

Graham Plastow

List of Publications by Year in descending order

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Version: 2024-02-01

162
papers

7,249
citations

76196

40
h-index

64668

79
g-index

164
all docs

164
docs citations

164
times ranked

7086
citing authors

#	ARTICLE	IF	CITATIONS
1	Phenotypic effect of a single nucleotide polymorphism on SSC7 on fetal outcomes in PRRSV-2 infected gilts. <i>Livestock Science</i> , 2022, 255, 104800.	0.6	6
2	Breeding for disease resilience: opportunities to manage polymicrobial challenge and improve commercial performance in the pig industry. <i>CABI Agriculture and Bioscience</i> , 2022, 3, 6.	1.1	12
3	Integrative analyses of genomic and metabolomic data reveal genetic mechanisms associated with carcass merit traits in beef cattle. <i>Scientific Reports</i> , 2022, 12, 3389.	1.6	6
4	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>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
5	Signaling differences in peripheral blood mononuclear cells of high and low vaccine responders prior to, and following, vaccination in piglets. <i>Vaccine: X</i> , 2022, 11, 100167.	0.9	1
6	Genetic and phenotypic parameters for feed efficiency and component traits in American mink. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	3
7	Methane and carbon dioxide emissions and grazed forage intake from pregnant beef heifers previously classified for residual feed intake under drylot conditions. <i>Canadian Journal of Animal Science</i> , 2021, 101, 71-84.	0.7	3
8	MicroRNAomes of Cattle Intestinal Tissues Revealed Possible miRNA Regulated Mechanisms Involved in <i>Escherichia coli</i> O157 Fecal Shedding. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 634505.	1.8	6
9	Whole-Blood Transcriptome Analysis of Feedlot Cattle With and Without Bovine Respiratory Disease. <i>Frontiers in Genetics</i> , 2021, 12, 627623.	1.1	15
10	Abundance and Expression of Shiga Toxin Genes in <i>Escherichia coli</i> at the Recto-Anal Junction Relates to Host Immune Genes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 633573.	1.8	9
11	Genetic parameter estimations and genomic insights for teat and udder structure in young and mature Canadian Angus cows. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	2
12	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
13	Investigating the genetic architecture of disease resilience in pigs by genome-wide association studies of complete blood count traits collected from a natural disease challenge model. <i>BMC Genomics</i> , 2021, 22, 535.	1.2	4
14	Natural versus induced estrus indicators of Holstein heifers determined by an automated activity monitoring system. <i>Livestock Science</i> , 2021, 249, 104514.	0.6	1
15	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
16	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
17	The potential for mitigation of methane emissions in ruminants through the application of metagenomics, metabolomics, and other -OMICS technologies. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	8
18	Purebred-crossbred genetic parameters for reproductive traits in swine. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	2

