438	Origin and dispersal of early domestic pigs in northern China. Scientific Reports, 2017, 7, 5602.	1.6	32

#	Article	IF	CITATIONS
439	Variation in Recombination Rate and Its Genetic Determinism in Sheep Populations. Genetics, 2017, 207, 767-784.	1.2	55
440	Taste, nutrient sensing and feed intake in pigs (130 years of research: then, now and future). Animal Feed Science and Technology, 2017, 233, 3-12.	1.1	27
441	Evolutionary Relationships and Taxonomy of Suidae and Tayassuidae. , 0, , 1-19.		4
442	A History of Pig Domestication: New Ways of Exploring a Complex Process. , 0, , 39-48.		8
443	Conservation of Wild Pigs and Peccaries. , 0, , 277-290.		2
444	A Genomic Perspective on Wild Boar Demography and Evolution. , 0, , 376-387.		3
445	Miss Piggy on the catwalk again. Blood, 2017, 130, 2153-2154.	0.6	0
446	Clinical veterinary proteomics: Techniques and approaches to decipher the animal plasma proteome. Veterinary Journal, 2017, 230, 6-12.	0.6	16
447	Relapsed/refractory HL: FDG-PET is the trump card. Blood, 2017, 130, 2154-2155.	0.6	2
448	Gene expression profile changes in the jejunum of weaned piglets after oral administration of Lactobacillus or an antibiotic. Scientific Reports, 2017, 7, 15816.	1.6	17
449	Genome-wide DNA methylation analysis of the porcine hypothalamus-pituitary-ovary axis. Scientific Reports, 2017, 7, 4277.	1.6	25
450	Genomic selection for crossbred performance accounting for breed-specific effects. Genetics Selection Evolution, 2017, 49, 51.	1.2	39
451	The wolf reference genome sequence (Canis lupus lupus) and its implications for Canis spp. population genomics. BMC Genomics, 2017, 18, 495.	1.2	73
452	Genetic analysis of teat number in pigs reveals some developmental pathways independent of vertebra number and several loci which only affect a specific side. Genetics Selection Evolution, 2017, 49, 4.	1.2	39
453	Genetic diversity, extent of linkage disequilibrium and persistence of gametic phase in Canadian pigs. BMC Genetics, 2017, 18, 6.	2.7	34
454	Transcriptome analysis of coding and long non-coding RNAs highlights the regulatory network of cascade initiation of permanent molars in miniature pigs. BMC Genomics, 2017, 18, 148.	1.2	24
455	Genome-wide association study confirm major QTL for backfat fatty acid composition on SSC14 in Duroc pigs. BMC Genomics, 2017, 18, 369.	1.2	36
456	A high-quality annotated transcriptome of swine peripheral blood. BMC Genomics, 2017, 18, 479.	1.2	7

	CITATION RE	PORT	
#	Article	IF	CITATIONS
457	Origin of the retroviruses: when, where, and how?. Current Opinion in Virology, 2017, 25, 23-27.	2.6	65
458	Distinguishing migration events of different timing for wild boar in the Balkans. Journal of Biogeography, 2017, 44, 259-270.	1.4	14
459	The â€~heritability' of domestication and its functional partitioning in the pig. Heredity, 2017, 118, 160-168.	1.2	7
460	Genome-wide association study for ham weight loss at first salting in Italian Large White pigs: towards the genetic dissection of a key trait for dry-cured ham production. Animal Genetics, 2017, 48, 103-107.	0.6	18
461	Next generation semiconductor based sequencing of bitter taste receptor genes in different pig populations and association analysis using a selective DNA pool-seq approach. Animal Genetics, 2017, 48, 97-102.	0.6	14
462	Comprehensive variation discovery and recovery of missing sequence in the pig genome using multiple de novo assemblies. Genome Research, 2017, 27, 865-874.	2.4	116
463	Comparison of Single Genome and Allele Frequency Data Reveals Discordant Demographic Histories. G3: Genes, Genomes, Genetics, 2017, 7, 3605-3620.	0.8	70
464	Whole-genome resequencing reveals candidate mutations for pig prolificacy. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20172437.	1.2	17
465	Gene engineering in swine for agriculture. Journal of Integrative Agriculture, 2017, 16, 2792-2804.	1.7	3
466	Future livestock breeding: Precision breeding based on multi-omics information and population personalization. Journal of Integrative Agriculture, 2017, 16, 2784-2791.	1.7	12
467	Including crossbred pigs in the genomic relationship matrix through utilization of both linkage disequilibrium and linkage analysis1. Journal of Animal Science, 2017, 95, 5197-5207.	0.2	14
468	Comparative transcriptomics of 5 high-altitude vertebrates and their low-altitude relatives. GigaScience, 2017, 6, 1-9.	3.3	50
469	Genome-wide SNP data unveils the globalization of domesticated pigs. Genetics Selection Evolution, 2017, 49, 71.	1.2	114
470	Genome-wide association studies and meta-analysis reveal novel quantitative trait loci and pleiotropic loci for swine head-related traits1,2. Journal of Animal Science, 2017, 95, 2354-2366.	0.2	4
471	Using markers with large effect in genetic and genomic predictions1. Journal of Animal Science, 2017, 95, 59-71.	0.2	24
472	Correlations of genes expression in PPAR signalling pathway with porcine meat quality traits. Czech Journal of Animal Science, 2016, 61, 333-339.	0.5	10
473	The Importance of Endophenotypes to Evaluate the Relationship between Genotype and External Phenotype. International Journal of Molecular Sciences, 2017, 18, 472.	1.8	23
474	The Oncopig Cancer Model as a Complementary Tool for Phenotypic Drug Discovery. Frontiers in Pharmacology, 2017, 8, 894.	1.6	14

#	Article	IF	CITATIONS
475	The porcine translational research database: a manually curated, genomics and proteomics-based research resource. BMC Genomics, 2017, 18, 643.	1.2	55
476	Pilot study of large-scale production of mutant pigs by ENU mutagenesis. ELife, 2017, 6, .	2.8	32
477	The MeLiM Minipig: An Original Spontaneous Model to Explore Cutaneous Melanoma Genetic Basis. Frontiers in Genetics, 2017, 8, 146.	1.1	18
478	Structure and Function of the Fecal Microbiota in Diarrheic Neonatal Piglets. Frontiers in Microbiology, 2017, 8, 502.	1.5	103
479	The Oncopig Cancer Model: An Innovative Large Animal Translational Oncology Platform. Frontiers in Oncology, 2017, 7, 190.	1.3	92
480	Epigenetics of Livestock Breeding. , 2017, , 441-463.		5
481	Porcine to Human Heart Transplantation: Is Clinical Application Now Appropriate?. Journal of Immunology Research, 2017, 2017, 1-11.	0.9	27
482	Genome-wide analysis of structural variants reveals genetic differences in Chinese pigs. PLoS ONE, 2017, 12, e0186721.	1.1	7
483	A viral metagenomic approach on a non-metagenomic experiment: Mining next generation sequencing datasets from pig DNA identified several porcine parvoviruses for a retrospective evaluation of viral infections. PLoS ONE, 2017, 12, e0179462.	1.1	9
484	Precision engineering for PRRSV resistance in pigs: Macrophages from genome edited pigs lacking CD163 SRCR5 domain are fully resistant to both PRRSV genotypes while maintaining biological function. PLoS Pathogens, 2017, 13, e1006206.	2.1	282
485	Use of haplotypes to identify regions harbouring lethal recessive variants in pigs. Genetics Selection Evolution, 2017, 49, 57.	1.2	8
486	Fine mapping of a QTL affecting levels of skatole on pig chromosome 7. BMC Genetics, 2017, 18, 85.	2.7	6
487	The porcine virome and xenotransplantation. Virology Journal, 2017, 14, 171.	1.4	37
488	Modulation of the main porcine enteric neuropeptides by a single low-dose of lipopolysaccharide (LPS) Salmonella Enteritidis. Gut Pathogens, 2017, 9, 73.	1.6	12
489	042 Genome-wide association of myoglobin concentrations in pork loins. Journal of Animal Science, 2017, 95, 20-20.	0.2	2
490	A systematic survey to identify lethal recessive variation in highly managed pig populations. BMC Genomics, 2017, 18, 858.	1.2	37
491	Genetically Tailored Pig Models for Translational Biomedical Research. , 2017, , 671-701.		2
492	Loss-of-function myostatin mutation increases insulin sensitivity and browning of white fat in Meishan pigs. Oncotarget, 2017, 8, 34911-34922.	0.8	45

#	Article	IF	CITATIONS
493	The IICR (inverse instantaneous coalescence rate) as a summary of genomic diversity: insights into demographic inference and model choice. Heredity, 2018, 120, 13-24.	1.2	74
494	Porcine cluster of differentiation (CD) markers 2018 update. Research in Veterinary Science, 2018, 118, 199-246.	0.9	31
495	Infectious disease risks in xenotransplantation. American Journal of Transplantation, 2018, 18, 1857-1864.	2.6	84
496	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. Nature Communications, 2018, 9, 859.	5.8	126
497	Molecular population structure for feral swine in the United States. Journal of Wildlife Management, 2018, 82, 821-832.	0.7	17
498	Transformation of animal genomics by next-generation sequencing technologies: a decade of challenges and their impact on genetic architecture. Critical Reviews in Biotechnology, 2018, 38, 1157-1175.	5.1	33
499	Genomic Selection. Population Genomics, 2018, , 427-480.	0.2	4
500	Mammalian genomic regulatory regions predicted by utilizing human genomics, transcriptomics, and epigenetics data. GigaScience, 2018, 7, 1-17.	3.3	27
501	Low-pass single-chromosome sequencing of human small supernumerary marker chromosomes (sSMCs) and Apodemus B chromosomes. Chromosoma, 2018, 127, 301-311.	1.0	18
502	Proteomics in Domestic Animals: from Farm to Systems Biology. , 2018, , .		4
503	The Use of Proteomics to Study Biomarkers of Stress and Welfare in Farm Animals. , 2018, , 339-360.		1
504	Genetically engineered pigs as models for human disease. DMM Disease Models and Mechanisms, 2018, 11, .	1.2	155
505	Are Nonsense Alleles of Drosophila melanogaster Genes under Any Selection?. Genome Biology and Evolution, 2018, 10, 1012-1018.	1.1	3
506	DNA methylation changes and evolution of RNA-based duplication inSus scrofa: based on a two-step strategy. Epigenomics, 2018, 10, 199-218.	1.0	6
507	Inferring the evolution of the major histocompatibility complex of wild pigs and peccaries using hybridisation DNA capture-based sequencing. Immunogenetics, 2018, 70, 401-417.	1.2	6
508	Decellularised conjunctiva for ocular surface reconstruction. Acta Biomaterialia, 2018, 67, 259-269.	4.1	30
509	Elevated Proportions of Deleterious Genetic Variation in Domestic Animals and Plants. Genome Biology and Evolution, 2018, 10, 276-290.	1.1	75
510	Branched-chain amino acid ratios modulate lipid metabolism in adipose tissues of growing pigs. Journal of Functional Foods, 2018, 40, 614-624.	1.6	22

