

# Martien A M Groenen

## List of Publications by Year in descending order

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Version: 2024-02-01

293  
papers

21,384  
citations

10351

72  
h-index

12233

133  
g-index

304  
all docs

304  
docs citations

304  
times ranked

14933  
citing authors

#	ARTICLE	IF	CITATIONS
1	Familial follicular cell thyroid carcinomas in a large number of Dutch German longhaired pointers. <i>Veterinary and Comparative Oncology</i> , 2022, 20, 227-234.	0.8	4
2	Assessing the genomic diversity and relatedness in 10 Canadian heritage chicken lines using whole-genome sequence data. <i>Journal of Animal Breeding and Genetics</i> , 2022, , .	0.8	1
3	Fine Mapping of a Major Backfat QTL Reveals a Causal Regulatory Variant Affecting the CCND2 Gene. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	9
4	The Visayan Warty Pig ( <i>Sus cebifrons</i> ) Genome Provides Insight Into Chromosome Evolution and Sensory Adaptation in Pigs. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	3
5	Genetic consequences of long-term small effective population size in the critically endangered pygmy hog. <i>Evolutionary Applications</i> , 2021, 14, 710-720.	1.5	19
6	Heterogeneity of a dwarf phenotype in Dutch traditional chicken breeds revealed by genomic analyses. <i>Evolutionary Applications</i> , 2021, 14, 1095-1108.	1.5	7
7	Parallel Genomic Changes Drive Repeated Evolution of Placentas in Live-Bearing Fish. <i>Molecular Biology and Evolution</i> , 2021, 38, 2627-2638.	3.5	11
8	Human pathways in animal models: possibilities and limitations. <i>Nucleic Acids Research</i> , 2021, 49, 1859-1871.	6.5	35
9	Organoids: a promising new in vitro platform in livestock and veterinary research. <i>Veterinary Research</i> , 2021, 52, 43.	1.1	29
10	A natural knockout of the <i>MYO7A</i> gene leads to pre-weaning mortality in pigs. <i>Animal Genetics</i> , 2021, 52, 514-517.	0.6	5
11	Deleterious Mutations in the TPO Gene Associated with Familial Thyroid Follicular Cell Carcinoma in Dutch German Longhaired Pointers. <i>Genes</i> , 2021, 12, 997.	1.0	5
12	Accelerated discovery of functional genomic variation in pigs. <i>Genomics</i> , 2021, 113, 2229-2239.	1.3	16
13	A 12 kb multi-allelic copy number variation encompassing a GC gene enhancer is associated with mastitis resistance in dairy cattle. <i>PLoS Genetics</i> , 2021, 17, e1009331.	1.5	25
14	Introgression contributes to distribution of structural variations in cattle. <i>Genomics</i> , 2021, 113, 3092-3102.	1.3	7
15	Time Course Transcriptomic Study Reveals the Gene Regulation During Liver Development and the Correlation With Abdominal Fat Weight in Chicken. <i>Frontiers in Genetics</i> , 2021, 12, 723519.	1.1	9
16	CNVranger: association analysis of CNVs with gene expression and quantitative phenotypes. <i>Bioinformatics</i> , 2020, 36, 972-973.	1.8	17
17	The type of bottleneck matters: Insights into the deleterious variation landscape of small managed populations. <i>Evolutionary Applications</i> , 2020, 13, 330-341.	1.5	36
18	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. <i>PLoS Genetics</i> , 2020, 16, e1009027.	1.5	7