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19	Economic comparison of an ear tag automated activity monitor for estrus detection with timed-AI in Holstein heifers. <i>Theriogenology</i> , 2021, 175, 155-162.	0.9	0
20	Heritability and genetic correlations of plasma metabolites of pigs with production, resilience and carcass traits under natural polymicrobial disease challenge. <i>Scientific Reports</i> , 2021, 11, 20628.	1.6	6
21	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
22	Identification of candidate genes and enriched biological functions for feed efficiency traits by integrating plasma metabolites and imputed whole genome sequence variants in beef cattle. <i>BMC Genomics</i> , 2021, 22, 823.	1.2	6
23	Relationship between indirect genetic effects for growth, environmental enrichment, coping style and sex with the serum metabolome profile of pigs. <i>Scientific Reports</i> , 2021, 11, 23377.	1.6	2
24	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
25	Estimation of genetic parameters and trends for growth traits in Hays Converter cattle using multiple-trait and random regression models. <i>Livestock Science</i> , 2020, 241, 104245.	0.6	1
26	Performance and optimization of an ear tag automated activity monitor for estrus prediction in dairy heifers. <i>Theriogenology</i> , 2020, 155, 197-204.	0.9	12
27	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
28	Discovery of Predictors of <i>Mycoplasma hyopneumoniae</i> Vaccine Response Efficiency in Pigs: 16S rRNA Gene Fecal Microbiota Analysis. <i>Microorganisms</i> , 2020, 8, 1151.	1.6	10
29	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
30	Candidate serum metabolite biomarkers of residual feed intake and carcass merit in sheep. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	19
31	Kinome profiling of peripheral blood mononuclear cells collected prior to vaccination reveals biomarkers and potential mechanisms of vaccine unresponsiveness in pigs. <i>Scientific Reports</i> , 2020, 10, 11546.	1.6	7
32	Genomic Heritability and Genome-Wide Association Studies of Plasma Metabolites in Crossbred Beef Cattle. <i>Frontiers in Genetics</i> , 2020, 11, 538600.	1.1	9
33	Longitudinal blood transcriptomic analysis to identify molecular regulatory patterns of bovine respiratory disease in beef cattle. <i>Genomics</i> , 2020, 112, 3968-3977.	1.3	21
34	Genetic architecture of quantitative traits in beef cattle revealed by genome wide association studies of imputed whole genome sequence variants: I: feed efficiency and component traits. <i>BMC Genomics</i> , 2020, 21, 36.	1.2	49
35	Genetic architecture of quantitative traits in beef cattle revealed by genome wide association studies of imputed whole genome sequence variants: II: carcass merit traits. <i>BMC Genomics</i> , 2020, 21, 38.	1.2	33
36	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

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37	Genetic parameter estimation for sensory traits in longissimus muscle and their association with pH and intramuscular fat in pork chops. <i>Livestock Science</i> , 2020, 238, 104080.	0.6	1
38	Genetic parameters and purebred crossbred genetic correlations for growth, meat quality, and carcass traits in pigs. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	6
39	154 A genetic marker for PRRS resistance has no adverse effect on economically important traits in pigs. <i>Journal of Animal Science</i> , 2020, 98, 145-145.	0.2	1
40	Host genetics influence the rumen microbiota and heritable rumen microbial features associate with feed efficiency in cattle. <i>Microbiome</i> , 2019, 7, 92.	4.9	230
41	Characterization of whole blood transcriptome and early-life fecal microbiota in high and low responder pigs before, and after vaccination for <i>Mycoplasma hyopneumoniae</i> . <i>Vaccine</i> , 2019, 37, 1743-1755.	1.7	16
42	Comparison of the nasopharyngeal bacterial microbiota of beef calves raised without the use of antimicrobials between healthy calves and those diagnosed with bovine respiratory disease. <i>Veterinary Microbiology</i> , 2019, 231, 56-62.	0.8	33
43	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
44	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
45	Modeling heterotic effects in beef cattle using genome-wide SNP-marker genotypes1. <i>Journal of Animal Science</i> , 2018, 96, 830-845.	0.2	20
46	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
47	Genomic evaluation of feed efficiency component traits in Duroc pigs using 80K, 650K and whole-genome sequence variants. <i>Genetics Selection Evolution</i> , 2018, 50, 14.	1.2	57
48	Interactions of the Hindgut Mucosa-Associated Microbiome with Its Host Regulate Shedding of <i>Escherichia coli</i> O157:H7 by Cattle. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	24
49	Genome-wide association studies to identify quantitative trait loci affecting milk production traits in water buffalo. <i>Journal of Dairy Science</i> , 2018, 101, 433-444.	1.4	70
50	Putative Loci Causing Early Embryonic Mortality in Duroc Swine. <i>Frontiers in Genetics</i> , 2018, 9, 655.	1.1	3
51	Evolution of the nasopharyngeal bacterial microbiota of beef calves from spring processing to 40 days after feedlot arrival. <i>Veterinary Microbiology</i> , 2018, 225, 139-148.	0.8	30
52	Synaptogyrin-2 influences replication of Porcine circovirus 2. <i>PLoS Genetics</i> , 2018, 14, e1007750.	1.5	28
53	Genome-wide association scan for heterotic quantitative trait loci in multi-breed and crossbred beef cattle. <i>Genetics Selection Evolution</i> , 2018, 50, 48.	1.2	37
54	Integrating RNA-seq and GWAS reveals novel genetic mutations for buffalo reproductive traits. <i>Animal Reproduction Science</i> , 2018, 197, 290-295.	0.5	7