#	Article	IF	CITATIONS
511	Nextâ€generation metrics for monitoring genetic erosion within populations of conservation concern. Evolutionary Applications, 2018, 11, 1066-1083.	1.5	93
512	Historical demography of common carp estimated from individuals collected from various parts of the world using the pairwise sequentially markovian coalescent approach. Genetica, 2018, 146, 235-241.	0.5	11
513	Genome-wide association of changes in swine feeding behaviour due to heat stress. Genetics Selection Evolution, 2018, 50, 11.	1.2	35
514	Effects and biotransformation of the mycotoxin deoxynivalenol in growing pigs fed with naturally contaminated pelleted grains with and without the addition of <i>Coriobacteriaceum</i> DSM 11798. Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment, 2018. 35. 1394-1409.	1.1	15
515	Evolution, regulation, and function of porcine selenogenome. Free Radical Biology and Medicine, 2018, 127, 116-123.	1.3	26
516	No Gut No Gain! Enteral Bile Acid Treatment Preserves Gut Growth but Not Parenteral Nutrition–Associated Liver Injury in a Novel Extensive Short Bowel Animal Model. Journal of Parenteral and Enteral Nutrition, 2018, 42, 1238-1251.	1.3	15
517	Transcriptome differences in frontal cortex between wild boar and domesticated pig. Animal Science Journal, 2018, 89, 848-857.	0.6	11
518	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes. Genome Research, 2018, 28, 448-459.	2.4	99
519	Downregulation of Aquaporins (AQP1 and AQP5) and Na,K-ATPase in Porcine Reproductive and Respiratory Syndrome Virus-Infected Pig Lungs. Inflammation, 2018, 41, 1104-1114.	1.7	17
520	Branchedâ€chain amino acid ratios in lowâ€protein diets regulate the free amino acid profile and the expression of hepatic fatty acid metabolismâ€related genes in growing pigs. Journal of Animal Physiology and Animal Nutrition, 2018, 102, e43-e51.	1.0	10
521	Polymorphism and peptide-binding specificities of porcine major histocompatibility complex (MHC) class I molecules. Molecular Immunology, 2018, 93, 236-245.	1.0	19
522	Determination of complete sequence information of the human ABO blood group orthologous gene in pigs and breed difference in blood type frequencies. Gene, 2018, 640, 1-5.	1.0	10
523	Combined GWAS and LDLA approaches to improve genome-wide quantitative trait loci detection affecting carcass and meat quality traits in pig. Meat Science, 2018, 135, 148-158.	2.7	18
524	Characterisation of the porcine eyeball as an in-vitro model for dry eye. Contact Lens and Anterior Eye, 2018, 41, 13-17.	0.8	29
525	Genotypingâ€byâ€sequencing through transcriptomics: implementation in a range of crop species with varying reproductive habits and ploidy levels. Plant Biotechnology Journal, 2018, 16, 877-889.	4.1	45
526	Deregulation of obesity-relevant genes is associated with progression in BMI and the amount of adipose tissue in pigs. Molecular Genetics and Genomics, 2018, 293, 129-136.	1.0	6
527	Genomic Analysis of Demographic History and Ecological Niche Modeling in the Endangered Sumatran Rhinoceros Dicerorhinus sumatrensis. Current Biology, 2018, 28, 70-76.e4.	1.8	57
528	Contribution of the swine model in the study of human sexually transmitted infections. Infection, Genetics and Evolution, 2018, 66, 346-360.	1.0	22

#	Article	IF	CITATIONS
529	Automatic delineation of brain regions on MRI and PET images from the pig. Journal of Neuroscience Methods, 2018, 294, 51-58.	1.3	27
530	Porcine Y-chromosome variation is consistent with the occurrence of paternal gene flow from non-Asian to Asian populations. Heredity, 2018, 120, 63-76.	1.2	14
531	Analysis of Pig Vomeronasal Receptor Type 1 (V1R) Promoter Region Reveals a Common Promoter Motif but Poor CpG Islands. Animal Biotechnology, 2018, 29, 293-300.	0.7	7
532	Genome-Wide Association of Myoglobin Concentrations in Pork Loins. Meat and Muscle Biology, 2018, 2, .	0.7	4
533	Genome-wide differences in DNA methylation changes in caprine ovaries between oestrous and dioestrous phases. Journal of Animal Science and Biotechnology, 2018, 9, 85.	2.1	28
534	Porcine single nucleotide polymorphisms and their functional effect: an update. BMC Research Notes, 2018, 11, 860.	0.6	12
535	Genome-wide detection of selective signatures in a Duroc pig population. Journal of Integrative Agriculture, 2018, 17, 2528-2535.	1.7	14
536	Reconstruction of avian ancestral karyotypes reveals differences in the evolutionary history of macro- and microchromosomes. Genome Biology, 2018, 19, 155.	3.8	44
537	Comparative demography elucidates the longevity of parasitic and symbiotic relationships. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20181032.	1.2	14
538	Introgression of Chinese haplotypes contributed to the improvement of Danish Duroc pigs. Evolutionary Applications, 2019, 12, 292-300.	1.5	5
539	Of Mice, Dogs, Pigs, and Men: Choosing the Appropriate Model for Immuno-Oncology Research. ILAR Journal, 2018, 59, 247-262.	1.8	40
540	Genome-wide epigenetic landscape of pig lincRNAs and their evolution during porcine domestication. Epigenomics, 2018, 10, 1603-1618.	1.0	3
541	Chromosome-level assembly reveals extensive rearrangement in saker falcon and budgerigar, but not ostrich, genomes. Genome Biology, 2018, 19, 171.	3.8	65
542	The evolutionary dynamics of microRNAs in domestic mammals. Scientific Reports, 2018, 8, 17050.	1.6	17
543	Copy number variation in the MSRB3 gene enlarges porcine ear size through a mechanism involving miR-584-5p. Genetics Selection Evolution, 2018, 50, 72.	1.2	37
544	Distinct Patterns of PPARÎ ³ Promoter Usage, Lipid Degradation Activity, and Gene Expression in Subcutaneous Adipose Tissue of Lean and Obese Swine. International Journal of Molecular Sciences, 2018, 19, 3892.	1.8	8
545	Nucleotide Sequences of Porcine α1 and α2 Chains of Type I Collagen cDNA and Their Different Expression Levels in Tissues. Japan Agricultural Research Quarterly, 2018, 52, 149-154.	0.1	2
546	Livestock 2.0 – genome editing for fitter, healthier, and more productive farmed animals. Genome Biology, 2018, 19, 204.	3.8	114

#	Article	IF	Citations
547	Sequence variation, evolutionary constraint, and selection at the CD163 gene in pigs. Genetics Selection Evolution, 2018, 50, 69.	1.2	11
548	Editorial: Building Strategies for Porcine Cancer Models. Frontiers in Genetics, 2018, 9, 377.	1.1	1
549	Analysis of porcine body size variation using re-sequencing data of miniature and large pigs. BMC Genomics, 2018, 19, 687.	1.2	12
550	Comprehensive inbred variation discovery in Bama pigs using de novo assemblies. Gene, 2018, 679, 81-89.	1.0	9
551	<scp>PERV</scp> ading strategies and infectious risk for clinical xenotransplantation. Xenotransplantation, 2018, 25, e12402.	1.6	15
552	Imputation-Based Whole-Genome Sequence Association Study Reveals Constant and Novel Loci for Hematological Traits in a Large-Scale Swine F2 Resource Population. Frontiers in Genetics, 2018, 9, 401.	1.1	28
553	Sequence Composition and Evolution of Mammalian B Chromosomes. Genes, 2018, 9, 490.	1.0	16
554	Sequencing through thick and thin: Historiographical and philosophical implications. Studies in History and Philosophy of Science Part C:Studies in History and Philosophy of Biological and Biomedical Sciences, 2018, 72, 10-27.	0.8	8
555	Genome-wide DNA methylation profiles of porcine ovaries in estrus and proestrus. Physiological Genomics, 2018, 50, 714-723.	1.0	6
556	Porcine endogenous retroviruses: Quantification of the copy number in cell lines, pig breeds, and organs. Xenotransplantation, 2018, 25, e12445.	1.6	40
557	Genomic responses to selection for tame/aggressive behaviors in the silver fox (<i>Vulpes vulpes</i>) Tj ETQq0 () 0 rgBT /C 3.3)verlock 10 T 64
558	Balancing selection on a recessive lethal deletion with pleiotropic effects on two neighboring genes in the porcine genome. PLoS Genetics, 2018, 14, e1007661.	1.5	39
559	Genomic structure and expression of the porcine ACTC1 gene. Czech Journal of Animal Science, 2018, 63, 371-378.	0.5	1
560	The Histone Deacetylase Inhibitor, CI994, Improves Nuclear Reprogramming and In Vitro Developmental Potential of Cloned Pig Embryos. Cellular Reprogramming, 2018, 20, 205-213.	0.5	15
561	Evidence of evolutionary history and selective sweeps in the genome of Meishan pig reveals its genetic and phenotypic characterization. GigaScience, 2018, 7, .	3.3	56
562	IFN-λ and microRNAs are important modulators of the pulmonary innate immune response against influenza A (H1N2) infection in pigs. PLoS ONE, 2018, 13, e0194765.	1.1	24
563	Identification of Differentially Expressed Genes in Porcine Ovaries at Proestrus and Estrus Stages Using RNA-Seq Technique. BioMed Research International, 2018, 2018, 1-8.	0.9	12
564	Transcriptome Analysis Reveals Dynamic Gene Expression Profiles in Porcine Alveolar Macrophages in Response to the Chinese Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus. BioMed Research International, 2018, 2018, 1-23.	0.9	24

#	Article	IF	CITATIONS
565	Expression and Regulation Profile of Mature MicroRNA in the Pig: Relevance to Xenotransplantation. BioMed Research International, 2018, 2018, 1-9.	0.9	11
566	The unique evolution of the pig LRC, a single KIR but expansion of LILR and a novel Ig receptor family. Immunogenetics, 2018, 70, 661-669.	1.2	15
567	Transgenerational and Epigenetic Impacts of Environmental Exposures in Male Reproduction. , 2018, , 634-641.		0
568	RNA-Seq based transcriptome of whole blood from immunocompetent pigs (Sus scrofa) experimentally infected with Mycoplasma suis strain Illinois. Veterinary Research, 2018, 49, 49.	1.1	33
569	Material Characterization of Hardening Soft Sponge Featuring MR Fluid and Application of 6-DOF MR Haptic Master for Robot-Assisted Surgery. Materials, 2018, 11, 1268.	1.3	15
570	Genome-wide detection of selection signatures in Chinese indigenous Laiwu pigs revealed candidate genes regulating fat deposition in muscle. BMC Genetics, 2018, 19, 31.	2.7	40
571	Highâ€quality wholeâ€genome sequence of an abundant Holarctic odontocete, the harbour porpoise (<i>Phocoena phocoena</i>). Molecular Ecology Resources, 2018, 18, 1469-1481.	2.2	11
572	Comparative transcriptome analysis of the invasive weed Mikania micrantha with its native congeners provides insights into genetic basis underlying successful invasion. BMC Genomics, 2018, 19, 392.	1.2	19
573	A translational model of chronic kidney disease in swine. American Journal of Physiology - Renal Physiology, 2018, 315, F364-F373.	1.3	37
575	Development of Immune Cells in the Intestinal Mucosa Can Be Affected by Intensive and Extensive Farm Environments, and Antibiotic Use. Frontiers in Immunology, 2018, 9, 1061.	2.2	6
576	Genetically Induced Tumors in the Oncopig Model Invoke an Antitumor Immune Response Dominated by Cytotoxic CD8β+ T Cells and Differentiated γδT Cells Alongside a Regulatory Response Mediated by FOXP3+ T Cells and Immunoregulatory Molecules. Frontiers in Immunology, 2018, 9, 1301.	2.2	15
577	Linkage disequilibrium pattern and genomeâ€wide association mapping for meat traits in multiple porcine F ₂ crosses. Animal Genetics, 2018, 49, 403-412.	0.6	9
578	Role of Biotechnology in the Agrofood Industry. , 2018, , 1-26.		0
579	Gene expression profiles of germ-free and conventional piglets from the same litter. Scientific Reports, 2018, 8, 10745.	1.6	26
580	Population Genomics of Ungulates. Population Genomics, 2018, , 185-209.	0.2	4
581	Selective constraints in coldâ€region wild boars may defuse the effects of small effective population size on molecular evolution of mitogenomes. Ecology and Evolution, 2018, 8, 8102-8114.	0.8	19
582	The cell reâ€associationâ€based wholeâ€tooth regeneration strategies in large animal, <i>Sus scrofa</i> . Cell Proliferation, 2018, 51, e12479.	2.4	27
583	Population size may shape the accumulation of functional mutations following domestication. BMC Evolutionary Biology, 2018, 18, 4.	3.2	15

