List of Publications by Year in descending order

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		26630	28297
155	12,314	56	105
papers	citations	h-index	g-index
170	170	170	10006
172	172	172	10336
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Stem cell-derived porcine macrophages as a new platform for studying host-pathogen interactions. BMC Biology, 2022, 20, 14.	3.8	3
2	Profiling of open chromatin in developing pig (<i>Sus scrofa</i>) muscle to identify regulatory regions. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	13
3	A chromosome-level genome assembly for the Pacific oyster <i>Crassostrea gigas</i> . GigaScience, 2021, 10, .	6.4	88
4	Characterisation of autophagy disruption in the ileum of pigs infected with Lawsonia intracellularis. Veterinary Research Communications, 2021, , 1.	1.6	1
5	From FAANG to fork: application of highly annotated genomes to improve farmed animal production. Genome Biology, 2020, 21, 285.	8.8	74
6	Global Analysis of Transcription Start Sites in the New Ovine Reference Genome (Oar rambouillet) Tj ETQq0 0 0 r	gBT /Overl	ock 10 Tf 50
7	Illuminating the dark side of the human transcriptome with long read transcript sequencing. BMC Genomics, 2020, 21, 751.	2.8	97
8	Whole genome analysis of water buffalo and global cattle breeds highlights convergent signatures of domestication. Nature Communications, 2020, 11, 4739.	12.8	50
9	An improved pig reference genome sequence to enable pig genetics and genomics research. GigaScience, 2020, 9, .	6.4	187
10	Metagenomic sequencing of clinical samples reveals a single widespread clone of Lawsonia intracellularis responsible for porcine proliferative enteropathy. Microbial Genomics, 2020, 6, .	2.0	2
11	A Gene Expression Atlas of the Domestic Water Buffalo (Bubalus bubalis). Frontiers in Genetics, 2019, 10, 668.	2.3	49
12	Balancing selection at a premature stop mutation in the myostatin gene underlies a recessive leg weakness syndrome in pigs. PLoS Genetics, 2019, 15, e1007759.	3.5	31
13	Comprehensive Transcriptional Profiling of the Gastrointestinal Tract of Ruminants from Birth to Adulthood Reveals Strong Developmental Stage Specific Gene Expression. G3: Genes, Genomes, Genetics, 2019, 9, 359-373.	1.8	48
14	Functional Annotation of the Transcriptome of the Pig, Sus scrofa, Based Upon Network Analysis of an RNAseq Transcriptional Atlas. Frontiers in Genetics, 2019, 10, 1355.	2.3	42
15	Livestock 2.0 – genome editing for fitter, healthier, and more productive farmed animals. Genome Biology, 2018, 19, 204.	8.8	114
16	Pigs Lacking the Scavenger Receptor Cysteine-Rich Domain 5 of CD163 Are Resistant to Porcine Reproductive and Respiratory Syndrome Virus 1 Infection. Journal of Virology, 2018, 92, .	3.4	149

17	Normalized long read RNA sequencing in chicken reveals transcriptome complexity similar to human. BMC Genomics, 2017, 18, 323.	2.8	129
18	Isolation of subtelomeric sequences of porcine chromosomes for translocation screening reveals	1.7	25

Isolation of subtelomeric sequences of porcine chromosomes for translocation screening reveals errors in the pig genome assembly. Animal Genetics, 2017, 48, 395-403. 1.7 18