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55	Efficacy of genetic parameter estimation of pork loin quality of crossbred commercial pigs using technological quality measurements of frozen and unfrozen product. <i>Canadian Journal of Animal Science</i> , 2018, 98, 453-462.	0.7	1
56	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
57	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
58	Genome-Wide SNP Data Revealed the Extent of Linkage Disequilibrium, Persistence of Phase and Effective Population Size in Purebred and Crossbred Buffalo Populations. <i>Frontiers in Genetics</i> , 2018, 9, 688.	1.1	23
59	Genetic diversity, breed composition and admixture of Kenyan domestic pigs. <i>PLoS ONE</i> , 2018, 13, e0190080.	1.1	44
60	Novel insights into host responses and reproductive pathophysiology of porcine reproductive and respiratory syndrome caused by PRRSV-2. <i>Veterinary Microbiology</i> , 2017, 209, 114-123.	0.8	48
61	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
62	Trust and Consumer Preferences for Pig Production Attributes in Canada. <i>Canadian Journal of Agricultural Economics</i> , 2017, 65, 477-514.	1.2	12
63	Host genetics of response to porcine reproductive and respiratory syndrome in nursery pigs. <i>Veterinary Microbiology</i> , 2017, 209, 107-113.	0.8	24
64	Host mechanisms involved in cattle <i>Escherichia coli</i> O157 shedding: a fundamental understanding for reducing foodborne pathogen in food animal production. <i>Scientific Reports</i> , 2017, 7, 7630.	1.6	15
65	Comparative transcriptomic analysis of porcine peripheral blood reveals differentially expressed genes from the cytokine-cytokine receptor interaction pathway related to health status. <i>Genome</i> , 2017, 60, 1021-1028.	0.9	12
66	Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture. <i>BMC Genomics</i> , 2017, 18, 484.	1.2	99
67	Genomewide association of piglet responses to infection with one of two porcine reproductive and respiratory syndrome virus isolates1. <i>Journal of Animal Science</i> , 2017, 95, 16-38.	0.2	26
68	Livestock metabolomics and the livestock metabolome: A systematic review. <i>PLoS ONE</i> , 2017, 12, e0177675.	1.1	226
69	Genomewide association of piglet responses to infection with one of two porcine reproductive and respiratory syndrome virus isolates. <i>Journal of Animal Science</i> , 2017, 95, 16.	0.2	13
70	Use of Genomic Tools to Improve Cattle Health in the Context of Infectious Diseases. <i>Frontiers in Genetics</i> , 2016, 7, 30.	1.1	23
71	History of the Hays Converter. <i>Canadian Journal of Animal Science</i> , 2016, 96, 471-477.	0.7	2
72	A genome-wide association study of fetal response to type 2 porcine reproductive and respiratory syndrome virus challenge. <i>Scientific Reports</i> , 2016, 6, 20305.	1.6	19

