

Martien A M Groenen

List of Publications by Year in descending order

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293
papers

21,384
citations

10373

72
h-index

12258

133
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304
all docs

304
docs citations

304
times ranked

14933
citing authors

#	ARTICLE	IF	CITATIONS
1	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 2004, 432, 695-716.	13.7	2,421
2	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	13.7	1,190
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.	1.1	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.	3.3	548
5	The PiGMaP consortium linkage map of the pig (<i>Sus scrofa</i>). <i>Mammalian Genome</i> , 1995, 6, 157-175.	1.0	475
6	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004, 432, 717-722.	13.7	391
7	A consensus linkage map of the chicken genome. <i>Genome Research</i> , 2000, 10, 137-47.	2.4	357
8	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (<i>Meleagris gallopavo</i>): Genome Assembly and Analysis. <i>PLoS Biology</i> , 2010, 8, e1000475.	2.6	348
9	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015, 16, 57.	3.8	331
10	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. <i>Nature Genetics</i> , 2013, 45, 776-783.	9.4	327
11	Empirical Evaluation of Genetic Clustering Methods Using Multilocus Genotypes From 20 Chicken Breeds. <i>Genetics</i> , 2001, 159, 699-713.	1.2	306
12	First report on chicken genes and chromosomes 2000. <i>Cytogenetic and Genome Research</i> , 2000, 90, 169-218.	0.6	299
13	Detection of Quantitative Trait Loci for Backfat Thickness and Intramuscular Fat Content in Pigs (<i>Sus</i>) Tj ETQq1 1 0,784314 rgBT /Ove 1.2 276		
14	Regions of Homozygosity in the Porcine Genome: Consequence of Demography and the Recombination Landscape. <i>PLoS Genetics</i> , 2012, 8, e1003100.	1.5	266
15	Genome-wide scan for body composition in pigs reveals important role of imprinting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 7947-7950.	3.3	264
16	Evidence of long-term gene flow and selection during domestication from analyses of Eurasian wild and domestic pig genomes. <i>Nature Genetics</i> , 2015, 47, 1141-1148.	9.4	263
17	A high-density SNP-based linkage map of the chicken genome reveals sequence features correlated with recombination rate. <i>Genome Research</i> , 2009, 19, 510-519.	2.4	261
18	Genome-wide assessment of worldwide chicken SNP genetic diversity indicates significant absence of rare alleles in commercial breeds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17312-17317.	3.3	230

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19	Signatures of Diversifying Selection in European Pig Breeds. <i>PLoS Genetics</i> , 2013, 9, e1003453.	1.5	228
20	Biodiversity of 52 chicken populations assessed by microsatellite typing of DNA pools. <i>Genetics Selection Evolution</i> , 2003, 35, 533-57.	1.2	209
21	A physical map of the chicken genome. <i>Nature</i> , 2004, 432, 761-764.	13.7	200
22	Pig Domestication and Human-Mediated Dispersal in Western Eurasia Revealed through Ancient DNA and Geometric Morphometrics. <i>Molecular Biology and Evolution</i> , 2013, 30, 824-832.	3.5	196
23	The development and characterization of a 60K SNP chip for chicken. <i>BMC Genomics</i> , 2011, 12, 274.	1.2	185
24	Evolutionary signals of selection on cognition from the great tit genome and methylome. <i>Nature Communications</i> , 2016, 7, 10474.	5.8	172
25	Microsatellite markers in common carp (<i>Cyprinus carpio</i> L.). <i>Animal Genetics</i> , 1997, 28, 129-134.	0.6	168
26	Recent natural selection causes adaptive evolution of an avian polygenic trait. <i>Science</i> , 2017, 358, 365-368.	6.0	161
27	Genetic Mapping of Quantitative Trait Loci Affecting Susceptibility to Marek's Disease Virus Induced Tumors in F2 Intercross Chickens. <i>Genetics</i> , 1998, 148, 349-360.	1.2	156
28	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.	1.2	150
29	Two-dimensional screening of the Wageningen chicken BAC library. <i>Mammalian Genome</i> , 2000, 11, 360-363.	1.0	141
30	Genome sequencing reveals fine scale diversification and reticulation history during speciation in <i>Sus</i> . <i>Genome Biology</i> , 2013, 14, R107.	13.9	137
31	Genomic analysis reveals selection for Asian genes in European pigs following human-mediated introgression. <i>Nature Communications</i> , 2014, 5, 4392.	5.8	137
32	Second report on chicken genes and chromosomes 2005. <i>Cytogenetic and Genome Research</i> , 2005, 109, 415-479.	0.6	136
33	Genome-Wide Footprints of Pig Domestication and Selection Revealed through Massive Parallel Sequencing of Pooled DNA. <i>PLoS ONE</i> , 2011, 6, e14782.	1.1	135
34	Pig genome sequence - analysis and publication strategy. <i>BMC Genomics</i> , 2010, 11, 438.	1.2	132
35	Cloning and characterization of the acyl-coenzyme A: 6-aminopenicillanic-acid-acyltransferase gene of <i>Penicillium chrysogenum</i> . <i>Gene</i> , 1989, 83, 291-300.	1.0	130
36	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.	1.2	128