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19	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
20	Genome-wide SNP data unveils the globalization of domesticated pigs. Genetics Selection Evolution, 2017, 49, 71.	3.0	114
21	A high resolution atlas of gene expression in the domestic sheep (Ovis aries). PLoS Genetics, 2017, 13, e1006997.	3.5	210
22	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.	4.7	282
23	Lawsonia intracellularis exploits β-catenin/Wnt and Notch signalling pathways during infection of intestinal crypt to alter cell homeostasis and promote cell proliferation. PLoS ONE, 2017, 12, e0173782.	2.5	33
24	Epithelial, metabolic and innate immunity transcriptomic signatures differentiating the rumen from other sheep and mammalian gastrointestinal tract tissues. PeerJ, 2016, 4, e1762.	2.0	87
25	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
26	<scp>GO</scp> â€ <scp>FAANG</scp> meeting: a Gathering On Functional Annotation of <scp>An</scp> imal Genomes. Animal Genetics, 2016, 47, 528-533.	1.7	65
27	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
28	Genome-wide association reveals QTL for growth, bone and in vivo carcass traits as assessed by computed tomography in Scottish Blackface lambs. Genetics Selection Evolution, 2016, 48, 11.	3.0	58
29	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 14–3–3 Proteins. Journal of Proteome Research, 2016, 15, 1388-1401.	3.7	13
30	Genomic diversity and differentiation of a managed island wild boar population. Heredity, 2016, 116, 60-67.	2.6	41
31	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. PLoS ONE, 2016, 11, e0152155.	2.5	12
32	OBITUARY Professor Stephen Bishop. Journal of Agricultural Science, 2015, 153, 957-958.	1.3	0
33	Efficiency of genomic prediction for boar taint reduction in Danish Landrace pigs. Animal Genetics, 2015, 46, 607-616.	1.7	7
34	Identification and annotation of conserved promoters and macrophage-expressed genes in the pig genome. BMC Genomics, 2015, 16, 970.	2.8	22
35	Identification of Low-Confidence Regions in the Pig Reference Genome (Sscrofa10.2). Frontiers in Genetics, 2015, 6, 338.	2.3	28
36	Exome Sequencing: Current and Future Perspectives. G3: Genes, Genomes, Genetics, 2015, 5, 1543-1550.	1.8	165

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37	Avianbase: a community resource for bird genomics. Genome Biology, 2015, 16, 21.	8.8	28
38	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	1.1	97
39	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. Genome Biology, 2015, 16, 57.	8.8	331
40	Lawsonia intracellularis infection of intestinal crypt cells is associated with specific depletion of secreted MUC2 in goblet cells. Veterinary Immunology and Immunopathology, 2015, 168, 61-67.	1.2	16
41	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
42	Beyond the whole genome consensus: Unravelling of PRRSV phylogenomics using next generation sequencing technologies. Virus Research, 2014, 194, 167-174.	2.2	10
43	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.	1.7	39
44	Development and validation of a high density SNP genotyping array for Atlantic salmon (Salmo salar). BMC Genomics, 2014, 15, 90.	2.8	219
45	Design and development of exome capture sequencing for the domestic pig (Sus scrofa). BMC Genomics, 2014, 15, 550.	2.8	24
46	Down-regulation of mechanisms involved in cell transport and maintenance of mucosal integrity in pigs infected with Lawsonia intracellularis. Veterinary Research, 2014, 45, 55.	3.0	20
47	Analysis of the genetics of boar taint reveals both single SNPs and regional effects. BMC Genomics, 2014, 15, 424.	2.8	30
48	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.	3.4	15
49	The sheep genome illuminates biology of the rumen and lipid metabolism. Science, 2014, 344, 1168-1173.	12.6	436
50	Structural and functional annotation of the porcine immunome. BMC Genomics, 2013, 14, 332.	2.8	203
51	The impact of breed and tissue compartment on the response of pig macrophages to lipopolysaccharide. BMC Genomics, 2013, 14, 581.	2.8	83
52	Signatures of Diversifying Selection in European Pig Breeds. PLoS Genetics, 2013, 9, e1003453.	3.5	228
53	Secreted Phosphoprotein 1 Expression in Endometrium and Placental Tissues of Hyperprolific Large White and Meishan Gilts1. Biology of Reproduction, 2013, 88, 120.	2.7	20
54	Genome sequencing reveals fine scale diversification and reticulation history during speciation in Sus. Genome Biology, 2013, 14, R107.	9.6	137