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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	<scp>GO</scp>â€œ<scp>FAANG</scp> meeting: a Gathering On Functional Annotation of <scp>An</scp>imal Genomes. <i>Animal Genetics</i> , 2016, 47, 528-533.	0.6	65
75	Accuracy of genomic predictions for feed efficiency traits of beef cattle using 50K and imputed HD genotypes1. <i>Journal of Animal Science</i> , 2016, 94, 1342-1353.	0.2	34
76	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
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	Genome-wide analysis of the transcriptional response to porcine reproductive and respiratory syndrome virus infection at the maternal/fetal interface and in the fetus. <i>BMC Genomics</i> , 2016, 17, 383.	1.2	26
79	Genome Wide Association Studies (GWAS) Identify QTL on SSC2 and SSC17 Affecting Loin Peak Shear Force in Crossbred Commercial Pigs. <i>PLoS ONE</i> , 2016, 11, e0145082.	1.1	6
80	Comparative Transcriptomic Analysis of Rectal Tissue from Beef Steers Revealed Reduced Host Immunity in Escherichia coli O157:H7 Super-Shedders. <i>PLoS ONE</i> , 2016, 11, e0151284.	1.1	18
81	Differences in Whole Blood Gene Expression Associated with Infection Time-Course and Extent of Fetal Mortality in a Reproductive Model of Type 2 Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) Infection. <i>PLoS ONE</i> , 2016, 11, e0153615.	1.1	13
82	Genome-wide whole blood microRNAome and transcriptome analyses reveal miRNA-mRNA regulated host response to foodborne pathogen Salmonella infection in swine. <i>Scientific Reports</i> , 2015, 5, 12620.	1.6	33
83	A large and diverse collection of bovine genome sequences from the Canadian Cattle Genome Project. <i>GigaScience</i> , 2015, 4, 49.	3.3	38
84	Transcriptomic and Epigenetic Profiling of the Lung of Influenza-Infected Pigs: A Comparison of Different Birth Weight and Susceptibility Groups. <i>PLoS ONE</i> , 2015, 10, e0138653.	1.1	5
85	Dominant Red Coat Color in Holstein Cattle Is Associated with a Missense Mutation in the Coatomer Protein Complex, Subunit Alpha (COPA) Gene. <i>PLoS ONE</i> , 2015, 10, e0128969.	1.1	30
86	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
87	Genome-wide association for heifer reproduction and calf performance traits in beef cattle. <i>Genome</i> , 2015, 58, 549-557.	0.9	17
88	Genomic Selection, a New Era for Pork Quality Improvement. <i>Springer Science Reviews</i> , 2015, 3, 27-37.	1.3	9
89	Genome-wide association studies (GWAS) identify a QTL close to PRKAG3 affecting meat pH and colour in crossbred commercial pigs. <i>BMC Genetics</i> , 2015, 16, 33.	2.7	33
90	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

