

Daniela Lourenço

List of Publications by Year in descending order

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115
papers

2,623
citations

172207

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123
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123
docs citations

123
times ranked

1402
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus1. Journal of Animal Science, 2015, 93, 2653-2662.	0.2	139
2	Weighting Strategies for Single-Step Genomic BLUP: An Iterative Approach for Accurate Calculation of GEBV and GWAS. Frontiers in Genetics, 2016, 7, 151.	1.1	131
3	Accurate genomic predictions for BCWD resistance in rainbow trout are achieved using low-density SNP panels: Evidence that long-range LD is a major contributing factor. Journal of Animal Breeding and Genetics, 2018, 135, 263-274.	0.8	105
4	Frequentist p-values for large-scale-single step genome-wide association, with an application to birth weight in American Angus cattle. Genetics Selection Evolution, 2019, 51, 28.	1.2	97
5	Current status of genomic evaluation. Journal of Animal Science, 2020, 98, .	0.2	90
6	The Dimensionality of Genomic Information and Its Effect on Genomic Prediction. Genetics, 2016, 203, 573-581.	1.2	81
7	Single-Step Genomic Evaluations from Theory to Practice: Using SNP Chips and Sequence Data in BLUP90. Genes, 2020, 11, 790.	1.0	77
8	Incorporation of causative quantitative trait nucleotides in single-step GBLUP. Genetics Selection Evolution, 2017, 49, 59.	1.2	73
9	Accuracy of estimated breeding values with genomic information on males, females, or both: an example on broiler chicken. Genetics Selection Evolution, 2015, 47, 56.	1.2	69
10	Implementation of genomic recursions in single-step genomic best linear unbiased predictor for US Holsteins with a large number of genotyped animals. Journal of Dairy Science, 2016, 99, 1968-1974.	1.4	66
11	Hot topic: Use of genomic recursions in single-step genomic best linear unbiased predictor (BLUP) with a large number of genotypes. Journal of Dairy Science, 2015, 98, 4090-4094.	1.4	60
12	Methods for genomic evaluation of a relatively small genotyped dairy population and effect of genotyped cow information in multiparity analyses. Journal of Dairy Science, 2014, 97, 1742-1752.	1.4	57
13	Dimensionality of genomic information and performance of the Algorithm for Proven and Young for different livestock species. Genetics Selection Evolution, 2016, 48, 82.	1.2	56
14	Accuracies of genomic prediction of feed efficiency traits using different prediction and validation methods in an experimental Nelore cattle population1. Journal of Animal Science, 2016, 94, 3613-3623.	0.2	55
15	Development of genomic predictions for harvest and carcass weight in channel catfish. Genetics Selection Evolution, 2018, 50, 66.	1.2	54
16	Are evaluations on young genotyped animals benefiting from the past generations?. Journal of Dairy Science, 2014, 97, 3930-3942.	1.4	53
17	Implications of <scp>SNP</scp> weighting on single-step genomic predictions for different reference population sizes. Journal of Animal Breeding and Genetics, 2017, 134, 463-471.	0.8	47
18	Invited review: Advances and applications of random regression models: From quantitative genetics to genomics. Journal of Dairy Science, 2019, 102, 7664-7683.	1.4	46

