Jack C M Dekkers

List of Publications by Year
in descending order

137 papers	5,186 citations	87888 38 h-index	102487 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. Genetics Selection Evolution, 2022, 54, 11.	3.0	0
2	Predictions of the accuracy of genomic prediction: connecting R2, selection index theory, and Fisher information. Genetics Selection Evolution, 2022, 54, 13.	3.0	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. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	7
4	Ten simple rules to ruin a collaborative environment. PLoS Computational Biology, 2022, 18, e1009957.	3.2	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. Virus Research, 2022, 316, 198809.	2.2	1
6	Application of Bayesian genomic prediction methods to genome-wide association analyses. Genetics Selection Evolution, 2022, 54, 31.	3.0	3
7	Gene expression in tonsils in swine following infection with porcine reproductive and respiratory syndrome virus. BMC Veterinary Research, 2021, 17, 88.	1.9	12
8	Cross-validation of best linear unbiased predictions of breeding values using an efficient leave-one-out strategy. Journal of Animal Breeding and Genetics, 2021, 138, 519-527.	2.0	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. Journal of Animal Science, 2021, 99, .	0.5	2
10	Distinct transcriptomic response to Newcastle disease virus infection during heat stress in chicken tracheal epithelial tissue. Scientific Reports, 2021, 11, 7450.	3.3	4
11	Proliferation of peripheral blood mononuclear cells from healthy piglets after mitogen stimulation as indicators of disease resilience. Journal of Animal Science, 2021, 99, .	0.5	5
12	Predicting the accuracy of genomic predictions. Genetics Selection Evolution, 2021, 53, 55.	3.0	17
13	Host Genetics of Response to Porcine Reproductive and Respiratory Syndrome in Sows: Reproductive Performance. Frontiers in Genetics, 2021, 12, 707870.	2.3	1
14	Quantitative analysis of the blood transcriptome of young healthy pigs and its relationship with subsequent disease resilience. BMC Genomics, 2021, 22, 614.	2.8	9
15	Host Genetics of Response to Porcine Reproductive and Respiratory Syndrome in Sows: Antibody Response as an Indicator Trait for Improved Reproductive Performance. Frontiers in Genetics, 2021, 12, 707873.	2.3	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. Journal of Animal Science, 2021, 99, .	0.5	6
17	Genetic parameters of drinking and feeding traits of wean-to-finish pigs under a polymicrobial natural disease challenge. Journal of Animal Science and Biotechnology, 2021, 12, 105.	5.3	4
18	Thyroid hormone suppression in feeder pigs following polymicrobial or porcine reproductive and respiratory syndrome virus-2 challenge. Journal of Animal Science, 2021, 99, .	0.5	4

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19	Multiple trait breeding programs with genotype-by-environment interactions based on reaction norms, with application to genetic improvement of disease resilience. Genetics Selection Evolution, 2021, 53, 93.	3.0	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. Genetics Selection Evolution, 2021, 53, 91.	3.0	3
21	Investigating the relationship between vaginal microbiota and host genetics and their impact on immune response and farrowing traits in commercial gilts. Journal of Animal Breeding and Genetics, 2020, 137, 84-102.	2.0	16
22	Genetic Analysis of Antibody Response to Porcine Reproductive and Respiratory Syndrome Vaccination as an Indicator Trait for Reproductive Performance in Commercial Sows. Frontiers in Genetics, 2020, 11, 1011.	2.3	16
23	The genetic basis of natural antibody titers of young healthy pigs and relationships with disease resilience. BMC Genomics, 2020, 21, 648.	2.8	17
24	Phenotypic variability and population structure analysis of Tanzanian free-range local chickens. BMC Veterinary Research, 2020, 16, 360.	1.9	14
25	Genomic Analysis of IgG Antibody Response to Common Pathogens in Commercial Sows in Health-Challenged Herds. Frontiers in Genetics, 2020, 11, 593804.	2.3	4
26	Genetic Basis of Response of Ghanaian Local Chickens to Infection With a Lentogenic Newcastle Disease Virus. Frontiers in Genetics, 2020, 11, 739.	2.3	8
27	Genetic analysis of disease resilience in wean-to-finish pigs from a natural disease challenge model. Journal of Animal Science, 2020, 98, .	0.5	31
28	Transcriptome Analysis Reveals Inhibitory Effects of Lentogenic Newcastle Disease Virus on Cell Survival and Immune Function in Spleen of Commercial Layer Chicks. Genes, 2020, 11, 1003.	2.4	2
29	Novel Combined Tissue Transcriptome Analysis After Lentogenic Newcastle Disease Virus Challenge in Inbred Chicken Lines of Differential Resistance. Frontiers in Genetics, 2020, 11, 11.	2.3	14
30	Novel Engraftment and T Cell Differentiation of Human Hematopoietic Cells in ARTâˆ'/âˆ'IL2RGâˆ'/Y SCID Pigs. Frontiers in Immunology, 2020, 11, 100.	4.8	21
31	A biphasic curve for modeling, classifying, and predicting egg production in single cycle and molted flocks. Poultry Science, 2020, 99, 2007-2010.	3.4	2
32	Exploring Phenotypes for Disease Resilience in Pigs Using Complete Blood Count Data From a Natural Disease Challenge Model. Frontiers in Genetics, 2020, 11, 216.	2.3	14
33	CD3Îµ+ Cells in Pigs With Severe Combined Immunodeficiency Due to Defects in ARTEMIS. Frontiers in Immunology, 2020, 11, 510.	4.8	5
34	Autozygosity and Genetic Differentiation of Landrace and Large White Pigs as Revealed by the Genetic Analyses of Crossbreds. Frontiers in Genetics, 2019, 10, 739.	2.3	8
35	Genetic Analyses of Tanzanian Local Chicken Ecotypes Challenged with Newcastle Disease Virus. Genes, 2019, 10, 546.	2.4	20
36	Effect of a dual enteric and respiratory pathogen challenge on swine growth, efficiency, carcass composition, and pork quality1. Journal of Animal Science, 2019, 97, 4710-4720.	0.5	4