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91	Maternal and fetal predictors of fetal viral load and death in third trimester, type 2 porcine reproductive and respiratory syndrome virus infected pregnant gilts. <i>Veterinary Research</i> , 2015, 46, 107.	1.1	38
92	Variation in time and magnitude of immune response and viremia in experimental challenges with Porcine circovirus 2b. <i>BMC Veterinary Research</i> , 2014, 10, 286.	0.7	14
93	Reliability of molecular breeding values for Warner-Bratzler shear force and carcass traits of beef cattle – An independent validation study ¹ . <i>Journal of Animal Science</i> , 2014, 92, 2896-2904.	0.2	22
94	Analysis of biological networks and biological pathways associated with residual feed intake in beef cattle. <i>Animal Science Journal</i> , 2014, 85, 374-387.	0.6	67
95	Increasing gene discovery and coverage using RNA-seq of globin RNA reduced porcine blood samples. <i>BMC Genomics</i> , 2014, 15, 954.	1.2	43
96	Cytokine profiles in pregnant gilts experimentally infected with porcine reproductive and respiratory syndrome virus and relationships with viral load and fetal outcome. <i>Veterinary Research</i> , 2014, 45, 113.	1.1	25
97	Applications of genomics to improve livestock in the developing world. <i>Livestock Science</i> , 2014, 166, 76-83.	0.6	32
98	Single nucleotide polymorphisms for feed efficiency and performance in crossbred beef cattle. <i>BMC Genetics</i> , 2014, 15, 14.	2.7	47
99	Gene co-expression network analysis identifies porcine genes associated with variation in Salmonella shedding. <i>BMC Genomics</i> , 2014, 15, 452.	1.2	65
100	Associations between single nucleotide polymorphisms in 33 candidate genes and meat quality traits in commercial pigs. <i>Animal Genetics</i> , 2014, 45, 508-516.	0.6	22
101	MicroRNA Buffering and Altered Variance of Gene Expression in Response to Salmonella Infection. <i>PLoS ONE</i> , 2014, 9, e94352.	1.1	17
102	Variation in Fetal Outcome, Viral Load and ORF5 Sequence Mutations in a Large Scale Study of Phenotypic Responses to Late Gestation Exposure to Type 2 Porcine Reproductive and Respiratory Syndrome Virus. <i>PLoS ONE</i> , 2014, 9, e96104.	1.1	47
103	Sequence, Structural and Expression Divergence of Duplicate Genes in the Bovine Genome. <i>PLoS ONE</i> , 2014, 9, e102868.	1.1	13
104	Birth Weight, Intrauterine Growth Retardation and Fetal Susceptibility to Porcine Reproductive and Respiratory Syndrome Virus. <i>PLoS ONE</i> , 2014, 9, e109541.	1.1	23
105	Genetic and Phenotypic Correlations between Performance Traits with Meat Quality and Carcass Characteristics in Commercial Crossbred Pigs. <i>PLoS ONE</i> , 2014, 9, e110105.	1.1	42
106	Complicated Relationships: A Review of Biological Interaction Networks and Pathways in Animal Science. <i>Springer Science Reviews</i> , 2013, 1, 73-83.	1.3	3
107	Expansion of ruminant-specific microRNAs shapes target gene expression divergence between ruminant and non-ruminant species. <i>BMC Genomics</i> , 2013, 14, 609.	1.2	19
108	Genome-wide association analyses for carcass quality in crossbred beef cattle. <i>BMC Genetics</i> , 2013, 14, 80.	2.7	32

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109	Whole genome sequencing of Gir cattle for identifying polymorphisms and loci under selection. <i>Genome</i> , 2013, 56, 592-598.	0.9	63
110	Association analysis for feed efficiency traits in beef cattle using preserved haplotypes. <i>Genome</i> , 2013, 56, 586-591.	0.9	1
111	Genomic analyses identify distinct patterns of selection in domesticated pigs and Tibetan wild boars. <i>Nature Genetics</i> , 2013, 45, 1431-1438.	9.4	472
112	Genome-wide association analyses for growth and feed efficiency traits in beef cattle ¹ . <i>Journal of Animal Science</i> , 2013, 91, 3612-3633.	0.2	76
113	Effect of temperature and pH on postmortem color development of porcine M. longissimus dorsi and M. semimembranosus. <i>Journal of the Science of Food and Agriculture</i> , 2013, 93, 1206-1210.	1.7	5
114	Livestock and the promise of genomics. <i>Genome</i> , 2013, 56, 556-566.	0.9	6
115	Genome Sequence and Assembly of <i>Bos indicus</i> . <i>Journal of Heredity</i> , 2012, 103, 342-348.	1.0	106
116	Linkage disequilibrium in Angus, Charolais, and Crossbred beef cattle. <i>Frontiers in Genetics</i> , 2012, 3, 152.	1.1	93
117	Impact of selection for residual feed intake on breeding soundness and reproductive performance of bulls on pasture-based multisire mating ¹ . <i>Journal of Animal Science</i> , 2012, 90, 2963-2969.	0.2	31
118	An atlas of DNA methylomes in porcine adipose and muscle tissues. <i>Nature Communications</i> , 2012, 3, 850.	5.8	152
119	Developing a genome-wide selection model for genetic improvement of residual feed intake and carcass merit in a beef cattle breeding program. <i>Science Bulletin</i> , 2012, 57, 2741-2746.	1.7	4
120	Structural analysis of MHC alleles in an RSV tumour regression chicken using a BAC library. <i>Animal Genetics</i> , 2012, 43, 348-351.	0.6	10
121	Estimating Animal Abundance in Ground Beef Batches Assayed with Molecular Markers. <i>PLoS ONE</i> , 2012, 7, e34191.	1.1	2
122	Associations of marker panel scores with feed intake and efficiency traits in beef cattle using preselected single nucleotide polymorphisms ¹ . <i>Journal of Animal Science</i> , 2011, 89, 3362-3371.	0.2	14
123	Effect of different ingredients on color and oxidative characteristics of high pressure processed chicken breast meat with special emphasis on use of β -glucan as a partial salt replacer. <i>Innovative Food Science and Emerging Technologies</i> , 2011, 12, 244-254.	2.7	25
124	Genomic Diversity in Pig (<i>Sus scrofa</i>) and its Comparison with Human and other Livestock. <i>Current Genomics</i> , 2011, 12, 138-146.	0.7	32
125	Identification of candidate markers on bovine chromosome 14 (BTA14) under milk production trait quantitative trait loci in Holstein. <i>Journal of Animal Breeding and Genetics</i> , 2011, 128, 305-313.	0.8	10
126	Mapping QTL in the porcine MHC region affecting fatness and growth traits in a Meishan/Large White composite population. <i>Animal Genetics</i> , 2011, 42, 83-85.	0.6	9