ARTICLE IF CITATIONS # De novo assembly of mitochondrial genomes provides insights into genetic diversity and molecular 584 0.5 4 evolution in wild boars and domestic pigs. Genetica, 2018, 146, 277-285. Feedomics: Promises for food security with sustainable food animal production. TrAC - Trends in 5.8 Analytical Chemistry, 2018, 107, 130-141. Weighted single-step GWAS and gene network analysis reveal new candidate genes for semen traits in 586 1.2 49 pigs. Genetics Selection Evolution, 2018, 50, 40. Genome-wide scanning reveals genetic diversity and signatures of selection in Chinese indigenous 587 cattle breeds. Livestock Science, 2018, 216, 100-108. Differential gene expression patterns in vein regions susceptible versus resistant to neointimal 588 1.0 4 hyperplasia. Physiological Genomics, 2018, 50, 615-627. Type I interferon suppression-negative and host mRNA nuclear retention-negative mutation in $nsp1\hat{l}^2$ confers attenuation of porcine reproductive and respiratory syndrome virus in pigs. Virology, 2018, 1.1 517, 177-187. Using Huntingtin Knock-In Minipigs to Fill the Gap Between Mouse Models and Patients with 590 1.5 0 Huntington's Disease. Neuroscience Bulletin, 2018, 34, 870-872. How to estimate kinship. Molecular Ecology, 2018, 27, 4121-4135. 591 2.0 87 Comparative gene expression profiling of pigâ€derived <scp>iPSC</scp>â€like cells: Effects of induced 592 pluripotency on expression of porcine endogenous retrovirus (PERV). Xenotransplantation, 2018, 25, 1.6 14 e12429. Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. Annual Review of 3.8 143 Ecology, Evolution, and Systematics, 2018, 49, 433-456. X-ray Crystallographic Characterization of the Swine MHC I Molecule SLA-3*0202 Complexed with 594 0.1 0 IAV-HA Nonapeptide. Crystallography Reports, 2018, 63, 428-432. Long non-coding RNAs and mRNAs profiling during spleen development in pig. PLoS ONE, 2018, 13, 595 1.1 29 e0193552. RAPID COMMUNICATION: A haplotype information theory method reveals genes of evolutionary 596 0.2 3 interest in European vs. Asian pigs1. Journal of Animal Science, 2018, 96, 3064-3069. A controllable tactile device for human-like tissue realization using smart magneto-rheological fluids: fabrication and modeling. Smart Materials and Structures, 2018, 27, 065015. 1.8 Deleterious alleles in the context of domestication, inbreeding, and selection. Evolutionary 598 1.5 94 Applications, 2019, 12, 6-17. Contribution of DNA methylation in chronic stressâ€induced cardiac remodeling and arrhythmias in 599 14 mice. FASEB Journal, 2019, 33, 12240-12252. Population Genomics Analysis Revealed Origin and High-altitude Adaptation of Tibetan Pigs. Scientific 600 1.6 44 Reports, 2019, 9, 11463. High-throughput metagenome analysis of the Sarcoptes scabiei internal microbiota and in-situ 1.6 identification of intestinal Streptomyces sp.. Scientific Reports, 2019, 9, 11744.

ARTICLE IF CITATIONS A Genomics Perspective on Pig Domestication., 0,,. 602 3 Autozygosity and Genetic Differentiation of Landrace and Large White Pigs as Revealed by the Genetic 1.1 Analyses of Crossbreds. Frontiers in Genetics, 2019, 10, 739. Contemporary Demographic Reconstruction Methods Are Robust to Genome Assembly Quality: A Case 604 3.5 84 Study in Tasmanian Devils. Molecular Biology and Evolution, 2019, 36, 2906-2921. Comprehensive Profiles of mRNAs and miRNAs Reveal Molecular Characteristics of Multiple Organ 1.1 Physiologies and Development in Pigs. Frontiers in Genetics, 2019, 10, 756. Development and Genome Sequencing of a Laboratory-Inbred Miniature Pig Facilitates Study of Human 606 1.9 31 Diabetic Disease. IScience, 2019, 19, 162-176. Utilizing Human Dermal Fibroblast Heterogeneity in Autologous Dermal Fibroblast Therapy: An Overcomplicated Strategy or a Promising Approach?. Anatomical Record, 2019, 302, 2126-2131. 0.8 Porcine Interferon Complex and Co-Evolution with Increasing Viral Pressure after Domestication. 608 1.5 17 Viruses, 2019, 11, 555. The Melding of Drug Screening Platforms for Melanoma. Frontiers in Oncology, 2019, 9, 512. 609 1.3 20 RepSox Increases Porcine Cloning Efficiency by Improving Pluripotency of Donor Nuclei. Cellular 610 0.5 2 Reprogramming, 2019, 21, 181-186. Improving accuracy of direct and maternal genetic effects in genomic evaluations using pooled boar 0.2 semen: a simulation study1. Journal of Animal Science, 2019, 97, 3237-3245. Avian Chromosomal Evolution., 2019,, 69-92. 612 4 Comparing interspecific socio-communicative skills of socialized juvenile dogs and miniature pigs. Animal Cognition, 2019, 22, 917-929. A swine model of soy protein–induced food allergenicity: implications in human and swine nutrition. 614 0.8 11 Animal Frontiers, 2019, 9, 52-59. Developmental atlas of the RNA editome in Sus scrofa skeletal muscle. DNA Research, 2019, 26, 261-272. 1.5 Genome-Wide Single-Nucleotide Polymorphism Data Unveil Admixture of Chinese Indigenous Chicken 617 1.1 24 Breeds with Commercial Breeds. Genome Biology and Evolution, 2019, 11, 1847-1856. Dietary apple polyphenols supplementation enhances antioxidant capacity and improves lipid metabolism in weaned piglets. Journal of Animal Physiology and Animal Nútrition, 2019, 103, 1512-1520. Mitochondrial DNA diversity and origin of indigenous pigs in South China and their contribution to 619 1.7 14 western modern pig breeds. Journal of Integrative Agriculture, 2019, 18, 2338-2350. A functional regulatory variant of MYH3 influences muscle fiber-type composition and intramuscular 1.5 fat content in pigs. PLoS Genetics, 2019, 15, e1008279.

#	Article	IF	CITATIONS
621	Development of retrotransposons insertion polymorphic markers and application in the genetic variation evaluation of Chinese Bama miniature pigs. Canadian Journal of Animal Science, 2019, , .	0.7	0
622	TaqMan probe realâ€time polymerase chain reaction targeting the ATPase 6 gene for the detection of pork adulteration in meat and meatballs. Journal of Food Safety, 2019, 39, e12715.	1.1	11
623	Landscape of Loci and Candidate Genes for Muscle Fatty Acid Composition in Pigs Revealed by Multiple Population Association Analysis. Frontiers in Genetics, 2019, 10, 1067.	1.1	7
624	A Survey of Copy Number Variation in the Porcine Genome Detected From Whole-Genome Sequence. Frontiers in Genetics, 2019, 10, 737.	1.1	16
625	Transcription analysis of the response of the porcine adrenal cortex to a single subclinical dose of lipopolysaccharide from Salmonella Enteritidis. International Journal of Biological Macromolecules, 2019, 141, 1228-1245.	3.6	5
626	Genomic diversity, linkage disequilibrium and selection signatures in European local pig breeds assessed with a high density SNP chip. Scientific Reports, 2019, 9, 13546.	1.6	78
627	Penaeid shrimp genome provides insights into benthic adaptation and frequent molting. Nature Communications, 2019, 10, 356.	5.8	328
628	Tracking diphyodont development in miniature pig in vitro and in vivo. Biology Open, 2019, 8, .	0.6	8
629	Imputation to whole-genome sequence using multiple pig populations and its use in genome-wide association studies. Genetics Selection Evolution, 2019, 51, 2.	1.2	54
630	Eutherian third-party data gene collections. Gene Reports, 2019, 16, 100414.	0.4	4
631	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. Science, 2019, 364, .	6.0	266
632	Biological adaptations in the Arctic cervid, the reindeer (<i>Rangifer tarandus</i>). Science, 2019, 364, ·	6.0	58
633	The Biomineralization Proteome: Protein Complexity for a Complex Bioceramic Assembly Process. Proteomics, 2019, 19, e1900036.	1.3	36
634	Epigenetics and heritable phenotypic variations in livestock. , 2019, , 283-313.		0
635	No imprinted XIST expression in pigs: biallelic XIST expression in early embryos and random X inactivation in placentas. Cellular and Molecular Life Sciences, 2019, 76, 4525-4538.	2.4	10
636	Earlier demethylation of myogenic genes contributes to embryonic precocious terminal differentiation of myoblasts in miniature pigs. FASEB Journal, 2019, 33, 9638-9655.	0.2	11
637	Retrotransposons evolution and impact on IncRNA and protein coding genes in pigs. Mobile DNA, 2019, 10, 19.	1.3	22
638	Genome-Wide Investigation and Functional Analysis of Sus scrofa RNA Editing Sites across Eleven Tissues. Genes, 2019, 10, 327.	1.0	12

#	Article	IF	CITATIONS
639	Improved annotation of the domestic pig genome through integration of Iso-Seq and RNA-seq data. BMC Genomics, 2019, 20, 344.	1.2	80
640	Subclinical lipopolysaccharide from Salmonella Enteritidis induces neuropeptide dysregulation in the spinal cord and the dorsal root ganglia. BMC Neuroscience, 2019, 20, 18.	0.8	3
641	Genomic analysis on pygmy hog reveals extensive interbreeding during wild boar expansion. Nature Communications, 2019, 10, 1992.	5.8	38
642	Dynamic Transcriptome Analysis Reveals Potential Long Non-coding RNAs Governing Postnatal Pineal Development in Pig. Frontiers in Genetics, 2019, 10, 409.	1.1	17
643	Animal models of arrhythmia: classic electrophysiology to genetically modified large animals. Nature Reviews Cardiology, 2019, 16, 457-475.	6.1	131
644	Translating Human Cancer Sequences Into Personalized Porcine Cancer Models. Frontiers in Oncology, 2019, 9, 105.	1.3	10
645	Porcine Models of Pancreatic Cancer. Frontiers in Oncology, 2019, 9, 144.	1.3	30
646	Balancing selection at a premature stop mutation in the myostatin gene underlies a recessive leg weakness syndrome in pigs. PLoS Genetics, 2019, 15, e1007759.	1.5	31
647	Assessing Sus scrofa diversity among continental United States, and Pacific islands populations using molecular markers from a gene banks collection. Scientific Reports, 2019, 9, 3173.	1.6	6
648	Effects of heterozygosity on performance of purebred and crossbred pigs. Genetics Selection Evolution, 2019, 51, 8.	1.2	26
649	Non-murine models to investigate tumor-immune interactions in head and neck cancer. Oncogene, 2019, 38, 4902-4914.	2.6	12
650	Examination of the temporal and spatial dynamics of the gut microbiome in newborn piglets reveals distinct microbial communities in six intestinal segments. Scientific Reports, 2019, 9, 3453.	1.6	59
651	Whole-Genome Resequencing Identifies KIT New Alleles That Affect Coat Color Phenotypes in Pigs. Frontiers in Genetics, 2019, 10, 218.	1.1	17
652	The regulatory actions of retinoic acid on M2 polarization of porcine macrophages. Developmental and Comparative Immunology, 2019, 98, 20-33.	1.0	26
653	Proposed U.S. regulation of gene-edited food animals is not fit for purpose. Npj Science of Food, 2019, 3, 3.	2.5	27
654	Gestational diabetes promotes germ cell cCyst breakdown and primordial follicle formation in newborn mice via the AKT signaling pathway. PLoS ONE, 2019, 14, e0215007.	1.1	3
655	The identification of differentially expressed genes between extremes of placental efficiency in maternal line gilts on day 95 of gestation. BMC Genomics, 2019, 20, 254.	1.2	11
656	Characterization of whole blood transcriptome and early-life fecal microbiota in high and low responder pigs before, and after vaccination for Mycoplasma hyopneumoniae. Vaccine, 2019, 37, 1743-1755.	1.7	16

#	Article	IF	CITATIONS
657	Analysis of Anasplatyrhynchos genome resequencing data reveals genetic signatures of artificial selection. PLoS ONE, 2019, 14, e0211908.	1.1	3
658	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. Genome Research, 2019, 29, 576-589.	2.4	39
659	Sexual Dimorphism in Immune Development and in Response to Nutritional Intervention in Neonatal Piglets. Frontiers in Immunology, 2019, 10, 2705.	2.2	21
660	A Porcine <i>Ex Vivo</i> Lung Perfusion Model To Investigate Bacterial Pathogenesis. MBio, 2019, 10, .	1.8	19
661	The Value of Reference Genomes in the Conservation of Threatened Species. Genes, 2019, 10, 846.	1.0	113
662	A mutation in MAP2 is associated with prenatal hair follicle density. FASEB Journal, 2019, 33, 14479-14490.	0.2	4
663	Effects of Dietary Apple Polyphenols Supplementation on Hepatic Fat Deposition and Antioxidant Capacity in Finishing Pigs. Animals, 2019, 9, 937.	1.0	12
664	Demographic Histories and Genome-Wide Patterns of Divergence in Incipient Species of Shorebirds. Frontiers in Genetics, 2019, 10, 919.	1.1	14
665	MiR-144-3p Enhances Cardiac Fibrosis After Myocardial Infarction by Targeting PTEN. Frontiers in Cell and Developmental Biology, 2019, 7, 249.	1.8	40
666	Cytokine gene expression assay as a diagnostic tool for detection of Mycobacterium bovis infection in warthogs (Phacochoerus africanus). Scientific Reports, 2019, 9, 16525.	1.6	7
667	Biochemical and biomechanical comparisions of decellularized scaffolds derived from porcine subcutaneous and visceral adipose tissue. Journal of Tissue Engineering, 2019, 10, 204173141988816.	2.3	17
668	Unlocking the origins and biology of domestic animals using ancient DNA and paleogenomics. BMC Biology, 2019, 17, 98.	1.7	48
669	Infection in xenotransplantation: opportunities and challenges. Current Opinion in Organ Transplantation, 2019, 24, 527-534.	0.8	22
670	Chromosome-level genome assembly for giant panda provides novel insights into Carnivora chromosome evolution. Genome Biology, 2019, 20, 267.	3.8	31
671	Comparative Anatomy of the Mammalian Corneal Subbasal Nerve Plexus. , 2019, 60, 4972.		22
672	Hydrogel from Acellular Porcine Adipose Tissue Accelerates Wound Healing by Inducing Intradermal Adipocyte Regeneration. Journal of Investigative Dermatology, 2019, 139, 455-463.	0.3	27
673	Functional Annotation of Animal Genomes (FAANG): Current Achievements and Roadmap. Annual Review of Animal Biosciences, 2019, 7, 65-88.	3.6	172
674	Whole-Genome Sequencing of Three Native Cattle Breeds Originating From the Northernmost Cattle Farming Regions. Frontiers in Genetics, 2018, 9, 728.	1.1	57

