

Jack C M Dekkers

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7926839/publications.pdf>

Version: 2024-02-01

137
papers

5,186
citations

87843

38
h-index

102432

66
g-index

145
all docs

145
docs citations

145
times ranked

4262
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic analysis of disease resilience of wean-to-finish pigs under a natural disease challenge model using reaction norms. <i>Genetics Selection Evolution</i> , 2022, 54, 11.	1.2	0
2	Predictions of the accuracy of genomic prediction: connecting R ² , selection index theory, and Fisher information. <i>Genetics Selection Evolution</i> , 2022, 54, 13.	1.2	2
3	Genome-wide association study of disease resilience traits from a natural polymicrobial disease challenge model in pigs identifies the importance of the major histocompatibility complex region. <i>C3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
4	Ten simple rules to ruin a collaborative environment. <i>PLoS Computational Biology</i> , 2022, 18, e1009957.	1.5	1
5	Effect of the host genotype at a Porcine Reproductive and Respiratory Syndrome (PRRS) resistance marker on evolution of the modified-live PRRS vaccine virus in pigs. <i>Virus Research</i> , 2022, 316, 198809.	1.1	1
6	Application of Bayesian genomic prediction methods to genome-wide association analyses. <i>Genetics Selection Evolution</i> , 2022, 54, 31.	1.2	3
7	Gene expression in tonsils in swine following infection with porcine reproductive and respiratory syndrome virus. <i>BMC Veterinary Research</i> , 2021, 17, 88.	0.7	12
8	Cross-validation of best linear unbiased predictions of breeding values using an efficient leave-one-out strategy. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 519-527.	0.8	16
9	Genomics of response to porcine reproductive and respiratory syndrome virus in purebred and crossbred sows: antibody response and performance following natural infection vs. vaccination. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	2
10	Distinct transcriptomic response to Newcastle disease virus infection during heat stress in chicken tracheal epithelial tissue. <i>Scientific Reports</i> , 2021, 11, 7450.	1.6	4
11	Proliferation of peripheral blood mononuclear cells from healthy piglets after mitogen stimulation as indicators of disease resilience. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	5
12	Predicting the accuracy of genomic predictions. <i>Genetics Selection Evolution</i> , 2021, 53, 55.	1.2	17
13	Host Genetics of Response to Porcine Reproductive and Respiratory Syndrome in Sows: Reproductive Performance. <i>Frontiers in Genetics</i> , 2021, 12, 707870.	1.1	1
14	Quantitative analysis of the blood transcriptome of young healthy pigs and its relationship with subsequent disease resilience. <i>BMC Genomics</i> , 2021, 22, 614.	1.2	9
15	Host Genetics of Response to Porcine Reproductive and Respiratory Syndrome in Sows: Antibody Response as an Indicator Trait for Improved Reproductive Performance. <i>Frontiers in Genetics</i> , 2021, 12, 707873.	1.1	4
16	Associations of natural variation in the CD163 and other candidate genes on host response of nursery pigs to porcine reproductive and respiratory syndrome virus infection. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	6
17	Genetic parameters of drinking and feeding traits of wean-to-finish pigs under a polymicrobial natural disease challenge. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 105.	2.1	4
18	Thyroid hormone suppression in feeder pigs following polymicrobial or porcine reproductive and respiratory syndrome virus-2 challenge. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	4