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37	Genome-Wide Characterization of Selection Signatures and Runs of Homozygosity in Ugandan Goat Breeds. <i>Frontiers in Genetics</i> , 2018, 9, 318.	1.1	126
38	Molecular Cytogenetic Definition of the Chicken Genome: The First Complete Avian Karyotype. <i>Genetics</i> , 2004, 166, 1367-1373.	1.2	122
39	The nucleotide sequence of bovine MHC class IIDQB andDRB genes. <i>Immunogenetics</i> , 1990, 31, 37-44.	1.2	120
40	Whole genome comparative studies between chicken and turkey and their implications for avian genome evolution. <i>BMC Genomics</i> , 2008, 9, 168.	1.2	119
41	Linkage Disequilibrium Decay and Haplotype Block Structure in the Pig. <i>Genetics</i> , 2008, 179, 569-579.	1.2	118
42	Evolutionary dynamics of copy number variation in pig genomes in the context of adaptation and domestication. <i>BMC Genomics</i> , 2013, 14, 449.	1.2	118
43	Genome-wide single nucleotide polymorphism analysis reveals recent genetic introgression from domestic pigs into Northwest European wild boar populations. <i>Molecular Ecology</i> , 2013, 22, 856-866.	2.0	117
44	Whole genome scan in chickens for quantitative trait loci affecting growth and feed efficiency. <i>Poultry Science</i> , 1999, 78, 15-23.	1.5	114
45	Genome-wide SNP data unveils the globalization of domesticated pigs. <i>Genetics Selection Evolution</i> , 2017, 49, 71.	1.2	114
46	Detection and characterization of quantitative trait loci for growth and reproduction traits in pigs. <i>Livestock Science</i> , 2001, 72, 185-198.	1.2	112
47	A Comprehensive Microsatellite Linkage Map of the Chicken Genome. <i>Genomics</i> , 1998, 49, 265-274.	1.3	111
48	Genetic diversity within and between European pig breeds using microsatellite markers. <i>Animal Genetics</i> , 2006, 37, 189-198.	0.6	110
49	The nucleotide sequence of the bovine MHC class II alpha genes: DRA, DQA, andDYA. <i>Immunogenetics</i> , 1990, 31, 29-36.	1.2	103
50	Fine mapping and imprinting analysis for fatness trait QTLs in pigs. <i>Mammalian Genome</i> , 2000, 11, 656-661.	1.0	103
51	Partial duplication of the PRLR and SPEF2 genes at the late feathering locus in chicken. <i>BMC Genomics</i> , 2008, 9, 391.	1.2	102
52	A decade of pig genome sequencing: a window on pig domestication and evolution. <i>Genetics Selection Evolution</i> , 2016, 48, 23.	1.2	102
53	Ancient pigs reveal a near-complete genomic turnover following their introduction to Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17231-17238.	3.3	101
54	Genetic Resources, Genome Mapping and Evolutionary Genomics of the Pig (<i>Sus scrofa</i>). <i>International Journal of Biological Sciences</i> , 2007, 3, 153-165.	2.6	100

