

# Alan L Archibald

## List of Publications by Year in descending order

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155  
papers

12,314  
citations

26630

56  
h-index

28297

105  
g-index

172  
all docs

172  
docs citations

172  
times ranked

10336  
citing authors

#	ARTICLE	IF	CITATIONS
1	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	27.8	1,190
2	A regulatory mutation in IGF2 causes a major QTL effect on muscle growth in the pig. <i>Nature</i> , 2003, 425, 832-836.	27.8	791
3	Design of a High Density SNP Genotyping Assay in the Pig Using SNPs Identified and Characterized by Next Generation Sequencing Technology. <i>PLoS ONE</i> , 2009, 4, e6524.	2.5	568
4	Strong signatures of selection in the domestic pig genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19529-19536.	7.1	548
5	The PiGMap consortium linkage map of the pig ( <i>Sus scrofa</i> ). <i>Mammalian Genome</i> , 1995, 6, 157-175.	2.2	475
6	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	12.6	436
7	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015, 16, 57.	8.8	331
8	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. <i>PLoS Pathogens</i> , 2017, 13, e1006206.	4.7	282
9	Signatures of Diversifying Selection in European Pig Breeds. <i>PLoS Genetics</i> , 2013, 9, e1003453.	3.5	228
10	Development and validation of a high density SNP genotyping array for Atlantic salmon ( <i>Salmo salar</i> ). <i>BMC Genomics</i> , 2014, 15, 90.	2.8	219
11	A high resolution atlas of gene expression in the domestic sheep ( <i>Ovis aries</i> ). <i>PLoS Genetics</i> , 2017, 13, e1006997.	3.5	210
12	Structural and functional annotation of the porcine immunome. <i>BMC Genomics</i> , 2013, 14, 332.	2.8	203
13	A gene expression atlas of the domestic pig. <i>BMC Biology</i> , 2012, 10, 90.	3.8	199
14	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020, 9, .	6.4	187
15	The sheep genome reference sequence: a work in progress. <i>Animal Genetics</i> , 2010, 41, 449-453.	1.7	173
16	Somatic Cell Nuclear Transfer in the Pig: Control of Pronuclear Formation and Integration with Improved Methods for Activation and Maintenance of Pregnancy <sup>1</sup> . <i>Biology of Reproduction</i> , 2002, 66, 642-650.	2.7	165
17	Exome Sequencing: Current and Future Perspectives. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1543-1550.	1.8	165
18	A high density recombination map of the pig reveals a correlation between sex-specific recombination and GC content. <i>BMC Genomics</i> , 2012, 13, 586.	2.8	150

