Mario P L Calus

List of Publications by Year
in descending order

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	Whole-Genome Regression and Prediction Methods Applied to Plant and Animal Breeding. Genetics, 2013, 193, 327-345.	1.2	732
2	A reaction norm model for genomic selection using high-dimensional genomic and environmental data. Theoretical and Applied Genetics, 2014, 127, 595-607.	1.8	439
3	Genomic Prediction in Animals and Plants: Simulation of Data, Validation, Reporting, and Benchmarking. Genetics, 2013, 193, 347-365.	1.2	370
4	Accuracy of Genomic Selection Using Different Methods to Define Haplotypes. Genetics, 2008, 178, 553-561.	1.2	308
5	Reliability of direct genomic values for animals with different relationships within and to the reference population. Journal of Dairy Science, 2012, 95, 389-400.	1.4	256
6	Accuracy of multi-trait genomic selection using different methods. Genetics Selection Evolution, 2011, 43, 26.	1.2	239
7	The Effect of Linkage Disequilibrium and Family Relationships on the Reliability of Genomic Prediction. Genetics, 2013, 193, 621-631.	1.2	161
8	Genetic parameters for predicted methane production and potential for reducing enteric emissions through genomic selection. Journal of Dairy Science, 2011, 94, 6122-6134.	1.4	160
9	Estimation of inbreeding using pedigree, 50k SNP chip genotypes and full sequence data in three cattle breeds. BMC Genetics, 2015, 16, 88.	2.7	135
10	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. Journal of Animal Breeding and Genetics, 2007, 124, 362-368.	0.8	114
11	Influence of Herd Environment on Health and Fertility and Their Relationship with Milk Production. Journal of Dairy Science, 2005, 88, 335-347.	1.4	111
12	Genomic prediction using imputed whole-genome sequence data in Holstein Friesian cattle. Genetics Selection Evolution, 2015, 47, 71.	1.2	104
13	Genetic Correlations Between Milk Production and Health and Fertility Depending on Herd Environment. Journal of Dairy Science, 2006, 89, 1765-1775.	1.4	90
14	Genomic prediction using preselected DNA variants from a GWAS with whole-genome sequence data in Holstein–Friesian cattle. Genetics Selection Evolution, 2016, 48, 95.	1.2	89
15	Imputation of genotypes with low-density chips and its effect on reliability of direct genomic values in Dutch Holstein cattle. Journal of Dairy Science, 2012, 95, 876-889.	1.4	86
16	Genotype Ã— Environment Interaction for Protein Yield in Dutch Dairy Cattle as Quantified by Different Models. Journal of Dairy Science, 2002, 85, 3115-3123.	1.4	84
17	Estimation of Environmental Sensitivity of Genetic Merit for Milk Production Traits Using a Random Regression Model. Journal of Dairy Science, 2003, 86, 3756-3764.	1.4	82
18	Genomic and pedigree-based genetic parameters for scarcely recorded traits when some animals are genotyped. Journal of Dairy Science, 2011, 94, 4189-4197.	1.4	78