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37	Genetics and Genomic Regions Affecting Response to Newcastle Disease Virus Infection under Heat Stress in Layer Chickens. Genes, 2019, 10, 61.	2.4	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. Virus Research, 2019, 267, 21-25.	2.2	6
39	Genetics of male reproductive performance in White Leghorns. Poultry Science, 2019, 98, 2729-2733.	3.4	6
40	The effects of a globin blocker on the resolution of 3′mRNA sequencing data in porcine blood. BMC Genomics, 2019, 20, 741.	2.8	4
41	The effect of a porcine reproductive and respiratory syndrome outbreak on genetic parameters and reaction norms for reproductive performance in pigs1. Journal of Animal Science, 2019, 97, 1101-1116.	0.5	5
42	Identification of factors associated with virus level in tonsils of pigs experimentally infected with porcine reproductive and respiratory syndrome virus1. Journal of Animal Science, 2019, 97, 536-547.	0.5	9
43	Effect of lower-energy, higher-fiber diets on pigs divergently selected for residual feed intake when fed higher-energy, lower-fiber diets1. Journal of Animal Science, 2018, 96, 1221-1236.	0.5	16
44	Transcriptome Analysis in Spleen Reveals Differential Regulation of Response to Newcastle Disease Virus in Two Chicken Lines. Scientific Reports, 2018, 8, 1278.	3.3	54
45	Genomic prediction of piglet response to infection with one of two porcine reproductive and respiratory syndrome virus isolates. Genetics Selection Evolution, 2018, 50, 3.	3.0	8
46	Novel analysis of the Harderian gland transcriptome response to Newcastle disease virus in two inbred chicken lines. Scientific Reports, 2018, 8, 6558.	3.3	27
47	Association of Candidate Genes with Response to Heat and Newcastle Disease Virus. Genes, 2018, 9, 560.	2.4	12
48	Integrated Proteomic and Transcriptomic Analysis of Differential Expression of Chicken Lung Tissue in Response to NDV Infection during Heat Stress. Genes, 2018, 9, 579.	2.4	24
49	Harnessing longitudinal information to identify genetic variation in tolerance of pigs to Porcine Reproductive and Respiratory Syndrome virus infection. Genetics Selection Evolution, 2018, 50, 50.	3.0	11
50	Metabolic adaptation of pigs to a Mycoplasma hyopneumoniae and Lawsonia intracellularis dual challenge1. Journal of Animal Science, 2018, 96, 3196-3207.	0.5	7
51	Genome-wide mapping of quantitative trait loci in admixed populations using mixed linear model and Bayesian multiple regression analysis. Genetics Selection Evolution, 2018, 50, 32.	3.0	20
52	Genetic Analysis of a Commercial Egg Laying Line Challenged With Newcastle Disease Virus. Frontiers in Genetics, 2018, 9, 326.	2.3	20
53	Genetic relationships of antibody response, viremia level, and weight gain in pigs experimentally infected with porcine reproductive and respiratory syndrome virus1. Journal of Animal Science, 2018, 96, 3565-3581.	0.5	14
54	Novel Resilience Phenotypes Using Feed Intake Data From a Natural Disease Challenge Model in Wean-to-Finish Pigs. Frontiers in Genetics, 2018, 9, 660.	2.3	85