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19	Application of single-step genomic evaluation using multiple-trait random regression test-day models in dairy cattle. <i>Journal of Dairy Science</i> , 2019, 102, 2365-2377.	1.4	45
20	Crossbreed evaluations in single-step genomic best linear unbiased predictor using adjusted realized relationship matrices1. <i>Journal of Animal Science</i> , 2016, 94, 909-919.	0.2	44
21	Genetics and genomics of reproductive disorders in Canadian Holstein cattle. <i>Journal of Dairy Science</i> , 2019, 102, 1341-1353.	1.4	44
22	Controlling bias in genomic breeding values for young genotyped bulls. <i>Journal of Dairy Science</i> , 2019, 102, 9956-9970.	1.4	43
23	Genome-wide association for milk production traits and somatic cell score in different lactation stages of Ayrshire, Holstein, and Jersey dairy cattle. <i>Journal of Dairy Science</i> , 2019, 102, 8159-8174.	1.4	42
24	Genome-Wide Association Analysis With a 50K Transcribed Gene SNP-Chip Identifies QTL Affecting Muscle Yield in Rainbow Trout. <i>Frontiers in Genetics</i> , 2018, 9, 387.	1.1	39
25	Whole-genome mapping of quantitative trait loci and accuracy of genomic predictions for resistance to columnaris disease in two rainbow trout breeding populations. <i>Genetics Selection Evolution</i> , 2019, 51, 42.	1.2	39
26	Alternative SNP weighting for single-step genomic best linear unbiased predictor evaluation of stature in US Holsteins in the presence of selected sequence variants. <i>Journal of Dairy Science</i> , 2019, 102, 10012-10019.	1.4	37
27	Comparison of genomic predictions for lowly heritable traits using multi-step and single-step genomic best linear unbiased predictor in Holstein cattle. <i>Journal of Dairy Science</i> , 2018, 101, 8076-8086.	1.4	36
28	Genome-wide identification of loci associated with growth in rainbow trout. <i>BMC Genomics</i> , 2020, 21, 209.	1.2	34
29	Genetic evaluations for growth heat tolerance in Angus cattle1. <i>Journal of Animal Science</i> , 2016, 94, 4143-4150.	0.2	33
30	Changes in genetic parameters for fitness and growth traits in pigs under genomic selection. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	33
31	Using single-step genomic best linear unbiased predictor to enhance the mitigation of seasonal losses due to heat stress in pigs. <i>Journal of Animal Science</i> , 2016, 94, 5004-5013.	0.2	29
32	Single-step genome-wide association for longitudinal traits of Canadian Ayrshire, Holstein, and Jersey dairy cattle. <i>Journal of Dairy Science</i> , 2019, 102, 9995-10011.	1.4	29
33	Genome-Wide Association Study Identifies Genomic Loci Affecting Filet Firmness and Protein Content in Rainbow Trout. <i>Frontiers in Genetics</i> , 2019, 10, 386.	1.1	28
34	Validation of single-step GBLUP genomic predictions from threshold models using the linear regression method: An application in chicken mortality. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 4-13.	0.8	28
35	Selection of core animals in the Algorithm for Proven and Young using a simulation model. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 545-552.	0.8	25
36	Accuracy of genomic BLUP when considering a genomic relationship matrix based on the number of the largest eigenvalues: a simulation study. <i>Genetics Selection Evolution</i> , 2019, 51, 75.	1.2	23

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37	Investigating conception rate for beef service sires bred to dairy cows and heifers. <i>Journal of Dairy Science</i> , 2020, 103, 10374-10382.	1.4	23
38	Modeling response to heat stress in pigs from nucleus and commercial farms in different locations in the United States1. <i>Journal of Animal Science</i> , 2016, 94, 4789-4798.	0.2	21
39	Reaction norm for yearling weight in beef cattle using single-step genomic evaluation1. <i>Journal of Animal Science</i> , 2018, 96, 27-34.	0.2	21
40	Bias in heritability estimates from genomic restricted maximum likelihood methods under different genotyping strategies. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 40-50.	0.8	21
41	Sexual dimorphism in livestock species selected for economically important traits1. <i>Journal of Animal Science</i> , 2016, 94, 3684-3692.	0.2	20
42	Accuracy of breeding values in small genotyped populations using different sources of external information – A simulation study. <i>Journal of Dairy Science</i> , 2017, 100, 395-401.	1.4	20
43	Crossbred evaluations using single-step genomic BLUP and algorithm for proven and young with different sources of data1. <i>Journal of Animal Science</i> , 2019, 97, 1513-1522.	0.2	20
44	Genomic prediction of lactation curves for milk, fat, protein, and somatic cell score in Holstein cattle. <i>Journal of Dairy Science</i> , 2019, 102, 452-463.	1.4	20
45	Genomic investigation of milk production in Italian buffalo. <i>Italian Journal of Animal Science</i> , 2021, 20, 539-547.	0.8	20
46	Heritability and response to selection for carcass weight and growth in the Delta Select strain of channel catfish, <i>Ictalurus punctatus</i> . <i>Aquaculture</i> , 2020, 515, 734507.	1.7	18
47	Genomic predictions for fillet yield and firmness in rainbow trout using reduced-density SNP panels. <i>BMC Genomics</i> , 2021, 22, 92.	1.2	18
48	Bias in genomic predictions by mating practices for linear type traits in a large-scale genomic evaluation. <i>Journal of Dairy Science</i> , 2021, 104, 662-677.	1.4	17
49	Beef trait genetic parameters based on old and recent data and its implications for genomic predictions in Italian Simmental cattle. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	16
50	Prediction accuracy for a simulated maternally affected trait of beef cattle using different genomic evaluation models1. <i>Journal of Animal Science</i> , 2013, 91, 4090-4098.	0.2	15
51	Genomic predictions in purebreds with a multibreed genomic relationship matrix1. <i>Journal of Animal Science</i> , 2019, 97, 4418-4427.	0.2	14
52	Indirect predictions with a large number of genotyped animals using the algorithm for proven and young. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	14
53	Emerging issues in genomic selection. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	14
54	Application of single step genomic BLUP under different uncertain paternity scenarios using simulated data. <i>PLoS ONE</i> , 2017, 12, e0181752.	1.1	14