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19	Improved accuracy of genomic prediction for dry matter intake of dairy cattle from combined European and Australian data sets. Journal of Dairy Science, 2012, 95, 6103-6112.	1.4	64
20	Accuracy of genomic prediction using imputed whole‐genome sequence data in white layers. Journal of Animal Breeding and Genetics, 2016, 133, 167-179.	0.8	61
21	Genetic parameters across lactation for feed intake, fat- and protein-corrected milk, and liveweight in first-parity Holstein cattle. Journal of Dairy Science, 2014, 97, 5851-5862.	1.4	60
22	Empirical and deterministic accuracies of across-population genomic prediction. Genetics Selection Evolution, 2015, 47, 5.	1.2	60
23	An Equation to Predict the Accuracy of Genomic Values by Combining Data from Multiple Traits, Populations, or Environments. Genetics, 2016, 202, 799-823.	1.2	54
24	Genomic prediction of dry matter intake in dairy cattle from an international data set consisting of research herds in Europe, North America, and Australasia. Journal of Dairy Science, 2015, 98, 6522-6534.	1.4	52
25	Effects of the number of markers per haplotype and clustering of haplotypes on the accuracy of QTL mapping and prediction of genomic breeding values. Genetics Selection Evolution, 2009, 41, 11.	1.2	51
26	Predicted accuracy of and response to genomic selection for new traits in dairy cattle. Animal, 2013, 7, 183-191.	1.3	51
27	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
28	Impact of QTL properties on the accuracy of multi-breed genomic prediction. Genetics Selection Evolution, 2015, 47, 42.	1.2	49
29	Effects of data structure on the estimation of covariance functions to describe genotype by environment interactions in a reaction norm model. Genetics Selection Evolution, 2004, 36, 489-507.	1.2	48
30	Long-term response to genomic selection: effects of estimation method and reference population structure for different genetic architectures. Genetics Selection Evolution, 2012, 44, 3.	1.2	47
31	The effect of rare alleles on estimated genomic relationships from whole genome sequence data. BMC Genetics, 2015, 16, 24.	2.7	46
32	Assigning breed origin to alleles in crossbred animals. Genetics Selection Evolution, 2016, 48, 61.	1.2	45
33	Multi-population Genomic Relationships for Estimating Current Genetic Variances Within and Genetic Correlations Between Populations. Genetics, 2017, 207, 503-515.	1.2	43
34	Associations Among Descriptors of Herd Management and Phenotypic and Genetic Levels of Health and Fertility. Journal of Dairy Science, 2005, 88, 2178-2189.	1.4	42
35	Sensitivity of methods for estimating breeding values using genetic markers to the number of QTL and distribution of QTL variance. Genetics Selection Evolution, 2010, 42, 9.	1.2	41
36	Genomic selection on breeding time in a wild bird population. Evolution Letters, 2019, 3, 142-151.	1.6	40

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37	Predicting energy balance for dairy cows using high-density single nucleotide polymorphism information. Journal of Dairy Science, 2010, 93, 2757-2764.	1.4	39
38	Genomic evaluation for a three-way crossbreeding system considering breed-of-origin of alleles. Genetics Selection Evolution, 2017, 49, 75.	1.2	39
39	Combining cow and bull reference populations to increase accuracy of genomic prediction and genome-wide association studies. Journal of Dairy Science, 2013, 96, 6703-6715.	1.4	38
40	Identification of Mendelian inconsistencies between SNP and pedigree information of sibs. Genetics Selection Evolution, 2011, 43, 34.	1.2	37
41	Efficient genomic prediction based on whole-genome sequence data using split-and-merge Bayesian variable selection. Genetics Selection Evolution, 2016, 48, 49.	1.2	36
42	Short communication: Milk fat composition of 4 cattle breeds in the Netherlands. Journal of Dairy Science, 2011, 94, 1021-1025.	1.4	35
43	Selection of SNP from 50K and 777K arrays to predict breed of origin in cattle1. Journal of Animal Science, 2013, 91, 5128-5134.	0.2	34
44	Breeding Value Estimation for Fat Percentage Using Dense Markers on Bos taurus Autosome 14. Journal of Dairy Science, 2007, 90, 4821-4829.	1.4	33
45	Whole-genome sequence data uncover loss of genetic diversity due to selection. Genetics Selection Evolution, 2016, 48, 33.	1.2	33
46	SNPrune: an efficient algorithm to prune large SNP array and sequence datasets based on high linkage disequilibrium. Genetics Selection Evolution, 2018, 50, 34.	1.2	33
47	Empirical determination of breed-of-origin of alleles in three-breed cross pigs. Genetics Selection Evolution, 2016, 48, 55.	1.2	31
48	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. Journal of Dairy Science, 2014, 97, 1799-1811.	1.4	29
49	The impact of genotyping different groups of animals on accuracy when moving from traditional to genomic selection. Journal of Dairy Science, 2012, 95, 5412-5421.	1.4	28
50	Plasma Proteome Profiles Associated with Diet-Induced Metabolic Syndrome and the Early Onset of Metabolic Syndrome in a Pig Model. PLoS ONE, 2013, 8, e73087.	1.1	27
51	Benefits of Dominance over Additive Models for the Estimation of Average Effects in the Presence of Dominance. G3: Genes, Genomes, Genetics, 2017, 7, 3405-3414.	0.8	27
52	Validation of simultaneous deregression of cow and bull breeding values and derivation of appropriate weights. Journal of Dairy Science, 2016, 99, 6403-6419.	1.4	26
53	Breeding Top Genotypes and Accelerating Response to Recurrent Selection by Selecting Parents with Greater Gametic Variance. Genetics, 2020, 214, 91-107.	1.2	26
54	Genotype by Environment Interaction for Somatic Cell Score Across Bulk Milk Somatic Cell Count and Days in Milk. Journal of Dairy Science, 2006, 89, 4846-4857.	1.4	25