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55	A nested mixture model for genomic prediction using whole-genome SNP genotypes. PLoS ONE, 2018, 13, e0194683.	2.5	9
56	Genetic basis of resistance to avian influenza in different commercial varieties of layer chickens. Poultry Science, 2018, 97, 3421-3428.	3.4	11
57	Novel Mechanisms Revealed in the Trachea Transcriptome of Resistant and Susceptible Chicken Lines following Infection with Newcastle Disease Virus. Vaccine Journal, 2017, 24, .	3.1	53
58	Genetic architecture of gene expression underlying variation in host response to porcine reproductive and respiratory syndrome virus infection. Scientific Reports, 2017, 7, 46203.	3.3	32
59	Application of Whole-Genome Prediction Methods for Genome-Wide Association Studies: A Bayesian Approach. Journal of Agricultural, Biological, and Environmental Statistics, 2017, 22, 172-193.	1.4	60
60	Host genetics of response to porcine reproductive and respiratory syndrome in nursery pigs. Veterinary Microbiology, 2017, 209, 107-113.	1.9	24
61	Pigs with Severe Combined Immunodeficiency Are Impaired in Controlling Influenza A Virus Infection. Journal of Innate Immunity, 2017, 9, 193-202.	3.8	12
62	Use of multi-trait and random regression models to identify genetic variation in tolerance to porcine reproductive and respiratory syndrome virus. Genetics Selection Evolution, 2017, 49, 37.	3.0	20
63	A high-quality annotated transcriptome of swine peripheral blood. BMC Genomics, 2017, 18, 479.	2.8	7
64	A Hypothesis and Review of the Relationship between Selection for Improved Production Efficiency, Coping Behavior, and Domestication. Frontiers in Genetics, 2017, 8, 134.	2.3	29
65	Effects of Diet and Genetics on Growth Performance of Pigs in Response to Repeated Exposure to Heat Stress. Frontiers in Genetics, 2017, 8, 155.	2.3	21
66	T Cell Lymphoma and Leukemia in Severe Combined Immunodeficiency Pigs following Bone Marrow Transplantation: A Case Report. Frontiers in Immunology, 2017, 8, 813.	4.8	18
67	Resistant and susceptible chicken lines show distinctive responses to Newcastle disease virus infection in the lung transcriptome. BMC Genomics, 2017, 18, 989.	2.8	54
68	Genomic regions associated with host response to porcine reproductive and respiratory syndrome vaccination and co-infection in nursery pigs. BMC Genomics, 2017, 18, 865.	2.8	18
69	Antigenic and Biological Characterization of ORF2â€"6 Variants at Early Times Following PRRSV Infection. Viruses, 2017, 9, 113.	3.3	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. PLoS ONE, 2016, 11, e0152496.	2.5	83
71	Post-weaning blood transcriptomic differences between Yorkshire pigs divergently selected for residual feed intake. BMC Genomics, 2016, 17, 73.	2.8	53
72	NK cells are intrinsically functional in pigs with Severe Combined Immunodeficiency (SCID) caused by spontaneous mutations in the Artemis gene. Veterinary Immunology and Immunopathology, 2016, 175, 1-6.	1.2	29