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55	Comparative Analysis of Monocyte Subsets in the Pig. Journal of Immunology, 2013, 190, 6389-6396.	0.8	91
56	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.	7.1	548
57	USP18 restricts PRRSV growth through alteration of nuclear translocation of NF-κB p65 and p50 in MARC-145 cells. Virus Research, 2012, 169, 264-267.	2.2	22
58	Analyses of pig genomes provide insight into porcine demography and evolution. Nature, 2012, 491, 393-398.	27.8	1,190
59	Development of a genetic tool for product regulation in the diverse British pig breed market. BMC Genomics, 2012, 13, 580.	2.8	35
60	A high density recombination map of the pig reveals a correlation between sex-specific recombination and GC content. BMC Genomics, 2012, 13, 586.	2.8	150
61	A gene expression atlas of the domestic pig. BMC Biology, 2012, 10, 90.	3.8	199
62	Pig Bone Marrow-Derived Macrophages Resemble Human Macrophages in Their Response to Bacterial Lipopolysaccharide. Journal of Immunology, 2012, 188, 3382-3394.	0.8	147
63	Detection of a quantitative trait locus associated with resistance to Ascaris suum infection in pigs. International Journal for Parasitology, 2012, 42, 383-391.	3.1	15
64	Evaluation of approaches for identifying population informative markers from high density SNP Chips. BMC Genetics, 2011, 12, 45.	2.7	83
65	Mapping QTL in the porcine MHC region affecting fatness and growth traits in a Meishan/Large White composite population. Animal Genetics, 2011, 42, 83-85.	1.7	9
66	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
67	Novel gene expression responses in the ovine abomasal mucosa to infection with the gastric nematode Teladorsagia circumcincta. Veterinary Research, 2011, 42, 78.	3.0	23
68	Characterisation of five candidate genes within the ETEC F4ab/ac candidate region in pigs. BMC Research Notes, 2011, 4, 225.	1.4	18
69	The future of animal production: improving productivity and sustainability. Journal of Agricultural Science, 2011, 149, 9-16.	1.3	61
70	The receptor locus for Escherichia coli F4ab/F4ac in the pig maps distal to the MUC4–LMLN region. Mammalian Genome, 2011, 22, 122-129.	2.2	33
71	Host inhibits replication of European porcine reproductive and respiratory syndrome virus in macrophages by altering differential regulation of type-I interferon transcriptional response. Immunogenetics, 2011, 63, 437-448.	2.4	27
72	Genetic and expression analysis of cattle identifies candidate genes in pathways responding to <i>Trypanosoma congolense</i> infection. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9304-9309.	7.1	92