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19	From FAANG to fork: application of highly annotated genomes to improve farmed animal production. <i>Genome Biology</i> , 2020, 21, 285.	3.8	74
20	RNA-Seq Analysis Reveals Hub Genes Involved in Chicken Intramuscular Fat and Abdominal Fat Deposition During Development. <i>Frontiers in Genetics</i> , 2020, 11, 1009.	1.1	25
21	Genome-Wide Assessment of DNA Methylation in Chicken Cardiac Tissue Exposed to Different Incubation Temperatures and CO2 Levels. <i>Frontiers in Genetics</i> , 2020, 11, 558189.	1.1	11
22	Quantitative genetics of wing morphology in the parasitoid wasp <i>Nasonia vitripennis</i> : hosts increase sibling similarity. <i>Heredity</i> , 2020, 125, 40-49.	1.2	6
23	pCADD: SNV prioritisation in <i>Sus scrofa</i> . <i>Genetics Selection Evolution</i> , 2020, 52, 4.	1.2	21
24	Altered Hippocampal Epigenetic Regulation Underlying Reduced Cognitive Development in Response to Early Life Environmental Insults. <i>Genes</i> , 2020, 11, 162.	1.0	8
25	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
26	Impact of genotype, body weight and sex on the prenatal muscle transcriptome of Iberian pigs. <i>PLoS ONE</i> , 2020, 15, e0227861.	1.1	12
27	Parallel Genetic Origin of Foot Feathering in Birds. <i>Molecular Biology and Evolution</i> , 2020, 37, 2465-2476.	3.5	19
28	The Genomes of the Livebearing Fish Species <i>Poeciliopsis retropinna</i> and <i>Poeciliopsis turrubarensis</i> Reflect Their Different Reproductive Strategies. <i>Molecular Biology and Evolution</i> , 2020, 37, 1376-1386.	3.5	8
29	Functional and population genetic features of copy number variations in two dairy cattle populations. <i>BMC Genomics</i> , 2020, 21, 89.	1.2	19
30	Developments in genetic modification of cattle and implications for regulation, safety and traceability. <i>Frontiers of Agricultural Science and Engineering</i> , 2020, 7, 136.	0.9	7
31	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
32	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
33	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
34	Prioritizing sequence variants in conserved non-coding elements in the chicken genome using chCADD. , 2020, 16, e1009027.		0
35	Deleterious alleles in the context of domestication, inbreeding, and selection. <i>Evolutionary Applications</i> , 2019, 12, 6-17.	1.5	94
36	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

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37	The genome of the live-bearing fish <i>Heterandria formosa</i> implicates a role of conserved vertebrate genes in the evolution of placental fish. <i>BMC Evolutionary Biology</i> , 2019, 19, 156.	3.2	7
38	Detection of a Frameshift Deletion in the SPTBN4 Gene Leads to Prevention of Severe Myopathy and Postnatal Mortality in Pigs. <i>Frontiers in Genetics</i> , 2019, 10, 1226.	1.1	6
39	Genomic relatedness and diversity of Swedish native cattle breeds. <i>Genetics Selection Evolution</i> , 2019, 51, 56.	1.2	31
40	Response to Perrier and Charmantier: On the importance of time scales when studying adaptive evolution. <i>Evolution Letters</i> , 2019, 3, 248-253.	1.6	1
41	The Genomic Complexity of a Large Inversion in Great Tits. <i>Genome Biology and Evolution</i> , 2019, 11, 1870-1881.	1.1	15
42	Genomic analysis on pygmy hog reveals extensive interbreeding during wild boar expansion. <i>Nature Communications</i> , 2019, 10, 1992.	5.8	38
43	Loss of function mutations in essential genes cause embryonic lethality in pigs. <i>PLoS Genetics</i> , 2019, 15, e1008055.	1.5	46
44	Deciphering the patterns of genetic admixture and diversity in southern European cattle using genome-wide SNPs. <i>Evolutionary Applications</i> , 2019, 12, 951-963.	1.5	22
45	Exploring the unmapped DNA and RNA reads in a songbird genome. <i>BMC Genomics</i> , 2019, 20, 19.	1.2	21
46	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
47	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. <i>Molecular Ecology Resources</i> , 2018, 18, 877-891.	2.2	36
48	Genome-wide population structure and admixture analysis reveals weak differentiation among Ugandan goat breeds. <i>Animal Genetics</i> , 2018, 49, 59-70.	0.6	34
49	The impact of genome editing on the introduction of monogenic traits in livestock. <i>Genetics Selection Evolution</i> , 2018, 50, 18.	1.2	21
50	A survey of functional genomic variation in domesticated chickens. <i>Genetics Selection Evolution</i> , 2018, 50, 17.	1.2	27
51	CNVs are associated with genomic architecture in a songbird. <i>BMC Genomics</i> , 2018, 19, 195.	1.2	11
52	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
53	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
54	A Novel Loss-of-Function Variant in Transmembrane Protein 263 (TMEM263) of Autosomal Dwarfism in Chicken. <i>Frontiers in Genetics</i> , 2018, 9, 193.	1.1	17