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19	A large duplication associated with dominant white color in pigs originated by homologous recombination between LINE elements flanking KIT. <i>Mammalian Genome</i> , 2002, 13, 569-577.	2.2	149
20	Pigs Lacking the Scavenger Receptor Cysteine-Rich Domain 5 of CD163 Are Resistant to Porcine Reproductive and Respiratory Syndrome Virus 1 Infection. <i>Journal of Virology</i> , 2018, 92, .	3.4	149
21	Cosegregation of porcine malignant hyperthermia and a probable causal mutation in the skeletal muscle ryanodine receptor gene in backcross families. <i>Genomics</i> , 1991, 11, 744-750.	2.9	147
22	Pig Bone Marrow-Derived Macrophages Resemble Human Macrophages in Their Response to Bacterial Lipopolysaccharide. <i>Journal of Immunology</i> , 2012, 188, 3382-3394.	0.8	147
23	Comparative Genome Organization of Vertebrates. <i>Mammalian Genome</i> , 1996, 7, 717-734.	2.2	146
24	Genome sequencing reveals fine scale diversification and reticulation history during speciation in <i>Sus</i> . <i>Genome Biology</i> , 2013, 14, R107.	9.6	137
25	Pig genome sequence - analysis and publication strategy. <i>BMC Genomics</i> , 2010, 11, 438.	2.8	132
26	A high utility integrated map of the pig genome. <i>Genome Biology</i> , 2007, 8, R139.	9.6	130
27	Normalized long read RNA sequencing in chicken reveals transcriptome complexity similar to human. <i>BMC Genomics</i> , 2017, 18, 323.	2.8	129
28	Combined Analyses of Data From Quantitative Trait Loci Mapping Studies: Chromosome 4 Effects on Porcine Growth and Fatness. <i>Genetics</i> , 2000, 155, 1369-1378.	2.9	128
29	Targeting expression to the mammary gland: intronic sequences can enhance the efficiency of gene expression in transgenic mice. <i>Transgenic Research</i> , 1991, 1, 3-13.	2.4	127
30	Genome-wide SNP data unveils the globalization of domesticated pigs. <i>Genetics Selection Evolution</i> , 2017, 49, 71.	3.0	114
31	Livestock 2.0 “ genome editing for fitter, healthier, and more productive farmed animals. <i>Genome Biology</i> , 2018, 19, 204.	8.8	114
32	CpG islands of chicken are concentrated on microchromosomes. <i>Nature Genetics</i> , 1996, 12, 321-324.	21.4	113
33	Complete nucleotide sequence of the murine H-2k $\kappa$ gene. Comparison of three H-2K locus alleles. <i>Nucleic Acids Research</i> , 1984, 12, 9473-9487.	14.5	112
34	Genetic diversity within and between European pig breeds using microsatellite markers. <i>Animal Genetics</i> , 2006, 37, 189-198.	1.7	110
35	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	1.1	97
36	Illuminating the dark side of the human transcriptome with long read transcript sequencing. <i>BMC Genomics</i> , 2020, 21, 751.	2.8	97

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37	Swine Genome Sequencing Consortium (SGSC): A Strategic Roadmap for Sequencing The Pig Genome. <i>Comparative and Functional Genomics</i> , 2005, 6, 251-255.	2.0	93
38	Genetic and expression analysis of cattle identifies candidate genes in pathways responding to <i>Trypanosoma congolense</i> infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9304-9309.	7.1	92
39	Comparative Analysis of Monocyte Subsets in the Pig. <i>Journal of Immunology</i> , 2013, 190, 6389-6396.	0.8	91
40	A chromosome-level genome assembly for the Pacific oyster <i>Crassostrea gigas</i> . <i>GigaScience</i> , 2021, 10, .	6.4	88
41	Mapping Quantitative Trait Loci Affecting Female Reproductive Traits on Porcine Chromosome 81. <i>Biology of Reproduction</i> , 2003, 68, 2172-2179.	2.7	87
42	Epithelial, metabolic and innate immunity transcriptomic signatures differentiating the rumen from other sheep and mammalian gastrointestinal tract tissues. <i>PeerJ</i> , 2016, 4, e1762.	2.0	87
43	Mapping of quantitative trait loci on porcine chromosome 4. <i>Animal Genetics</i> , 1998, 29, 415-424.	1.7	86
44	Gene Transfer into Sheep. <i>Nature Biotechnology</i> , 1988, 6, 179-183.	17.5	83
45	Evaluation of approaches for identifying population informative markers from high density SNP Chips. <i>BMC Genetics</i> , 2011, 12, 45.	2.7	83
46	The impact of breed and tissue compartment on the response of pig macrophages to lipopolysaccharide. <i>BMC Genomics</i> , 2013, 14, 581.	2.8	83
47	Innate Immune Responses to Replication of Porcine Reproductive And Respiratory Syndrome Virus in Isolated Swine Alveolar Macrophages. <i>Viral Immunology</i> , 2007, 20, 105-118.	1.3	82
48	Characterization of 24 porcine (dA-dC)n-(dT-dG)n microsatellites: genotyping of unrelated animals from four breeds and linkage studies. <i>Mammalian Genome</i> , 1993, 4, 187-192.	2.2	81
49	Assignment of 19 porcine type I loci by somatic cell hybrid analysis detects new regions of conserved synteny between human and pig. <i>Mammalian Genome</i> , 1996, 7, 275-279.	2.2	75
50	From FAANG to fork: application of highly annotated genomes to improve farmed animal production. <i>Genome Biology</i> , 2020, 21, 285.	8.8	74
51	Linkage and comparative mapping of the locus controlling susceptibility towards <i>E. coli</i> F4ab/ac diarrhoea in pigs. <i>Cytogenetic and Genome Research</i> , 2003, 102, 157-162.	1.1	69
52	Detection of quantitative trait loci for androstenone, skatole and boar taint in a cross between Large White and Meishan pigs. <i>Animal Genetics</i> , 2005, 36, 14-22.	1.7	66
53	Quantitative trait loci for production traits in pigs: a combined analysis of two Meishan × Large White populations. <i>Animal Genetics</i> , 2008, 39, 486-495.	1.7	65
54	GOFAANG meeting: a Gathering On Functional Annotation of Animal Genomes. <i>Animal Genetics</i> , 2016, 47, 528-533.	1.7	65