#	Article	IF	CITATIONS
675	Whole-Tooth Regeneration by Allogeneic Cell Reassociation in Pig Jawbone. Tissue Engineering - Part A, 2019, 25, 1202-1212.	1.6	19
676	High doses of ANP and BNP exacerbate lipolysis in humans and the lipolytic effect of BNP is associated with cardiac triglyceride content in pigs. Peptides, 2019, 112, 43-47.	1.2	6
677	Building a livestock genetic and genomic information knowledgebase through integrative developments of Animal QTLdb and CorrDB. Nucleic Acids Research, 2019, 47, D701-D710.	6.5	268
678	Generation by somatic cell nuclear transfer of GGTA1 knockout pigs expressing soluble human TNFRI-Fc and human HO-1. Transgenic Research, 2019, 28, 91-102.	1.3	12
679	Harnessing genomic information for livestock improvement. Nature Reviews Genetics, 2019, 20, 135-156.	7.7	262
680	The combination of metformin and 2â€deoxyglucose significantly inhibits cyst formation in miniature pigs with polycystic kidney disease. British Journal of Pharmacology, 2019, 176, 711-724.	2.7	49
681	The first comprehensive description of the expression profile of genes involved in differential body growth and the immune system of the Jeju Native Pig and miniature pig. Amino Acids, 2019, 51, 495-511.	1.2	7
682	Whole-genome analysis of structural variations between Xiang pigs with larger litter sizes and those with smaller litter sizes. Genomics, 2019, 111, 310-319.	1.3	11
683	Phylogenomic Resolution of the Cetacean Tree of Life Using Target Sequence Capture. Systematic Biology, 2020, 69, 479-501.	2.7	160
684	Preclinical study for treatment of hypospadias by advanced therapy medicinal products. World Journal of Urology, 2020, 38, 2115-2122.	1.2	11
685	Building a sequence map of the pig pan-genome from multiple de novo assemblies and Hi-C data. Science China Life Sciences, 2020, 63, 750-763.	2.3	47
686	An assessment of genetic diversity and population structures of fifteen Vietnamese indigenous pig breeds for supporting the decision making on conservation strategies. Tropical Animal Health and Production, 2020, 52, 1033-1041.	0.5	5
687	Detection of homozygous genotypes for a putatively lethal recessive mutation in the porcine argininosuccinate synthase 1 (<i>ASS1</i>) gene. Animal Genetics, 2020, 51, 106-110.	0.6	2
688	Predicting survival and longevity of sows using purebred and crossbred data1. Translational Animal Science, 2020, 4, 993-1005.	0.4	2
689	Revisiting the Pig IGHC Gene Locus in Different Breeds Uncovers Nine Distinct IGHG Genes. Journal of Immunology, 2020, 205, 2137-2145.	0.4	7
690	African Swine Fever Circulation among Free-Ranging Pigs in Sardinia: Data from the Eradication Program. Vaccines, 2020, 8, 549.	2.1	25
691	Functional signatures of evolutionarily young CTCF binding sites. BMC Biology, 2020, 18, 132.	1.7	9
692	The untold story between enhancers and skeletal muscle development. Journal of Integrative Agriculture, 2020, 19, 2137-2149.	1.7	0

#	Article	IF	CITATIONS
693	Genomic diversity revealed by whole-genome sequencing in three Danish commercial pig breeds. Journal of Animal Science, 2020, 98, .	0.2	9
694	PRE-1 Revealed Previous Unknown Introgression Events in Eurasian Boars during the Middle Pleistocene. Genome Biology and Evolution, 2020, 12, 1751-1764.	1.1	9
696	Genetic architecture of individual variation in recombination rate on the X chromosome in cattle. Heredity, 2020, 125, 304-316.	1.2	10
697	Genetic origins and diversity of bushpigs from Madagascar (Potamochoerus larvatus, family Suidae). Scientific Reports, 2020, 10, 20629.	1.6	5
698	Phylogeography of feral Monteiro pig in the Brazilian Pantanal Ecosystem. Genetica, 2020, 148, 183-193.	0.5	3
699	Selective sweep analysis reveals extensive parallel selection traits between large white and Duroc pigs. Evolutionary Applications, 2020, 13, 2807-2820.	1.5	14
700	<i>RAB37</i> multiple alleles, transcription activation and evolution in mammals. International Journal of Biological Sciences, 2020, 16, 2964-2973.	2.6	2
701	Inclusion of endophenotypes in a standard GWAS facilitate a detailed mechanistic understanding of genetic elements that control blood lipid levels. Scientific Reports, 2020, 10, 18434.	1.6	5
702	Next-generation sequencing in veterinary medicine - a review. Veterinarska Stanica, 2020, 51, 175-185.	0.1	0
703	Asia-wide phylogeography of wild boar (Sus scrofa) based on mitochondrial DNA and Y-chromosome: Revising the migration routes of wild boar in Asia. PLoS ONE, 2020, 15, e0238049.	1.1	23
704	Identification of Signatures of Selection by Whole-Genome Resequencing of a Chinese Native Pig. Frontiers in Genetics, 2020, 11, 566255.	1.1	20
705	Wholeâ€genome sequencing reveals breedâ€differential CNVs between Tongcheng and Large White pigs. Animal Genetics, 2020, 51, 940-944.	0.6	7
706	Improving read alignment through the generation of alternative reference via iterative strategy. Scientific Reports, 2020, 10, 18712.	1.6	3
707	Evaluation of un-methylated DNA enrichment in sequencing of African swine fever virus complete genome. Journal of Virological Methods, 2020, 285, 113959.	1.0	3
708	Dietary Ferulic Acid Supplementation Improves Antioxidant Capacity and Lipid Metabolism in Weaned Piglets. Nutrients, 2020, 12, 3811.	1.7	30
709	Proteomic characterisation of drug metabolising enzymes and drug transporters in pig liver. Xenobiotica, 2020, 50, 1208-1219.	0.5	4
710	Potentiation of IL-4 Signaling by Retinoic Acid in Intestinal Epithelial Cells and Macrophages—Mechanisms and Targets. Frontiers in Immunology, 2020, 11, 605.	2.2	11
711	The Domestication Makeup: Evolution, Survival, and Challenges. Frontiers in Ecology and Evolution, 2020, 8, .	1.1	29

#	ARTICLE	IF	Citations
712	Mutations in Domestic Animals Disrupting or Creating Pigmentation Patterns. Frontiers in Ecology and Evolution, 2020, 8, .	1.1	3
713	Genome-wide detection of selective signatures in a Jinhua pig population. Journal of Integrative Agriculture, 2020, 19, 1314-1322.	1.7	7
714	Impaired Tâ€cell responses in domestic pigs and wild boar upon infection with a highly virulent African swine fever virus strain. Transboundary and Emerging Diseases, 2020, 67, 3016-3032.	1.3	31
715	Whole genome sequence analysis reveals genetic structure and X-chromosome haplotype structure in indigenous Chinese pigs. Scientific Reports, 2020, 10, 9433.	1.6	11
716	Cytogenetic Characterization of a Small Evolutionary Rearrangement Involving Chromosomes BTA21 and OAR18. Cytogenetic and Genome Research, 2020, 160, 193-198.	0.6	2
717	Genome sequence and comparative analysis of reindeer (Rangifer tarandus) in northern Eurasia. Scientific Reports, 2020, 10, 8980.	1.6	30
718	Transcription from a gene desert in a melanoma porcine model. Molecular Genetics and Genomics, 2020, 295, 1239-1252.	1.0	1
719	An improved pig reference genome sequence to enable pig genetics and genomics research. GigaScience, 2020, 9, .	3.3	187
720	Porcine cancer models: potential tools to enhance cancer drug trials. Expert Opinion on Drug Discovery, 2020, 15, 893-902.	2.5	8
721	Spatial genetic structure and historical demography of East Asian wild boar. Animal Genetics, 2020, 51, 557-567.	0.6	9
722	From Beef to Bees: High-Throughput Kinome Analysis to Understand Host Responses of Livestock Species to Infectious Diseases and Industry-Associated Stress. Frontiers in Immunology, 2020, 11, 765.	2.2	6
723	A transcriptional landscape of 28 porcine tissues obtained by super deepSAGE sequencing. BMC Genomics, 2020, 21, 229.	1.2	5
724	Development of Molecular Markers Based on the L1 Retrotransposon Insertion Polymorphisms in Pigs (Sus scrofa) and Their Association with Economic Traits. Russian Journal of Genetics, 2020, 56, 183-191.	0.2	5
725	Genetic improvement of livestock, from conventional breeding to biotechnological approaches. , 2020, , 393-405.		5
726	Swine Disease Models for Optimal Vascular Engineering. Annual Review of Biomedical Engineering, 2020, 22, 25-49.	5.7	19
727	Introgression of Eastern Chinese and Southern Chinese haplotypes contributes to the improvement of fertility and immunity in European modern pigs. GigaScience, 2020, 9, .	3.3	31
728	Modelling the shape of the pig scapula. Genetics Selection Evolution, 2020, 52, 36.	1.2	1
729	Xeno-organ donor pigs with multiple genetic modifications – the more the better?. Current Opinion in Genetics and Development, 2020, 64, 60-65.	1.5	22

#	Article	IF	CITATIONS
730	Assessing the evolutionary persistence of ecological relationships: A review and preview. Infection, Genetics and Evolution, 2020, 84, 104441.	1.0	4
731	Molecular cloning, sequence characteristics, and tissue expression analysis of glucagon receptor gene in Bama minipig. Canadian Journal of Animal Science, 2020, 100, 536-546.	0.7	0
732	pCADD: SNV prioritisation in Sus scrofa. Genetics Selection Evolution, 2020, 52, 4.	1.2	21
733	Altered Hippocampal Epigenetic Regulation Underlying Reduced Cognitive Development in Response to Early Life Environmental Insults. Genes, 2020, 11, 162.	1.0	8
734	Modern genetic and genomic improvement of the pig. , 2020, , 249-262.		6
735	Porcine models for studying complications and organ crosstalk in diabetes mellitus. Cell and Tissue Research, 2020, 380, 341-378.	1.5	54
736	Mechanism of nonthermal induction of apoptosis by highâ€intensity focused electromagnetic procedure: Biochemical investigation in a porcine model. Journal of Cosmetic Dermatology, 2020, 19, 605-611.	0.8	17
737	Porcine Liver Anatomy Applied to Biomedicine. Journal of Surgical Research, 2020, 250, 70-79.	0.8	22
738	Polymorphism of the alpha-1-fucosyltransferase (FUT1) gene in several wild boar (Sus scrofa) populations in France and link to edema disease. Research in Veterinary Science, 2020, 131, 78-86.	0.9	5
739	Systematic alteration of ATAC-seq for profiling open chromatin in cryopreserved nuclei preparations from livestock tissues. Scientific Reports, 2020, 10, 5230.	1.6	26
740	Robotically handled whole-tissue culture system for the screening of oral drug formulations. Nature Biomedical Engineering, 2020, 4, 544-559.	11.6	35
741	Robotic screening of intestinal drug absorption. Nature Biomedical Engineering, 2020, 4, 485-486.	11.6	3
742	Whole genome resequencing reveals an association of ABCC4 variants with preaxial polydactyly in pigs. BMC Genomics, 2020, 21, 268.	1.2	3
743	iTRAQ-based Quantitative Proteomics Analysis Identifies Host Pathways Modulated during Toxoplasma gondii Infection in Swine. Microorganisms, 2020, 8, 518.	1.6	8
744	Beyond tradition and convention: benefits of non-traditional model organisms in cancer research. Cancer and Metastasis Reviews, 2021, 40, 47-69.	2.7	11
745	Vertebrate Chromosome Evolution. Annual Review of Animal Biosciences, 2021, 9, 1-27.	3.6	34
746	Genetic Engineering of Livestock: The Opportunity Cost of Regulatory Delay. Annual Review of Animal Biosciences, 2021, 9, 453-478.	3.6	34
747	Genetic consequences of longâ€ŧerm small effective population size in the critically endangered pygmy hog. Evolutionary Applications, 2021, 14, 710-720.	1.5	19

