

# Larry A Kuehn

## List of Publications by Year in descending order

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Version: 2024-02-01

136  
papers

3,695  
citations

182225  
30  
h-index

190340  
53  
g-index

136  
all docs

136  
docs citations

136  
times ranked

3643  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | Genetic parameters, heterosis, and breed effects for body condition score and mature cow weight in beef cattle. <i>Journal of Animal Science</i> , 2022, 100, .  | 0.2 | 6         |
| 2  | Influence of environmental factors and genetic variation on mitochondrial DNA copy number. <i>Journal of Animal Science</i> , 2022, 100, .   | 0.2 | 6         |
| 3  | Breeding Sustainable Beef Cows: Reducing Weight and Increasing Productivity. <i>Animals</i> , 2022, 12, 1745.  | 1.0 | 1         |
| 4  | A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i> . <i>Journal of Heredity</i> , 2021, 112, 184-191.   | 1.0 | 25        |
| 5  | Genetic changes in beef cow traits following selection for calving ease. <i>Translational Animal Science</i> , 2021, 5, txab009.   | 0.4 | 1         |
| 6  | A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . <i>Journal of Heredity</i> , 2021, 112, 174-183.   | 1.0 | 14        |
| 7  | Evaluating Accuracy of DNA Pool Construction Based on White Blood Cell Counts. <i>Frontiers in Genetics</i> , 2021, 12, 635846.  | 1.1 | 3         |
| 8  | Using Genomics to Measure Phenomics: Repeatability of Bull Prolificacy in Multiple-Bull Pastures. <i>Agriculture (Switzerland)</i> , 2021, 11, 603.  | 1.4 | 2         |
| 9  | Breed and heterotic effects for mature weight in beef cattle. <i>Journal of Animal Science</i> , 2021, 99, .   | 0.2 | 8         |
| 10 | Detection of bovine inflammatory cytokines IL-1 $\beta$ , IL-6, and TNF- $\alpha$ with a multiplex electrochemiluminescent assay platform. <i>Veterinary Immunology and Immunopathology</i> , 2021, 237, 110274. | 0.5 | 2         |
| 11 | Accuracy of GEBV of sires based on pooled allele frequency of their progeny. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .   | 0.8 | 3         |
| 12 | Transcriptome profiles of the skeletal muscle of mature cows during feed restriction and realimentation. <i>BMC Research Notes</i> , 2021, 14, 361.  | 0.6 | 0         |
| 13 | Estimation of Pool Construction and Technical Error. <i>Agriculture (Switzerland)</i> , 2021, 11, 1091.  | 1.4 | 2         |
| 14 | Hematology parameters as potential indicators of feed efficiency in pigs. <i>Translational Animal Science</i> , 2021, 5, txab219.  | 0.4 | 4         |
| 15 | Lamb wool shedding is a good predictor of ewe wool shedding. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 365-373.  | 0.8 | 3         |
| 16 | Classification of 16S rRNA reads is improved using a niche-specific database constructed by near-full length sequencing. <i>PLoS ONE</i> , 2020, 15, e0235498.   | 1.1 | 11        |
| 17 | Genomic Breed Composition of Selection Signatures in Brangus Beef Cattle. <i>Frontiers in Genetics</i> , 2020, 11, 710.  | 1.1 | 21        |
| 18 | Influence of host genetics in shaping the rumen bacterial community in beef cattle. <i>Scientific Reports</i> , 2020, 10, 15101.   | 1.6 | 35        |