#	ARTICLE	IF	CITATIONS
19	Multiple trait breeding programs with genotype-by-environment interactions based on reaction norms, with application to genetic improvement of disease resilience. <i>Genetics Selection Evolution</i> , 2021, 53, 93.	1.2	3
20	Further host-genomic characterization of total antibody response to PRRSV vaccination and its relationship with reproductive performance in commercial sows: genome-wide haplotype and zygosity analyses. <i>Genetics Selection Evolution</i> , 2021, 53, 91.	1.2	3
21	Investigating the relationship between vaginal microbiota and host genetics and their impact on immune response and farrowing traits in commercial gilts. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 84-102.	0.8	16
22	Genetic Analysis of Antibody Response to Porcine Reproductive and Respiratory Syndrome Vaccination as an Indicator Trait for Reproductive Performance in Commercial Sows. <i>Frontiers in Genetics</i> , 2020, 11, 1011.	1.1	16
23	The genetic basis of natural antibody titers of young healthy pigs and relationships with disease resilience. <i>BMC Genomics</i> , 2020, 21, 648.	1.2	17
24	Phenotypic variability and population structure analysis of Tanzanian free-range local chickens. <i>BMC Veterinary Research</i> , 2020, 16, 360.	0.7	14
25	Genomic Analysis of IgG Antibody Response to Common Pathogens in Commercial Sows in Health-Challenged Herds. <i>Frontiers in Genetics</i> , 2020, 11, 593804.	1.1	4
26	Genetic Basis of Response of Ghanaian Local Chickens to Infection With a Lentogenic Newcastle Disease Virus. <i>Frontiers in Genetics</i> , 2020, 11, 739.	1.1	8
27	Genetic analysis of disease resilience in wean-to-finish pigs from a natural disease challenge model. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	31
28	Transcriptome Analysis Reveals Inhibitory Effects of Lentogenic Newcastle Disease Virus on Cell Survival and Immune Function in Spleen of Commercial Layer Chicks. <i>Genes</i> , 2020, 11, 1003.	1.0	2
29	Novel Combined Tissue Transcriptome Analysis After Lentogenic Newcastle Disease Virus Challenge in Inbred Chicken Lines of Differential Resistance. <i>Frontiers in Genetics</i> , 2020, 11, 11.	1.1	14
30	Novel Engraftment and T Cell Differentiation of Human Hematopoietic Cells in ART ^Δ /IL2RG ^Δ /Y SCID Pigs. <i>Frontiers in Immunology</i> , 2020, 11, 100.	2.2	21
31	A biphasic curve for modeling, classifying, and predicting egg production in single cycle and molted flocks. <i>Poultry Science</i> , 2020, 99, 2007-2010.	1.5	2
32	Exploring Phenotypes for Disease Resilience in Pigs Using Complete Blood Count Data From a Natural Disease Challenge Model. <i>Frontiers in Genetics</i> , 2020, 11, 216.	1.1	14
33	CD3 ⁺ Cells in Pigs With Severe Combined Immunodeficiency Due to Defects in ARTEMIS. <i>Frontiers in Immunology</i> , 2020, 11, 510.	2.2	5
34	Autozygosity and Genetic Differentiation of Landrace and Large White Pigs as Revealed by the Genetic Analyses of Crossbreds. <i>Frontiers in Genetics</i> , 2019, 10, 739.	1.1	8
35	Genetic Analyses of Tanzanian Local Chicken Ecotypes Challenged with Newcastle Disease Virus. <i>Genes</i> , 2019, 10, 546.	1.0	20
36	Effect of a dual enteric and respiratory pathogen challenge on swine growth, efficiency, carcass composition, and pork quality ¹ . <i>Journal of Animal Science</i> , 2019, 97, 4710-4720.	0.2	4