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55	Use of a single-step approach for integrating foreign information into national genomic evaluation in Holstein cattle. <i>Journal of Dairy Science</i> , 2019, 102, 8175-8183.	1.4	13
56	Modeling honey yield, defensive and swarming behaviors of Italian honey bees (<i>Apis mellifera</i>) Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 702	2.7	13
57	Investigating pig survival in different production phases using genomic models. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	13
58	Use of genomic recursions and algorithm for proven and young animals for single-step genomic <sc>BLUP</sc> analyses – a simulation study. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 340-345.	0.8	12
59	Genomic analysis of cow mortality and milk production using a threshold-linear model. <i>Journal of Dairy Science</i> , 2017, 100, 7295-7305.	1.4	12
60	Estimating the effect of the deleterious recessive haplotypes AH1 and AH2 on reproduction performance of Ayrshire cattle. <i>Journal of Dairy Science</i> , 2019, 102, 5315-5322.	1.4	12
61	Variance and covariance estimates for resistance to bacterial cold water disease and columnaris disease in two rainbow trout breeding populations1. <i>Journal of Animal Science</i> , 2019, 97, 1124-1132.	0.2	12
62	Core-dependent changes in genomic predictions using the Algorithm for Proven and Young in single-step genomic best linear unbiased prediction. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	12
63	Variance components using genomic information for 2 functional traits in Italian Simmental cattle: Calving interval and lactation persistency. <i>Journal of Dairy Science</i> , 2020, 103, 5227-5233.	1.4	11
64	Accounting for Population Structure and Phenotypes From Relatives in Association Mapping for Farm Animals: A Simulation Study. <i>Frontiers in Genetics</i> , 2021, 12, 642065.	1.1	11
65	Investigating the persistence of accuracy of genomic predictions over time in broilers. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	11
66	Technical note: Avoiding the direct inversion of the numerator relationship matrix for genotyped animals in single-step genomic best linear unbiased prediction solved with the preconditioned conjugate gradient1. <i>Journal of Animal Science</i> , 2017, 95, 49-52.	0.2	10
67	Applying the Metafounders Approach for Genomic Evaluation in a Multibreed Beef Cattle Population. <i>Frontiers in Genetics</i> , 2020, 11, 556399.	1.1	9
68	Performances of Adaptive MultiBLUP, Bayesian regressions, and weighted-GBLUP approaches for genomic predictions in Belgian Blue beef cattle. <i>BMC Genomics</i> , 2020, 21, 545.	1.2	9
69	Reducing computational cost of large-scale genomic evaluation by using indirect genomic prediction. <i>JDS Communications</i> , 2021, 2, 356-360.	0.5	9
70	Invited review: Unknown-parent groups and metafounders in single-step genomic BLUP. <i>Journal of Dairy Science</i> , 2022, 105, 923-939.	1.4	9
71	Relationships among mortality, performance, and disorder traits in broiler chickens: a genetic and genomic approach. <i>Poultry Science</i> , 2018, 97, 1511-1518.	1.5	8
72	Regional and seasonal analyses of weights in growing Angus cattle1. <i>Journal of Animal Science</i> , 2016, 94, 4369-4375.	0.2	7