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|----|---|-----|-----------|
| 19 | Assessment of Imputation from Low-Pass Sequencing to Predict Merit of Beef Steers. <i>Genes</i> , 2020, 11, 1312.   | 1.0 | 55        |
| 20 | Ruminal transcript abundance of the centromere-associated protein E gene may influence residual feed intake in beef steers. <i>Animal Genetics</i> , 2020, 51, 453-456.                               | 0.6 | 1         |
| 21 | Genomic prediction using pooled data in a single-step genomic best linear unbiased prediction framework. <i>Journal of Animal Science</i> , 2020, 98, .   | 0.2 | 8         |
| 22 | Heritability and genetic correlations of feed intake, body weight gain, residual gain, and residual feed intake of beef cattle as heifers and cows. <i>Journal of Animal Science</i> , 2020, 98, .    | 0.2 | 34        |
| 23 | Dynamics of genomic architecture during composite breed development in cattle. <i>Animal Genetics</i> , 2020, 51, 224-234.  | 0.6 | 23        |
| 24 | Longitudinal study of humoral immunity to bovine coronavirus, virus shedding, and treatment for bovine respiratory disease in pre-weaned beef calves. <i>BMC Veterinary Research</i> , 2019, 15, 161. | 0.7 | 24        |
| 25 | Microbiome of the upper nasal cavity of beef calves prior to weaning <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2019, 97, 2368-2375.   | 0.2 | 8         |
| 26 | Validation of <sc>SNP</sc> associations with bovine ovulation and twinning rate. <i>Animal Genetics</i> , 2019, 50, 259-261.  | 0.6 | 3         |
| 27 | Comparison of different functions to describe growth from weaning to maturity in crossbred beef cattle <sup>1</sup> . <i>Journal of Animal Science</i> , 2019, 97, 1523-1533.                         | 0.2 | 10        |
| 28 | Characterization of water intake and water efficiency in beef cattle <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2019, 97, 4770-4782.   | 0.2 | 19        |
| 29 | Genetic correlations among weight and cumulative productivity of crossbred beef cows <sup>1</sup> . <i>Journal of Animal Science</i> , 2019, 97, 63-77.   | 0.2 | 15        |
| 30 | Using SNP Weights Derived From Gene Expression Modules to Improve GWAS Power for Feed Efficiency in Pigs. <i>Frontiers in Genetics</i> , 2019, 10, 1339.  | 1.1 | 11        |
| 31 | Rumen bacterial community structure impacts feed efficiency in beef cattle. <i>Journal of Animal Science</i> , 2018, 96, 1045-1058.   | 0.2 | 71        |
| 32 | Reducing the period of data collection for intake and gain to improve response to selection for feed efficiency in beef cattle. <i>Journal of Animal Science</i> , 2018, 96, 854-866.                 | 0.2 | 8         |
| 33 | Genome-wide association study for feed efficiency traits using SNP and haplotype models <sup>1</sup> . <i>Journal of Animal Science</i> , 2018, 96, 2086-2098.  | 0.2 | 10        |
| 34 | Complete blood count data and leukocyte expression of cytokine genes and cytokine receptor genes associated with bovine respiratory disease in calves. <i>BMC Research Notes</i> , 2018, 11, 786.     | 0.6 | 15        |
| 35 | Environmental effects on water intake and water intake prediction in growing beef cattle <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2018, 96, 4368-4384.                                     | 0.2 | 29        |
| 36 | Genetic variation in humoral response to an <i>Escherichia coli</i> O157:H7 vaccine in beef cattle. <i>PLoS ONE</i> , 2018, 13, e0197347.   | 1.1 | 1         |