#	ARTICLE	IF	CITATIONS
37	Genetics and Genomic Regions Affecting Response to Newcastle Disease Virus Infection under Heat Stress in Layer Chickens. <i>Genes</i> , 2019, 10, 61.	1.0	19
38	Infectivity of GII.4 human norovirus does not differ between T-B-NK+ severe combined immunodeficiency (SCID) and non-SCID gnotobiotic pigs, implicating the role of NK cells in mediation of human norovirus infection. <i>Virus Research</i> , 2019, 267, 21-25.	1.1	6
39	Genetics of male reproductive performance in White Leghorns. <i>Poultry Science</i> , 2019, 98, 2729-2733.	1.5	6
40	The effects of a globin blocker on the resolution of 3â€™ mRNA sequencing data in porcine blood. <i>BMC Genomics</i> , 2019, 20, 741.	1.2	4
41	The effect of a porcine reproductive and respiratory syndrome outbreak on genetic parameters and reaction norms for reproductive performance in pigs1. <i>Journal of Animal Science</i> , 2019, 97, 1101-1116.	0.2	5
42	Identification of factors associated with virus level in tonsils of pigs experimentally infected with porcine reproductive and respiratory syndrome virus1. <i>Journal of Animal Science</i> , 2019, 97, 536-547.	0.2	9
43	Effect of lower-energy, higher-fiber diets on pigs divergently selected for residual feed intake when fed higher-energy, lower-fiber diets1. <i>Journal of Animal Science</i> , 2018, 96, 1221-1236.	0.2	16
44	Transcriptome Analysis in Spleen Reveals Differential Regulation of Response to Newcastle Disease Virus in Two Chicken Lines. <i>Scientific Reports</i> , 2018, 8, 1278.	1.6	54
45	Genomic prediction of piglet response to infection with one of two porcine reproductive and respiratory syndrome virus isolates. <i>Genetics Selection Evolution</i> , 2018, 50, 3.	1.2	8
46	Novel analysis of the Harderian gland transcriptome response to Newcastle disease virus in two inbred chicken lines. <i>Scientific Reports</i> , 2018, 8, 6558.	1.6	27
47	Association of Candidate Genes with Response to Heat and Newcastle Disease Virus. <i>Genes</i> , 2018, 9, 560.	1.0	12
48	Integrated Proteomic and Transcriptomic Analysis of Differential Expression of Chicken Lung Tissue in Response to NDV Infection during Heat Stress. <i>Genes</i> , 2018, 9, 579.	1.0	24
49	Harnessing longitudinal information to identify genetic variation in tolerance of pigs to Porcine Reproductive and Respiratory Syndrome virus infection. <i>Genetics Selection Evolution</i> , 2018, 50, 50.	1.2	11
50	Metabolic adaptation of pigs to a <i>Mycoplasma hyopneumoniae</i> and <i>Lawsonia intracellularis</i> dual challenge1. <i>Journal of Animal Science</i> , 2018, 96, 3196-3207.	0.2	7
51	Genome-wide mapping of quantitative trait loci in admixed populations using mixed linear model and Bayesian multiple regression analysis. <i>Genetics Selection Evolution</i> , 2018, 50, 32.	1.2	20
52	Genetic Analysis of a Commercial Egg Laying Line Challenged With Newcastle Disease Virus. <i>Frontiers in Genetics</i> , 2018, 9, 326.	1.1	20
53	Genetic relationships of antibody response, viremia level, and weight gain in pigs experimentally infected with porcine reproductive and respiratory syndrome virus1. <i>Journal of Animal Science</i> , 2018, 96, 3565-3581.	0.2	14
54	Novel Resilience Phenotypes Using Feed Intake Data From a Natural Disease Challenge Model in Wean-to-Finish Pigs. <i>Frontiers in Genetics</i> , 2018, 9, 660.	1.1	85

#	ARTICLE	IF	CITATIONS
55	A nested mixture model for genomic prediction using whole-genome SNP genotypes. <i>PLoS ONE</i> , 2018, 13, e0194683.	1.1	9
56	Genetic basis of resistance to avian influenza in different commercial varieties of layer chickens. <i>Poultry Science</i> , 2018, 97, 3421-3428.	1.5	11
57	Novel Mechanisms Revealed in the Trachea Transcriptome of Resistant and Susceptible Chicken Lines following Infection with Newcastle Disease Virus. <i>Vaccine Journal</i> , 2017, 24, .	3.2	53
58	Genetic architecture of gene expression underlying variation in host response to porcine reproductive and respiratory syndrome virus infection. <i>Scientific Reports</i> , 2017, 7, 46203.	1.6	32
59	Application of Whole-Genome Prediction Methods for Genome-Wide Association Studies: A Bayesian Approach. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2017, 22, 172-193.	0.7	60
60	Host genetics of response to porcine reproductive and respiratory syndrome in nursery pigs. <i>Veterinary Microbiology</i> , 2017, 209, 107-113.	0.8	24
61	Pigs with Severe Combined Immunodeficiency Are Impaired in Controlling Influenza A Virus Infection. <i>Journal of Innate Immunity</i> , 2017, 9, 193-202.	1.8	12
62	Use of multi-trait and random regression models to identify genetic variation in tolerance to porcine reproductive and respiratory syndrome virus. <i>Genetics Selection Evolution</i> , 2017, 49, 37.	1.2	20
63	A high-quality annotated transcriptome of swine peripheral blood. <i>BMC Genomics</i> , 2017, 18, 479.	1.2	7
64	A Hypothesis and Review of the Relationship between Selection for Improved Production Efficiency, Coping Behavior, and Domestication. <i>Frontiers in Genetics</i> , 2017, 8, 134.	1.1	29
65	Effects of Diet and Genetics on Growth Performance of Pigs in Response to Repeated Exposure to Heat Stress. <i>Frontiers in Genetics</i> , 2017, 8, 155.	1.1	21
66	T Cell Lymphoma and Leukemia in Severe Combined Immunodeficiency Pigs following Bone Marrow Transplantation: A Case Report. <i>Frontiers in Immunology</i> , 2017, 8, 813.	2.2	18
67	Resistant and susceptible chicken lines show distinctive responses to Newcastle disease virus infection in the lung transcriptome. <i>BMC Genomics</i> , 2017, 18, 989.	1.2	54
68	Genomic regions associated with host response to porcine reproductive and respiratory syndrome vaccination and co-infection in nursery pigs. <i>BMC Genomics</i> , 2017, 18, 865.	1.2	18
69	Antigenic and Biological Characterization of ORF2-6 Variants at Early Times Following PRRSV Infection. <i>Viruses</i> , 2017, 9, 113.	1.5	17
70	Genome-Wide Association Study Singles Out SCD and LEPR as the Two Main Loci Influencing Intramuscular Fat Content and Fatty Acid Composition in Duroc Pigs. <i>PLoS ONE</i> , 2016, 11, e0152496.	1.1	83
71	Post-weaning blood transcriptomic differences between Yorkshire pigs divergently selected for residual feed intake. <i>BMC Genomics</i> , 2016, 17, 73.	1.2	53
72	NK cells are intrinsically functional in pigs with Severe Combined Immunodeficiency (SCID) caused by spontaneous mutations in the Artemis gene. <i>Veterinary Immunology and Immunopathology</i> , 2016, 175, 1-6.	0.5	29