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55	Assessing the contribution of breeds to genetic diversity in conservation schemes. <i>Genetics Selection Evolution</i> , 2002, 34, 613-33.	1.2	98
56	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	0.6	97
57	A genome-wide association study on androstenone levels in pigs reveals a cluster of candidate genes on chromosome 6. <i>BMC Genetics</i> , 2010, 11, 42.	2.7	96
58	Adult porcine genome-wide DNA methylation patterns support pigs as a biomedical model. <i>BMC Genomics</i> , 2015, 16, 743.	1.2	96
59	Deleterious alleles in the context of domestication, inbreeding, and selection. <i>Evolutionary Applications</i> , 2019, 12, 6-17.	1.5	94
60	Biodiversity of pig breeds from China and Europe estimated from pooled DNA samples: differences in microsatellite variation between two areas of domestication. <i>Genetics Selection Evolution</i> , 2008, 40, 103-28.	1.2	89
61	The Chicken Leukocyte Receptor Complex: A Highly Diverse Multigene Family Encoding at Least Six Structurally Distinct Receptor Types. <i>Journal of Immunology</i> , 2005, 175, 385-393.	0.4	88
62	Conservation genomic analysis of domestic and wild pig populations from the Iberian Peninsula. <i>BMC Genetics</i> , 2013, 14, 106.	2.7	87
63	Mapping quantitative trait loci affecting feather pecking behavior and stress response in laying hens. <i>Poultry Science</i> , 2003, 82, 1215-1222.	1.5	85
64	Copy number variation in the speciation of pigs: a possible prominent role for olfactory receptors. <i>BMC Genomics</i> , 2015, 16, 330.	1.2	85
65	The Evolution of Suidae. <i>Annual Review of Animal Biosciences</i> , 2016, 4, 61-85.	3.6	85
66	Biodiversity of pig breeds from China and Europe estimated from pooled DNA samples: differences in microsatellite variation between two areas of domestication. <i>Genetics Selection Evolution</i> , 2008, 40, 103-128.	1.2	84
67	Whole genome scan for quantitative trait loci affecting body weight in chickens using a three generation design. <i>Livestock Science</i> , 1998, 54, 133-150.	1.2	83
68	Genetic origin, admixture and population history of aurochs (<i>Bos primigenius</i>) and primitive European cattle. <i>Heredity</i> , 2017, 118, 169-176.	1.2	80
69	Preliminary Linkage Map of the Chicken (<i>Gallus domesticus</i>) Genome Based on Microsatellite Markers: 77 New Markers Mapped. <i>Poultry Science</i> , 1996, 75, 746-754.	1.5	79
70	Localization to chicken Chromosome 5 of a novel locus determining salmonellosis resistance. <i>Immunogenetics</i> , 2001, 53, 786-791.	1.2	79
71	Detection and Localization of Quantitative Trait Loci Affecting Fatness in Broilers. <i>Poultry Science</i> , 2004, 83, 295-301.	1.5	77
72	Signatures of Selection in the Genomes of Commercial and Non-Commercial Chicken Breeds. <i>PLoS ONE</i> , 2012, 7, e32720.	1.1	77