#	ARTICLE	IF	CITATIONS
748	Selection and introgression facilitated the adaptation of Chinese native endangered cattle in extreme environments. Evolutionary Applications, 2021, 14, 860-873.	1.5	11
749	Historical range expansion and biological changes of Sus scrofa corresponding to domestication and feralization. Mammal Research, 2021, 66, 1-12.	0.6	10
750	Development of Wild Boar Species-Specific DNA Markers for a Potential Quality Control and Traceability Method in Meat Products. Food Analytical Methods, 2021, 14, 18-27.	1.3	4
751	Genomics for Food Security With Efficient and Sustainable Livestock Production. , 2021, , 229-244.		1
752	A specific promoter-type in ribonuclease L gene is associated with phagocytic activity in pigs. Journal of Veterinary Medical Science, 2021, 83, 1407-1415.	0.3	0
754	Homozygosity Mapping Reveals Population History and Trait Architecture in Self-Incompatible Pear (Pyrus spp.). Frontiers in Plant Science, 2020, 11, 590846.	1.7	7
755	A comprehensive epigenome atlas reveals DNA methylation regulating skeletal muscle development. Nucleic Acids Research, 2021, 49, 1313-1329.	6.5	68
756	A new duck genome reveals conserved and convergently evolved chromosome architectures of birds and mammals. GigaScience, 2021, 10, .	3.3	36
757	Origin and distribution of ancient Thai pig lineages. International Journal of Osteoarchaeology, 2021, 31, 406-416.	0.6	1
759	Specification and epigenomic resetting of the pig germline exhibit conservation with the human lineage. Cell Reports, 2021, 34, 108735.	2.9	43
760	Comparative Mapping of the Macrochromosomes of Eight Avian Species Provides Further Insight into Their Phylogenetic Relationships and Avian Karyotype Evolution. Cells, 2021, 10, 362.	1.8	13
762	Human pathways in animal models: possibilities and limitations. Nucleic Acids Research, 2021, 49, 1859-1871.	6.5	35
763	Divergence at mitochondrial and ribosomal loci indicates the split between Asian and European populations of Trichinella spiralis occurred prior to swine domestication. Infection, Genetics and Evolution, 2021, 88, 104705.	1.0	5
765	Biological mechanisms of growth performance and meat quality in porcine muscle tissue. Animal Biotechnology, 2022, 33, 1246-1254.	0.7	3
766	Application of Animal Models in Cancer Research: Recent Progress and Future Prospects. Cancer Management and Research, 2021, Volume 13, 2455-2475.	0.9	61
768	Transcriptional regulation of alcohol induced liver fibrosis in a translational porcine hepatocellular carcinoma model. Biochimie, 2021, 182, 73-84.	1.3	7
769	Construction of Whole Genomes from Scaffolds Using Single Cell Strand-Seq Data. International Journal of Molecular Sciences, 2021, 22, 3617.	1.8	5
770	Classical, Molecular, and Genomic Cytogenetics of the Pig, a Clinical Perspective. Animals, 2021, 11, 1257.	1.0	6

#	Article	IF	Citations
771	Genetic parameters and genomic prediction for feed intake recorded at the group and individual level in different production systems for growing pigs. Genetics Selection Evolution, 2021, 53, 33.	1.2	3
772	Genetic Architecture Underlying Nascent Speciation—The Evolution of Eurasian Pigs under Domestication. Molecular Biology and Evolution, 2021, 38, 3556-3566.	3.5	3
773	Genome-wide association and transcriptome studies identify candidate genes and pathways for feed conversion ratio in pigs. BMC Genomics, 2021, 22, 294.	1.2	11
774	Porcine germline genome engineering. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	17
775	Chapter 2: Function and regulation of porcine selenogenome and selenoproteome. , 2021, , 39-59.		14
776	The Meishan pig genome reveals structural variationâ€mediated gene expression and phenotypic divergence underlying Asian pig domestication. Molecular Ecology Resources, 2021, 21, 2077-2092.	2.2	20
777	Toward Genome-Based Selection in Asian Seabass: What Can We Learn From Other Food Fishes and Farm Animals?. Frontiers in Genetics, 2021, 12, 506754.	1.1	8
778	Genetic Diversity and Population Structures in Chinese Miniature Pigs Revealed by SINE Retrotransposon Insertion Polymorphisms, a New Type of Genetic Markers. Animals, 2021, 11, 1136.	1.0	9
779	Exploring the genetic features and signatures of selection in South China indigenous pigs. Journal of Integrative Agriculture, 2021, 20, 1359-1371.	1.7	9
780	Perspective: Humanized Pig Models of Bladder Cancer. Frontiers in Molecular Biosciences, 2021, 8, 681044.	1.6	3
781	Genomics of Adaptations in Ungulates. Animals, 2021, 11, 1617.	1.0	3
782	Variability in porcine microRNA genes and its association with mRNA expression and lipid phenotypes. Genetics Selection Evolution, 2021, 53, 43.	1.2	4
783	SINE jumping contributes to large-scale polymorphisms in the pig genomes. Mobile DNA, 2021, 12, 17.	1.3	21
784	Genomic Analysis Reveals Human-Mediated Introgression From European Commercial Pigs to Henan Indigenous Pigs. Frontiers in Genetics, 2021, 12, 705803.	1.1	1
785	A Mix of Old British and Modern European Breeds: Genomic Prediction of Breed Composition of Smallholder Pigs in Uganda. Frontiers in Genetics, 2021, 12, 676047.	1.1	7
786	Large-scale genomic analysis reveals the genetic cost of chicken domestication. BMC Biology, 2021, 19, 118.	1.7	22
787	A pig BodyMap transcriptome reveals diverse tissue physiologies and evolutionary dynamics of transcription. Nature Communications, 2021, 12, 3715.	5.8	60
788	Porcine models of acute kidney injury. American Journal of Physiology - Renal Physiology, 2021, 320, F1030-F1044.	1.3	10

#	Article	IF	CITATIONS
789	A DNA Regulatory Element Haplotype at Zinc Finger Genes Is Associated with Host Resilience to Small Ruminant Lentivirus in Two Sheep Populations. Animals, 2021, 11, 1907.	1.0	1
790	Long-term, multidomain analyses to identify the breed and allelic effects in MSTN-edited pigs to overcome lameness and sustainably improve nutritional meat production. Science China Life Sciences, 2022, 65, 362-375.	2.3	19
791	A porcine brain-wide RNA editing landscape. Communications Biology, 2021, 4, 717.	2.0	5
792	Interspecies chimeras as a platform for exogenic organ production and transplantation. Experimental Biology and Medicine, 2021, 246, 1838-1844.	1.1	4
793	Porcine pancreatic ductal epithelial cells transformed with KRASG12D and SV40T are tumorigenic. Scientific Reports, 2021, 11, 13436.	1.6	5
794	Different Proportions of Branched-Chain Amino Acids Modulate Lipid Metabolism in a Finishing Pig Model. Journal of Agricultural and Food Chemistry, 2021, 69, 7037-7048.	2.4	28
796	Single-cell atlas of domestic pig cerebral cortex and hypothalamus. Science Bulletin, 2021, 66, 1448-1461.	4.3	20
797	Exogenous LIN28 Is Required for the Maintenance of Self-Renewal and Pluripotency in Presumptive Porcine-Induced Pluripotent Stem Cells. Frontiers in Cell and Developmental Biology, 2021, 9, 709286.	1.8	8
798	Do Pleistocene rock paintings depict Sulawesi warty pigs (Sus celebensis) with a domestication character?. Archaeology in Oceania, 2021, 56, 149.	0.3	4
799	Accelerated deciphering of the genetic architecture of agricultural economic traits in pigs using a low-coverage whole-genome sequencing strategy. GigaScience, 2021, 10, .	3.3	34
800	Maternal lineage of Nicobari pig (<i>Sus scrofa nicobaricus</i>) correlated with migration of <i>Nicobarese</i> , a native tribal population of Andaman and Nicobar Islands, India. Animal Biotechnology, 2023, 34, 156-165.	0.7	3
801	Genome-wide scan for selection signatures based on whole-genome re-sequencing in Landrace and Yorkshire pigs. Journal of Integrative Agriculture, 2021, 20, 1898-1906.	1.7	6
802	Genome-wide analysis of genetic diversity and artificial selection in Large White pigs in Russia. PeerJ, 2021, 9, e11595.	0.9	5
803	Genome-Wide Association Study Based on Random Regression Model Reveals Candidate Genes Associated with Longitudinal Data in Chinese Simmental Beef Cattle. Animals, 2021, 11, 2524.	1.0	6
804	Human-Mediated Admixture and Selection Shape the Diversity on the Modern Swine (<i>Sus scrofa</i>) Y Chromosomes. Molecular Biology and Evolution, 2021, 38, 5051-5065.	3.5	9
805	An overview of in vitro, ex vivo and in vivo models for studying the transport of drugs across intestinal barriers. Advanced Drug Delivery Reviews, 2021, 175, 113795.	6.6	69
806	Ancient Faunal History Revealed by Interdisciplinary Biomolecular Approaches. Diversity, 2021, 13, 370.	0.7	7
807	Single Nucleotide Polymorphisms of Immunity-Related Genes and Their Effects on Immunophenotypes in Different Pig Breeds. Genes, 2021, 12, 1377.	1.0	2

ARTICLE IF CITATIONS # A Genome-Wide CRISPR/Cas9 Screen Reveals the Requirement of Host Sphingomyelin Synthase 1 for 808 1.5 9 Infection with Pseudorabies Virus Mutant gDâ€"Pass. Viruses, 2021, 13, 1574. Epigenetic clock and DNA methylation analysis of porcine models of aging and obesity. GeroScience, 809 2.1 2021, 43, 2467-2483. Sexually Dimorphic Transcriptomic Changes of Developing Fetal Brain Reveal Signaling Pathways and 810 1.8 10 Marker Genes of Brain Cells in Domestic Pigs. Cells, 2021, 10, 2439. NOD2 Genotypes Affect the Symptoms and Mortality in the Porcine Circovirus 2-Spreading Pig Population. Genes, 2021, 12, 1424. Characteristics of faecal bacterial flora and volatile fatty acids in Min pig, Landrace pig, and 812 1.2 6 Yorkshire pig. Electronic Journal of Biotechnology, 2021, 53, 33-43. Effect of dietary leucine supplementation on skeletal muscle fiber type transformation in weaning piglets. Animal Biotechnology, 2021, , 1-9. Accurate determination of meat mass fractions using DNA measurements for quantifying meat 814 1.38 adulteration by digital PCR. International Journal of Food Science and Technology, 2021, 56, 6345-6358. Swine models for translational oncological research: an evolving landscape and regulatory 1.0 considerations. Mammalian Genome, 2022, 33, 230-240. 816 The genome of the naturally evolved obesity-prone Ossabaw miniature pig. IScience, 2021, 24, 103081. 1.9 9 The Quest for Genes Involved in Adaptation to Climate Change in Ruminant Livestock. Animals, 2021, 11, 1.0 2833. Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. Cell, 2021, 818 13.5 49 184, 4874-4885.e16. Assessment of Mosaicism and Detection of Cryptic Alleles in CRISPR/Cas9-Engineered Neurofibromatosis Type 1 and TP53 Mutant Porcine Models Reveals Overlooked Challenges in Precision 1.1 Modeling of Human Diseases. Frontiers in Genetics, 2021, 12, 721045. Revisiting the evolutionary history of domestic and wild ducks based on genomic analyses. Zoological 820 0.9 13 Research, 2021, 42, 43-50. Improvement, identification, and target prediction for miRNAs in the porcine genome by using massive, 0.2 public high-throughput sequencing data. Journal of Animal Science, 2021, 99, . Integrated hybrid <i>de novo</i> assembly technologies to obtain high-quality pig genome using short 822 3.2 3 and long reads. Briefings in Bioinformatics, 2021, 22, . Decoding Coalescent Hidden Markov Models in Linear Time. Lecture Notes in Computer Science, 2014, 1.0 8394, 100-114. Ussing Chamber., 2015, , 263-273. 824 17 Genetically Engineered Large Animals in Biomedicine., 2018, , 169-214.