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73	Estimating dominance genetic variances for growth traits in American Angus males using genomic models. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	7
74	Determining the stability of accuracy of genomic estimated breeding values in future generations in commercial pig populations. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	7
75	Technical note: Impact of pedigree depth on convergence of single-step genomic BLUP in a purebred swine population1. <i>Journal of Animal Science</i> , 2017, 95, 3391-3395.	0.2	6
76	Genome-wide scan for common variants associated with intramuscular fat and moisture content in rainbow trout. <i>BMC Genomics</i> , 2020, 21, 529.	1.2	6
77	Changes in genomic predictions when new information is added. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	6
78	A Comprehensive Comparison of Haplotype-Based Single-Step Genomic Predictions in Livestock Populations With Different Genetic Diversity Levels: A Simulation Study. <i>Frontiers in Genetics</i> , 2021, 12, 729867.	1.1	6
79	Impact of including information from bulls and their daughters in the training population of multiple-step genomic evaluations in dairy cattle: A simulation study. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 441-452.	0.8	5
80	A comprehensive study on size and definition of the core group in the proven and young algorithm for single-step GBLUP. <i>Genetics Selection Evolution</i> , 2022, 54, .	1.2	5
81	On the equivalence between marker effect models and breeding value models and direct genomic values with the Algorithm for Proven and Young. <i>Genetics Selection Evolution</i> , 2022, 54, .	1.2	5
82	Investigation of β -hydroxybutyrate in early lactation of Simmental cows: Genetic parameters and genomic predictions. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 708-718.	0.8	4
83	Detecting effective starting point of genomic selection by divergent trends from best linear unbiased prediction and single-step genomic best linear unbiased prediction in pigs, beef cattle, and broilers. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	4
84	DESEMPENHO PRODUTIVO DE VACAS GIROLANDO ESTIMADO PELO MODELO DE WOOD AJUSTADO POR METODOLOGIA BAYESIANA. <i>Archives of Veterinary Science</i> , 2016, 21, .	0.1	4
85	Validation of single-step genomic predictions using the linear regression method for milk yield and heat tolerance in a Thai-Holstein population. <i>Veterinary World</i> , 2021, 14, 3119-3125.	0.7	4
86	Past, present, and future developments in single-step genomic models. <i>Italian Journal of Animal Science</i> , 2022, 21, 673-685.	0.8	4
87	Improving accuracy of direct and maternal genetic effects in genomic evaluations using pooled boar semen: a simulation study1. <i>Journal of Animal Science</i> , 2019, 97, 3237-3245.	0.2	3
88	Indirect genomic predictions for milk yield in crossbred Holstein-Jersey dairy cattle. <i>Journal of Dairy Science</i> , 2021, 104, 5728-5737.	1.4	3
89	Inclusion of sire by herd interaction effect in the genomic evaluation for weaning weight of American Angus. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	3
90	International bull evaluations by genomic BLUP with a prediction population. <i>Journal of Dairy Science</i> , 2019, 102, 2330-2335.	1.4	2