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73	Using genome-wide measures of coancestry to maintain diversity and fitness in endangered and domestic pig populations. <i>Genome Research</i> , 2015, 25, 970-981.	2.4	77
74	A whole-genome scan for quantitative trait loci affecting teat number in pigs. <i>Journal of Animal Science</i> , 2001, 79, 2320.	0.2	75
75	Genome-wide SNP detection in the great tit (<i>Parus major</i>) using high throughput sequencing. <i>Molecular Ecology</i> , 2010, 19, 89-99.	2.0	75
76	From FAANG to fork: application of highly annotated genomes to improve farmed animal production. <i>Genome Biology</i> , 2020, 21, 285.	3.8	74
77	Large scale single nucleotide polymorphism discovery in unsequenced genomes using second generation high throughput sequencing technology: applied to turkey. <i>BMC Genomics</i> , 2009, 10, 479.	1.2	73
78	Whole genome scan in chickens for quantitative trait loci affecting carcass traits. <i>Poultry Science</i> , 1999, 78, 1091-1099.	1.5	72
79	Comparison of linkage disequilibrium and haplotype diversity on macro- and microchromosomes in chicken. <i>BMC Genetics</i> , 2009, 10, 86.	2.7	72
80	The complete sequence of the gene encoding bovine β -casein. <i>Gene</i> , 1993, 123, 187-193.	1.0	71
81	The IGF2-intron3-G3072A substitution explains a major imprinted QTL effect on backfat thickness in a Meishan–European white pig intercross. <i>Genetical Research</i> , 2004, 84, 95-101.	0.3	70
82	The Genome of Winter Moth (<i>Operophtera brumata</i>) Provides a Genomic Perspective on Sexual Dimorphism and Phenology. <i>Genome Biology and Evolution</i> , 2015, 7, 2321-2332.	1.1	70
83	Microsatellite Polymorphism in Commercial Broiler and Layer Lines Estimated Using Pooled Blood Samples. <i>Poultry Science</i> , 1996, 75, 904-909.	1.5	69
84	A genome-wide scan for signatures of directional selection in domesticated pigs. <i>BMC Genomics</i> , 2015, 16, 130.	1.2	67
85	GO–FAANG meeting: a Gathering On Functional Annotation of Animal Genomes. <i>Animal Genetics</i> , 2016, 47, 528-533.	0.6	65
86	Distribution and Functionality of Copy Number Variation across European Cattle Populations. <i>Frontiers in Genetics</i> , 2017, 8, 108.	1.1	65
87	Genome wide SNP discovery, analysis and evaluation in mallard (<i>Anas platyrhynchos</i>). <i>BMC Genomics</i> , 2011, 12, 150.	1.2	63
88	Whole genome SNP discovery and analysis of genetic diversity in Turkey (<i>Meleagris gallopavo</i>). <i>BMC Genomics</i> , 2012, 13, 391.	1.2	63
89	Replicated analysis of the genetic architecture of quantitative traits in two wild great tit populations. <i>Molecular Ecology</i> , 2015, 24, 6148-6162.	2.0	61
90	Accuracy of genomic prediction using imputed whole-genome sequence data in white layers. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 167-179.	0.8	61