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73	Genetic and genomic basis of antibody response to porcine reproductive and respiratory syndrome (PRRS) in gilts and sows. Genetics Selection Evolution, 2016, 48, 51.	3.0	24
74	Effect of selection for residual feed intake during the grow/finish phase of production on sow reproductive performance and lactation efficiency1. Journal of Animal Science, 2016, 94, 4120-4132.	0.5	19
75	Comparison of host genetic factors influencing pig response to infection with two North American isolates of porcine reproductive and respiratory syndrome virus. Genetics Selection Evolution, 2016, 48, 43.	3.0	37
76	Effects of number of training generations on genomic prediction for various traits in a layer chicken population. Genetics Selection Evolution, 2016, 48, 22.	3.0	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. BMC Genomics, 2016, 17, 196.	2.8	24
78	Mixture models detect large effect QTL better than GBLUP and result in more accurate and persistent predictions. Journal of Animal Science and Biotechnology, 2016, 7, 7.	5.3	23
79	Response and inbreeding from a genomic selection experiment in layer chickens. Genetics Selection Evolution, 2015, 47, 59.	3.0	67
80	Identification of a putative quantitative trait nucleotide in guanylate binding protein 5 for host response to PRRS virus infection. BMC Genomics, 2015, 16, 412.	2.8	75
81	Linkage disequilibrium in crossbred and pure line chickens. Genetics Selection Evolution, 2015, 47, 11.	3.0	43
82	Whole blood microarray analysis of pigs showing extreme phenotypes after a porcine reproductive and respiratory syndrome virus infection. BMC Genomics, 2015, 16, 516.	2.8	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. Vaccine Journal, 2015, 22, 1244-1254.	3.1	27
84	Not All SCID Pigs Are Created Equally: Two Independent Mutations in the <i>Artemis</i> Gene Cause SCID in Pigs. Journal of Immunology, 2015, 195, 3171-3179.	0.8	43
85	Porcine reproductive and respiratory syndrome virus replication and quasispecies evolution in pigs that lack adaptive immunity. Virus Research, 2015, 195, 246-249.	2.2	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. Animal Genetics, 2014, 45, 48-58.	1.7	61
87	Applied Animal Genomics: Results from the Field. Annual Review of Animal Biosciences, 2014, 2, 105-139.	7.4	102
88	Genetic analysis of reproductive traits and antibody response in a PRRS outbreak herd1. Journal of Animal Science, 2014, 92, 2905-2921.	0.5	58
89	Genome-wide association and genomic prediction for host response to porcine reproductive and respiratory syndrome virus infection. Genetics Selection Evolution, 2014, 46, 18.	3.0	75
90	Genomic selection of purebred animals for crossbred performance in the presence of dominant gene action. Genetics Selection Evolution, 2013, 45, 11.	3.0	79

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91	Pedigree and genomic analyses of feed consumption and residual feed intake in laying hens. Poultry Science, 2013, 92, 2270-2275.	3.4	25
92	Genome-Wide Association Study for Marek's Disease Mortality in Layer Chickens. Avian Diseases, 2013, 57, 395-400.	1.0	22
93	Whole Genome Association Studies of Residual Feed Intake and Related Traits in the Pig. PLoS ONE, 2013, 8, e61756.	2.5	104
94	A Least Squares Regression Model to Detect Quantitative Trait Loci with Polar Overdominance in a Cross of Outbred Breeds: Simulation. Asian-Australasian Journal of Animal Sciences, 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. Journal of Animal Science, 2012, 90, 127-141.	0.5	22
96	A Hierarchical Semiparametric Model for Incorporating Intergene Information for Analysis of Genomic Data. Biometrics, 2012, 68, 1168-1177.	1.4	2
97	Human Xenografts Are Not Rejected in a Naturally Occurring Immunodeficient Porcine Line: A Human Tumor Model in Pigs. BioResearch Open Access, 2012, 1, 63-68.	2.6	39
98	Control of porcine reproductive and respiratory syndrome (PRRS) through genetic improvements in disease resistance and tolerance. Frontiers in Genetics, 2012, 3, 260.	2.3	92
99	Improved Estimation of the Noncentrality Parameter Distribution from a Large Number of <i>t</i>â€Statistics, with Applications to False Discovery Rate Estimation in Microarray Data Analysis. Biometrics, 2012, 68, 1178-1187.	1.4	4
100	A Fast EM Algorithm for BayesA-Like Prediction of Genomic Breeding Values. PLoS ONE, 2012, 7, e49157.	2.5	27
101	Application of Genomics Tools to Animal Breeding. Current Genomics, 2012, 13, 207-212.	1.6	97
102	Genetic analysis of longitudinal measurements of performance traits in selection lines for residual feed intake in Yorkshire swine1. Journal of Animal Science, 2011, 89, 1270-1280.	0.5	14
103	Persistence of accuracy of genomic estimated breeding values over generations in layer chickens. Genetics Selection Evolution, 2011, 43, 23.	3.0	86
104	Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. Genetics Selection Evolution, 2011, 43, 40.	3.0	174
105	Breeding value prediction for production traits in layer chickens using pedigree or genomic relationships in a reduced animal model. Genetics Selection Evolution, 2011, 43, 5.	3.0	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. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2010, 298, R494-R507.	1.8	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. Physiological Genomics, 2010, 41, 254-268.	2.3	16
108	Variance model selection with application to joint analysis of multiple microarray datasets under false discovery rate control. Statistics and Its Interface, 2010, 3, 477-491.	0.3	4