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|----|---|-----|-----------|
| 37 | Test duration for water intake, ADG, and DMI in beef cattle <sup>1</sup> . <i>Journal of Animal Science</i> , 2018, 96, 3043-3054.  | 0.2 | 9         |
| 38 | RNA-Seq Meta-analysis identifies genes in skeletal muscle associated with gain and intake across a multi-season study of crossbred beef steers. <i>BMC Genomics</i> , 2018, 19, 430.  | 1.2 | 21        |
| 39 | Association of Circulating Transfer RNA fragments with antibody response to <i>Mycoplasma bovis</i> in beef cattle. <i>BMC Veterinary Research</i> , 2018, 14, 89.  | 0.7 | 3         |
| 40 | Evaluating the microbiome of two sampling locations in the nasal cavity of cattle with bovine respiratory disease complex (BRDC) <sup>1</sup> . <i>Journal of Animal Science</i> , 2018, 96, 1281-1287.   | 0.2 | 22        |
| 41 | Relationships between the genes expressed in the mesenteric adipose tissue of beef cattle and feed intake and gain. <i>Animal Genetics</i> , 2017, 48, 386-394.   | 0.6 | 14        |
| 42 | Evaluation of the effect of serum antibody abundance against bovine coronavirus on bovine coronavirus shedding and risk of respiratory tract disease in beef calves from birth through the first five weeks in a feedlot. <i>American Journal of Veterinary Research</i> , 2017, 78, 1065-1076. | 0.3 | 13        |
| 43 | The impact of the bovine faecal microbiome on <i>Escherichia coli</i> O157:H7 prevalence and enumeration in naturally infected cattle. <i>Journal of Applied Microbiology</i> , 2017, 123, 1027-1042.   | 1.4 | 9         |
| 44 | Linkage disequilibrium among commonly genotyped SNP variants detected from bull sequence. <i>Animal Genetics</i> , 2017, 48, 516-522.   | 0.6 | 5         |
| 45 | Ruminal expression of the <i>NQO1</i> , <i>RGS5</i> , and <i>ACAT1</i> genes may be indicators of feed efficiency in beef steers. <i>Animal Genetics</i> , 2017, 48, 90-92.   | 0.6 | 10        |
| 46 | Effect of abomasal butyrate infusion on gene expression in the duodenum of lambs. <i>Journal of Animal Science</i> , 2017, 95, 1191-1196.   | 0.2 | 4         |
| 47 | Analysis of the gut bacterial communities in beef cattle and their association with feed intake, growth, and efficiency <sup>1,2,3</sup> . <i>Journal of Animal Science</i> , 2017, 95, 3215-3224.  | 0.2 | 48        |
| 48 | Association of preweaning and weaning serum cortisol and metabolites with ADG and incidence of respiratory disease in beef cattle. <i>Journal of Animal Science</i> , 2017, 95, 5012-5019.  | 0.2 | 7         |
| 49 | Differential expression of genes related to gain and intake in the liver of beef cattle. <i>BMC Research Notes</i> , 2017, 10, 1.   | 0.6 | 268       |
| 50 | Endocannabinoid concentrations in plasma during the finishing period are associated with feed efficiency and carcass composition of beef cattle <sup>1</sup> . <i>Journal of Animal Science</i> , 2017, 95, 4568-4574.  | 0.2 | 2         |
| 51 | Evaluating a New Shade for Feedlot Cattle Performance and Heat Stress. <i>Transactions of the ASABE</i> , 2017, 60, 1301-1311.  | 1.1 | 4         |
| 52 | Analysis of the gut bacterial communities in beef cattle and their association with feed intake, growth, and efficiency. <i>Journal of Animal Science</i> , 2017, 95, 3215.   | 0.2 | 25        |
| 53 | Genetic variance and covariance and breed differences for feed intake and average daily gain to improve feed efficiency in growing cattle. <i>Journal of Animal Science</i> , 2017, 95, 1444.   | 0.2 | 2         |
| 54 | Microbial community profiles of the jejunum from steers differing in feed efficiency <sup>1,2,3</sup> . <i>Journal of Animal Science</i> , 2016, 94, 327-338.   | 0.2 | 62        |