#	Article	IF	CITATIONS
826	Porcine cytokines, chemokines and growth factors: 2019 update. Research in Veterinary Science, 2020, 131, 266-300.	0.9	14
827	L'axe tube digestif-cerveau : avancées récentes obtenues sur un modÓle d'obésité chez le porc. De L'Academie Nationale De Medecine, 2013, 197, 1683-1699.	Bulletin 0.0	2
828	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
829	Plastic pigs and public secrets in translational neonatology in Denmark. Palgrave Communications, 2020, 6, .	4.7	1
830	Porcine endogenous retrovirus-A/C: biochemical properties of its integrase and susceptibility to raltegravir. Journal of General Virology, 2015, 96, 3124-3130.	1.3	10
845	A porcine model of phenylketonuria generated by CRISPR/Cas9 genome editing. JCI Insight, 2020, 5, .	2.3	29
847	Neonatal and infant immunity for tuberculosis vaccine development: importance of age-matched animal models. DMM Disease Models and Mechanisms, 2020, 13, .	1.2	7
848	Prediction of Altered 3′- UTR miRNA-Binding Sites from RNA-Seq Data: The Swine Leukocyte Antigen Complex (SLA) as a Model Region. PLoS ONE, 2012, 7, e48607.	1.1	15
849	A High Throughput Genotyping Approach Reveals Distinctive Autosomal Genetic Signatures for European and Near Eastern Wild Boar. PLoS ONE, 2013, 8, e55891.	1.1	27
850	A Further Look at Porcine Chromosome 7 Reveals VRTN Variants Associated with Vertebral Number in Chinese and Western Pigs. PLoS ONE, 2013, 8, e62534.	1.1	64
851	Production of Cloned Pigs with Targeted Attenuation of Gene Expression. PLoS ONE, 2013, 8, e64613.	1.1	11
852	Identification of the Porcine XIST Gene and Its Differential CpG Methylation Status in Male and Female Pig Cells. PLoS ONE, 2013, 8, e73677.	1.1	9
853	Genome-Wide Estimates of Coancestry and Inbreeding in a Closed Herd of Ancient Iberian Pigs. PLoS ONE, 2013, 8, e78314.	1.1	43
854	Single Intraperitoneal Injection of Monocrotaline as a Novel Large Animal Model of Chronic Pulmonary Hypertension in Tibet Minipigs. PLoS ONE, 2013, 8, e78965.	1.1	9
855	NHE Isoform Switching and KChIP2 Upregulation in Aging Porcine Atria. PLoS ONE, 2013, 8, e82951.	1.1	2
856	Enhancing Genome-Wide Copy Number Variation Identification by High Density Array CGH Using Diverse Resources of Pig Breeds. PLoS ONE, 2014, 9, e87571.	1.1	36
857	A Draft De Novo Genome Assembly for the Northern Bobwhite (Colinus virginianus) Reveals Evidence for a Rapid Decline in Effective Population Size Beginning in the Late Pleistocene. PLoS ONE, 2014, 9, e90240.	1.1	34
858	Contemporary Genetic Structure, Phylogeography and Past Demographic Processes of Wild Boar Sus scrofa Population in Central and Eastern Europe. PLoS ONE, 2014, 9, e91401.	1.1	33

#	Article	IF	CITATIONS
859	Frequent Loss and Alteration of the MOXD2 Gene in Catarrhines and Whales: A Possible Connection with the Evolution of Olfaction. PLoS ONE, 2014, 9, e104085.	1.1	7
860	A Genome-Wide Association Study Reveals Dominance Effects on Number of Teats in Pigs. PLoS ONE, 2014, 9, e105867.	1.1	59
861	A Deep Catalog of Autosomal Single Nucleotide Variation in the Pig. PLoS ONE, 2015, 10, e0118867.	1.1	22
862	CRISPR/Cas9 as Tool for Functional Study of Genes Involved in Preimplantation Embryo Development. PLoS ONE, 2015, 10, e0120501.	1.1	14
863	piRNAs from Pig Testis Provide Evidence for a Conserved Role of the Piwi Pathway in Post-Transcriptional Gene Regulation in Mammals. PLoS ONE, 2015, 10, e0124860.	1.1	48
864	The Porcine TSPY Gene Is Tricopy but Not a Copy Number Variant. PLoS ONE, 2015, 10, e0131745.	1.1	5
865	De Novo Transcriptome Assembly of the Chinese Swamp Buffalo by RNA Sequencing and SSR Marker Discovery. PLoS ONE, 2016, 11, e0147132.	1.1	43
866	Identification of Copy Number Variations in Xiang and Kele Pigs. PLoS ONE, 2016, 11, e0148565.	1.1	31
867	The Intestinal Eukaryotic Virome in Healthy and Diarrhoeic Neonatal Piglets. PLoS ONE, 2016, 11, e0151481.	1.1	28
868	Consequences of Epistasis on Growth in an Erhualian × White Duroc Pig Cross. PLoS ONE, 2017, 12, e0162045.	1.1	5
869	Joint Profiling of miRNAs and mRNAs Reveals miRNA Mediated Gene Regulation in the Göttingen Minipig Obesity Model. PLoS ONE, 2016, 11, e0167285.	1.1	14
870	β2-microglobulin gene duplication in cetartiodactyla remains intact only in pigs and possibly confers selective advantage to the species. PLoS ONE, 2017, 12, e0182322.	1.1	8
871	Biomarkers for tissue engineering of the tendon-bone interface. PLoS ONE, 2018, 13, e0189668.	1.1	23
872	Genome-wide analysis reveals selection for Chinese Rongchang pigs. Frontiers of Agricultural Science and Engineering, 2017, 4, 319.	0.9	2
873	Base editing in pigs for precision breeding. Frontiers of Agricultural Science and Engineering, 2020, 7, 161.	0.9	6
874	Integrated analysis of mRNA and miRNA expression profiles in livers of Yimeng black pigs with extreme phenotypes for backfat thickness. Oncotarget, 2017, 8, 114787-114800.	0.8	9
875	Importance of genomic research in studying the history of development of domestic animals. Molekuliarnaia Genetika, Mikrobiologiia I Virusologiia, 2016, 34, 123.	0.1	1
876	Endogenous Retroviruses in Domestic Animals. Current Genomics, 2014, 15, 256-265.	0.7	16

	CITATION	LEPURT	
#	Article	IF	CITATIONS
877	The Challenge of Genome Sequence Assembly. Open Bioinformatics Journal, 2018, 11, 231-239.	1.0	4
878	å^©ç""基å›ç»"å¦å'Œè½¬å½•组å¦å^†æžæŒ–æŽ~与å·′马香猪早熟相å³çš"候选基å›. Zoolo	gica d. Rese	arch,92018, 3
879	Constructing Proteome Reference Map of the Porcine Jejunal Cell Line (IPEC-J2) by Label-Free Mass Spectrometry. Journal of Microbiology and Biotechnology, 2016, 26, 1124-1131.	0.9	3
880	Use of genetically-engineered pig donors in islet transplantation. World Journal of Transplantation, 2015, 5, 243.	0.6	24
881	Computational Prediction of Alzheimer's and Parkinson's Disease MicroRNAs in Domestic Animals. Asian-Australasian Journal of Animal Sciences, 2016, 29, 782-792.	2.4	3
882	Genome analysis of Yucatan miniature pigs to assess their potential as biomedical model animals. Asian-Australasian Journal of Animal Sciences, 2019, 32, 290-296.	2.4	11
883	Analysis of allele-specific expression using RNA-seq of the Korean native pig and Landrace reciprocal cross. Asian-Australasian Journal of Animal Sciences, 2019, 32, 1816-1825.	2.4	5
884	Characterization of PSPA Cell Differentiation,an Established Pig Preadipocyte Cell Line as an In Vitro Model for Pig Fat Development. Japan Agricultural Research Quarterly, 2015, 49, 85-90.	0.1	3
885	Freeze-thaw decellularization of the trabecular meshwork in an <i>ex vivo</i> eye perfusion model. PeerJ, 2017, 5, e3629.	0.9	26
886	Divergent and convergent evolution of housekeeping genes in human–pig lineage. PeerJ, 2018, 6, e4840.	0.9	19
887	Genes of the pig, <i>Sus scrofa</i> , reconstructed with EvidentialGene. PeerJ, 2019, 7, e6374.	0.9	40
888	An association analysis between a polymorphism in the SEC24A gene and lipid traits recorded in Duroc pigs. Italian Journal of Animal Science, 2021, 20, 1444-1451.	0.8	0
889	A Deeper Insight into Evolutionary Patterns and Phylogenetic History of ASFV Epidemics in Sardinia (Italy) through Extensive Genomic Sequencing. Viruses, 2021, 13, 1994.	1.5	15
890	Detecting the selection signatures in Chinese Duroc,Landrace, Yorkshire, Liangshan, and Qingyu pigs. Functional and Integrative Genomics, 2021, 21, 655-664.	1.4	4
891	First Genomic Evidence of Dual African Swine Fever Virus Infection: Case Report from Recent and Historical Outbreaks in Sardinia. Viruses, 2021, 13, 2145.	1.5	4
892	Single-step genomic evaluation with metafounders for feed conversion ratio and average daily gain in Danish Landrace and Yorkshire pigs. Genetics Selection Evolution, 2021, 53, 79.	1.2	5
893	Generation of pig primary fibroblast cells harboring defective <i>MC</i> 4R genes by <i>N</i> -ethyl- <i>N</i> -nitrosourea mutagenesis: A gene-driven, nontransgenic approach to pig improvement. American Journal of Molecular Biology, 2013, 03, 139-147.	0.1	0
894	Advanced Technologies and Agriculture: Genomics, Nanotechnology, and Beyond. , 2014, , 274-288.		0

#	Article	IF	CITATIONS
895	Genomics of Food Animals. , 2014, , 433-453.		0
896	Diversification of Southeast Asian mammals during the Quaternary glaciation: insights from the genomic era. Biodiversity Science, 2014, 22, 40.	0.2	0
899	Current knowledge and future prospect of the genome structure analysis of immune-related genes in swine Journal of Animal Genetics, 2015, 43, 13-23.	0.5	0
900	Current Status of Cattle Genome Sequencing and Analysis using Next Generation Sequencing. Journal of Life Science, 2015, 25, 349-356.	0.2	2
901	Genetic diversity of domestic pigs in Tierralta (Colombia) using microsatellites. Revista Colombiana De Ciencias Pecuarias, 2015, 28, .	0.4	0
904	A data filtering to utilizing Human Methylation arrays in genome-wide study of bovine DNA methylation. Journal of Animal Genetics, 2016, 44, 45-52.	0.5	3
905	Strategies to avoid drowning in the deep sequencing data flood. Animal Reproduction, 2016, 13, 153-159.	0.4	0
913	Polymorphism in the intron 20 of porcine O-linked N-acetylglucosamine transferase. Asian-Australasian Journal of Animal Sciences, 2017, 30, 1086-1092.	2.4	1
925	A Study on the Conceptual Composition Scale Development for the Prevention of Child Abuse and PR Communication Strategy. Journal of Public Relations, 2018, 22, 30-69.	0.2	0
927	In silico approaches to discover the functional impact of non-synonymous single nucleotide polymorphisms in selective sweep regions of the Landrace genome. Asian-Australasian Journal of Animal Sciences, 2018, 31, 1980-1990.	2.4	0
928	Development and Genome Sequence of a Laboratory-Inbred Miniature Pig Facilitate Study of Human Diabetic Disease. SSRN Electronic Journal, 0, , .	0.4	0
929	Progress in plant genome sequencing: research directions. Vavilovskii Zhurnal Genetiki I Selektsii, 2019, 23, 38-48.	0.4	4
930	Detection of genome-wide structural variations in the Shanghai Holstein cattle population using next-generation sequencing. Asian-Australasian Journal of Animal Sciences, 2019, 32, 320-333.	2.4	3
931	Pigs as model systems for biomedical research. Bioscientifica Proceedings, 0, , .	1.0	1
938	Confirmation of differentiation clusters' and endoglin markers preset in porcine buccal mucosa cells. Medical Journal of Cell Biology (discontinued), 2020, 8, 118-123.	0.2	0
939	Animal Models in Toxicologic Research: Pig. , 2022, , 751-776.		0
940	Locus-specific analysis of DNA methylation patterns in cloned and <i>in vitro</i> fertilized porcine embryos. Journal of Reproduction and Development, 2020, 66, 505-514.	0.5	4
941	Tools for Molecular Studies in Xenotransplantation. Methods in Molecular Biology, 2020, 2110, 27-45.	0.4	0