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109	Microarray gene expression profiles of fasting induced changes in liver and adipose tissues of pigs expressing the melanocortin-4 receptor D298N variant. Physiological Genomics, 2009, 38, 98-111.	2.3	44
110	The effect of heritability estimates on high-density single nucleotide polymorphism analyses with related animals1. Journal of Animal Science, 2009, 87, 868-875.	0.5	8
111	Factors Affecting Accuracy From Genomic Selection in Populations Derived From Multiple Inbred Lines: A Barley Case Study. Genetics, 2009, 182, 355-364.	2.9	362
112	Genomic selection of purebreds for crossbred performance. Genetics Selection Evolution, 2009, 41, 12.	3.0	158
113	Extent and consistency of linkage disequilibrium and identification of DNA markers for production and egg quality traits in commercial layer chicken populations. BMC Genomics, 2009, 10, S2.	2.8	44
114	ANEXdb: an integrated animal ANnotation and microarray EXpression database. Mammalian Genome, 2009, 20, 768-777.	2.2	28
115	Linkage Disequilibrium in Related Breeding Lines of Chickens. Genetics, 2007, 177, 2161-2169.	2.9	90
116	Global transcriptional response of porcine mesenteric lymph nodes to Salmonella enterica serovar Typhimurium. Genomics, 2007, 90, 72-84.	2.9	36
117	Marker-assisted selection for commercial crossbred performance1. Journal of Animal Science, 2007, 85, 2104-2114.	0.5	130
118	Prediction of response to marker‑assisted and genomic selection using selection index theory. Journal of Animal Breeding and Genetics, 2007, 124, 331-341.	2.0	305
119	Associations of myostatin gene polymorphisms with performance and mortality traits in broiler chickens. Genetics Selection Evolution, 2007, 39, 73-89.	3.0	39
120	Interval mapping of quantitative trait loci with selective DNA pooling data. Genetics Selection Evolution, 2007, 39, 685-709.	3.0	13
121	Genomic selection for marker-assisted improvement in line crosses. Theoretical and Applied Genetics, 2007, 115, 665-674.	3.6	41
122	Identification of errors and factors associated with errors in data from electronic swine feeders1. Journal of Animal Science, 2005, 83, 969-982.	0.5	58
123	Combined line-cross and half-sib QTL analysis of crosses between outbred lines. Genetical Research, 2005, 85, 235-248.	0.9	43
124	Investigation of Obesity Candidate Genes On Porcine Fat Deposition Quantitative Trait Loci Regions. Obesity, 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. Genetics Selection Evolution, 2004, 36, 395-414.	3.0	1
126	Polar overdominant inheritance of a DLK1 polymorphism is associated with growth and fatness in pigs. Mammalian Genome, 2004, 15, 552-9.	2.2	54

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127	The effect of using approximate gametic variance covariance matrices on marker assisted selection by BLUP. Genetics Selection Evolution, 2004, 36, 29-48.	3.0	6
128	Optimizing purebred selection for crossbred performance using QTL with different degrees of dominance. Genetics Selection Evolution, 2004, 36, 297-324.	3.0	20
129	Tests of candidate genes in breed cross populations for QTL mapping in livestock. Mammalian Genome, 2003, 14, 472-482.	2.2	27
130	A comparison of alternative methods to compute conditional genotype probabilities for genetic evaluation with finite locus models. Genetics Selection Evolution, 2003, 35, 585-604.	3.0	5
131	A method to optimize selection on multiple identified quantitative trait loci. Genetics Selection Evolution, 2002, 34, 145-70.	3.0	30
132	Optimal selection on two quantitative trait loci with linkage. Genetics Selection Evolution, 2002, 34, 171-92.	3.0	14
133	The use of molecular genetics in the improvement of agricultural populations. Nature Reviews Genetics, 2002, 3, 22-32.	16.3	519
134	Application of the False Discovery Rate to Quantitative Trait Loci Interval Mapping With Multiple Traits. Genetics, 2002, 161, 905-914.	2.9	22
135	Potential gain from optimizing multigeneration selection on an identified quantitative trait locus.. Journal of Animal Science, 2001, 79, 2975.	0.5	21
136	Power of quantitative trait locus mapping for polygenic binary traits using generalized and regression interval mapping in multi-family half-sib designs. Genetical Research, 2000, 76, 305-317.	0.9	34
137	Least Squares Interval Mapping of Quantitative Trait Loci Under the Infinitesimal Genetic Model in Outbred Populations. Genetics, 1998, 148, 495-505.	2.9	16