

Mario P L Calus

List of Publications by Year in descending order

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134
papers

6,152
citations

101384

36
h-index

85405

71
g-index

143
all docs

143
docs citations

143
times ranked

4342
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Prediction performance of linear models and gradient boosting machine on complex phenotypes in outbred mice. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, . | 0.8 | 7 |
| 2 | The long-term effects of genomic selection: 1. Response to selection, additive genetic variance, and genetic architecture. <i>Genetics Selection Evolution</i> , 2022, 54, 19. | 1.2 | 11 |
| 3 | Estimation of dam line composition of 3-way crossbred animals using genomic information. <i>Genetics Selection Evolution</i> , 2022, 54, . | 1.2 | 3 |
| 4 | Impact of genomic preselection on subsequent genetic evaluations with ssGBLUP using real data from pigs. <i>Genetics Selection Evolution</i> , 2022, 54, . | 1.2 | 1 |
| 5 | Factors affecting accuracy of estimated effective number of chromosome segments for numerically small breeds. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 151-160. | 0.8 | 3 |
| 6 | Predicting the purebred-crossbred genetic correlation from the genetic variance components in the parental lines. <i>Genetics Selection Evolution</i> , 2021, 53, 10. | 1.2 | 4 |
| 7 | Assessing the genetic background and genomic relatedness of red cattle populations originating from Northern Europe. <i>Genetics Selection Evolution</i> , 2021, 53, 23. | 1.2 | 15 |
| 8 | Technical note: Genetic groups in single-step single nucleotide polymorphism best linear unbiased predictor. <i>Journal of Dairy Science</i> , 2021, 104, 3298-3303. | 1.4 | 10 |
| 9 | Relatedness between numerically small Dutch Red dairy cattle populations and possibilities for multibreed genomic prediction. <i>Journal of Dairy Science</i> , 2021, 104, 4498-4506. | 1.4 | 3 |
| 10 | Review: optimizing genomic selection for crossbred performance by model improvement and data collection. <i>Journal of Animal Science</i> , 2021, 99, . | 0.2 | 11 |
| 11 | The impact of direct-maternal genetic correlations on international beef cattle evaluations for Limousin weaning weight. <i>Journal of Animal Science</i> , 2021, 99, . | 0.2 | 3 |
| 12 | Persistence of functional microbiota composition across generations. <i>Scientific Reports</i> , 2021, 11, 19007. | 1.6 | 3 |
| 13 | Avoiding preselection bias in subsequent single-step genomic BLUP evaluations of genomically preselected animals. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 432-441. | 0.8 | 9 |
| 14 | Prediction of nutrient digestibility in grower-finisher pigs based on faecal microbiota composition. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 23-35. | 0.8 | 12 |
| 15 | Breeding Top Genotypes and Accelerating Response to Recurrent Selection by Selecting Parents with Greater Gametic Variance. <i>Genetics</i> , 2020, 214, 91-107. | 1.2 | 26 |
| 16 | Single-step genome-wide association studies (GWAS) and post-GWAS analyses to identify genomic regions and candidate genes for milk yield in Brazilian Girolando cattle. <i>Journal of Dairy Science</i> , 2020, 103, 10347-10360. | 1.4 | 15 |
| 17 | Optimizing genomic reference populations to improve crossbred performance. <i>Genetics Selection Evolution</i> , 2020, 52, 65. | 1.2 | 8 |
| 18 | Investigating the impact of preselection on subsequent single-step genomic BLUP evaluation of preselected animals. <i>Genetics Selection Evolution</i> , 2020, 52, 42. | 1.2 | 16 |