#	ARTICLE	IF	CITATIONS
73	Genetic and genomic basis of antibody response to porcine reproductive and respiratory syndrome (PRRS) in gilts and sows. <i>Genetics Selection Evolution</i> , 2016, 48, 51.	1.2	24
74	Effect of selection for residual feed intake during the grow/finish phase of production on sow reproductive performance and lactation efficiency ¹ . <i>Journal of Animal Science</i> , 2016, 94, 4120-4132.	0.2	19
75	Comparison of host genetic factors influencing pig response to infection with two North American isolates of porcine reproductive and respiratory syndrome virus. <i>Genetics Selection Evolution</i> , 2016, 48, 43.	1.2	37
76	Effects of number of training generations on genomic prediction for various traits in a layer chicken population. <i>Genetics Selection Evolution</i> , 2016, 48, 22.	1.2	19
77	Bioinformatic analyses in early host response to Porcine Reproductive and Respiratory Syndrome virus (PRRSV) reveals pathway differences between pigs with alternate genotypes for a major host response QTL. <i>BMC Genomics</i> , 2016, 17, 196.	1.2	24
78	Mixture models detect large effect QTL better than GBLUP and result in more accurate and persistent predictions. <i>Journal of Animal Science and Biotechnology</i> , 2016, 7, 7.	2.1	23
79	Response and inbreeding from a genomic selection experiment in layer chickens. <i>Genetics Selection Evolution</i> , 2015, 47, 59.	1.2	67
80	Identification of a putative quantitative trait nucleotide in guanylate binding protein 5 for host response to PRRS virus infection. <i>BMC Genomics</i> , 2015, 16, 412.	1.2	75
81	Linkage disequilibrium in crossbred and pure line chickens. <i>Genetics Selection Evolution</i> , 2015, 47, 11.	1.2	43
82	Whole blood microarray analysis of pigs showing extreme phenotypes after a porcine reproductive and respiratory syndrome virus infection. <i>BMC Genomics</i> , 2015, 16, 516.	1.2	13
83	Vaccination with a Porcine Reproductive and Respiratory Syndrome (PRRS) Modified Live Virus Vaccine Followed by Challenge with PRRS Virus and Porcine Circovirus Type 2 (PCV2) Protects against PRRS but Enhances PCV2 Replication and Pathogenesis Compared to Results for Nonvaccinated Cochallenged Controls. <i>Vaccine Journal</i> , 2015, 22, 1244-1254.	3.2	27
84	Not All SCID Pigs Are Created Equally: Two Independent Mutations in the <i>Artemis</i> Gene Cause SCID in Pigs. <i>Journal of Immunology</i> , 2015, 195, 3171-3179.	0.4	43
85	Porcine reproductive and respiratory syndrome virus replication and quasispecies evolution in pigs that lack adaptive immunity. <i>Virus Research</i> , 2015, 195, 246-249.	1.1	11
86	Validation and further characterization of a major quantitative trait locus associated with host response to experimental infection with porcine reproductive and respiratory syndrome virus. <i>Animal Genetics</i> , 2014, 45, 48-58.	0.6	61
87	Applied Animal Genomics: Results from the Field. <i>Annual Review of Animal Biosciences</i> , 2014, 2, 105-139.	3.6	102
88	Genetic analysis of reproductive traits and antibody response in a PRRS outbreak herd ¹ . <i>Journal of Animal Science</i> , 2014, 92, 2905-2921.	0.2	58
89	Genome-wide association and genomic prediction for host response to porcine reproductive and respiratory syndrome virus infection. <i>Genetics Selection Evolution</i> , 2014, 46, 18.	1.2	75
90	Genomic selection of purebred animals for crossbred performance in the presence of dominant gene action. <i>Genetics Selection Evolution</i> , 2013, 45, 11.	1.2	79