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127	Developing marker-assisted models for evaluating growth traits in Canadian beef cattle genetic improvement. <i>Livestock Science</i> , 2011, 138, 62-68.	0.6	10
128	The use of β -glucan as a partial salt replacer in high pressure processed chicken breast meat. <i>Food Chemistry</i> , 2011, 129, 768-776.	4.2	66
129	Optimizing a beef production system using specialized sire and dam lines. <i>Canadian Journal of Animal Science</i> , 2011, 91, 353-361.	0.7	9
130	Accuracy of genomic breeding values for residual feed intake in crossbred beef cattle ¹ . <i>Journal of Animal Science</i> , 2011, 89, 3353-3361.	0.2	45
131	Genetic parameters and genotype \times environment interaction for feed efficiency traits in steers fed grower and finisher diets ¹ . <i>Journal of Animal Science</i> , 2011, 89, 3394-3400.	0.2	21
132	Genotypes of chicken major histocompatibility complex B locus associated with regression of Rous sarcoma virus J-strain tumors. <i>Poultry Science</i> , 2010, 89, 651-657.	1.5	12
133	Identification of SNPs in porcine genes expressed during porcine respiratory and reproductive syndrome virus infection. <i>Animal Genetics</i> , 2009, 40, 580-582.	0.6	5
134	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	6.0	746
135	Quantitative Trait Loci Affecting Rous Sarcoma Virus Induced Tumor Regression Trait in F2 Intercross Chickens. <i>Asian-Australasian Journal of Animal Sciences</i> , 2009, 22, 1359-1365.	2.4	1
136	Impact of genomics on animal agriculture and opportunities for animal health. <i>Trends in Biotechnology</i> , 2008, 26, 21-25.	4.9	26
137	Relationships between biochemical characteristics and meat quality of Longissimus thoracis and Semimembranosus muscles in five porcine lines. <i>Meat Science</i> , 2008, 80, 927-933.	2.7	47
138	A Naturally Occurring Variant of Porcine Mx1 Associated with Increased Susceptibility to Influenza Virus In Vitro. <i>Biochemical Genetics</i> , 2007, 45, 11-24.	0.8	51
139	Single nucleotide polymorphism identification, linkage and radiation hybrid mapping of the porcine pituitary adenylate cyclase-activating polypeptide type I receptor gene to chromosome 18. <i>Journal of Animal Breeding and Genetics</i> , 2006, 123, 414-418.	0.8	6
140	Genetic diversity in European pigs utilizing amplified fragment length polymorphism markers. <i>Animal Genetics</i> , 2006, 37, 232-238.	0.6	31
141	Commercial pigs: an untapped resource for human obesity research?. <i>Drug Discovery Today</i> , 2006, 11, 475-477.	3.2	27
142	Functional Implication of an Arg307Gly Substitution in Corticosteroid-Binding Globulin, a Candidate Gene for a Quantitative Trait Locus Associated With Cortisol Variability and Obesity in Pig. <i>Genetics</i> , 2006, 173, 2143-2149.	1.2	28
143	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
144	Using commercial pigs in the search for genes behind human obesity. <i>Nature Reviews Genetics</i> , 2005, 6, 248-248.	7.7	2