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73	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
74	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. BMC Genomics, 2010, 11, 361.	2.8	10
75	Pig genome sequence - analysis and publication strategy. BMC Genomics, 2010, 11, 438.	2.8	132
76	Refined candidate region specified by haplotype sharing for <i>Escherichia coli</i> F4ab/F4ac susceptibility alleles in pigs. Animal Genetics, 2010, 41, 21-25.	1.7	27
77	The sheep genome reference sequence: a work in progress. Animal Genetics, 2010, 41, 449-453.	1.7	173
78	A Comprehensive Genetic Analysis of Candidate Genes Regulating Response to Trypanosoma congolense Infection in Mice. PLoS Neglected Tropical Diseases, 2010, 4, e880.	3.0	14
79	Design of a High Density SNP Genotyping Assay in the Pig Using SNPs Identified and Characterized by Next Generation Sequencing Technology. PLoS ONE, 2009, 4, e6524.	2.5	568
80	Comparative genomics of Toll-like receptor signalling in five species. BMC Genomics, 2009, 10, 216.	2.8	36
81	A Pstl RFLP at the porcine orosomucoid locus (ORM). Animal Genetics, 2009, 25, 285-285.	1.7	4
82	Refined localization of the <i>Escherichia coli</i> F4ab/F4ac receptor locus on pig chromosome 13. Animal Genetics, 2009, 40, 749-752.	1.7	24
83	Functional analysis of the porcine USP18 and its role during porcine arterivirus replication. Gene, 2009, 439, 35-42.	2.2	12
84	An animal model to evaluate the function and regulation of the adaptively evolving stress protein SEP53 in oesophageal bile damage responses. Cell Stress and Chaperones, 2008, 13, 375-385.	2.9	8
85	The cholecystokinin type A receptor g.179A>G polymorphism affects feeding rate. Animal Genetics, 2008, 39, 187-188.	1.7	10
86	Characterization of the porcine <i>KIT ligand</i> gene: expression analysis, genomic structure, polymorphism detection and association with coat colour traits. Animal Genetics, 2008, 39, 217-224.	1.7	16
87	Quantitative trait loci for production traits in pigs: a combined analysis of two Meishanâ€f×â€fLarge White populations. Animal Genetics, 2008, 39, 486-495.	1.7	65
88	Innate Immune Responses to Replication of Porcine Reproductive And Respiratory Syndrome Virus in Isolated Swine Alveolar Macrophages. Viral Immunology, 2007, 20, 105-118.	1.3	82
89	A high utility integrated map of the pig genome. Genome Biology, 2007, 8, R139.	9.6	130
90	Genetic Perspectives on Host Responses to Porcine Reproductive and Respiratory Syndrome (PRRS). Viral Immunology, 2007, 20, 343-358.	1.3	61

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91	QTL modulating ear size and erectness in pigs. Animal Genetics, 2007, 38, 222-226.	1.7	30
92	Livestock genomics: bridging the gap between mice and men. Trends in Biotechnology, 2007, 25, 483-489.	9.3	17
93	Genetic diversity within and between European pig breeds using microsatellite markers. Animal Genetics, 2006, 37, 189-198.	1.7	110
94	Genetic diversity in European pigs utilizing amplified fragment length polymorphism markers. Animal Genetics, 2006, 37, 232-238.	1.7	31
95	Assessment of SULT1A1, CYP2A6 and CYP2C18 as candidate genes for elevated backfat skatole levels in commercial and experimental pig populations. Animal Genetics, 2006, 37, 521-522.	1.7	9
96	Identification of a single killer immunoglobulin-like receptor (KIR) gene in the porcine leukocyte receptor complex on chromosome 6q. Immunogenetics, 2006, 58, 481-486.	2.4	32
97	A Polymorphism in the 5′-Untranslated Region of the Porcine Cholecystokinin Type A Receptor Gene Affects Feed Intake and Growth. Genetics, 2006, 174, 1555-1563.	2.9	21
98	Macrophage Transcriptional Responses following In Vitro Infection with a Highly Virulent African Swine Fever Virus Isolate. Journal of Virology, 2006, 80, 10514-10521.	3.4	51
99	Detection of quantitative trait loci for androstenone, skatole and boar taint in a cross between Large White and Meishan pigs. Animal Genetics, 2005, 36, 14-22.	1.7	66
100	Cloning and mapping of the porcine cytochrome-p450 2E1 gene and its association with skatole levels in the domestic pig. Animal Genetics, 2005, 36, 417-422.	1.7	31
101	Swine Genome Sequencing Consortium (SGSC): A Strategic Roadmap for Sequencing The Pig Genome. Comparative and Functional Genomics, 2005, 6, 251-255.	2.0	93
102	A QTL affecting daily feed intake maps to Chromosome 2 in pigs. Mammalian Genome, 2005, 16, 464-470.	2.2	31
103	An assessment of European pig diversity using molecular markers: Partitioning of diversity among breeds. Conservation Genetics, 2005, 6, 729-741.	1.5	40
104	Molecular cloning, characterization, and chromosomal assignment of porcine cationic amino acid transporter-1. Genomics, 2005, 85, 352-359.	2.9	13
105	High-resolution comparative mapping of pig Chromosome 4, emphasizing the FAT1 region. Mammalian Genome, 2004, 15, 717-731.	2.2	25
106	A regulatory mutation in IGF2 causes a major QTL effect on muscle growth in the pig. Nature, 2003, 425, 832-836.	27.8	791
107	Mapping Quantitative Trait Loci Affecting Female Reproductive Traits on Porcine Chromosome 81. Biology of Reproduction, 2003, 68, 2172-2179.	2.7	87
108	Linkage and comparative mapping of the locus controlling susceptibility towards <i>E. coli</i> F4ab/ac diarrhoea in pigs. Cytogenetic and Genome Research, 2003, 102, 157-162.	1.1	69