#	ARTICLE	IF	CITATIONS
91	Pedigree and genomic analyses of feed consumption and residual feed intake in laying hens. <i>Poultry Science</i> , 2013, 92, 2270-2275.	1.5	25
92	Genome-Wide Association Study for Marek's Disease Mortality in Layer Chickens. <i>Avian Diseases</i> , 2013, 57, 395-400.	0.4	22
93	Whole Genome Association Studies of Residual Feed Intake and Related Traits in the Pig. <i>PLoS ONE</i> , 2013, 8, e61756.	1.1	104
94	A Least Squares Regression Model to Detect Quantitative Trait Loci with Polar Overdominance in a Cross of Outbred Breeds: Simulation. <i>Asian-Australasian Journal of Animal Sciences</i> , 2013, 26, 1536-1544.	2.4	1
95	Bayesian analysis of the effect of selection for residual feed intake on growth and feed intake curves in Yorkshire swine1. <i>Journal of Animal Science</i> , 2012, 90, 127-141.	0.2	22
96	A Hierarchical Semiparametric Model for Incorporating Intergene Information for Analysis of Genomic Data. <i>Biometrics</i> , 2012, 68, 1168-1177.	0.8	2
97	Human Xenografts Are Not Rejected in a Naturally Occurring Immunodeficient Porcine Line: A Human Tumor Model in Pigs. <i>BioResearch Open Access</i> , 2012, 1, 63-68.	2.6	39
98	Control of porcine reproductive and respiratory syndrome (PRRS) through genetic improvements in disease resistance and tolerance. <i>Frontiers in Genetics</i> , 2012, 3, 260.	1.1	92
99	Improved Estimation of the Noncentrality Parameter Distribution from a Large Number of t -Statistics, with Applications to False Discovery Rate Estimation in Microarray Data Analysis. <i>Biometrics</i> , 2012, 68, 1178-1187.	0.8	4
100	A Fast EM Algorithm for BayesA-Like Prediction of Genomic Breeding Values. <i>PLoS ONE</i> , 2012, 7, e49157.	1.1	27
101	Application of Genomics Tools to Animal Breeding. <i>Current Genomics</i> , 2012, 13, 207-212.	0.7	97
102	Genetic analysis of longitudinal measurements of performance traits in selection lines for residual feed intake in Yorkshire swine1. <i>Journal of Animal Science</i> , 2011, 89, 1270-1280.	0.2	14
103	Persistence of accuracy of genomic estimated breeding values over generations in layer chickens. <i>Genetics Selection Evolution</i> , 2011, 43, 23.	1.2	86
104	Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. <i>Genetics Selection Evolution</i> , 2011, 43, 40.	1.2	174
105	Breeding value prediction for production traits in layer chickens using pedigree or genomic relationships in a reduced animal model. <i>Genetics Selection Evolution</i> , 2011, 43, 5.	1.2	130
106	Gene expression profiling of the short-term adaptive response to acute caloric restriction in liver and adipose tissues of pigs differing in feed efficiency. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2010, 298, R494-R507.	0.9	83
107	Gene expression in hypothalamus, liver, and adipose tissues and food intake response to melanocortin-4 receptor agonist in pigs expressing melanocortin-4 receptor mutations. <i>Physiological Genomics</i> , 2010, 41, 254-268.	1.0	16
108	Variance model selection with application to joint analysis of multiple microarray datasets under false discovery rate control. <i>Statistics and Its Interface</i> , 2010, 3, 477-491.	0.2	4