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91	New microsatellite markers in chicken optimized for automated fluorescent genotyping. <i>Animal Genetics</i> , 1997, 28, 427-437.	0.6	60
92	Porcine colonization of the Americas: a 60k SNP story. <i>Heredity</i> , 2013, 110, 321-330.	1.2	58
93	DNA sequences at the ends of the genome of bacteriophage Mu essential for transposition.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1985, 82, 2087-2091.	3.3	57
94	The design and cross-population application of a genome-wide SNP chip for the great tit <i>Parus major</i> . <i>Molecular Ecology Resources</i> , 2012, 12, 753-770.	2.2	56
95	Identification of genes regulating growth and fatness traits in pig through hypothalamic transcriptome analysis. <i>Physiological Genomics</i> , 2014, 46, 195-206.	1.0	56
96	Large scale variation in DNA copy number in chicken breeds. <i>BMC Genomics</i> , 2013, 14, 398.	1.2	55
97	Replicated high-density genetic maps of two great tit populations reveal fine-scale genomic departures from sex-equal recombination rates. <i>Heredity</i> , 2014, 112, 307-316.	1.2	53
98	Untangling the hybrid nature of modern pig genomes: a mosaic derived from biogeographically distinct and highly divergent <i>Sus scrofa</i> populations. <i>Molecular Ecology</i> , 2014, 23, 4089-4102.	2.0	52
99	Multiple octamer binding sites in the promoter region of the bovine κ -Casein gene. <i>Nucleic Acids Research</i> , 1992, 20, 4311-4318.	6.5	51
100	FISH on avian lampbrush chromosomes produces higher resolution gene mapping. <i>Genetica</i> , 2006, 128, 241-251.	0.5	50
101	Identification of high utility SNPs for population assignment and traceability purposes in the pig using high-throughput sequencing. <i>Animal Genetics</i> , 2011, 42, 613-620.	0.6	49
102	Two genes involved in penicillin biosynthesis are linked in a 5.1 kb <i>Sall</i> fragment in the genome of <i>Penicillium chrysogenum</i> . <i>Molecular Genetics and Genomics</i> , 1989, 218, 572-576.	2.4	47
103	Confirmation of quantitative trait loci affecting fatness in chickens. <i>Genetics Selection Evolution</i> , 2005, 37, 215-28.	1.2	47
104	Extent of linkage disequilibrium in chicken. <i>Cytogenetic and Genome Research</i> , 2007, 117, 338-345.	0.6	47
105	Regional differences in recombination hotspots between two chicken populations. <i>BMC Genetics</i> , 2010, 11, 11.	2.7	47
106	A history of hybrids? Genomic patterns of introgression in the True Geese. <i>BMC Evolutionary Biology</i> , 2017, 17, 201.	3.2	47
107	Comparative analysis of chicken chromosome 28 provides new clues to the evolutionary fragility of gene-rich vertebrate regions. <i>Genome Research</i> , 2007, 17, 1603-1613.	2.4	46
108	Widespread horizontal genomic exchange does not erode species barriers among sympatric ducks. <i>BMC Evolutionary Biology</i> , 2012, 12, 45.	3.2	46

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109	Loss of function mutations in essential genes cause embryonic lethality in pigs. <i>PLoS Genetics</i> , 2019, 15, e1008055.	1.5	46
110	Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. <i>BMC Genomics</i> , 2013, 14, 148.	1.2	45
111	The X Chromosome harbors quantitative trait loci for backfat thickness and intramuscular fat content in pigs. <i>Mammalian Genome</i> , 2000, 11, 800-802.	1.0	44
112	Application of massive parallel sequencing to whole genome SNP discovery in the porcine genome. <i>BMC Genomics</i> , 2009, 10, 374.	1.2	44
113	Whole-genome sequence analysis reveals differences in population management and selection of European low-input pig breeds. <i>BMC Genomics</i> , 2014, 15, 601.	1.2	44
114	Impact of neonatal iron deficiency on hippocampal DNA methylation and gene transcription in a porcine biomedical model of cognitive development. <i>BMC Genomics</i> , 2016, 17, 856.	1.2	44
115	Chicken Ig-Like Receptor B2, a Member of a Multigene Family, Is Mainly Expressed on B Lymphocytes, Recruits Both Src Homology 2 Domain Containing Protein Tyrosine Phosphatase (SHP)-1 and SHP-2, and Inhibits Proliferation. <i>Journal of Immunology</i> , 2004, 173, 7385-7393.	0.4	42
116	Characterization of a GlyCAM1-like gene (glycosylation-dependent cell adhesion molecule 1) which is highly and specifically expressed in the lactating bovine mammary gland. <i>Gene</i> , 1995, 158, 189-195.	1.0	41
117	Accuracy of Predicted Genomic Breeding Values in Purebred and Crossbred Pigs. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1575-1583.	0.8	41
118	Genomic diversity and differentiation of a managed island wild boar population. <i>Heredity</i> , 2016, 116, 60-67.	1.2	41
119	Regulation of expression of milk protein genes: a review. <i>Livestock Science</i> , 1994, 38, 61-78.	1.2	40
120	An assessment of European pig diversity using molecular markers: Partitioning of diversity among breeds. <i>Conservation Genetics</i> , 2005, 6, 729-741.	0.8	40
121	Genetic consequences of breaking migratory traditions in barnacle geese <i>Branta leucopsis</i> . <i>Molecular Ecology</i> , 2013, 22, 5835-5847.	2.0	40
122	Multicolour fluorescent detection and mapping of AFLP markers in chicken (<i>Gallus domesticus</i>). <i>Animal Genetics</i> , 1999, 30, 274-285.	0.6	39
123	The Gene Orders on Human Chromosome 15 and Chicken Chromosome 10 Reveal Multiple Inter- and Intrachromosomal Rearrangements. <i>Molecular Biology and Evolution</i> , 2001, 18, 2102-2109.	3.5	39
124	A tree of geese: A phylogenomic perspective on the evolutionary history of True Geese. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 303-313.	1.2	39
125	Balancing selection on a recessive lethal deletion with pleiotropic effects on two neighboring genes in the porcine genome. <i>PLoS Genetics</i> , 2018, 14, e1007661.	1.5	39
126	Genomic analysis on pygmy hog reveals extensive interbreeding during wild boar expansion. <i>Nature Communications</i> , 2019, 10, 1992.	5.8	38

