

# Graham Plastow

## List of Publications by Year in descending order

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162  
papers

7,249  
citations

76294

40  
h-index

64755

79  
g-index

164  
all docs

164  
docs citations

164  
times ranked

7086  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	6.0	746
2	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
3	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
4	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
5	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
6	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
7	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
8	Livestock metabolomics and the livestock metabolome: A systematic review. <i>PLoS ONE</i> , 2017, 12, e0177675.	1.1	226
9	Evidence for New Alleles in the Protein Kinase Adenosine Monophosphate-Activated $\beta$ 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
10	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
11	An atlas of DNA methylomes in porcine adipose and muscle tissues. <i>Nature Communications</i> , 2012, 3, 850.	5.8	152
12	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
13	Genome Sequence and Assembly of <i>Bos indicus</i> . <i>Journal of Heredity</i> , 2012, 103, 342-348.	1.0	106
14	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
15	Linkage disequilibrium in Angus, Charolais, and Crossbred beef cattle. <i>Frontiers in Genetics</i> , 2012, 3, 152.	1.1	93
16	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
17	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
18	Genome-wide association analyses for growth and feed efficiency traits in beef cattle1. <i>Journal of Animal Science</i> , 2013, 91, 3612-3633.	0.2	76

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19	Identification of a putative quantitative trait nucleotide in guanylate binding protein 5 for host response to PRRS virus infection. BMC Genomics, 2015, 16, 412.	1.2	75
20	Genome-wide association studies to identify quantitative trait loci affecting milk production traits in water buffalo. Journal of Dairy Science, 2018, 101, 433-444.	1.4	70
21	Investigation of Obesity Candidate Genes On Porcine Fat Deposition Quantitative Trait Loci Regions. Obesity, 2004, 12, 1981-1994.	4.0	68
22	Analysis of biological networks and biological pathways associated with residual feed intake in beef cattle. Animal Science Journal, 2014, 85, 374-387.	0.6	67
23	The use of Î²-glucan as a partial salt replacer in high pressure processed chicken breast meat. Food Chemistry, 2011, 129, 768-776.	4.2	66
24	Gene co-expression network analysis identifies porcine genes associated with variation in Salmonella shedding. BMC Genomics, 2014, 15, 452.	1.2	65
25	<sc>GO</sc>â€™<sc>FAANG</sc> meeting: a Gathering On Functional Annotation of <sc>Animal Genomes. Animal Genetics, 2016, 47, 528-533.	0.6	65
26	Whole genome sequencing of Gir cattle for identifying polymorphisms and loci under selection. Genome, 2013, 56, 592-598.	0.9	63
27	Candidate Gene Analysis for Quantitative Traits Using the Transmission Disequilibrium Test: The Example of the Melanocortin 4-Receptor in Pigs. Genetics, 2003, 164, 637-644.	1.2	60
28	Genomic evaluation of feed efficiency component traits in Duroc pigs using 80K, 650K and whole-genome sequence variants. Genetics Selection Evolution, 2018, 50, 14.	1.2	57
29	A Naturally Occurring Variant of Porcine Mx1 Associated with Increased Susceptibility to Influenza Virus In Vitro. Biochemical Genetics, 2007, 45, 11-24.	0.8	51
30	The potential impact of current animal research on the meat industry and consumer attitudes towards meat. Meat Science, 2003, 63, 79-88.	2.7	50
31	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. BMC Genomics, 2020, 21, 36.	1.2	49
32	Novel insights into host responses and reproductive pathophysiology of porcine reproductive and respiratory syndrome caused by PRRSV-2. Veterinary Microbiology, 2017, 209, 114-123.	0.8	48
33	Relationships between biochemical characteristics and meat quality of Longissimus thoracis and Semimembranosus muscles in five porcine lines. Meat Science, 2008, 80, 927-933.	2.7	47
34	Single nucleotide polymorphisms for feed efficiency and performance in crossbred beef cattle. BMC Genetics, 2014, 15, 14.	2.7	47
35	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. PLoS ONE, 2014, 9, e96104.	1.1	47
36	A Sensitive Method for Detecting Variation in Copy Numbers of Duplicated Genes. Genome Research, 2003, 13, 2171-2177.	2.4	46