		CITATION REPO	RT	
#	Article	IF		Citations
944	Comparative genomic analysis of eutherian interferon genes. Genomics, 2020, 112, 4749-42	759. 1.	3	2
946	Advancing swine models for human health and diseases. Missouri Medicine, 2013, 110, 212	-5. 0.	.3	35
947	Evolutionary and Functional Analysis of Korean Native Pig Using Single Nucleotide Polymorp Molecules and Cells, 2020, 43, 728-738.	hisms. 1.	0	0
948	Longâ€read assembly of the Chinese indigenous Ningxiang pig genome and identification of variations in fat metabolism among different breeds. Molecular Ecology Resources, 2022, 22	genetic 2, 1508-1520. 2.	2	9
949	Coarse root distribution of Vatica pauciflora (Korth.) Blume in different soil slopes as reveale root detector. IOP Conference Series: Earth and Environmental Science, 2021, 918, 012046	d by o.	.2	2
950	The genome variation and developmental transcriptome maps reveal genetic differentiation muscle in pigs. PLoS Genetics, 2021, 17, e1009910.	of skeletal 1.	5	22
951	circRNAome profiling reveals circFgfr2 regulates myogenesis and muscle regeneration via a loop. Journal of Cachexia, Sarcopenia and Muscle, 2022, 13, 696-712.	eedback 2.	.9	28
952	Importance of the pig as a human biomedical model. Science Translational Medicine, 2021,	13, eabd5758. 5.	8	234
953	Aptamer-based factor IXa inhibition preserves hemostasis and prevents thrombosis in a pigle ECMO. Molecular Therapy - Nucleic Acids, 2022, 27, 524-534.	t model of 2.	3	5
954	Analysis Polyadenylation Signal Usage in Sus scrofa. Animals, 2022, 12, 194.	1.	0	1
955	Transcriptome and Metabolome Integration Provides New Insights Into the Regulatory Netw Tibetan Pig Alveolar Type II Epithelial Cells in Response to Hypoxia. Frontiers in Genetics, 202 812411.	orks of 22, 13, 1.	1	5
956	Targeted myostatin loss-of-function mutation increases type II muscle fibers in Meishan pigs of Integrative Agriculture, 2022, 21, 188-198.	. Journal 1.	7	5
957	Genetic Diversity, Admixture and Analysis of Homozygous-by-Descent (HBD) Segments of R Boar. Biology, 2022, 11, 203.	ussian Wild 1.	3	2
958	Metabolic programming in the offspring after gestational overfeeding in the mother: toward neonatal rescuing with metformin in a swine model. International Journal of Obesity, 2022, 4 1018-1026.	16, 1.	6	3
959	What does the PERV copy number tell us?. Xenotransplantation, 2022, 29, e12732.	1.	6	2
961	Large Animal Models of Breast Cancer. Frontiers in Oncology, 2022, 12, 788038.	1.	3	13
962	Foundations of Molecular Genetics: From Major Genes to Genomics. , 2022, , 1-12.			0
963	Adaptive Cellular Immunity against African Swine Fever Virus Infections. Pathogens, 2022, 1	1, 274. 1.	2	21

		TATION REPORT	
#	Article	IF	Citations
964	Experimental Nuclear Medicine Meets Tumor Biology. Pharmaceuticals, 2022, 15, 227.	1.7	4
965	Limited environmental stability of infectious porcine endogenous retrovirus type C; Usage of reverse transcriptase in combination with viral RNA as markers for infectious virus. Xenotransplantation, 2022, , e12738.	1.6	1
966	Comparison of the choice of animals for re-sequencing in two maternal pig lines. Genetics Selection Evolution, 2022, 54, 16.	1.2	1
967	Revisiting the Evolutionary History of Pigs via De Novo Mutation Rate Estimation in A Three-generation Pedigree. Genomics, Proteomics and Bioinformatics, 2022, 20, 1040-1052.	3.0	9
968	Comparative Transcriptome Analysis Provides Insight into Spatio-Temporal Expression Characteristics and Genetic Regulatory Network in Postnatal Developing Subcutaneous and Visceral Fat of Bama Pig. Frontiers in Genetics, 2022, 13, 844833.	. 1.1	4
969	Genomeâ€wide analysis suggests multiple domestication events of Chinese local pigs. Animal Genetic 2022, 53, 293-306.	cs, 0.6	5
970	Insights on the historical biogeography of Philippine domestic pigs and its relationship with continental domestic pigs and wild boars. PLoS ONE, 2022, 17, e0254299.	1.1	7
971	The de novo assembly of a European wild boar genome revealed unique patterns of chromosomal structural variations and segmental duplications. Animal Genetics, 2022, 53, 281-292.	0.6	6
972	The transcriptome from asexual to sexual in vitro development of Cystoisospora suis (Apicomplexa:) ⁻	[j ETQq0 0 0 rgBT /0	Dverlock 10 Tf
973	Comparison of the Effects of Inorganic or Amino Acid-Chelated Zinc on Mouse Myoblast Growth in vitro and Growth Performance and Carcass Traits in Growing-Finishing Pigs. Frontiers in Nutrition, 2022, 9, 857393.	1.6	6
974	AMG487 inhibits PRRSV replication and ameliorates lung injury in pig lung xenografts by down-regulating the expression of ANXA2. Antiviral Research, 2022, 202, 105314.	1.9	4
975	Sequence polymorphisms of PR39 cathelicidins and extensive copy variations in commercial pig breed Gene, 2022, 822, 146323.	ls. 1.0	2
976	Ancient DNA reveals the maternal genetic history of East Asian domestic pigs. Journal of Genetics and Genomics, 2022, 49, 537-546.	1.7	4
977	Scan of the endogenous retrovirus sequences across the swine genome and survey of their copy number variation and sequence diversity among various Chinese and Western pig breeds. Zoological Research, 2022, 43, 423-441.	0.9	5
978	Chloride channel accessory 1 gene deficiency causes selective loss of mucus production in a new pig model. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2022, 322, L842-L85	2. ^{1.3}	5
979	Gene Cloning, Tissue Expression Profiles and Antiviral Activities of Interferon-β from Two Chinese Miniature Pig Breeds. Veterinary Sciences, 2022, 9, 190.	0.6	1
980	Genomic consequences of a century of inbreeding and isolation in the Danish wild boar population. Evolutionary Applications, 2022, 15, 954-966.	1.5	0
1033	Genomic Prediction Methods Accounting for Nonadditive Genetic Effects. Methods in Molecular Biology, 2022, 2467, 219-243.	0.4	3

#	Article	IF	CITATIONS
1035	Qualitative Attributes of Commercial Pig Meat from an Italian Native Breed: The Nero d'Abruzzo. Foods, 2022, 11, 1297.	1.9	4
1036	3D chromatin remodelling in the germ line modulates genome evolutionary plasticity. Nature Communications, 2022, 13, 2608.	5.8	10
1037	From bats to pangolins: new insights into species differences in the structure and function of the immune system. Innate Immunity, 2022, 28, 107-121.	1.1	4
1039	Nonsense Mutations in Eukaryotes. Biochemistry (Moscow), 2022, 87, 400-412.	0.7	1
1040	Comparative and quantitative morphology of the pig and wild boar cerebellum for identifying possible effects of domestication. Annals of Anatomy, 2022, , 151957.	1.0	0
1042	Association Studies and Genomic Prediction for Genetic Improvements in Agriculture. Frontiers in Plant Science, 2022, 13, .	1.7	2
1043	Microfluidic and Static Organotypic Culture Systems to Support Ex Vivo Spermatogenesis From Prepubertal Porcine Testicular Tissue: A Comparative Study. Frontiers in Physiology, 2022, 13, .	1.3	5
1044	The Visayan Warty Pig (<i>Sus cebifrons</i>) Genome Provides Insight Into Chromosome Evolution and Sensory Adaptation in Pigs. Molecular Biology and Evolution, 2022, 39, .	3.5	3
1045	Integrated Omics Analysis Reveals Alterations in the Intestinal Microbiota and Metabolites of Piglets After Starvation. Frontiers in Microbiology, 0, 13, .	1.5	0
1046	Population structure of 3907 worldwide pigs and the introgression of Chinese indigenous pigs by European pigs. Animal Genetics, 2022, 53, 599-612.	0.6	2
1047	Functional genomics of reproduction in pigs: Are we there yet?. Molecular Reproduction and Development, 2023, 90, 436-444.	1.0	1
1048	Maternal and Fetal Bile Acid Homeostasis Regulated by Sulfated Progesterone Metabolites through FXR Signaling Pathway in a Pregnant Sow Model. International Journal of Molecular Sciences, 2022, 23, 6496.	1.8	5
1049	Detection of non-reference porcine endogenous retrovirus loci in the Vietnamese native pig genome. Scientific Reports, 2022, 12, .	1.6	2
1050	Endothelial cell heterogeneity and microglia regulons revealed by a pig cell landscape at single-cell level. Nature Communications, 2022, 13, .	5.8	22
1051	The Boar War: Five Hot Factors Unleashing Boar Expansion and Related Emergency. Land, 2022, 11, 887.	1.2	17
1052	Warthog Genomes Resolve an Evolutionary Conundrum and Reveal Introgression of Disease Resistance Genes. Molecular Biology and Evolution, 2022, 39, .	3.5	11
1053	Imputation of Ancient Whole Genome Sus scrofa DNA Introduces Biases Toward Main Population Components in the Reference Panel. Frontiers in Genetics, 0, 13, .	1.1	3
1054	Comparative transcriptome analysis on the mangrove Acanthus ilicifolius and its two terrestrial relatives provides insights into adaptation to intertidal habitats. Gene, 2022, 839, 146730.	1.0	3