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55	Consequences for diversity when prioritizing animals for conservation with pedigree or genomic information. Journal of Animal Breeding and Genetics, 2011, 128, 473-481.	0.8	25
56	Accuracy of genomic prediction of purebreds for cross bred performance in pigs. Journal of Animal Breeding and Genetics, 2016, 133, 443-451.	0.8	24
57	Genomic prediction for crossbred performance using metafounders1. Journal of Animal Science, 2019, 97, 548-558.	0.2	24
58	Imputation of non-genotyped individuals based on genotyped relatives: assessing the imputation accuracy of a real case scenario in dairy cattle. Genetics Selection Evolution, 2014, 46, 6.	1.2	23
59	Evaluation of genomic selection for replacement strategies using selection index theory. Journal of Dairy Science, 2015, 98, 6499-6509.	1.4	23
60	The Importance of Endophenotypes to Evaluate the Relationship between Genotype and External Phenotype. International Journal of Molecular Sciences, 2017, 18, 472.	1.8	23
61	Effect of enlarging the reference population with (un)genotyped animals on the accuracy of genomic selection in dairy cattle. Journal of Dairy Science, 2011, 94, 431-441.	1.4	22
62	The association between somatic cell count patterns and milk production prior to mastitis. Livestock Science, 2005, 96, 291-299.	1.2	21
63	Human-Mediated Introgression of Haplotypes in a Modern Dairy Cattle Breed. Genetics, 2018, 209, 1305-1317.	1.2	21
64	Effects of Management and Genetics on Udder Health and Milk Composition in Dairy Cows. Journal of Dairy Science, 2007, 90, 229-238.	1.4	20
65	Estimation of prediction error variances via Monte Carlo sampling methods using different formulations of the prediction error variance. Genetics Selection Evolution, 2009, 41, 23.	1.2	20
66	Pedigree‐and marker‐based methods in the estimation of genetic diversity in small groups of Holstein cattle. Journal of Animal Breeding and Genetics, 2012, 129, 195-205.	0.8	20
67	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
68	The Impact of Non-additive Effects on the Genetic Correlation Between Populations. G3: Genes, Genomes, Genetics, 2020, 10, 783-795.	0.8	20
69	Imputation of missing single nucleotide polymorphism genotypes using a multivariate mixed model framework1. Journal of Animal Science, 2011, 89, 2042-2049.	0.2	19
70	Unraveling the genetic architecture of environmental variance of somatic cell score using high-density single nucleotide polymorphism and cow data from experimental farms. Journal of Dairy Science, 2013, 96, 7306-7317.	1.4	19
71	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
72	Genomic Evaluation for a Crossbreeding System Implementing Breed-of-Origin for Targeted Markers. Frontiers in Genetics, 2019, 10, 418.	1.1	19