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37	Accuracy of genomic breeding values for residual feed intake in crossbred beef cattle <sup>1</sup> . <i>Journal of Animal Science</i> , 2011, 89, 3353-3361.	0.2	45
38	Genetic diversity, breed composition and admixture of Kenyan domestic pigs. <i>PLoS ONE</i> , 2018, 13, e0190080.	1.1	44
39	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
40	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
41	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
42	A large and diverse collection of bovine genome sequences from the Canadian Cattle Genome Project. <i>GigaScience</i> , 2015, 4, 49.	3.3	38
43	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
44	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
45	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
46	Accuracy of genomic predictions for feed efficiency traits of beef cattle using 50K and imputed HD genotypes <sup>1</sup> . <i>Journal of Animal Science</i> , 2016, 94, 1342-1353.	0.2	34
47	Genome-wide whole blood microRNAome and transcriptome analyses reveal miRNA-mRNA regulated host response to foodborne pathogen <i>Salmonella</i> infection in swine. <i>Scientific Reports</i> , 2015, 5, 12620.	1.6	33
48	Genome-wide association studies (GWAS) identify a QTL close to PRKAG3 affecting meat pH and colour in crossbred commercial pigs. <i>BMC Genomics</i> , 2015, 16, 33.	2.7	33
49	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
50	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
51	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
52	Genome-wide association analyses for carcass quality in crossbred beef cattle. <i>BMC Genomics</i> , 2013, 14, 80.	2.7	32
53	Applications of genomics to improve livestock in the developing world. <i>Livestock Science</i> , 2014, 166, 76-83.	0.6	32
54	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

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55	Genetic diversity in European pigs utilizing amplified fragment length polymorphism markers. <i>Animal Genetics</i> , 2006, 37, 232-238.	0.6	31
56	Impact of selection for residual feed intake on breeding soundness and reproductive performance of bulls on pasture-based multisire mating <sup>1</sup> . <i>Journal of Animal Science</i> , 2012, 90, 2963-2969.	0.2	31
57	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
58	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
59	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
60	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
61	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
62	Synaptogyrin-2 influences replication of Porcine circovirus 2. <i>PLoS Genetics</i> , 2018, 14, e1007750.	1.5	28
63	Commercial pigs: an untapped resource for human obesity research?. <i>Drug Discovery Today</i> , 2006, 11, 475-477.	3.2	27
64	Impact of genomics on animal agriculture and opportunities for animal health. <i>Trends in Biotechnology</i> , 2008, 26, 21-25.	4.9	26
65	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
66	Genomewide association of piglet responses to infection with one of two porcine reproductive and respiratory syndrome virus isolates <sup>1</sup> . <i>Journal of Animal Science</i> , 2017, 95, 16-38.	0.2	26
67	Effect of different ingredients on color and oxidative characteristics of high pressure processed chicken breast meat with special emphasis on use of $\beta$ -glucan as a partial salt replacer. <i>Innovative Food Science and Emerging Technologies</i> , 2011, 12, 244-254.	2.7	25
68	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
69	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
70	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
71	Host genetics of response to porcine reproductive and respiratory syndrome in nursery pigs. <i>Veterinary Microbiology</i> , 2017, 209, 107-113.	0.8	24
72	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

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73	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
74	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
75	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
76	Reliability of molecular breeding values for Warner-Bratzler shear force and carcass traits of beef cattle – An independent validation study <sup>1</sup> . <i>Journal of Animal Science</i> , 2014, 92, 2896-2904.	0.2	22
77	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
78	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
79	Genetic parameters and genotype × environment interaction for feed efficiency traits in steers fed grower and finisher diets <sup>1</sup> . <i>Journal of Animal Science</i> , 2011, 89, 3394-3400.	0.2	21
80	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
81	IDENTIFICATION OF THREE SNPs IN THE PORCINE MYOSTATIN GENE (MSTN). <i>Animal Biotechnology</i> , 2002, 13, 173-178.	0.7	20
82	Modeling heterotic effects in beef cattle using genome-wide SNP-marker genotypes <sup>1</sup> . <i>Journal of Animal Science</i> , 2018, 96, 830-845.	0.2	20
83	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
84	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
85	Candidate serum metabolite biomarkers of residual feed intake and carcass merit in sheep. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	19
86	Comparative Transcriptomic Analysis of Rectal Tissue from Beef Steers Revealed Reduced Host Immunity in <i>Escherichia coli</i> O157:H7 Super-Shedders. <i>PLoS ONE</i> , 2016, 11, e0151284.	1.1	18
87	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
88	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
89	Genome-wide association for heifer reproduction and calf performance traits in beef cattle. <i>Genome</i> , 2015, 58, 549-557.	0.9	17
90	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