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127	A systematic survey to identify lethal recessive variation in highly managed pig populations. BMC Genomics, 2017, 18, 858.	1.2	37
128	A high-density SNP chip for genotyping great tit (<i>Parus major</i>) populations and its application to studying the genetic architecture of exploration behaviour. Molecular Ecology Resources, 2018, 18, 877-891.	2.2	36
129	The type of bottleneck matters: Insights into the deleterious variation landscape of small managed populations. Evolutionary Applications, 2020, 13, 330-341.	1.5	36
130	Comparative analysis of the natriuretic peptide precursor gene cluster in vertebrates reveals loss of ANF and retention of CNP-3 in chicken. Developmental Dynamics, 2005, 233, 1076-1082.	0.8	35
131	A Novel Activating Chicken IgY FcR Is Related to Leukocyte Receptor Complex (LRC) Genes but Is Located on a Chromosomal Region Distinct from the LRC and FcR Gene Clusters. Journal of Immunology, 2009, 182, 1533-1540.	0.4	35
132	A SNP based linkage map of the turkey genome reveals multiple intrachromosomal rearrangements between the Turkey and Chicken genomes. BMC Genomics, 2010, 11, 647.	1.2	35
133	Development of a genetic tool for product regulation in the diverse British pig breed market. BMC Genomics, 2012, 13, 580.	1.2	35
134	Human pathways in animal models: possibilities and limitations. Nucleic Acids Research, 2021, 49, 1859-1871.	6.5	35
135	The Imprinted Gene DIO3 Is a Candidate Gene for Litter Size in Pigs. PLoS ONE, 2012, 7, e31825.	1.1	35
136	The HMGI-C gene is a likely candidate for the autosomal dwarf locus in the chicken. , 1998, 89, 295-300.		34
137	Systematic differences in the response of genetic variation to pedigree and genome-based selection methods. Heredity, 2014, 113, 503-513.	1.2	34
138	Genome-wide population structure and admixture analysis reveals weak differentiation among Ugandan goat breeds. Animal Genetics, 2018, 49, 59-70.	0.6	34
139	Identification of quantitative trait loci for receiving pecks in young and adult laying hens. Poultry Science, 2003, 82, 1661-1667.	1.5	33
140	Segregation distortion in chicken and the evolutionary consequences of female meiotic drive in birds. Heredity, 2010, 105, 290-298.	1.2	33
141	Centromere positions in chicken and Japanese quail chromosomes: de novo centromere formation versus pericentric inversions. Chromosome Research, 2012, 20, 1017-1032.	1.0	33
142	Mining for single nucleotide polymorphisms in pig genome sequence data. BMC Genomics, 2009, 10, 4.	1.2	32
143	Functional genes mapped on the chicken genome. Animal Genetics, 1995, 26, 73-78.	0.6	32
144	East Asian contributions to Dutch traditional and western commercial chickens inferred from mtDNA analysis. Animal Genetics, 2011, 42, 125-133.	0.6	32