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|----|---|-----|-----------|
| 55 | Profile of the Spleen Transcriptome in Beef Steers with Variation in Gain and Feed Intake. <i>Frontiers in Genetics</i> , 2016, 7, 127.   | 1.1 | 14        |
| 56 | Association of MicroRNAs with Antibody Response to <i>Mycoplasma bovis</i> in Beef Cattle. <i>PLoS ONE</i> , 2016, 11, e0161651.  | 1.1 | 17        |
| 57 | Breed effects and genetic parameter estimates for calving difficulty and birth weight in a multibreed population <sup>1</sup> . <i>Journal of Animal Science</i> , 2016, 94, 1857-1864. | 0.2 | 22        |
| 58 | Differential gene expression in the duodenum, jejunum and ileum among crossbred beef steers with divergent gain and feed intake phenotypes. <i>Animal Genetics</i> , 2016, 47, 408-427. | 0.6 | 42        |
| 59 | Genomewide association study of liver abscess in beef cattle <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2016, 94, 490-499.   | 0.2 | 9         |
| 60 | Transcriptome differences in the rumen of beef steers with variation in feed intake and gain. <i>Gene</i> , 2016, 586, 12-26.   | 1.0 | 45        |
| 61 | Estimating heritability of wool shedding in a crossbred ewe population. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 396-403.  | 0.8 | 7         |
| 62 | Cecum microbial communities from steers differing in feed efficiency <sup>1,2,3</sup> . <i>Journal of Animal Science</i> , 2015, 93, 5327-5340.   | 0.2 | 58        |
| 63 | Evaluation of single nucleotide polymorphisms in chromosomal regions impacting pregnancy status in cattle. <i>Journal of Animal Science</i> , 2015, 93, 978.                            | 0.2 | 4         |
| 64 | Relationship of leptin concentrations with feed intake, growth, and efficiency in finishing beef steers. <i>Journal of Animal Science</i> , 2015, 93, 4401-4407.                        | 0.2 | 12        |
| 65 | A survey of polymorphisms detected from sequences of popular beef breeds <sup>1,2,3</sup> . <i>Journal of Animal Science</i> , 2015, 93, 5128-5143.                                     | 0.2 | 36        |
| 66 | Genomewide association study of lung lesions in cattle using sample pooling. <i>Journal of Animal Science</i> , 2015, 93, 956.  | 0.2 | 21        |
| 67 | Rumen Microbiome from Steers Differing in Feed Efficiency. <i>PLoS ONE</i> , 2015, 10, e0129174.  | 1.1 | 307       |
| 68 | Estimation of breed-specific heterosis effects for birth, weaning, and yearling weight in cattle <sup>1</sup> . <i>Journal of Animal Science</i> , 2015, 93, 46-52.                     | 0.2 | 53        |
| 69 | Differences in transcript abundance of genes on BTA15 located within a region associated with gain in beef steers. <i>Gene</i> , 2015, 572, 42-48.                                      | 1.0 | 7         |
| 70 | Seasonal variation in vitamin D status of beef cattle reared in the central United States. <i>Domestic Animal Endocrinology</i> , 2015, 52, 71-74.                                      | 0.8 | 21        |
| 71 | Microbial community profiles of the colon from steers differing in feed efficiency. <i>SpringerPlus</i> , 2015, 4, 454.   | 1.2 | 52        |
| 72 | Genetic markers that influence feed efficiency phenotypes also affect cattle temperament as measured by flight speed. <i>Animal Genetics</i> , 2015, 46, 60-64.                         | 0.6 | 13        |