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91	MicroRNA Buffering and Altered Variance of Gene Expression in Response to Salmonella Infection. PLoS ONE, 2014, 9, e94352.	1.1	17
92	Characterization of whole blood transcriptome and early-life fecal microbiota in high and low responder pigs before, and after vaccination for Mycoplasma hyopneumoniae. Vaccine, 2019, 37, 1743-1755.	1.7	16
93	Host mechanisms involved in cattle Escherichia coli O157 shedding: a fundamental understanding for reducing foodborne pathogen in food animal production. Scientific Reports, 2017, 7, 7630.	1.6	15
94	Whole-Blood Transcriptome Analysis of Feedlot Cattle With and Without Bovine Respiratory Disease. Frontiers in Genetics, 2021, 12, 627623.	1.1	15
95	Associations of marker panel scores with feed intake and efficiency traits in beef cattle using preselected single nucleotide polymorphisms <sup>1</sup> . Journal of Animal Science, 2011, 89, 3362-3371.	0.2	14
96	Variation in time and magnitude of immune response and viremia in experimental challenges with Porcine circovirus 2b. BMC Veterinary Research, 2014, 10, 286.	0.7	14
97	Genetic relationships of antibody response, viremia level, and weight gain in pigs experimentally infected with porcine reproductive and respiratory syndrome virus <sup>1</sup> . Journal of Animal Science, 2018, 96, 3565-3581.	0.2	14
98	Exploring Phenotypes for Disease Resilience in Pigs Using Complete Blood Count Data From a Natural Disease Challenge Model. Frontiers in Genetics, 2020, 11, 216.	1.1	14
99	Sequence, Structural and Expression Divergence of Duplicate Genes in the Bovine Genome. PLoS ONE, 2014, 9, e102868.	1.1	13
100	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. PLoS ONE, 2016, 11, e0153615.	1.1	13
101	Genomewide association of piglet responses to infection with one of two porcine reproductive and respiratory syndrome virus isolates. Journal of Animal Science, 2017, 95, 16.	0.2	13
102	Genotypes of chicken major histocompatibility complex B locus associated with regression of Rous sarcoma virus J-strain tumors. Poultry Science, 2010, 89, 651-657.	1.5	12
103	Trust and Consumer Preferences for Pig Production Attributes in Canada. Canadian Journal of Agricultural Economics, 2017, 65, 477-514.	1.2	12
104	Comparative transcriptomic analysis of porcine peripheral blood reveals differentially expressed genes from the cytokine-cytokine receptor interaction pathway related to health status. Genome, 2017, 60, 1021-1028.	0.9	12
105	Performance and optimization of an ear tag automated activity monitor for estrus prediction in dairy heifers. Theriogenology, 2020, 155, 197-204.	0.9	12
106	Breeding for disease resilience: opportunities to manage polymicrobial challenge and improve commercial performance in the pig industry. CABI Agriculture and Bioscience, 2022, 3, 6.	1.1	12
107	Identification of candidate markers on bovine chromosome 14 (BTA14) under milk production trait quantitative trait loci in Holstein. Journal of Animal Breeding and Genetics, 2011, 128, 305-313.	0.8	10
108	Developing marker-assisted models for evaluating growth traits in Canadian beef cattle genetic improvement. Livestock Science, 2011, 138, 62-68.	0.6	10

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109	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
110	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
111	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
112	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
113	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
114	Genomic Selection, a New Era for Pork Quality Improvement. <i>Springer Science Reviews</i> , 2015, 3, 27-37.	1.3	9
115	Identification of factors associated with virus level in tonsils of pigs experimentally infected with porcine reproductive and respiratory syndrome virus 1. <i>Journal of Animal Science</i> , 2019, 97, 536-547.	0.2	9
116	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
117	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
118	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
119	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
120	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
121	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
122	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
123	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
124	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
125	Livestock and the promise of genomics. <i>Genome</i> , 2013, 56, 556-566.	0.9	6
126	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



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127	Genetic parameters and purebredâ€™crossbred genetic correlations for growth, meat quality, and carcass traits in pigs. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	6
128	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
129	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
130	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
131	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
132	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
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	Effect of temperature and <scp>pH</scp> 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
135	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
136	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
137	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
138	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
139	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
140	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
141	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
142	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
143	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
144	Putative Loci Causing Early Embryonic Mortality in Duroc Swine. <i>Frontiers in Genetics</i> , 2018, 9, 655.	1.1	3

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145	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
146	Genetic and phenotypic parameters for feed efficiency and component traits in American mink. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	3
147	History of the Hays Converter. <i>Canadian Journal of Animal Science</i> , 2016, 96, 471-477.	0.7	2
148	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
149	Purebred-crossbred genetic parameters for reproductive traits in swine. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	2
150	Using commercial pigs in the search for genes behind human obesity. <i>Nature Reviews Genetics</i> , 2005, 6, 248-248.	7.7	2
151	Estimating Animal Abundance in Ground Beef Batches Assayed with Molecular Markers. <i>PLoS ONE</i> , 2012, 7, e34191.	1.1	2
152	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
153	ELISA detection of restriction site polymorphisms in the pig ryanodine receptor locus. <i>Mammalian Genome</i> , 1998, 9, 629-632.	1.0	1
154	Association analysis for feed efficiency traits in beef cattle using preserved haplotypes. <i>Genome</i> , 2013, 56, 586-591.	0.9	1
155	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
156	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
157	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
158	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
159	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
160	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
161	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
162	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