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55	Early and late feathering in turkey and chicken: same gene but different mutations. <i>Genetics Selection Evolution</i> , 2018, 50, 7.	1.2	11
56	Gene networks for total number born in pigs across divergent environments. <i>Mammalian Genome</i> , 2017, 28, 426-435.	1.0	3
57	Recent natural selection causes adaptive evolution of an avian polygenic trait. <i>Science</i> , 2017, 358, 365-368.	6.0	161
58	Oncopig Soft-Tissue Sarcomas Recapitulate Key Transcriptional Features of Human Sarcomas. <i>Scientific Reports</i> , 2017, 7, 2624.	1.6	27
59	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
60	Distinguishing migration events of different timing for wild boar in the Balkans. <i>Journal of Biogeography</i> , 2017, 44, 259-270.	1.4	14
61	Genome-wide SNP data unveils the globalization of domesticated pigs. <i>Genetics Selection Evolution</i> , 2017, 49, 71.	1.2	114
62	Distribution and Functionality of Copy Number Variation across European Cattle Populations. <i>Frontiers in Genetics</i> , 2017, 8, 108.	1.1	65
63	A history of hybrids? Genomic patterns of introgression in the True Geese. <i>BMC Evolutionary Biology</i> , 2017, 17, 201.	3.2	47
64	A systematic survey to identify lethal recessive variation in highly managed pig populations. <i>BMC Genomics</i> , 2017, 18, 858.	1.2	37
65	The Use of Genomics in Conservation Management of the Endangered Visayan Warty Pig ( <i>Sus</i> ). <i>Tj ETQq1 1 0.784314 rgBT /Overlook</i>	0.8	12
66	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
67	After genome-wide association studies: Gene networks elucidating candidate genes divergences for number of teats across two pig populations1. <i>Journal of Animal Science</i> , 2016, 94, 1446-1458.	0.2	11
68	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
69	Genome-wide single nucleotide polymorphism (SNP) identification and characterization in a non-model organism, the African buffalo ( <i>Syncerus caffer</i> ), using next generation sequencing. <i>Mammalian Biology</i> , 2016, 81, 595-603.	0.8	11
70	<sc>GO</sc>â€œ<sc>FAANG</sc> meeting: a Gathering On Functional Annotation of <sc>An</sc>imal Genomes. <i>Animal Genetics</i> , 2016, 47, 528-533.	0.6	65
71	Evidence for adaptation of porcine Toll-like receptors. <i>Immunogenetics</i> , 2016, 68, 179-189.	1.2	7
72	A decade of pig genome sequencing: a window on pig domestication and evolution. <i>Genetics Selection Evolution</i> , 2016, 48, 23.	1.2	102

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73	Evolutionary patterns of Toll-like receptor signaling pathway genes in the Suidae. <i>BMC Evolutionary Biology</i> , 2016, 16, 33.	3.2	8
74	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
75	Evolutionary signals of selection on cognition from the great tit genome and methylome. <i>Nature Communications</i> , 2016, 7, 10474.	5.8	172
76	The Evolution of Suidae. <i>Annual Review of Animal Biosciences</i> , 2016, 4, 61-85.	3.6	85
77	Genomic diversity and differentiation of a managed island wild boar population. <i>Heredity</i> , 2016, 116, 60-67.	1.2	41
78	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
79	Adult porcine genome-wide DNA methylation patterns support pigs as a biomedical model. <i>BMC Genomics</i> , 2015, 16, 743.	1.2	96
80	Accuracy of Predicted Genomic Breeding Values in Purebred and Crossbred Pigs. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1575-1583.	0.8	41
81	Adaptive Evolution of Toll-Like Receptors (TLRs) in the Family Suidae. <i>PLoS ONE</i> , 2015, 10, e0124069.	1.1	22
82	Accuracy of genomic prediction using deregressed breeding values estimated from purebred and crossbred offspring phenotypes in pigs1. <i>Journal of Animal Science</i> , 2015, 93, 3313-3321.	0.2	10
83	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
84	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
85	Population-level consequences of complementary sex determination in a solitary parasitoid. <i>BMC Evolutionary Biology</i> , 2015, 15, 98.	3.2	15
86	Artificial selection on introduced Asian haplotypes shaped the genetic architecture in European commercial pigs. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20152019.	1.2	25
87	Evolution of Tibetan wild boars. <i>Nature Genetics</i> , 2015, 47, 188-189.	9.4	10
88	TRES: Identification of Discriminatory and Informative SNPs from Population Genomic Data: Figure 1.. <i>Journal of Heredity</i> , 2015, 106, 672-676.	1.0	26
89	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	0.6	97
90	A genome-wide scan for signatures of directional selection in domesticated pigs. <i>BMC Genomics</i> , 2015, 16, 130.	1.2	67