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55	The ARKdb: genome databases for farmed and other animals. <i>Nucleic Acids Research</i> , 2001, 29, 106-110.	14.5	64
56	Genetic Perspectives on Host Responses to Porcine Reproductive and Respiratory Syndrome (PRRS). <i>Viral Immunology</i> , 2007, 20, 343-358.	1.3	61
57	The future of animal production: improving productivity and sustainability. <i>Journal of Agricultural Science</i> , 2011, 149, 9-16.	1.3	61
58	Genome-wide association reveals QTL for growth, bone and in vivo carcass traits as assessed by computed tomography in Scottish Blackface lambs. <i>Genetics Selection Evolution</i> , 2016, 48, 11.	3.0	58
59	A large-fragment porcine genomic library resource in a BAC vector. <i>Mammalian Genome</i> , 2000, 11, 811-814.	2.2	55
60	Macrophage Transcriptional Responses following In Vitro Infection with a Highly Virulent African Swine Fever Virus Isolate. <i>Journal of Virology</i> , 2006, 80, 10514-10521.	3.4	51
61	Whole genome analysis of water buffalo and global cattle breeds highlights convergent signatures of domestication. <i>Nature Communications</i> , 2020, 11, 4739.	12.8	50
62	A Gene Expression Atlas of the Domestic Water Buffalo ( <i>Bubalus bubalis</i> ). <i>Frontiers in Genetics</i> , 2019, 10, 668.	2.3	49
63	Comprehensive Transcriptional Profiling of the Gastrointestinal Tract of Ruminants from Birth to Adulthood Reveals Strong Developmental Stage Specific Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 359-373.	1.8	48
64	Functional Annotation of the Transcriptome of the Pig, <i>Sus scrofa</i> , Based Upon Network Analysis of an RNAseq Transcriptional Atlas. <i>Frontiers in Genetics</i> , 2019, 10, 1355.	2.3	42
65	Genomic diversity and differentiation of a managed island wild boar population. <i>Heredity</i> , 2016, 116, 60-67.	2.6	41
66	An assessment of European pig diversity using molecular markers: Partitioning of diversity among breeds. <i>Conservation Genetics</i> , 2005, 6, 729-741.	1.5	40
67	A genome-wide linkage analysis for reproductive traits in F2 Large White × Meishan cross gilts. <i>Animal Genetics</i> , 2014, 45, 191-197.	1.7	39
68	Comparative genomics of Toll-like receptor signalling in five species. <i>BMC Genomics</i> , 2009, 10, 216.	2.8	36
69	Development of a genetic tool for product regulation in the diverse British pig breed market. <i>BMC Genomics</i> , 2012, 13, 580.	2.8	35
70	The receptor locus for <i>Escherichia coli</i> F4ab/F4ac in the pig maps distal to the MUC4-LMLN region. <i>Mammalian Genome</i> , 2011, 22, 122-129.	2.2	33
71	<i>Lawsonia intracellularis</i> exploits $\beta$ -catenin/Wnt and Notch signalling pathways during infection of intestinal crypt to alter cell homeostasis and promote cell proliferation. <i>PLoS ONE</i> , 2017, 12, e0173782.	2.5	33
72	Production of pharmaceutical proteins in milk. <i>Experientia</i> , 1991, 47, 905-912.	1.2	32