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|----|---|-----|-----------|
| 19 | The Impact of Non-additive Effects on the Genetic Correlation Between Populations. G3: Genes, Genomes, Genetics, 2020, 10, 783-795. | 0.8 | 20 |
| 20 | Computational strategies for the preconditioned conjugate gradient method applied to ssSNPBLUP, with an application to a multivariate maternal model. Genetics Selection Evolution, 2020, 52, 24. | 1.2 | 16 |
| 21 | Impact of sub-setting the data of the main Limousin beef cattle population on the estimates of across-country genetic correlations. Genetics Selection Evolution, 2020, 52, 32. | 1.2 | 8 |
| 22 | Regulating appetite in broilers for improving body and muscle development – A review. Journal of Animal Physiology and Animal Nutrition, 2020, 104, 1819-1834. | 1.0 | 13 |
| 23 | Variance estimates are similar using pedigree or genomic relationships with or without the use of metafounders or the algorithm for proven and young animals1. Journal of Animal Science, 2020, 98, . | 0.2 | 17 |
| 24 | Validation of genomic predictions for body weight in broilers using crossbred information and considering breed-of-origin of alleles. Genetics Selection Evolution, 2019, 51, 38. | 1.2 | 19 |
| 25 | Impact of merging commercial breeding lines on the genetic diversity of Landrace pigs. Genetics Selection Evolution, 2019, 51, 60. | 1.2 | 18 |
| 26 | Genomic Evaluation for a Crossbreeding System Implementing Breed-of-Origin for Targeted Markers. Frontiers in Genetics, 2019, 10, 418. | 1.1 | 19 |
| 27 | Assessment of sire contribution and breed-of-origin of alleles in a three-way crossbred broiler dataset. Poultry Science, 2019, 98, 6270-6280. | 1.5 | 5 |
| 28 | A second-level diagonal preconditioner for single-step SNPBLUP. Genetics Selection Evolution, 2019, 51, 30. | 1.2 | 18 |
| 29 | Genomic selection on breeding time in a wild bird population. Evolution Letters, 2019, 3, 142-151. | 1.6 | 40 |
| 30 | Estimating the purebred-crossbred genetic correlation of body weight in broiler chickens with pedigree or genomic relationships. Genetics Selection Evolution, 2019, 51, 6. | 1.2 | 16 |
| 31 | Genomic prediction for crossbred performance using metafounders1. Journal of Animal Science, 2019, 97, 548-558. | 0.2 | 24 |
| 32 | Fecal microbial composition associated with variation in feed efficiency in pigs depends on diet and sex1. Journal of Animal Science, 2018, 96, 1405-1418. | 0.2 | 50 |
| 33 | Sparse single-step genomic BLUP in crossbreeding schemes1,2. Journal of Animal Science, 2018, 96, 2060-2073. | 0.2 | 14 |
| 34 | Multibreed genomic prediction using multitrait genomic residual maximum likelihood and multitask Bayesian variable selection. Journal of Dairy Science, 2018, 101, 4279-4294. | 1.4 | 20 |
| 35 | Which Individuals To Choose To Update the Reference Population? Minimizing the Loss of Genetic Diversity in Animal Genomic Selection Programs. G3: Genes, Genomes, Genetics, 2018, 8, 113-121. | 0.8 | 18 |
| 36 | Required properties for markers used to calculate unbiased estimates of the genetic correlation between populations. Genetics Selection Evolution, 2018, 50, 65. | 1.2 | 11 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | Impact of rare and low-frequency sequence variants on reliability of genomic prediction in dairy cattle. <i>Genetics Selection Evolution</i> , 2018, 50, 62. | 1.2 | 12 |
| 38 | Effects of alleles in crossbred pigs estimated for genomic prediction depend on their breed-of-origin. <i>BMC Genomics</i> , 2018, 19, 740. | 1.2 | 10 |
| 39 | The impact of using old germplasm on genetic merit and diversity – A cattle breed case study. <i>Journal of Animal Breeding and Genetics</i> , 2018, 135, 311-322. | 0.8 | 17 |
| 40 | Genomic Prediction Using Individual-Level Data and Summary Statistics from Multiple Populations. <i>Genetics</i> , 2018, 210, 53-69. | 1.2 | 15 |
| 41 | SNPrune: an efficient algorithm to prune large SNP array and sequence datasets based on high linkage disequilibrium. <i>Genetics Selection Evolution</i> , 2018, 50, 34. | 1.2 | 33 |
| 42 | Human-Mediated Introgression of Haplotypes in a Modern Dairy Cattle Breed. <i>Genetics</i> , 2018, 209, 1305-1317. | 1.2 | 21 |
| 43 | Prediction of the reliability of genomic breeding values for crossbred performance. <i>Genetics Selection Evolution</i> , 2017, 49, 43. | 1.2 | 12 |
| 44 | Accuracies of breeding values for dry matter intake using nongenotyped animals and predictor traits in different lactations. <i>Journal of Dairy Science</i> , 2017, 100, 9103-9114. | 1.4 | 10 |
| 45 | Benefits of Dominance over Additive Models for the Estimation of Average Effects in the Presence of Dominance. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3405-3414. | 0.8 | 27 |
| 46 | Multi-population Genomic Relationships for Estimating Current Genetic Variances Within and Genetic Correlations Between Populations. <i>Genetics</i> , 2017, 207, 503-515. | 1.2 | 43 |
| 47 | Conservation priorities for the different lines of Dutch Red and White Friesian cattle change when relationships with other breeds are taken into account. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 69-77. | 0.8 | 6 |
| 48 | The Importance of Endophenotypes to Evaluate the Relationship between Genotype and External Phenotype. <i>International Journal of Molecular Sciences</i> , 2017, 18, 472. | 1.8 | 23 |
| 49 | Contribution of rare and low-frequency whole-genome sequence variants to complex traits variation in dairy cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 60. | 1.2 | 15 |
| 50 | Genomic evaluation for a three-way crossbreeding system considering breed-of-origin of alleles. <i>Genetics Selection Evolution</i> , 2017, 49, 75. | 1.2 | 39 |
| 51 | Estimated allele substitution effects underlying genomic evaluation models depend on the scaling of allele counts. <i>Genetics Selection Evolution</i> , 2017, 49, 79. | 1.2 | 9 |
| 52 | Efficient genomic prediction based on whole-genome sequence data using split-and-merge Bayesian variable selection. <i>Genetics Selection Evolution</i> , 2016, 48, 49. | 1.2 | 36 |
| 53 | Accuracy of genomic prediction of purebreds for cross bred performance in pigs. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 443-451. | 0.8 | 24 |
| 54 | Genomic prediction using preselected DNA variants from a GWAS with whole-genome sequence data in Holstein – Friesian cattle. <i>Genetics Selection Evolution</i> , 2016, 48, 95. | 1.2 | 89 |