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145	Investigation of a peroxisome proliferator-activated receptor gamma haplotype effect on meat quality and carcass traits in pigs. <i>Animal Genetics</i> , 2004, 35, 238-241.	0.6	17
146	Investigation of Obesity Candidate Genes On Porcine Fat Deposition Quantitative Trait Loci Regions. <i>Obesity</i> , 2004, 12, 1981-1994.	4.0	68
147	Effects of breed, diet and muscle on fat deposition and eating quality in pigs. <i>Meat Science</i> , 2004, 67, 651-667.	2.7	341
148	Construction of a new porcine whole-genome framework map using a radiation hybrid panel. <i>Animal Genetics</i> , 2003, 34, 216-220.	0.6	21
149	The potential impact of current animal research on the meat industry and consumer attitudes towards meat. <i>Meat Science</i> , 2003, 63, 79-88.	2.7	50
150	Relationships of myosin heavy chain fibre types to meat quality traits in traditional and modern pigs. <i>Meat Science</i> , 2003, 64, 93-103.	2.7	173
151	A Sensitive Method for Detecting Variation in Copy Numbers of Duplicated Genes. <i>Genome Research</i> , 2003, 13, 2171-2177.	2.4	46
152	Candidate Gene Analysis for Quantitative Traits Using the Transmission Disequilibrium Test: The Example of the Melanocortin 4-Receptor in Pigs. <i>Genetics</i> , 2003, 164, 637-644.	1.2	60
153	IDENTIFICATION OF THREE SNPs IN THE PORCINE MYOSTATIN GENE (MSTN). <i>Animal Biotechnology</i> , 2002, 13, 173-178.	0.7	20
154	Mapping and investigation of the porcine major insulin sensitive glucose transport (SLC2A4/GLUT4) gene as a candidate gene for meat quality and carcass traits. <i>Journal of Animal Breeding and Genetics</i> , 2002, 119, 47-55.	0.8	9
155	Genetic variation in two conserved local Romanian pig breeds using type 1 DNA markers. <i>Genetics Selection Evolution</i> , 2001, 33, 417-32.	1.2	28
156	A Frameshift Mutation in <i>MC1R</i> and a High Frequency of Somatic Reversions Cause Black Spotting in Pigs. <i>Genetics</i> , 2001, 158, 779-785.	1.2	118
157	Evidence for New Alleles in the Protein Kinase Adenosine Monophosphate-Activated β 3-Subunit Gene Associated With Low Glycogen Content in Pig Skeletal Muscle and Improved Meat Quality. <i>Genetics</i> , 2001, 159, 1151-1162.	1.2	199
158	A missense variant of the porcine melanocortin-4 receptor (MC4R) gene is associated with fatness, growth, and feed intake traits. <i>Mammalian Genome</i> , 2000, 11, 131-135.	1.0	358
159	The Belt mutation in pigs is an allele at the Dominant white (<i>I/KIT</i>) locus. <i>Mammalian Genome</i> , 1999, 10, 1132-1136.	1.0	92
160	ELISA detection of restriction site polymorphisms in the pig ryanodine receptor locus. <i>Mammalian Genome</i> , 1998, 9, 629-632.	1.0	1
161	The estrogen receptor locus is associated with a major gene influencing litter size in pigs.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 201-205.	3.3	300
162	The ferrichrome receptor protein (tonA) of <i>Escherichia coli</i> synthesised as a precursor in vitro. <i>FEBS Letters</i> , 1981, 131, 262-264.	1.3	17