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73	Identification of a single killer immunoglobulin-like receptor (KIR) gene in the porcine leukocyte receptor complex on chromosome 6q. <i>Immunogenetics</i> , 2006, 58, 481-486.	2.4	32
74	Cloning and mapping of the porcine cytochrome-p450 2E1 gene and its association with skatole levels in the domestic pig. <i>Animal Genetics</i> , 2005, 36, 417-422.	1.7	31
75	A QTL affecting daily feed intake maps to Chromosome 2 in pigs. <i>Mammalian Genome</i> , 2005, 16, 464-470.	2.2	31
76	Genetic diversity in European pigs utilizing amplified fragment length polymorphism markers. <i>Animal Genetics</i> , 2006, 37, 232-238.	1.7	31
77	Balancing selection at a premature stop mutation in the myostatin gene underlies a recessive leg weakness syndrome in pigs. <i>PLoS Genetics</i> , 2019, 15, e1007759.	3.5	31
78	QTL modulating ear size and erectness in pigs. <i>Animal Genetics</i> , 2007, 38, 222-226.	1.7	30
79	Analysis of the genetics of boar taint reveals both single SNPs and regional effects. <i>BMC Genomics</i> , 2014, 15, 424.	2.8	30
80	The porcine gonadotropin-releasing hormone receptor gene (GNRHR): Genomic organization, polymorphisms, and association with the number of corpora lutea. <i>Genome</i> , 2001, 44, 7-12.	2.0	29
81	Identification of Low-Confidence Regions in the Pig Reference Genome (Sscrofa10.2). <i>Frontiers in Genetics</i> , 2015, 6, 338.	2.3	28
82	Avianbase: a community resource for bird genomics. <i>Genome Biology</i> , 2015, 16, 21.	8.8	28
83	The porcine gonadotropin-releasing hormone receptor gene ( <i>GNRHR</i> ): Genomic organization, polymorphisms, and association with the number of corpora lutea. <i>Genome</i> , 2001, 44, 7-12.	2.0	28
84	No detectable association of the ESR Pvu II mutation with sow productivity in a Meishan × Large White F2 population. <i>Animal Genetics</i> , 2002, 33, 448-450.	1.7	27
85	Refined candidate region specified by haplotype sharing for <i>Escherichia coli</i> F4ab/F4ac susceptibility alleles in pigs. <i>Animal Genetics</i> , 2010, 41, 21-25.	1.7	27
86	Host inhibits replication of European porcine reproductive and respiratory syndrome virus in macrophages by altering differential regulation of type-I interferon transcriptional response. <i>Immunogenetics</i> , 2011, 63, 437-448.	2.4	27
87	High-resolution comparative mapping of pig Chromosome 4, emphasizing the FAT1 region. <i>Mammalian Genome</i> , 2004, 15, 717-731.	2.2	25
88	Isolation of subtelomeric sequences of porcine chromosomes for translocation screening reveals errors in the pig genome assembly. <i>Animal Genetics</i> , 2017, 48, 395-403.	1.7	25
89	Farm animal genome databases. <i>Briefings in Bioinformatics</i> , 2000, 1, 151-160.	6.5	24
90	Refined localization of the <i>Escherichia coli</i> F4ab/F4ac receptor locus on pig chromosome 13. <i>Animal Genetics</i> , 2009, 40, 749-752.	1.7	24