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|----|--|-----|-----------|
| 73 | Investigation of bacterial diversity in the feces of cattle fed different diets <sup>1</sup> . <i>Journal of Animal Science</i> , 2014, 92, 683-694.   | 0.2 | 134       |
| 74 | MEAT SCIENCE AND MUSCLE BIOLOGY SYMPOSIUM: <i>Escherichia coli</i> O157:H7, diet, and fecal microbiome in beef cattle <sup>12</sup> . <i>Journal of Animal Science</i> , 2014, 92, 1345-1355.  | 0.2 | 19        |
| 75 | Effects of feeding dry-rolled corn-based diets with and without wet distillers grains with solubles and zilpaterol hydrochloride on performance, carcass characteristics, and heat stress in finishing beef steers <sup>1</sup> . <i>Journal of Animal Science</i> , 2014, 92, 4023-4033.                    | 0.2 | 13        |
| 76 | Beef cattle body temperature during climatic stress: a genome-wide association study. <i>International Journal of Biometeorology</i> , 2014, 58, 1665-1672.  | 1.3 | 53        |
| 77 | DNA polymorphisms and transcript abundance of PRKAG2 and phosphorylated AMP-activated protein kinase in the rumen are associated with gain and feed intake in beef steers. <i>Animal Genetics</i> , 2014, 45, 461-472.   | 0.6 | 7         |
| 78 | Use of ultrasound scanning and body condition score to evaluate composition traits in mature beef cows <sup>123</sup> . <i>Journal of Animal Science</i> , 2014, 92, 3868-3877.  | 0.2 | 7         |
| 79 | Deletion on chromosome 5 associated with decreased reproductive efficiency in female cattle <sup>1,2,3,4</sup> . <i>Journal of Animal Science</i> , 2014, 92, 1378-1384.   | 0.2 | 15        |
| 80 | Influence of dry matter intake, dry matter digestibility, and feeding behavior on body weight gain of beef steers <sup>1,2,3</sup> . <i>Journal of Animal Science</i> , 2014, 92, 3018-3025.   | 0.2 | 12        |
| 81 | Genomewide association study of reproductive efficiency in female cattle <sup>1,2,3,4</sup> . <i>Journal of Animal Science</i> , 2014, 92, 1945-1957.  | 0.2 | 29        |
| 82 | Incorporation of Genetic Technologies Associated with Applied Reproductive Technologies to Enhance World Food Production. <i>Advances in Experimental Medicine and Biology</i> , 2014, 752, 77-96.   | 0.8 | 5         |
| 83 | Comparison of molecular breeding values based on within- and across-breed training in beef cattle. <i>Genetics Selection Evolution</i> , 2013, 45, 30.   | 1.2 | 56        |
| 84 | A genomewide association study identified CYP2J2 as a gene controlling serum vitamin D status in beef cattle <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2013, 91, 3549-3556.  | 0.2 | 13        |
| 85 | Influence of Therapeutic Ceftiofur Treatments of Feedlot Cattle on Fecal and Hide Prevalences of Commensal <i>Escherichia coli</i> Resistant to Expanded-Spectrum Cephalosporins, and Molecular Characterization of Resistant Isolates. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2273-2283. | 1.4 | 31        |
| 86 | The change in differing leukocyte populations during vaccination to bovine respiratory disease and their correlations with lung scores, health records, and average daily gain <sup>1,2,3</sup> . <i>Journal of Animal Science</i> , 2013, 91, 3564-3573.  | 0.2 | 19        |
| 87 | Identification of an ionotropic glutamate receptor AMPA1/GRIA1 polymorphism in crossbred beef cows differing in fertility <sup>12</sup> . <i>Journal of Animal Science</i> , 2013, 91, 2640-2646.  | 0.2 | 17        |
| 88 | Imputation of microsatellite alleles from dense SNP genotypes for parentage verification across multiple <i>Bos taurus</i> and <i>Bos indicus</i> breeds. <i>Frontiers in Genetics</i> , 2013, 4, 176.   | 1.1 | 29        |
| 89 | Adipose and Muscle Tissue Gene Expression of Two Genes (NCAPG and LCORL) Located in a Chromosomal Region Associated with Cattle Feed Intake and Gain. <i>PLoS ONE</i> , 2013, 8, e80882.   | 1.1 | 58        |
| 90 | PHYSIOLOGY AND ENDOCRINOLOGY SYMPOSIUM: How single nucleotide polymorphism chips will advance our knowledge of factors controlling puberty and aid in selecting replacement beef females <sup>1,2,3,4</sup> . <i>Journal of Animal Science</i> , 2012, 90, 1152-1165.  | 0.2 | 43        |