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145	SNP marker detection and genotyping in tilapia. <i>Molecular Ecology Resources</i> , 2012, 12, 932-941.	2.2	32
146	Testing models of speciation from genome sequences: divergence and asymmetric admixture in <i>L. s. island</i> <i>S. outh</i> <i>E. ast</i> <i>A. sian</i> <i>S. us</i> species during the <i>P. lio</i> <i>P. leistocene</i> climatic fluctuations. <i>Molecular Ecology</i> , 2014, 23, 5566-5574.	2.0	32
147	Identification of QTLs Involved in Open-Field Behavior in Young and Adult Laying Hens. <i>Behavior Genetics</i> , 2004, 34, 325-333.	1.4	31
148	Genetic mapping of quantitative trait loci affecting susceptibility in chicken to develop pulmonary hypertension syndrome. <i>Animal Genetics</i> , 2005, 36, 468-476.	0.6	31
149	Genetic diversity in European pigs utilizing amplified fragment length polymorphism markers. <i>Animal Genetics</i> , 2006, 37, 232-238.	0.6	31
150	Genetic variances, heritabilities and maternal effects on body weight, breast meat yield, meat quality traits and the shape of the growth curve in turkey birds. <i>BMC Genetics</i> , 2011, 12, 14.	2.7	31
151	Genomic relatedness and diversity of Swedish native cattle breeds. <i>Genetics Selection Evolution</i> , 2019, 51, 56.	1.2	31
152	Mixed ancestry from wild and domestic lineages contributes to the rapid expansion of invasive feral swine. <i>Molecular Ecology</i> , 2020, 29, 1103-1119.	2.0	31
153	New Microsatellite Markers on the Linkage Map of the Chicken Genome. <i>Journal of Heredity</i> , 1994, 85, 410-413.	1.0	30
154	Comparative mapping of human Chromosome 19 with the chicken shows conserved synteny and gives an insight into chromosomal evolution. <i>Mammalian Genome</i> , 2002, 13, 310-315.	1.0	30
155	Detection of QTL for immune response to sheep red blood cells in laying hens. <i>Animal Genetics</i> , 2003, 34, 422-428.	0.6	30
156	Detection of different quantitative trait loci for antibody responses to keyhole limpet hemocyanin and <i>Mycobacterium butyricum</i> in two unrelated populations of laying hens. <i>Poultry Science</i> , 2003, 82, 1845-1852.	1.5	30
157	Detection of QTL for innate: Non-specific antibody levels binding LPS and LTA in two independent populations of laying hens. <i>Developmental and Comparative Immunology</i> , 2006, 30, 659-666.	1.0	30
158	Review of the initial validation and characterization of a 3K chicken SNP array. <i>World's Poultry Science Journal</i> , 2008, 64, 219-226.	1.4	30
159	Mapping of a site for packaging of bacteriophage Mu DNA. <i>Virology</i> , 1985, 144, 520-522.	1.1	29
160	QTL Mapping in chicken using a three generation full sib family structure of an extreme broiler X broiler cross. <i>Animal Biotechnology</i> , 1997, 8, 41-46.	0.7	29
161	Highly polymorphic microsatellite markers in poultry. <i>Animal Genetics</i> , 1993, 24, 441-443.	0.6	29
162	The effects of recent changes in breeding preferences on maintaining traditional Dutch chicken genomic diversity. <i>Heredity</i> , 2018, 121, 564-578.	1.2	29

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163	Organoids: a promising new in vitro platform in livestock and veterinary research. <i>Veterinary Research</i> , 2021, 52, 43.	1.1	29
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167	Polymorphic microsatellites developed by cross-species amplifications in common pheasant breeds. <i>Animal Genetics</i> , 2001, 32, 222-225.	0.6	27
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169	A survey of functional genomic variation in domesticated chickens. <i>Genetics Selection Evolution</i> , 2018, 50, 17.	1.2	27
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292	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
293	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0