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|----|---|-----|-----------|
| 55 | Validation of simultaneous deregression of cow and bull breeding values and derivation of appropriate weights. <i>Journal of Dairy Science</i> , 2016, 99, 6403-6419. | 1.4 | 26 |
| 56 | Genetic changes of survival traits over the past 25 yr in Dutch dairy cattle. <i>Journal of Dairy Science</i> , 2016, 99, 9810-9819. | 1.4 | 10 |
| 57 | Empirical determination of breed-of-origin of alleles in three-breed cross pigs. <i>Genetics Selection Evolution</i> , 2016, 48, 55. | 1.2 | 31 |
| 58 | Comparison of gene-based rare variant association mapping methods for quantitative traits in a bovine population with complex familial relationships. <i>Genetics Selection Evolution</i> , 2016, 48, 60. | 1.2 | 8 |
| 59 | Assigning breed origin to alleles in crossbred animals. <i>Genetics Selection Evolution</i> , 2016, 48, 61. | 1.2 | 45 |
| 60 | Genomic prediction of survival time in a population of brown laying hens showing cannibalistic behavior. <i>Genetics Selection Evolution</i> , 2016, 48, 68. | 1.2 | 15 |
| 61 | Whole-genome sequence data uncover loss of genetic diversity due to selection. <i>Genetics Selection Evolution</i> , 2016, 48, 33. | 1.2 | 33 |
| 62 | Accuracy of genomic prediction using imputed whole-genome sequence data in white layers. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 167-179. | 0.8 | 61 |
| 63 | An Equation to Predict the Accuracy of Genomic Values by Combining Data from Multiple Traits, Populations, or Environments. <i>Genetics</i> , 2016, 202, 799-823. | 1.2 | 54 |
| 64 | Ever-growing data sets pose (new) challenges to genomic prediction models. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 407-408. | 0.8 | 3 |
| 65 | Across population genomic prediction scenarios in which Bayesian variable selection outperforms GBLUP. <i>BMC Genetics</i> , 2015, 16, 146. | 2.7 | 18 |
| 66 | Heritability of milk fat composition is considerably lower for Meuse-Rhine-Yssel compared to Holstein Friesian cattle. <i>Livestock Science</i> , 2015, 180, 58-64. | 0.6 | 3 |
| 67 | Empirical and deterministic accuracies of across-population genomic prediction. <i>Genetics Selection Evolution</i> , 2015, 47, 5. | 1.2 | 60 |
| 68 | Evaluation of genomic selection for replacement strategies using selection index theory. <i>Journal of Dairy Science</i> , 2015, 98, 6499-6509. | 1.4 | 23 |
| 69 | The effect of rare alleles on estimated genomic relationships from whole genome sequence data. <i>BMC Genetics</i> , 2015, 16, 24. | 2.7 | 46 |
| 70 | Impact of QTL properties on the accuracy of multi-breed genomic prediction. <i>Genetics Selection Evolution</i> , 2015, 47, 42. | 1.2 | 49 |
| 71 | Estimation of inbreeding using pedigree, 50k SNP chip genotypes and full sequence data in three cattle breeds. <i>BMC Genetics</i> , 2015, 16, 88. | 2.7 | 135 |
| 72 | Accuracy of imputation using the most common sires as reference population in layer chickens. <i>BMC Genetics</i> , 2015, 16, 101. | 2.7 | 15 |