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|-----|---|-----|-----------|
| 91  | Accuracy of genomic breeding values in multibreed beef cattle populations derived from deregressed breeding values and phenotypes <sup>1,2</sup> . Journal of Animal Science, 2012, 90, 4177-4190.                                    | 0.2 | 50        |
| 92  | Genomics and the global beef cattle industry. Animal Production Science, 2012, 52, 92.  | 0.6 | 19        |
| 93  | Comparison of bacterial communities in faeces of beef cattle fed diets containing corn and wet distillersâ€™ grain with solubles. Letters in Applied Microbiology, 2012, 55, 109-114.   | 1.0 | 39        |
| 94  | Y are you not pregnant: Identification of Y chromosome segments in female cattle with decreased reproductive efficiency <sup>1,2,3,4</sup> . Journal of Animal Science, 2012, 90, 2142-2151.  | 0.2 | 30        |
| 95  | Associations of genetic markers in cattle receiving differing implant protocols <sup>1,2</sup> . Journal of Animal Science, 2012, 90, 2410-2423.  | 0.2 | 3         |
| 96  | The accuracies of DNA-based estimates of genetic merit derived from Angus or multibreed beef cattle training populations <sup>1,2,3</sup> . Journal of Animal Science, 2012, 90, 4191-4202.   | 0.2 | 8         |
| 97  | Evaluation of polymorphisms within the genes <i>GHSR</i> and <i>SLC2A2</i> that are within a region on bovine chromosome 1 (BTA1) previously associated with feed intake and weight gain. Animal Genetics, 2012, 43, 112-112.         | 0.6 | 1         |
| 98  | A region on BTA14 that includes the positional candidate genes <i>LYPLA1</i> , <i>XKR4</i> and <i>TMEM68</i> is associated with feed intake and growth phenotypes in cattle <sup>&gt;1</sup> . Animal Genetics, 2012, 43, 216-219.    | 0.6 | 57        |
| 99  | Genetic markers on <i>BTA</i> 14 predictive for residual feed intake in beef steers and their effects on carcass and meat quality traits. Animal Genetics, 2012, 43, 599-603.   | 0.6 | 10        |
| 100 | Evaluation of Bovine chemerin (RARRES2) Gene Variation on Beef Cattle Production Traits <sup>1</sup> . Frontiers in Genetics, 2012, 3, 39.  | 1.1 | 8         |
| 101 | Association, effects and validation of polymorphisms within the NCAPG - LCORL locus located on BTA6 with feed intake, gain, meat and carcass traits in beef cattle. BMC Genetics, 2011, 12, 103.                                      | 2.7 | 135       |
| 102 | Predicting breed composition using breed frequencies of 50,000 markers from the US Meat Animal Research Center 2,000 Bull Project <sup>1,2</sup> . Journal of Animal Science, 2011, 89, 1742-1750.                                    | 0.2 | 75        |
| 103 | Growth curves of crossbred cows sired by Hereford, Angus, Belgian Blue, Brahman, Boran, and Tuli bulls, and the fraction of mature body weight and height at puberty <sup>1,2</sup> . Journal of Animal Science, 2011, 89, 2373-2379. | 0.2 | 57        |
| 104 | Partial-genome evaluation of postweaning feed intake and efficiency of crossbred beef cattle <sup>1,2</sup> . Journal of Animal Science, 2011, 89, 1731-1741.   | 0.2 | 64        |
| 105 | Quantitative Genomics of Female Reproduction. , 2010, , 23-51.  |     | 1         |
| 106 | Postweaning growth and carcass traits in crossbred cattle from Hereford, Angus, Brangus, Beefmaster, Bonsmara, and Romosinuano maternal grandsires <sup>1,2</sup> . Journal of Animal Science, 2010, 88, 102-108.                     | 0.2 | 25        |
| 107 | Genomic regions associated with kyphosis in swine. BMC Genetics, 2010, 11, 112.   | 2.7 | 25        |
| 108 | Polymorphisms in <i>POMC</i> are not associated with dry matter intake and average daily gain phenotypes in beef cattle. Animal Genetics, 2010, 41, 669-669.  | 0.6 | 3         |