#	Article	IF	CITATIONS
1055	Determination of the genetic structure of pro-maternal pig breeds of Irish selection using mitochondrial DNA markers. The Animal Biology, 2022, 24, 3-8.	0.2	1
1057	Transcriptomics of meat quality. , 2022, , 337-391.		0
1058	Origin, evolution, and tissue-specific functions of the porcine repetitive element 1. Genetics Selection Evolution, 2022, 54, .	1.2	0
1060	Current Trends, Advances, and Challenges of Tissue Engineering-Based Approaches of Tooth Regeneration: A Review of the Literature. Current Stem Cell Research and Therapy, 2024, 19, 473-496.	0.6	2
1061	Progress and opportunities through use of genomics in animal production. Trends in Genetics, 2022, 38, 1228-1252.	2.9	5
1062	Evolutionary insights into porcine genomic structural variations based on a novelâ€constructed dataset from 24 worldwide diverse populations. Evolutionary Applications, 2022, 15, 1264-1280.	1.5	4
1063	Temperature acclimation in hot-spring snakes and the convergence of cold response. Innovation(China), 2022, 3, 100295.	5.2	5
1064	Mechanisms and strategies to promote cardiac xenotransplantation. Journal of Molecular and Cellular Cardiology, 2022, 172, 109-119.	0.9	5
1065	Long-range interaction within the chromatin domain determines regulatory patterns in porcine skeletal muscle. Genomics, 2022, 114, 110482.	1.3	1
1066	Epigenetics of Livestock Health, Production, and Breeding. , 2023, , 569-610.		1
			1
1067	Wild Boar Sus scrofa Linnaeus, 1758. Handbook of the Mammals of Europe, 2022, , 1-27.	0.1	3
1067 1068	Wild Boar Sus scrofa Linnaeus, 1758. Handbook of the Mammals of Europe, 2022, , 1-27. CRISPR/Cas-edited pigs for personalized medicine: more than preclinical test-system. Research Results in Pharmacology, 2022, 8, 87-98.	0.1	3
1067 1068 1069	Wild Boar Sus scrofa Linnaeus, 1758. Handbook of the Mammals of Europe, 2022, , 1-27. CRISPR/Cas-edited pigs for personalized medicine: more than preclinical test-system. Research Results in Pharmacology, 2022, 8, 87-98. The Role of the Environment in Shaping the Genomic Variation in an Insular Wild Boar Population. Diversity, 2022, 14, 774.	0.1 0.1 0.7	1 3 1 0
1067 1068 1069 1070	Wild Boar Sus scrofa Linnaeus, 1758. Handbook of the Mammals of Europe, 2022, , 1-27. CRISPR/Cas-edited pigs for personalized medicine: more than preclinical test-system. Research Results in Pharmacology, 2022, 8, 87-98. The Role of the Environment in Shaping the Genomic Variation in an Insular Wild Boar Population. Diversity, 2022, 14, 774. Current in Vitro and Animal Models for Understanding Foods: Human Gut–Microbiota Interactions. Journal of Agricultural and Food Chemistry, 2022, 70, 12733-12745.	0.1 0.1 0.7 2.4	1 3 1 0 5
1067 1068 1069 1070	Wild Boar Sus scrofa Linnaeus, 1758. Handbook of the Mammals of Europe, 2022, , 1-27. CRISPR/Cas-edited pigs for personalized medicine: more than preclinical test-system. Research Results in Pharmacology, 2022, 8, 87-98. The Role of the Environment in Shaping the Genomic Variation in an Insular Wild Boar Population. Diversity, 2022, 14, 774. Current in Vitro and Animal Models for Understanding Foods: Human Gut〓Microbiota Interactions. Journal of Agricultural and Food Chemistry, 2022, 70, 12733-12745. Evolution of the ancestral mammalian karyotype and syntenic regions. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	0.1 0.1 0.7 2.4 3.3	1 3 1 0 5 27
1067 1068 1069 1070 1071	Wild Boar Sus scrofa Linnaeus, 1758. Handbook of the Mammals of Europe, 2022, , 1-27. CRISPR/Cas-edited pigs for personalized medicine: more than preclinical test-system. Research Results in Pharmacology, 2022, 8, 87-98. The Role of the Environment in Shaping the Genomic Variation in an Insular Wild Boar Population. Diversity, 2022, 14, 774. Current in Vitro and Animal Models for Understanding Foods: Human Gut–Microbiota Interactions. Journal of Agricultural and Food Chemistry, 2022, 70, 12733-12745. Evolution of the ancestral mammalian karyotype and syntenic regions. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . Current approaches for the regeneration and reconstruction of ocular surface in dry eye. Frontiers in Medicine, 0, 9, .	0.1 0.1 0.7 2.4 3.3	1 3 1 0 5 27 1
1067 1068 1069 1070 1071 1072	Wild Boar Sus scrofa Linnaeus, 1758. Handbook of the Mammals of Europe, 2022, , 1-27. CRISPR/Cas-edited pigs for personalized medicine: more than preclinical test-system. Research Results in Pharmacology, 2022, 8, 87-98. The Role of the Environment in Shaping the Genomic Variation in an Insular Wild Boar Population. Diversity, 2022, 14, 774. Current in Vitro and Animal Models for Understanding Foods: Human Gut〓Microbiota Interactions. Journal of Agricultural and Food Chemistry, 2022, 70, 12733-12745. Evolution of the ancestral mammalian karyotype and syntenic regions. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . Current approaches for the regeneration and reconstruction of ocular surface in dry eye. Frontiers in Medicine, 0, 9, . Integration of multi-omics data reveals cis-regulatory variants that are associated with phenotypic differentiation of eastern from western pigs. Genetics Selection Evolution, 2022, 54, .	0.1 0.1 0.7 2.4 3.3 1.2 1.2	1 3 1 0 5 27 1 9

#	Article	IF	CITATIONS
1076	Comparative genomics of <i>Sarcoptes scabiei</i> provide new insights into adaptation to permanent parasitism and withinâ€host species divergence. Transboundary and Emerging Diseases, 2022, 69, 3468-3484.	1.3	4
1077	Effects of iron deficiency and iron supplementation at the host-microbiota interface: Could a piglet model unravel complexities of the underlying mechanisms?. Frontiers in Nutrition, 0, 9, .	1.6	3
1078	Exploring differentially expressed genes related to metabolism by RNA-Seq in porcine embryonic fibroblast after insulin treatment. Journal of Veterinary Science, 0, 23, .	0.5	0
1079	Genomeâ€wide association study and genomic prediction for intramuscular fat content in Suhuai pigs using imputed wholeâ€genome sequencing data. Evolutionary Applications, 2022, 15, 2054-2066.	1.5	4
1080	Transcriptome-Wide IncRNA and mRNA Profiling of Spleens from Meishan Pigs at Different Development Stages. Animals, 2022, 12, 2676.	1.0	1
1081	Current Analytical Methods and Research Trends Are Used to Identify Domestic Pig and Wild Boar DNA in Meat and Meat Products. Genes, 2022, 13, 1825.	1.0	2
1082	Gut microbiota involved in desulfation of sulfated progesterone metabolites: A potential regulation pathway of maternal bile acid homeostasis during pregnancy. Frontiers in Microbiology, 0, 13, .	1.5	1
1083	Introduced, Mixed, and Peripheral: Conservation of Mitochondrial-DNA Lineages in the Wild Boar (Sus) Tj ETQq1 1	0.784314	l ggBT /Ov <mark>e</mark> r
1084	De Novo Transcriptome Dataset Generation of the Swamp Buffalo Brain and Non-Brain Tissues. BioMed Research International, 2022, 2022, 1-15.	0.9	1
1085	Lost pigs of Angola: Whole genome sequencing reveals unique regions of selection with emphasis on metabolism and feed efficiency. Frontiers in Genetics, 0, 13, .	1.1	0
1086	Genetic architecture and selection of Anhui autochthonous pig population revealed by whole genome resequencing. Frontiers in Genetics, 0, 13, .	1.1	6
1088	Foundations of Molecular Genetics: From Major Genes to Genomics. , 2023, , 51-62.		0
1089	Understanding Mendelian errors in SNP arrays data using a Gochu Asturcelta pig pedigree: genomic alterations, family size and calling errors. Scientific Reports, 2022, 12, .	1.6	5
1090	Polymorphisms in Pattern Recognition Receptor Genes Are Associated with Respiratory Disease Severity in Pig Farms. Animals, 2022, 12, 3163.	1.0	1
1091	A Naturally Occurring Microhomology-Mediated Deletion of Three Genes in African Swine Fever Virus Isolated from Two Sardinian Wild Boars. Viruses, 2022, 14, 2524.	1.5	1
1092	The Innovative Informatics Approaches of High-Throughput Technologies in Livestock: Spearheading the Sustainability and Resiliency of Agrigenomics Research. Life, 2022, 12, 1893.	1.1	0
1093	Population Structure and Selection Signatures Underlying Domestication Inferred from Genome-Wide Copy Number Variations in Chinese Indigenous Pigs. Genes, 2022, 13, 2026.	1.0	2
1094	Segregation patterns and inheritance rate of copy number variations regions assessed in a Gochu Asturcelta pig pedigree. Gene, 2023, 854, 147111.	1.0	2

#	Article	IF	CITATIONS
1095	African Suid Genomes Provide Insights into the Local Adaptation to Diverse African Environments. Molecular Biology and Evolution, 2022, 39, .	3.5	9
1096	Humanising and dehumanising pigs in genomic and transplantation research. History and Philosophy of the Life Sciences, 2022, 44, .	0.6	7
1097	Assessing Population Structure and Signatures of Selection in Wanbei Pigs Using Whole Genome Resequencing Data. Animals, 2023, 13, 13.	1.0	4
1098	Genome Editing and Protein Energy Malnutrition. Advances in Experimental Medicine and Biology, 2023, , 215-232.	0.8	0
1099	Risks of Infectious Disease in Xenotransplantation. New England Journal of Medicine, 2022, 387, 2258-2267.	13.9	20
1102	Principles of 3D chromosome folding and evolutionary genome reshuffling in mammals. Cell Reports, 2022, 41, 111839.	2.9	10
1103	LncPLAAT3-AS Regulates PLAAT3-Mediated Adipocyte Differentiation and Lipogenesis in Pigs through miR-503-5p. Genes, 2023, 14, 161.	1.0	4
1104	Distinct traces of mixed ancestry in western commercial pig genomes following gene flow from Chinese indigenous breeds. Frontiers in Genetics, 0, 13, .	1.1	3
1105	Adult porcine (<i>Sus scrofa</i>) derived inner ear cells: Characteristics in inâ€vitro cultures. Anatomical Record, 2023, 306, 2119-2134.	0.8	0
1106	Spatial genetic structure of European wild boar, with inferences on late-Pleistocene and Holocene demographic history. Heredity, 2023, 130, 135-144.	1.2	5
1108	242. Genetic characterization of endangered indigenous pigs of Angola. , 2022, , .		0
1109	Genetic relationships of the Yucatan black hairless pig with Iberian breeds using single nucleotide polymorfisms. Brazilian Journal of Veterinary Research and Animal Science, 0, 60, e195697.	0.2	0
1110	Population differentiated copy number variation between Eurasian wild boar and domesticated pig populations. Scientific Reports, 2023, 13, .	1.6	0
1111	RNA-seq transcriptome profiling of pigs' liver in response to diet with different sources of fatty acids. Frontiers in Genetics, 0, 14, .	1.1	3
1112	Integrative single-cell RNA-seq and ATAC-seq analysis of myogenic differentiation in pig. BMC Biology, 2023, 21, .	1.7	9
1113	The Pig Community and Their Reference Genome. , 2023, , 159-201.		0
1114	Mitochondrial DNA Deficiency and Supplementation in Sus scrofa Oocytes Influence Transcriptome Profiles in Oocytes and Blastocysts. International Journal of Molecular Sciences, 2023, 24, 3783.	1.8	3
1116	Integrated analysis of methylation profiles and transcriptome of Marek's disease virus-infected chicken spleens reveal hypomethylation of CD4 and HMGB1 genes might promote Marek's disease tumorigenesis. Poultry Science, 2023, 102, 102594.	1.5	0

#	Article	IF	CITATIONS
1119	Inner Retinal Changes in Acute Experimental BRVO Treated With Bevacizumab or Triamcinolone Acetonide. Translational Vision Science and Technology, 2023, 12, 11.	1.1	0
1121	Transcriptomics and Selection Pressure Analysis Reveals the Influence Mechanism of PLIN1 Protein on the Development of Small Size in Min Pigs. International Journal of Molecular Sciences, 2023, 24, 3947.	1.8	1
1122	Novel Haplotype in the HHEX Gene Promoter Associated with Body Length in Pigs. Genes, 2023, 14, 511.	1.0	1
1123	Screening of candidate genes related to differences in growth and development between Chinese indigenous and Western pig breeds. Physiological Genomics, 2023, 55, 147-153.	1.0	3
1124	Detection of Genetic Differences between Holstein and Iranian North-West Indigenous Hybrid Cattles using Genomic Data. Research on Animal Production, 2022, 13, 175-186.	0.2	0
1125	Making Reference Genomes Useful: Annotation. , 2023, , 205-254.		0
1126	Spontaneous Sepsis in Adult Horses: From Veterinary to Human Medicine Perspectives. Cells, 2023, 12, 1052.	1.8	0
1127	Expression analysis of m6A-related genes in various tissues of Meishan pigs at different developmental stages. Revista Brasileira De Zootecnia, 2023, 52, .	0.3	0
1128	Methylation Genome-Wide Profiling in Lowly and Highly Efficient Somatic Cell Nuclear Transfer in Pigs. Applied Sciences (Switzerland), 2023, 13, 4798.	1.3	0
1135	Gentechnisch verÄ ¤ derte Großtiere in der Biomedizin. , 2023, , 189-239.		0
1147	Genomics for Sustainable Cured Pork Supply Chain. CSR, Sustainability, Ethics & Governance, 2023, , 51-72.	0.2	0
1151	Genome-Wide Copy Number Variation and Structural Variation: A Novel Tool for Improved Livestock Genomic Selection. Livestock Diseases and Management, 2023, , 75-88.	0.5	0
1156	Dangerous Viral Pathogens of Animal Origin: Risk and Biosecurity. , 2023, , 1563-1611.		0
1181	Protection of Cellular Antigens from Xenoreactive Responses as Overcoming Strategies. , 2024, , 189-218.		0
1182	Genome Editing and Transgenes in Pigs. , 2024, , 295-306.		0
1186	Tissue-based inÂvitro and exÂvivo models for intestinal permeability studies. , 2024, , 309-346.		0