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91	28 Genomic prediction for marbling score in Hanwoo cattle using sequence data. <i>Journal of Animal Science</i> , 2020, 98, 11-12.	0.2	2
92	193 Including causative variants into single step genomic BLUP. <i>Journal of Animal Science</i> , 2017, 95, 95-96.	0.2	1
93	Impact of embryo transfer phenotypic records on large-scale beef cattle genetic evaluations. <i>Revista Brasileira De Zootecnia</i> , 2018, 47, .	0.3	1
94	332 Indirect predictions based on SNP effects from GBLUP with increasing number of genotyped animals. <i>Journal of Animal Science</i> , 2019, 97, 49-49.	0.2	1
95	334 Investigating core-dependent changes in predictions using the algorithm for proven and young in ssGBLUP. <i>Journal of Animal Science</i> , 2019, 97, 50-50.	0.2	1
96	Effect of pond or strip spawning on growth and carcass yield of channel catfish progeny, <i>Ictalurus punctatus</i> . <i>Journal of the World Aquaculture Society</i> , 2020, 51, 407-417.	1.2	1
97	PSXII-37 Validation of single-step GBLUP genomic predictions from threshold models using the linear regression method: an application in chicken mortality. <i>Journal of Animal Science</i> , 2020, 98, 246-247.	0.2	1
98	Accuracy of genomic breeding values and predictive ability for postweaning liveweight and age at first calving in a Nellore cattle population with missing sire information. <i>Tropical Animal Health and Production</i> , 2021, 53, 432.	0.5	1
99	Impact of including the cause of missing records on genetic evaluations for growth in commercial pigs. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	1
100	335 Genomic predictions with a multi-breed genomic relationship matrix. <i>Journal of Animal Science</i> , 2019, 97, 49-50.	0.2	1
101	0303 Issues in commercial application of single-step genomic BLUP for genetic evaluation in American Angus. <i>Journal of Animal Science</i> , 2016, 94, 144-145.	0.2	1
102	25 Determining stability of genomic predictivity in future generations in commercial pig populations. <i>Journal of Animal Science</i> , 2020, 98, 21-21.	0.2	1
103	Development of genomic predictions for Angus cattle in Brazil incorporating genotypes from related American sires. <i>Journal of Animal Science</i> , 2022, , .	0.2	1
104	209 Prospecting genomic regions associated with columnaris disease in two rainbow trout breeding populations. <i>Journal of Animal Science</i> , 2017, 95, 103-104.	0.2	0
105	184 Impact of SNP selection on genomic prediction for different reference population sizes. <i>Journal of Animal Science</i> , 2017, 95, 91-91.	0.2	0
106	Optimized Histological Preparation of Ovary for Ovariole Counting in Africanized Honey Bee Queens (Hymenoptera: Apidae). <i>Journal of Insect Science</i> , 2019, 19, .	0.6	0
107	PSVIII-38 Genomic prediction for tick resistance in Angus cattle. <i>Journal of Animal Science</i> , 2019, 97, 263-263.	0.2	0
108	211 Changes in genetic parameters of fitness and growth traits under genomic selection in pigs. <i>Journal of Animal Science</i> , 2019, 97, 41-41.	0.2	0

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109	209 Genomic selection for multiple maternal and growth traits in large white pigs using Single-Step GBLUP. <i>Journal of Animal Science</i> , 2019, 97, 42-42.	0.2	0
110	22 Accuracy of indirect predictions for large datasets based on prediction error covariance of SNP effects from single-step GBLUP. <i>Journal of Animal Science</i> , 2020, 98, 6-7.	0.2	0
111	Introduction: ADSA and Interbull Joint Breeding and Genetics Symposia. <i>Journal of Dairy Science</i> , 2020, 103, 5275-5277.	1.4	0
112	Toxicity of β -1,3,6-galactans produced by <i>Diaporthe</i> sp. endophytes on <i>Metarhizium anisopliae</i> (Metschnikoff) Sorokin assessed by conidia germination speed parameter. <i>Bioscience Journal</i> , 2020, 36, .	0.4	0
113	294 Increased fluctuations of genetic evaluations with genomic information. <i>Journal of Animal Science</i> , 2020, 98, 32-33.	0.2	0
114	384 Genetic and Genomic Analysis in Livestock with Increasing Datasets. <i>Journal of Animal Science</i> , 2020, 98, 137-138.	0.2	0
115	31 Changes in genomic predictions when new data is included. <i>Journal of Animal Science</i> , 2020, 98, 7-8.	0.2	0