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73	Across population genomic prediction scenarios in which Bayesian variable selection outperforms GBLUP. BMC Genetics, 2015, 16, 146.	2.7	18
74	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
75	Impact of merging commercial breeding lines on the genetic diversity of Landrace pigs. Genetics Selection Evolution, 2019, 51, 60.	1.2	18
76	A second-level diagonal preconditioner for single-step SNPBLUP. Genetics Selection Evolution, 2019, 51, 30.	1.2	18
77	Genomic prediction based on data from three layer lines: a comparison between linear methods. Genetics Selection Evolution, 2014, 46, 57.	1.2	17
78	The impact of using old germplasm on genetic merit and diversity—A cattle breed case study. Journal of Animal Breeding and Genetics, 2018, 135, 311-322.	0.8	17
79	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
80	Differences in milk fat composition predicted by mid-infrared spectrometry among dairy cattle breeds in the Netherlands. Journal of Dairy Science, 2013, 96, 2570-2582.	1.4	16
81	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
82	Investigating the impact of preselection on subsequent single-step genomic BLUP evaluation of preselected animals. Genetics Selection Evolution, 2020, 52, 42.	1.2	16
83	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
84	Prediction of haplotypes for ungenotyped animals and its effect on marker-assisted breeding value estimation. Genetics Selection Evolution, 2010, 42, 10.	1.2	15
85	Accuracy of imputation using the most common sires as reference population in layer chickens. BMC Genetics, 2015, 16, 101.	2.7	15
86	Genomic prediction of survival time in a population of brown laying hens showing cannibalistic behavior. Genetics Selection Evolution, 2016, 48, 68.	1.2	15
87	Contribution of rare and low-frequency whole-genome sequence variants to complex traits variation in dairy cattle. Genetics Selection Evolution, 2017, 49, 60.	1.2	15
88	Genomic Prediction Using Individual-Level Data and Summary Statistics from Multiple Populations. Genetics, 2018, 210, 53-69.	1.2	15
89	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. Journal of Dairy Science, 2020, 103, 10347-10360.	1.4	15
90	Assessing the genetic background and genomic relatedness of red cattle populations originating from Northern Europe. Genetics Selection Evolution, 2021, 53, 23.	1.2	15

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91	Using selection index theory to estimate consistency of multi-locus linkage disequilibrium across populations. BMC Genetics, 2015, 16, 87.	2.7	14
92	Sparse single-step genomic BLUP in crossbreeding schemes1,2. Journal of Animal Science, 2018, 96, 2060-2073.	0.2	14
93	Estimation of Genetic Parameters for Milk Fat Depression in Dairy Cattle. Journal of Dairy Science, 2005, 88, 1166-1177.	1.4	13
94	Makeup of the genetic correlation between milk production traits using genome-wide single nucleotide polymorphism information. Journal of Dairy Science, 2012, 95, 2132-2143.	1.4	13
95	Right-hand-side updating for fast computing of genomic breeding values. Genetics Selection Evolution, 2014, 46, 24.	1.2	13
96	Regulating appetite in broilers for improving body and muscle development â€" A review. Journal of Animal Physiology and Animal Nutrition, 2020, 104, 1819-1834.	1.0	13
97	Prediction of the reliability of genomic breeding values for crossbred performance. Genetics Selection Evolution, 2017, 49, 43.	1.2	12
98	Impact of rare and low-frequency sequence variants on reliability of genomic prediction in dairy cattle. Genetics Selection Evolution, 2018, 50, 62.	1.2	12
99	Prediction of nutrient digestibility in growerâ€finisher pigs based on faecal microbiota composition. Journal of Animal Breeding and Genetics, 2020, 137, 23-35.	0.8	12
100	Required properties for markers used to calculate unbiased estimates of the genetic correlation between populations. Genetics Selection Evolution, 2018, 50, 65.	1.2	11
101	Review: optimizing genomic selection for crossbred performance by model improvement and data collection. Journal of Animal Science, 2021, 99, .	0.2	11
102	The long-term effects of genomic selection: 1. Response to selection, additive genetic variance, and genetic architecture. Genetics Selection Evolution, 2022, 54, 19.	1.2	11
103	Genomic prediction of breeding values using previously estimated SNP variances. Genetics Selection Evolution, 2014, 46, 52.	1.2	10
104	Genetic changes of survival traits over the past 25 yr in Dutch dairy cattle. Journal of Dairy Science, 2016, 99, 9810-9819.	1.4	10
105	Accuracies of breeding values for dry matter intake using nongenotyped animals and predictor traits in different lactations. Journal of Dairy Science, 2017, 100, 9103-9114.	1.4	10
106	Effects of alleles in crossbred pigs estimated for genomic prediction depend on their breed-of-origin. BMC Genomics, 2018, 19, 740.	1.2	10
107	Technical note: Genetic groups in single-step single nucleotide polymorphism best linear unbiased predictor. Journal of Dairy Science, 2021, 104, 3298-3303.	1.4	10
108	Estimating genomic breeding values from the QTL-MAS Workshop Data using a single SNP and haplotype/IBD approach. BMC Proceedings, 2009, 3, S10.	1.8	9