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91	Design and development of exome capture sequencing for the domestic pig ( <i>Sus scrofa</i> ). <i>BMC Genomics</i> , 2014, 15, 550.	2.8	24
92	Novel gene expression responses in the ovine abomasal mucosa to infection with the gastric nematode <i>Teladorsagia circumcincta</i> . <i>Veterinary Research</i> , 2011, 42, 78.	3.0	23
93	Localization of the PGD and TGF $\beta$ 1 loci to pig chromosome 6q. <i>Animal Genetics</i> , 1990, 21, 411-417.	1.7	22
94	USP18 restricts PRRSV growth through alteration of nuclear translocation of NF- $\kappa$ B p65 and p50 in MARC-145 cells. <i>Virus Research</i> , 2012, 169, 264-267.	2.2	22
95	Identification and annotation of conserved promoters and macrophage-expressed genes in the pig genome. <i>BMC Genomics</i> , 2015, 16, 970.	2.8	22
96	A Polymorphism in the 5' Untranslated Region of the Porcine Cholecystokinin Type A Receptor Gene Affects Feed Intake and Growth. <i>Genetics</i> , 2006, 174, 1555-1563.	2.9	21
97	Global Analysis of Transcription Start Sites in the New Ovine Reference Genome ( <i>Oar rambouillet</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	2.3	21
98	Secreted Phosphoprotein 1 Expression in Endometrium and Placental Tissues of Hyperproliferic Large White and Meishan Gilts. <i>Biology of Reproduction</i> , 2013, 88, 120.	2.7	20
99	Down-regulation of mechanisms involved in cell transport and maintenance of mucosal integrity in pigs infected with <i>Lawsonia intracellularis</i> . <i>Veterinary Research</i> , 2014, 45, 55.	3.0	20
100	Characterisation of five candidate genes within the ETEC F4ab/ac candidate region in pigs. <i>BMC Research Notes</i> , 2011, 4, 225.	1.4	18
101	CpG Islands of the Pig. <i>Genome Research</i> , 1997, 7, 924-931.	5.5	17
102	Livestock genomics: bridging the gap between mice and men. <i>Trends in Biotechnology</i> , 2007, 25, 483-489.	9.3	17
103	Characterization of the porcine <i>KIT</i> ligand gene: expression analysis, genomic structure, polymorphism detection and association with coat colour traits. <i>Animal Genetics</i> , 2008, 39, 217-224.	1.7	16
104	<i>Lawsonia intracellularis</i> infection of intestinal crypt cells is associated with specific depletion of secreted MUC2 in goblet cells. <i>Veterinary Immunology and Immunopathology</i> , 2015, 168, 61-67.	1.2	16
105	Detection of a quantitative trait locus associated with resistance to <i>Ascaris suum</i> infection in pigs. <i>International Journal for Parasitology</i> , 2012, 42, 383-391.	3.1	15
106	Genomic variation in macrophage-cultured European porcine reproductive and respiratory syndrome virus Olot/91 revealed using ultra-deep next generation sequencing. <i>Virology Journal</i> , 2014, 11, 42.	3.4	15
107	A Comprehensive Genetic Analysis of Candidate Genes Regulating Response to <i>Trypanosoma congolense</i> Infection in Mice. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e880.	3.0	14
108	Molecular cloning, characterization, and chromosomal assignment of porcine cationic amino acid transporter-1. <i>Genomics</i> , 2005, 85, 352-359.	2.9	13