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109	What Can the Genetics Revolution Offer the Meat Industry?. Outlook on Agriculture, 2003, 32, 219-226.	3.4	7
110	Somatic Cell Nuclear Transfer in the Pig: Control of Pronuclear Formation and Integration with Improved Methods for Activation and Maintenance of Pregnancy1. Biology of Reproduction, 2002, 66, 642-650.	2.7	165
111	A large duplication associated with dominant white color in pigs originated by homologous recombination between LINE elements flanking KIT. Mammalian Genome, 2002, 13, 569-577.	2.2	149
112	No detectable association of the ESR Pvu II mutation with sow productivity in a Meishan × Large White F2 population. Animal Genetics, 2002, 33, 448-450.	1.7	27
113	Assignment of the porcine GLUL gene to the distal end of chromosome 9q. Animal Genetics, 2002, 33, 315-316.	1.7	0
114	The porcine gonadotropin-releasing hormone receptor gene (GNRHR): Genomic organization, polymorphisms, and association with the number of corpora lutea. Genome, 2001, 44, 7-12.	2.0	29
115	The ARKdb: genome databases for farmed and other animals. Nucleic Acids Research, 2001, 29, 106-110.	14.5	64
116	Genetic and physical mapping, expression analysis and partial sequence of porcine PER1. Cytogenetic and Genome Research, 2001, 95, 82-84.	1.1	1
117	The Halothane Gene, Leanness and Stress Susceptibility in Pigs. , 2001, , 173-190.		2
118	The porcine gonadotropin-releasing hormone receptor gene (<i>GNRHR</i>): Genomic organization, polymorphisms, and association with the number of corpora lutea. Genome, 2001, 44, 7-12.	2.0	28
119	A large-fragment porcine genomic library resource in a BAC vector. Mammalian Genome, 2000, 11, 811-814.	2.2	55
120	Farm animal genome databases. Briefings in Bioinformatics, 2000, 1, 151-160.	6.5	24
121	Combined Analyses of Data From Quantitative Trait Loci Mapping Studies: Chromosome 4 Effects on Porcine Growth and Fatness. Genetics, 2000, 155, 1369-1378.	2.9	128
122	Physical mapping of porcine seasonality genes. Animal Biotechnology, 1999, 10, 143-146.	1.5	0
123	Mapping of quantitative trait loci on porcine chromosome 4. Animal Genetics, 1998, 29, 415-424.	1.7	86
124	Physical Mapping of the Murine Casein Locus Reveals the Gene Order as α-β-γ-ε-κ. DNA and Cell Biology, 1997, 16, 477-484.	1.9	12
125	The polymerase chain reaction. Livestock Science, 1997, 48, 79-80.	1.2	0
126	CpG Islands of the Pig. Genome Research, 1997, 7, 924-931.	5.5	17