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91	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
92	Accuracy of imputation using the most common sires as reference population in layer chickens. <i>BMC Genetics</i> , 2015, 16, 101.	2.7	15
93	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
94	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
95	A Genetic Linkage Map of Sole ( <i>Solea solea</i> ): A Tool for Evolutionary and Comparative Analyses of Exploited (Flat)Fishes. <i>PLoS ONE</i> , 2014, 9, e115040.	1.1	17
96	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
97	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
98	Identification of species-specific novel transcripts in pig reproductive tissues using RNA-seq. <i>Animal Genetics</i> , 2014, 45, 198-204.	0.6	22
99	Testing models of speciation from genome sequences: divergence and asymmetric admixture in Sland South-East Asian species during the Pliocene climatic fluctuations. <i>Molecular Ecology</i> , 2014, 23, 5566-5574.	2.0	32
100	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. <i>BMC Genetics</i> , 2014, 15, 4.	2.7	7
101	Systematic differences in the response of genetic variation to pedigree and genome-based selection methods. <i>Heredity</i> , 2014, 113, 503-513.	1.2	34
102	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
103	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
104	Genomic analysis reveals selection for Asian genes in European pigs following human-mediated introgression. <i>Nature Communications</i> , 2014, 5, 4392.	5.8	137
105	Asian low-androstenone haplotype on pig chromosome 6 does not unfavorably affect production and reproduction traits. <i>Animal Genetics</i> , 2014, 45, 874-877.	0.6	1
106	Hybrid origin of European commercial pigs examined by an in-depth haplotype analysis on chromosome 1. <i>Frontiers in Genetics</i> , 2014, 5, 442.	1.1	19
107	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
108	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

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109	Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. BMC Genomics, 2013, 14, 148.	1.2	45
110	Large scale variation in DNA copy number in chicken breeds. BMC Genomics, 2013, 14, 398.	1.2	55
111	Porcine colonization of the Americas: a 60k SNP story. Heredity, 2013, 110, 321-330.	1.2	58
112	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. Nature Genetics, 2013, 45, 776-783.	9.4	327
113	Signatures of Diversifying Selection in European Pig Breeds. PLoS Genetics, 2013, 9, e1003453.	1.5	228
114	Pig Domestication and Human-Mediated Dispersal in Western Eurasia Revealed through Ancient DNA and Geometric Morphometrics. Molecular Biology and Evolution, 2013, 30, 824-832.	3.5	196
115	Genome sequencing reveals fine scale diversification and reticulation history during speciation in Sus. Genome Biology, 2013, 14, R107.	13.9	137
116	Genetic consequences of breaking migratory traditions in barnacle geese <i>Branta leucopsis</i> . Molecular Ecology, 2013, 22, 5835-5847.	2.0	40
117	Conservation genomic analysis of domestic and wild pig populations from the Iberian Peninsula. BMC Genetics, 2013, 14, 106.	2.7	87
118	Regions of Homozygosity in the Porcine Genome: Consequence of Demography and the Recombination Landscape. PLoS Genetics, 2012, 8, e1003100.	1.5	266
119	Genetic correlation between heart ratio and body weight as a function of ascites frequency in broilers split up into sex and health status. Poultry Science, 2012, 91, 556-564.	1.5	13
120	Domesticated species form a treasure-trove for molecular characterization of Mendelian traits by exploiting the specific genetic structure of these species in across-breed genome wide association studies. Heredity, 2012, 109, 1-3.	1.2	9
121	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
122	Centromere positions in chicken and Japanese quail chromosomes: de novo centromere formation versus pericentric inversions. Chromosome Research, 2012, 20, 1017-1032.	1.0	33
123	Analyses of pig genomes provide insight into porcine demography and evolution. Nature, 2012, 491, 393-398.	13.7	1,190
124	Widespread horizontal genomic exchange does not erode species barriers among sympatric ducks. BMC Evolutionary Biology, 2012, 12, 45.	3.2	46
125	Whole genome SNP discovery and analysis of genetic diversity in Turkey ( <i>Meleagris gallopavo</i> ). BMC Genomics, 2012, 13, 391.	1.2	63
126	Development of a genetic tool for product regulation in the diverse British pig breed market. BMC Genomics, 2012, 13, 580.	1.2	35