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|----|---|-----|-----------|
| 73 | Using selection index theory to estimate consistency of multi-locus linkage disequilibrium across populations. <i>BMC Genetics</i> , 2015, 16, 87. | 2.7 | 14 |
| 74 | Genomic prediction using imputed whole-genome sequence data in Holstein Friesian cattle. <i>Genetics Selection Evolution</i> , 2015, 47, 71. | 1.2 | 104 |
| 75 | Genomic prediction of dry matter intake in dairy cattle from an international data set consisting of research herds in Europe, North America, and Australasia. <i>Journal of Dairy Science</i> , 2015, 98, 6522-6534. | 1.4 | 52 |
| 76 | Overlap in genomic variation associated with milk fat composition in Holstein Friesian and Dutch native dual-purpose breeds. <i>Journal of Dairy Science</i> , 2015, 98, 6510-6521. | 1.4 | 7 |
| 77 | Genomic prediction based on data from three layer lines using non-linear regression models. <i>Genetics Selection Evolution</i> , 2014, 46, 75. | 1.2 | 5 |
| 78 | Genomic prediction of breeding values using previously estimated SNP variances. <i>Genetics Selection Evolution</i> , 2014, 46, 52. | 1.2 | 10 |
| 79 | Genomic prediction based on data from three layer lines: a comparison between linear methods. <i>Genetics Selection Evolution</i> , 2014, 46, 57. | 1.2 | 17 |
| 80 | Right-hand-side updating for fast computing of genomic breeding values. <i>Genetics Selection Evolution</i> , 2014, 46, 24. | 1.2 | 13 |
| 81 | A comparison of principal component regression and genomic REML for genomic prediction across populations. <i>Genetics Selection Evolution</i> , 2014, 46, 60. | 1.2 | 9 |
| 82 | Consequences for diversity when animals are prioritized for conservation of the whole genome or of one specific allele. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 61-70. | 0.8 | 7 |
| 83 | A reaction norm model for genomic selection using high-dimensional genomic and environmental data. <i>Theoretical and Applied Genetics</i> , 2014, 127, 595-607. | 1.8 | 439 |
| 84 | Imputation of non-genotyped individuals based on genotyped relatives: assessing the imputation accuracy of a real case scenario in dairy cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 6. | 1.2 | 23 |
| 85 | Genetic parameters across lactation for feed intake, fat- and protein-corrected milk, and liveweight in first-parity Holstein cattle. <i>Journal of Dairy Science</i> , 2014, 97, 5851-5862. | 1.4 | 60 |
| 86 | Imputation of genotypes from low density (50,000 markers) to high density (700,000 markers) of cows from research herds in Europe, North America, and Australasia using 2 reference populations. <i>Journal of Dairy Science</i> , 2014, 97, 1799-1811. | 1.4 | 29 |
| 87 | Whole-Genome Regression and Prediction Methods Applied to Plant and Animal Breeding. <i>Genetics</i> , 2013, 193, 327-345. | 1.2 | 732 |
| 88 | Combining cow and bull reference populations to increase accuracy of genomic prediction and genome-wide association studies. <i>Journal of Dairy Science</i> , 2013, 96, 6703-6715. | 1.4 | 38 |
| 89 | Unraveling the genetic architecture of environmental variance of somatic cell score using high-density single nucleotide polymorphism and cow data from experimental farms. <i>Journal of Dairy Science</i> , 2013, 96, 7306-7317. | 1.4 | 19 |
| 90 | Differences in milk fat composition predicted by mid-infrared spectrometry among dairy cattle breeds in the Netherlands. <i>Journal of Dairy Science</i> , 2013, 96, 2570-2582. | 1.4 | 16 |