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109	Characterization of the Interactome of the Porcine Reproductive and Respiratory Syndrome Virus Nonstructural Protein 2 Reveals the Hyper Variable Region as a Binding Platform for Association with 14â€“3â€“3 Proteins. <i>Journal of Proteome Research</i> , 2016, 15, 1388-1401.	3.7	13
110	Profiling of open chromatin in developing pig ( <i>Sus scrofa</i> ) muscle to identify regulatory regions. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	13
111	5' and 3' SINE-PCR allows genotyping of pig families without cloning and sequencing steps. <i>Mammalian Genome</i> , 1993, 4, 243-246.	2.2	12
112	Physical Mapping of the Murine Casein Locus Reveals the Gene Order as $\hat{1}\pm\hat{1}^2\hat{1}^3\hat{1}\mu\hat{1}^6$ . <i>DNA and Cell Biology</i> , 1997, 16, 477-484.	1.9	12
113	Functional analysis of the porcine USP18 and its role during porcine arterivirus replication. <i>Gene</i> , 2009, 439, 35-42.	2.2	12
114	Genome-Wide Analysis in Swine Associates Corneal Graft Rejection with Donor-Recipient Mismatches in Three Novel Histocompatibility Regions and One Locus Homologous to the Mouse H-3 Locus. <i>PLoS ONE</i> , 2016, 11, e0152155.	2.5	12
115	Production of human $\hat{1}\pm\hat{1}$ antitrypsin in the milk of transgenic sheep and mice: Targeting expression of CDNA sequences to the mammary gland. <i>Animal Biotechnology</i> , 1991, 2, 161-176.	1.5	11
116	Methods of gene transfer and their potential use to modify milk composition. <i>Theriogenology</i> , 1990, 33, 113-123.	2.1	10
117	The cholecystokinin type A receptor g.179A>G polymorphism affects feeding rate. <i>Animal Genetics</i> , 2008, 39, 187-188.	1.7	10
118	Genotype and expression analysis of two inbred mouse strains and two derived congenic strains suggest that most gene expression is trans regulated and sensitive to genetic background. <i>BMC Genomics</i> , 2010, 11, 361.	2.8	10
119	Beyond the whole genome consensus: Unravelling of PRRSV phylogenomics using next generation sequencing technologies. <i>Virus Research</i> , 2014, 194, 167-174.	2.2	10
120	Mapping of the pig genome. <i>Current Opinion in Genetics and Development</i> , 1994, 4, 395-400.	3.3	9
121	Assessment of SULT1A1, CYP2A6 and CYP2C18 as candidate genes for elevated backfat skatole levels in commercial and experimental pig populations. <i>Animal Genetics</i> , 2006, 37, 521-522.	1.7	9
122	Porcine alpha $\hat{1}\hat{1}$ antitrypsin (PI): cDNA sequence, polymorphism and assignment to chromosome 7q2.4 $\hat{1}$ & q2.6. <i>Animal Genetics</i> , 1996, 27, 85-90.	1.7	9
123	Mapping QTL in the porcine MHC region affecting fatness and growth traits in a Meishan/Large White composite population. <i>Animal Genetics</i> , 2011, 42, 83-85.	1.7	9
124	Anchorage of an unassigned linkage group to pig Chromosome 10 with P1 clones. <i>Mammalian Genome</i> , 1994, 5, 646-648.	2.2	8
125	An animal model to evaluate the function and regulation of the adaptively evolving stress protein SEP53 in oesophageal bile damage responses. <i>Cell Stress and Chaperones</i> , 2008, 13, 375-385.	2.9	8
126	RFLP and linkage analysis of the porcine casein lociâ€“CASAS1, CASAS2, CASB and CASK. <i>Animal Genetics</i> , 1994, 25, 349-351.	1.7	8