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127	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
128	Signatures of Selection in the Genomes of Commercial and Non-Commercial Chicken Breeds. <i>PLoS ONE</i> , 2012, 7, e32720.	1.1	77
129	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
130	SNP marker detection and genotyping in tilapia. <i>Molecular Ecology Resources</i> , 2012, 12, 932-941.	2.2	32
131	The Imprinted Gene DIO3 Is a Candidate Gene for Litter Size in Pigs. <i>PLoS ONE</i> , 2012, 7, e31825.	1.1	35
132	The Development of a Genome Wide SNP Set for the Barnacle Goose <i>Branta leucopsis</i> . <i>PLoS ONE</i> , 2012, 7, e38412.	1.1	22
133	Prediction of Altered 3' UTR miRNA-Binding Sites from RNA-Seq Data: The Swine Leukocyte Antigen Complex (SLA) as a Model Region. <i>PLoS ONE</i> , 2012, 7, e48607.	1.1	15
134	The distal end of porcine chromosome 6p is involved in the regulation of skatole levels in boars. <i>BMC Genetics</i> , 2011, 12, 35.	2.7	20
135	Genome wide SNP discovery, analysis and evaluation in mallard ( <i>Anas platyrhynchos</i> ). <i>BMC Genomics</i> , 2011, 12, 150.	1.2	63
136	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
137	Regional Regulation of Transcription in the Bovine Genome. <i>PLoS ONE</i> , 2011, 6, e20413.	1.1	1
138	East Asian contributions to Dutch traditional and western commercial chickens inferred from mtDNA analysis. <i>Animal Genetics</i> , 2011, 42, 125-133.	0.6	32
139	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
140	Partial short-read sequencing of a highly inbred Iberian pig and genomics inference thereof. <i>Heredity</i> , 2011, 107, 256-264.	1.2	16
141	Whole genome QTL mapping for growth, meat quality and breast meat yield traits in turkey. <i>BMC Genetics</i> , 2011, 12, 61.	2.7	12
142	Number and mode of inheritance of QTL influencing backfat thickness on SSC2p in Sino-European pig pedigrees. <i>Genetics Selection Evolution</i> , 2011, 43, 11.	1.2	6
143	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
144	The development and characterization of a 60K SNP chip for chicken. <i>BMC Genomics</i> , 2011, 12, 274.	1.2	185

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145	Structural variation in the chicken genome identified by paired-end next-generation DNA sequencing of reduced representation libraries. <i>BMC Genomics</i> , 2011, 12, 94.	1.2	25
146	Combining two Meishan F2 crosses improves the detection of QTL on pig chromosomes 2, 4 and 6. <i>Genetics Selection Evolution</i> , 2010, 42, 42.	1.2	12
147	Regional regulation of transcription in the chicken genome. <i>BMC Genomics</i> , 2010, 11, 28.	1.2	7
148	Pig genome sequence - analysis and publication strategy. <i>BMC Genomics</i> , 2010, 11, 438.	1.2	132
149	A SNP based linkage map of the turkey genome reveals multiple intrachromosomal rearrangements between the Turkey and Chicken genomes. <i>BMC Genomics</i> , 2010, 11, 647.	1.2	35
150	Regional differences in recombination hotspots between two chicken populations. <i>BMC Genetics</i> , 2010, 11, 11.	2.7	47
151	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
152	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
153	Segregation distortion in chicken and the evolutionary consequences of female meiotic drive in birds. <i>Heredity</i> , 2010, 105, 290-298.	1.2	33
154	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
155	Precise Centromere Positioning on Chicken Chromosome 3. <i>Cytogenetic and Genome Research</i> , 2010, 129, 310-313.	0.6	17
156	The use of blood gas parameters to predict ascites susceptibility in juvenile broilers. <i>Poultry Science</i> , 2010, 89, 1684-1691.	1.5	17
157	Gene Expression in Chicken Reveals Correlation with Structural Genomic Features and Conserved Patterns of Transcription in the Terrestrial Vertebrates. <i>PLoS ONE</i> , 2010, 5, e11990.	1.1	20
158	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
159	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
160	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. <i>Journal of Immunology</i> , 2009, 182, 1533-1540.	0.4	35
161	Comparison of three microarray probe annotation pipelines: differences in strategies and their effect on downstream analysis. <i>BMC Proceedings</i> , 2009, 3, S1.	1.8	7
162	OligoRAP – an Oligo Re-Annotation Pipeline to improve annotation and estimate target specificity. <i>BMC Proceedings</i> , 2009, 3, S4.	1.8	9

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163	Microarray data mining using Bioconductor packages. BMC Proceedings, 2009, 3, S9.	1.8	9
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