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127	A consensus linkage map for swine chromosome 7. Animal Genetics, 1997, 28, 223-229.	1.7	5
128	Noah's ark on Fraser Island. Trends in Genetics, 1996, 12, 115-116.	6.7	0
129	Assignment of 19 porcine type I loci by somatic cell hybrid analysis detects new regions of conserved synteny between human and pig. Mammalian Genome, 1996, 7, 275-279.	2.2	75
130	Comparative Genome Organization of Vertebrates. Mammalian Genome, 1996, 7, 717-734.	2.2	146
131	CpG islands of chicken are concentrated on microchromosomes. Nature Genetics, 1996, 12, 321-324.	21.4	113
132	The porcine TTR locus maps to chromosome 6q. Animal Genetics, 1996, 27, 351-353.	1.7	4
133	Porcine alphaâ€l â€antitrypsin (PI): cDNA sequence, polymorphism and assignment to chromosome 7q2.4― > q2.6. Animal Genetics, 1996, 27, 85-90.	1.7	9
134	The PiGMaP consortium linkage map of the pig (Sus scrofa). Mammalian Genome, 1995, 6, 157-175.	2.2	475
135	Anchorage of an unassigned linkage group to pig Chromosome 10 with P1 clones. Mammalian Genome, 1994, 5, 646-648.	2.2	8
136	Livestock Genetics: Fat pigs can blame their genes. Current Biology, 1994, 4, 728-730.	3.9	4
137	Mapping of the pig genome. Current Opinion in Genetics and Development, 1994, 4, 395-400.	3.3	9
138	RFLP and linkage analysis of the porcine casein loci—CASAS1, CASAS2, CASB and CASK. Animal Genetics, 1994, 25, 349-351.	1.7	8
139	5? and 3? SINE-PCR allows genotyping of pig families without cloning and sequencing steps. Mammalian Genome, 1993, 4, 243-246.	2.2	12
140	Characterization of 24 porcine (dA-dC)n-(dT-dG)n microsatellites: genotyping of unrelated animals from four breeds and linkage studies. Mammalian Genome, 1993, 4, 187-192.	2.2	81
141	Mapping the Complex Genomes of Animals and Man. Outlook on Agriculture, 1993, 22, 79-84.	3.4	1
142	A porcine polymorphic microsatellite locus (<i>S0031</i>). Animal Genetics, 1993, 24, 70-70.	1.7	2
143	A Taql RFLP at the porcine thyroid stimulating hormone βâ€subunit locus (TSHB). Animal Genetics, 1992, 23, 567-567.	1.7	2
144	A Bam HI RFLP at the locus encoding the 65â€kDa regulatory subunit of porcine protein phosphatase 2A (PPP2ARB). Animal Genetics, 1992, 23, 568-568.	1.7	1

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145	Cosegregation of porcine malignant hyperthermia and a probable causal mutation in the skeletal muscle ryanodine receptor gene in backcross families. Genomics, 1991, 11, 744-750.	2.9	147
146	Production of pharmaceutical proteins in milk. Experientia, 1991, 47, 905-912.	1.2	32
147	Targeting expression to the mammary gland: intronic sequences can enhance the efficiency of gene expression in transgenic mice. Transgenic Research, 1991, 1, 3-13.	2.4	127
148	Production of human α1â€antitrypsin in the milk of transgenic sheep and mice: Targeting expression of CDNA sequences to the mammary gland. Animal Biotechnology, 1991, 2, 161-176.	1.5	11
149	Localization of the PGD and TGFβâ€l loci to pig chromosome 6q. Animal Genetics, 1990, 21, 411-417.	1.7	22
150	Methods of gene transfer and their potential use to modify milk composition. Theriogenology, 1990, 33, 113-123.	2.1	10
151	Progress on the halothane gene in pig. Animal Genetics, 1989, 20, 332-332.	1.7	1
152	Gene Transfer into Sheep. Nature Biotechnology, 1988, 6, 179-183.	17.5	83
153	A new allele at the <i>Pgd</i> locus in pigs. Animal Genetics, 1988, 19, 189-191.	1.7	2
154	A new transferrin allele in sheep. Animal Genetics, 1986, 17, 191-194.	1.7	2
155	Complete nucleotide sequence of the murine H-2kkgene. Comparison of three H-2K locus alleles. Nucleic Acids Research, 1984, 12, 9473-9487.	14.5	112