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|-----|---|-----|-----------|
| 109 | Contribution of genetic influences to animal-to-animal variation in myoglobin content and beef lean color stability <sup>1</sup> . <i>Journal of Animal Science</i> , 2010, 88, 1160-1167.  | 0.2 | 52        |
| 110 | Genome-wide association study of growth in crossbred beef cattle <sup>2</sup> . <i>Journal of Animal Science</i> , 2010, 88, 837-848.   | 0.2 | 168       |
| 111 | Connectedness in Targhee and Suffolk flocks participating in the United States National Sheep Improvement Program <sup>1</sup> . <i>Journal of Animal Science</i> , 2009, 87, 507-515.  | 0.2 | 13        |
| 112 | Confirmation of quantitative trait loci using a low-density single nucleotide polymorphism map for twinning and ovulation rate on bovine chromosome 5 <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2009, 87, 46-56.                  | 0.2 | 37        |
| 113 | A Limousin specific myostatin allele affects longissimus muscle area and fatty acid profiles in a Wagyu-Limousin F2 population <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2009, 87, 1576-1581.                                     | 0.2 | 25        |
| 114 | Genetic relationships of body composition, serum leptin, and age at puberty in gilts <sup>2</sup> . <i>Journal of Animal Science</i> , 2009, 87, 477-483.   | 0.2 | 38        |
| 115 | Evaluation of antral follicle count and ovarian morphology in crossbred beef cows: Investigation of influence of stage of the estrous cycle, age, and birth weight <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2009, 87, 1971-1980. | 0.2 | 126       |
| 116 | Genetic variation in the <i>mannosidase 2B2</i> gene and its association with ovulation rate in pigs. <i>Animal Genetics</i> , 2008, 39, 515-519.   | 0.6 | 11        |
| 117 | Changes in connectedness over time in alternative sheep sire referencing schemes <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2008, 86, 536-544.   | 0.2 | 25        |
| 118 | Experimental selection for calving ease and postnatal growth in seven cattle populations. II. Phenotypic differences <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2008, 86, 2103-2114.   | 0.2 | 18        |
| 119 | Assessing genetic gain, inbreeding, and bias attributable to different flock genetic means in alternative sheep sire referencing schemes <sup>1</sup> . <i>Journal of Animal Science</i> , 2008, 86, 526-535.                               | 0.2 | 8         |
| 120 | Opportunities for Collaborative Phenotyping for Disease Resistance Traits in a Large Beef Cattle Resource Population. <i>Developments in Biologicals</i> , 2008, 132, 327-330.  | 0.4 | 2         |
| 121 | Cytokine mRNA Expression in the Small Intestine of Weanling Pigs Fed Diets Supplemented with Specialized Protein or Peptide Sources. <i>Asian-Australasian Journal of Animal Sciences</i> , 2008, 21, 1800-1806.                            | 2.4 | 6         |
| 122 | Association of a single nucleotide polymorphism in SPP1 with growth traits and twinning in a cattle population selected for twinning rate <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2007, 85, 341-347.                            | 0.2 | 39        |
| 123 | Genetic (co)variance components for ewe productivity traits in Katahdin sheep <sup>1</sup> . <i>Journal of Animal Science</i> , 2007, 85, 60-68.  | 0.2 | 26        |
| 124 | Breeding objectives for Targhee sheep <sup>1</sup> . <i>Journal of Animal Science</i> , 2007, 85, 2815-2829.  | 0.2 | 28        |
| 125 | Detection of single nucleotide polymorphisms associated with ultrasonic backfat depth in a segregating Meishan × White Composite population <sup>1,2</sup> . <i>Journal of Animal Science</i> , 2007, 85, 1111-1119.                        | 0.2 | 21        |
| 126 | Genetic analysis of fibre characteristics in adult Targhee ewes and their relationship to breeding value estimates derived from yearling fleeces. <i>Small Ruminant Research</i> , 2007, 67, 164-172.                                       | 0.6 | 10        |



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|-----|---|-----|-----------|
| 127 | Managing the risk of comparing estimated breeding values across flocks or herds through connectedness: a review and application. <i>Genetics Selection Evolution</i> , 2007, 39, 225-247.                   | 1.2 | 29        |
| 128 | Antibody Response of Chickens to Sheep Red Blood Cells: Crosses Among Divergently Selected Lines and Relaxed Sublines. <i>Poultry Science</i> , 2006, 85, 1338-1341.  | 1.5 | 14        |
| 129 | Characterization of the aldo-keto reductase 1C gene cluster on pig chromosome 10: possible associations with reproductive traits. <i>BMC Veterinary Research</i> , 2006, 2, 28.                             | 0.7 | 24        |
| 130 | Response to intensity of reproduction in mouse lines resistant or susceptible to fescue toxicosis. <i>Journal of Animal Breeding and Genetics</i> , 2006, 123, 272-279.                                     | 0.8 | 0         |
| 131 | Adjustment of lamb birth and weaning weights for continuous effects of ewe age. <i>Animal Science</i> , 2005, 80, 241-248.  | 1.3 | 14        |
| 132 | Growth and hepatic vitrometabolism of ergotamine in mice divergently selected for response to endophyte toxicity. <i>Xenobiotica</i> , 2005, 35, 531-548.   | 0.5 | 16        |
| 133 | Effects of feeding endophyte-infected fescue seed on reproductive traits of male mice divergently selected for resistance or susceptibility to fescue toxicosis. <i>Theriogenology</i> , 2004, 61, 651-662. | 0.9 | 7         |
| 134 | Sleep time following anesthesia in mouse lines selected for resistance or susceptibility to fescue toxicosis. <i>Journal of Animal Science</i> , 2003, 81, 2562-2567.                                       | 0.2 | 8         |
| 135 | Genome-wide association study of reproductive efficiency in female cattle. <i>Journal of Animal Science</i> , 0, , .  | 0.2 | 0         |
| 136 | Effects of a Moderate or Aggressive Implant Strategy on the Rumen Microbiome and Metabolome in Steers. <i>Frontiers in Animal Science</i> , 0, 3, .   | 0.8 | 0         |