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|-----|--|-----|-----------|
| 91 | Genomic Prediction in Animals and Plants: Simulation of Data, Validation, Reporting, and Benchmarking. <i>Genetics</i> , 2013, 193, 347-365. | 1.2 | 370 |
| 92 | The Effect of Linkage Disequilibrium and Family Relationships on the Reliability of Genomic Prediction. <i>Genetics</i> , 2013, 193, 621-631. | 1.2 | 161 |
| 93 | Predicted accuracy of and response to genomic selection for new traits in dairy cattle. <i>Animal</i> , 2013, 7, 183-191. | 1.3 | 51 |
| 94 | Plasma Proteome Profiles Associated with Diet-Induced Metabolic Syndrome and the Early Onset of Metabolic Syndrome in a Pig Model. <i>PLoS ONE</i> , 2013, 8, e73087. | 1.1 | 27 |
| 95 | Selection of SNP from 50K and 777K arrays to predict breed of origin in cattle ¹ . <i>Journal of Animal Science</i> , 2013, 91, 5128-5134. | 0.2 | 34 |
| 96 | The impact of genotyping different groups of animals on accuracy when moving from traditional to genomic selection. <i>Journal of Dairy Science</i> , 2012, 95, 5412-5421. | 1.4 | 28 |
| 97 | Reliability of direct genomic values for animals with different relationships within and to the reference population. <i>Journal of Dairy Science</i> , 2012, 95, 389-400. | 1.4 | 256 |
| 98 | Imputation of genotypes with low-density chips and its effect on reliability of direct genomic values in Dutch Holstein cattle. <i>Journal of Dairy Science</i> , 2012, 95, 876-889. | 1.4 | 86 |
| 99 | Makeup of the genetic correlation between milk production traits using genome-wide single nucleotide polymorphism information. <i>Journal of Dairy Science</i> , 2012, 95, 2132-2143. | 1.4 | 13 |
| 100 | Improved accuracy of genomic prediction for dry matter intake of dairy cattle from combined European and Australian data sets. <i>Journal of Dairy Science</i> , 2012, 95, 6103-6112. | 1.4 | 64 |
| 101 | Pedigree- and marker-based methods in the estimation of genetic diversity in small groups of Holstein cattle. <i>Journal of Animal Breeding and Genetics</i> , 2012, 129, 195-205. | 0.8 | 20 |
| 102 | Long-term response to genomic selection: effects of estimation method and reference population structure for different genetic architectures. <i>Genetics Selection Evolution</i> , 2012, 44, 3. | 1.2 | 47 |
| 103 | Short communication: Milk fat composition of 4 cattle breeds in the Netherlands. <i>Journal of Dairy Science</i> , 2011, 94, 1021-1025. | 1.4 | 35 |
| 104 | Effect of enlarging the reference population with (un)genotyped animals on the accuracy of genomic selection in dairy cattle. <i>Journal of Dairy Science</i> , 2011, 94, 431-441. | 1.4 | 22 |
| 105 | Genomic and pedigree-based genetic parameters for scarcely recorded traits when some animals are genotyped. <i>Journal of Dairy Science</i> , 2011, 94, 4189-4197. | 1.4 | 78 |
| 106 | Genetic parameters for predicted methane production and potential for reducing enteric emissions through genomic selection. <i>Journal of Dairy Science</i> , 2011, 94, 6122-6134. | 1.4 | 160 |
| 107 | Consequences for diversity when prioritizing animals for conservation with pedigree or genomic information. <i>Journal of Animal Breeding and Genetics</i> , 2011, 128, 473-481. | 0.8 | 25 |
| 108 | Accuracy of multi-trait genomic selection using different methods. <i>Genetics Selection Evolution</i> , 2011, 43, 26. | 1.2 | 239 |