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109	A comparison of principal component regression and genomic REML for genomic prediction across populations. Genetics Selection Evolution, 2014, 46, 60.	1.2	9
110	Estimated allele substitution effects underlying genomic evaluation models depend on the scaling of allele counts. Genetics Selection Evolution, 2017, 49, 79.	1.2	9
111	Avoiding preselection bias in subsequent single‐step genomic BLUP evaluations of genomically preselected animals. Journal of Animal Breeding and Genetics, 2021, 138, 432-441.	0.8	9
112	Estimating genetic diversity across the neutral genome with the use of dense marker maps. Genetics Selection Evolution, 2010, 42, 12.	1.2	8
113	Comparison of gene-based rare variant association mapping methods for quantitative traits in a bovine population with complex familial relationships. Genetics Selection Evolution, 2016, 48, 60.	1.2	8
114	Optimizing genomic reference populations to improve crossbred performance. Genetics Selection Evolution, 2020, 52, 65.	1.2	8
115	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
116	Genetic evaluation of conformation traits using random contemporary groups and reducing the influence of parent averages. Livestock Science, 2001, 69, 129-137.	1.2	7
117	Comparison of analyses of the QTLMAS XIII common dataset. I: genomic selection. BMC Proceedings, 2010, 4, S1.	1.8	7
118	Simultaneous QTL detection and genomic breeding value estimation using high density SNP chips. BMC Proceedings, 2010, 4, S9.	1.8	7
119	Consequences for diversity when animals are prioritized for conservation of the whole genome or of one specific allele. Journal of Animal Breeding and Genetics, 2014, 131, 61-70.	0.8	7
120	Overlap in genomic variation associated with milk fat composition in Holstein Friesian and Dutch native dual-purpose breeds. Journal of Dairy Science, 2015, 98, 6510-6521.	1.4	7
121	Prediction performance of linear models and gradient boosting machine on complex phenotypes in outbred mice. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	7
122	Conservation priorities for the different lines of Dutch Red and White Friesian cattle change when relationships with other breeds are taken into account. Journal of Animal Breeding and Genetics, 2017, 134, 69-77.	0.8	6
123	Genomic prediction based on data from three layer lines using non-linear regression models. Genetics Selection Evolution, 2014, 46, 75.	1.2	5
124	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
125	Predicting the purebred-crossbred genetic correlation from the genetic variance components in the parental lines. Genetics Selection Evolution, 2021, 53, 10.	1.2	4
126	Including copy number variation in association studies to predict genotypic values. Genetical Research, 2010, 92, 115-125.	0.3	3

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127	Ever‑growing data sets pose (new) challenges to genomic prediction models. Journal of Animal Breeding and Genetics, 2015, 132, 407-408.	0.8	3
128	Heritability of milk fat composition is considerably lower for Meuse-Rhine-Yssel compared to Holstein Friesian cattle. Livestock Science, 2015, 180, 58-64.	0.6	3
129	Factors affecting accuracy of estimated effective number of chromosome segments for numerically small breeds. Journal of Animal Breeding and Genetics, 2021, 138, 151-160.	0.8	3
130	Relatedness between numerically small Dutch Red dairy cattle populations and possibilities for multibreed genomic prediction. Journal of Dairy Science, 2021, 104, 4498-4506.	1.4	3
131	The impact of direct-maternal genetic correlations on international beef cattle evaluations for Limousin weaning weight. Journal of Animal Science, 2021, 99, .	0.2	3
132	Persistence of functional microbiota composition across generations. Scientific Reports, 2021, 11, 19007.	1.6	3
133	Estimation of dam line composition of 3-way crossbred animals using genomic information. Genetics Selection Evolution, 2022, 54, .	1.2	3
134	Impact of genomic preselection on subsequent genetic evaluations with ssGBLUP using real data from pigs. Genetics Selection Evolution, 2022, 54, .	1.2	1