#	ARTICLE	IF	CITATIONS
109	Microarray gene expression profiles of fasting induced changes in liver and adipose tissues of pigs expressing the melanocortin-4 receptor D298N variant. <i>Physiological Genomics</i> , 2009, 38, 98-111.	1.0	44
110	The effect of heritability estimates on high-density single nucleotide polymorphism analyses with related animals ¹ . <i>Journal of Animal Science</i> , 2009, 87, 868-875.	0.2	8
111	Factors Affecting Accuracy From Genomic Selection in Populations Derived From Multiple Inbred Lines: A Barley Case Study. <i>Genetics</i> , 2009, 182, 355-364.	1.2	362
112	Genomic selection of purebreds for crossbred performance. <i>Genetics Selection Evolution</i> , 2009, 41, 12.	1.2	158
113	Extent and consistency of linkage disequilibrium and identification of DNA markers for production and egg quality traits in commercial layer chicken populations. <i>BMC Genomics</i> , 2009, 10, S2.	1.2	44
114	ANEXdb: an integrated animal ANnotation and microarray EXpression database. <i>Mammalian Genome</i> , 2009, 20, 768-777.	1.0	28
115	Linkage Disequilibrium in Related Breeding Lines of Chickens. <i>Genetics</i> , 2007, 177, 2161-2169.	1.2	90
116	Global transcriptional response of porcine mesenteric lymph nodes to <i>Salmonella enterica</i> serovar Typhimurium. <i>Genomics</i> , 2007, 90, 72-84.	1.3	36
117	Marker-assisted selection for commercial crossbred performance ¹ . <i>Journal of Animal Science</i> , 2007, 85, 2104-2114.	0.2	130
118	Prediction of response to marker-assisted and genomic selection using selection index theory. <i>Journal of Animal Breeding and Genetics</i> , 2007, 124, 331-341.	0.8	305
119	Associations of myostatin gene polymorphisms with performance and mortality traits in broiler chickens. <i>Genetics Selection Evolution</i> , 2007, 39, 73-89.	1.2	39
120	Interval mapping of quantitative trait loci with selective DNA pooling data. <i>Genetics Selection Evolution</i> , 2007, 39, 685-709.	1.2	13
121	Genomic selection for marker-assisted improvement in line crosses. <i>Theoretical and Applied Genetics</i> , 2007, 115, 665-674.	1.8	41
122	Identification of errors and factors associated with errors in data from electronic swine feeders ¹ . <i>Journal of Animal Science</i> , 2005, 83, 969-982.	0.2	58
123	Combined line-cross and half-sib QTL analysis of crosses between outbred lines. <i>Genetical Research</i> , 2005, 85, 235-248.	0.3	43
124	Investigation of Obesity Candidate Genes On Porcine Fat Deposition Quantitative Trait Loci Regions. <i>Obesity</i> , 2004, 12, 1981-1994.	4.0	68
125	A study on the minimum number of loci required for genetic evaluation using a finite locus model. <i>Genetics Selection Evolution</i> , 2004, 36, 395-414.	1.2	1
126	Polar overdominant inheritance of a DLK1 polymorphism is associated with growth and fatness in pigs. <i>Mammalian Genome</i> , 2004, 15, 552-9.	1.0	54

#	ARTICLE	IF	CITATIONS
127	The effect of using approximate gametic variance covariance matrices on marker assisted selection by BLUP. <i>Genetics Selection Evolution</i> , 2004, 36, 29-48.	1.2	6
128	Optimizing purebred selection for crossbred performance using QTL with different degrees of dominance. <i>Genetics Selection Evolution</i> , 2004, 36, 297-324.	1.2	20
129	Tests of candidate genes in breed cross populations for QTL mapping in livestock. <i>Mammalian Genome</i> , 2003, 14, 472-482.	1.0	27
130	A comparison of alternative methods to compute conditional genotype probabilities for genetic evaluation with finite locus models. <i>Genetics Selection Evolution</i> , 2003, 35, 585-604.	1.2	5
131	A method to optimize selection on multiple identified quantitative trait loci. <i>Genetics Selection Evolution</i> , 2002, 34, 145-70.	1.2	30
132	Optimal selection on two quantitative trait loci with linkage. <i>Genetics Selection Evolution</i> , 2002, 34, 171-92.	1.2	14
133	The use of molecular genetics in the improvement of agricultural populations. <i>Nature Reviews Genetics</i> , 2002, 3, 22-32.	7.7	519
134	Application of the False Discovery Rate to Quantitative Trait Loci Interval Mapping With Multiple Traits. <i>Genetics</i> , 2002, 161, 905-914.	1.2	22
135	Potential gain from optimizing multigeneration selection on an identified quantitative trait locus.. <i>Journal of Animal Science</i> , 2001, 79, 2975.	0.2	21
136	Power of quantitative trait locus mapping for polygenic binary traits using generalized and regression interval mapping in multi-family half-sib designs. <i>Genetical Research</i> , 2000, 76, 305-317.	0.3	34
137	Least Squares Interval Mapping of Quantitative Trait Loci Under the Infinitesimal Genetic Model in Outbred Populations. <i>Genetics</i> , 1998, 148, 495-505.	1.2	16