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|-----|---|-----|-----------|
| 109 | Identification of Mendelian inconsistencies between SNP and pedigree information of sibs. <i>Genetics Selection Evolution</i> , 2011, 43, 34. | 1.2 | 37 |
| 110 | Imputation of missing single nucleotide polymorphism genotypes using a multivariate mixed model framework1. <i>Journal of Animal Science</i> , 2011, 89, 2042-2049. | 0.2 | 19 |
| 111 | Including copy number variation in association studies to predict genotypic values. <i>Genetical Research</i> , 2010, 92, 115-125. | 0.3 | 3 |
| 112 | Comparison of analyses of the QTLMAS XIII common dataset. I: genomic selection. <i>BMC Proceedings</i> , 2010, 4, S1. | 1.8 | 7 |
| 113 | Simultaneous QTL detection and genomic breeding value estimation using high density SNP chips. <i>BMC Proceedings</i> , 2010, 4, S9. | 1.8 | 7 |
| 114 | Sensitivity of methods for estimating breeding values using genetic markers to the number of QTL and distribution of QTL variance. <i>Genetics Selection Evolution</i> , 2010, 42, 9. | 1.2 | 41 |
| 115 | Prediction of haplotypes for ungenotyped animals and its effect on marker-assisted breeding value estimation. <i>Genetics Selection Evolution</i> , 2010, 42, 10. | 1.2 | 15 |
| 116 | Estimating genetic diversity across the neutral genome with the use of dense marker maps. <i>Genetics Selection Evolution</i> , 2010, 42, 12. | 1.2 | 8 |
| 117 | Predicting energy balance for dairy cows using high-density single nucleotide polymorphism information. <i>Journal of Dairy Science</i> , 2010, 93, 2757-2764. | 1.4 | 39 |
| 118 | Effects of the number of markers per haplotype and clustering of haplotypes on the accuracy of QTL mapping and prediction of genomic breeding values. <i>Genetics Selection Evolution</i> , 2009, 41, 11. | 1.2 | 51 |
| 119 | Estimation of prediction error variances via Monte Carlo sampling methods using different formulations of the prediction error variance. <i>Genetics Selection Evolution</i> , 2009, 41, 23. | 1.2 | 20 |
| 120 | Estimating genomic breeding values from the QTL-MAS Workshop Data using a single SNP and haplotype/IBD approach. <i>BMC Proceedings</i> , 2009, 3, S10. | 1.8 | 9 |
| 121 | Accuracy of Genomic Selection Using Different Methods to Define Haplotypes. <i>Genetics</i> , 2008, 178, 553-561. | 1.2 | 308 |
| 122 | Breeding Value Estimation for Fat Percentage Using Dense Markers on <i>Bos taurus</i> Autosome 14. <i>Journal of Dairy Science</i> , 2007, 90, 4821-4829. | 1.4 | 33 |
| 123 | Effects of Management and Genetics on Udder Health and Milk Composition in Dairy Cows. <i>Journal of Dairy Science</i> , 2007, 90, 229-238. | 1.4 | 20 |
| 124 | Accuracy of breeding values when using and ignoring the polygenic effect in genomic breeding value estimation with a marker density of one SNP per cM. <i>Journal of Animal Breeding and Genetics</i> , 2007, 124, 362-368. | 0.8 | 114 |
| 125 | Genotype by Environment Interaction for Somatic Cell Score Across Bulk Milk Somatic Cell Count and Days in Milk. <i>Journal of Dairy Science</i> , 2006, 89, 4846-4857. | 1.4 | 25 |
| 126 | Genetic Correlations Between Milk Production and Health and Fertility Depending on Herd Environment. <i>Journal of Dairy Science</i> , 2006, 89, 1765-1775. | 1.4 | 90 |

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|-----|---|-----|-----------|
| 127 | The association between somatic cell count patterns and milk production prior to mastitis. <i>Livestock Science</i> , 2005, 96, 291-299. | 1.2 | 21 |
| 128 | Influence of Herd Environment on Health and Fertility and Their Relationship with Milk Production. <i>Journal of Dairy Science</i> , 2005, 88, 335-347. | 1.4 | 111 |
| 129 | Estimation of Genetic Parameters for Milk Fat Depression in Dairy Cattle. <i>Journal of Dairy Science</i> , 2005, 88, 1166-1177. | 1.4 | 13 |
| 130 | Associations Among Descriptors of Herd Management and Phenotypic and Genetic Levels of Health and Fertility. <i>Journal of Dairy Science</i> , 2005, 88, 2178-2189. | 1.4 | 42 |
| 131 | Effects of data structure on the estimation of covariance functions to describe genotype by environment interactions in a reaction norm model. <i>Genetics Selection Evolution</i> , 2004, 36, 489-507. | 1.2 | 48 |
| 132 | Estimation of Environmental Sensitivity of Genetic Merit for Milk Production Traits Using a Random Regression Model. <i>Journal of Dairy Science</i> , 2003, 86, 3756-3764. | 1.4 | 82 |
| 133 | Genotype \times Environment Interaction for Protein Yield in Dutch Dairy Cattle as Quantified by Different Models. <i>Journal of Dairy Science</i> , 2002, 85, 3115-3123. | 1.4 | 84 |
| 134 | Genetic evaluation of conformation traits using random contemporary groups and reducing the influence of parent averages. <i>Livestock Science</i> , 2001, 69, 129-137. | 1.2 | 7 |