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127	What Can the Genetics Revolution Offer the Meat Industry?. Outlook on Agriculture, 2003, 32, 219-226.	3.4	7
128	Efficiency of genomic prediction for boar taint reduction in Danish Landrace pigs. Animal Genetics, 2015, 46, 607-616.	1.7	7
129	Effects of porcine reproductive and respiratory syndrome virus infection on the performance of pregnant gilts and growing pigs. Animal Production Science, 2010, 50, 890.	1.3	6
130	Distinct functional enrichment of transcriptional signatures in pigs with high and low IFN-gamma responses after vaccination with a porcine reproductive and respiratory syndrome virus (PRRSV). Veterinary Research, 2016, 47, 104.	3.0	6
131	Combining laboratory and mathematical models to infer mechanisms underlying kinetic changes in macrophage susceptibility to an RNA virus. BMC Systems Biology, 2016, 10, 101.	3.0	6
132	A consensus linkage map for swine chromosome 7. Animal Genetics, 1997, 28, 223-229.	1.7	5
133	Quasispecies evolution of the prototypical genotype 1 porcine reproductive and respiratory syndrome virus early during in vivo infection is rapid and tissue specific. Archives of Virology, 2017, 162, 2203-2210.	2.1	5
134	Livestock Genetics: Fat pigs can blame their genes. Current Biology, 1994, 4, 728-730.	3.9	4
135	A PstI RFLP at the porcine orosomucoid locus (ORM). Animal Genetics, 2009, 25, 285-285.	1.7	4
136	The porcine TTR locus maps to chromosome 6q. Animal Genetics, 1996, 27, 351-353.	1.7	4
137	An intronic polymorphism in the porcine <i>IRF7</i> gene is associated with better health and immunity of the host during <i>Sarcocystis</i> infection, and affects interferon signalling. Animal Genetics, 2011, 42, 386-394.	1.7	4
138	Complete Genome Sequence of a Pathogenic Genotype 1 Subtype 3 Porcine Reproductive and Respiratory Syndrome Virus (Strain SU1-Bel) from Pig Primary Tissue. Genome Announcements, 2015, 3, .	0.8	3
139	Stem cell-derived porcine macrophages as a new platform for studying host-pathogen interactions. BMC Biology, 2022, 20, 14.	3.8	3
140	A new transferrin allele in sheep. Animal Genetics, 1986, 17, 191-194.	1.7	2
141	A new allele at the <i>Pgd</i> locus in pigs. Animal Genetics, 1988, 19, 189-191.	1.7	2
142	A TaqI RFLP at the porcine thyroid stimulating hormone $\beta$ -subunit locus (TSHB). Animal Genetics, 1992, 23, 567-567.	1.7	2
143	A porcine polymorphic microsatellite locus ( <i>S0031</i> ). Animal Genetics, 1993, 24, 70-70.	1.7	2
144	The Halothane Gene, Leanness and Stress Susceptibility in Pigs. , 2001, , 173-190.		2

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145	Metagenomic sequencing of clinical samples reveals a single widespread clone of <i>Lawsonia intracellularis</i> responsible for porcine proliferative enteropathy. <i>Microbial Genomics</i> , 2020, 6, .	2.0	2
146	Mapping the Complex Genomes of Animals and Man. <i>Outlook on Agriculture</i> , 1993, 22, 79-84.	3.4	1
147	Genetic and physical mapping, expression analysis and partial sequence of porcine PER1. <i>Cytogenetic and Genome Research</i> , 2001, 95, 82-84.	1.1	1
148	Progress on the halothane gene in pig. <i>Animal Genetics</i> , 1989, 20, 332-332.	1.7	1
149	A Bam HI RFLP at the locus encoding the 65 kDa regulatory subunit of porcine protein phosphatase 2A (PPP2ARB). <i>Animal Genetics</i> , 1992, 23, 568-568.	1.7	1
150	Characterisation of autophagy disruption in the ileum of pigs infected with <i>Lawsonia intracellularis</i> . <i>Veterinary Research Communications</i> , 2021, , 1.	1.6	1
151	Noah's ark on Fraser Island. <i>Trends in Genetics</i> , 1996, 12, 115-116.	6.7	0
152	The polymerase chain reaction. <i>Livestock Science</i> , 1997, 48, 79-80.	1.2	0
153	Physical mapping of porcine seasonality genes. <i>Animal Biotechnology</i> , 1999, 10, 143-146.	1.5	0
154	Assignment of the porcine GLUL gene to the distal end of chromosome 9q. <i>Animal Genetics</i> , 2002, 33, 315-316.	1.7	0
155	OBITUARY Professor Stephen Bishop. <i>Journal of Agricultural Science</i> , 2015, 153, 957-958.	1.3	0