

Daniela Lourenço

List of Publications by Year in descending order

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115
papers

2,623
citations

172457

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233421

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123
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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. <i>Journal of Animal Science</i> , 2015, 93, 2653-2662.	0.5	139
2	Weighting Strategies for Single-Step Genomic BLUP: An Iterative Approach for Accurate Calculation of GEBV and GWAS. <i>Frontiers in Genetics</i> , 2016, 7, 151.	2.3	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. <i>Journal of Animal Breeding and Genetics</i> , 2018, 135, 263-274.	2.0	105
4	Frequentist p-values for large-scale-single step genome-wide association, with an application to birth weight in American Angus cattle. <i>Genetics Selection Evolution</i> , 2019, 51, 28.	3.0	97
5	Current status of genomic evaluation. <i>Journal of Animal Science</i> , 2020, 98, .	0.5	90
6	The Dimensionality of Genomic Information and Its Effect on Genomic Prediction. <i>Genetics</i> , 2016, 203, 573-581.	2.9	81
7	Single-Step Genomic Evaluations from Theory to Practice: Using SNP Chips and Sequence Data in BLUP90. <i>Genes</i> , 2020, 11, 790.	2.4	77
8	Incorporation of causative quantitative trait nucleotides in single-step GBLUP. <i>Genetics Selection Evolution</i> , 2017, 49, 59.	3.0	73
9	Accuracy of estimated breeding values with genomic information on males, females, or both: an example on broiler chicken. <i>Genetics Selection Evolution</i> , 2015, 47, 56.	3.0	69
10	Implementation of genomic recursions in single-step genomic best linear unbiased predictor for US Holsteins with a large number of genotyped animals. <i>Journal of Dairy Science</i> , 2016, 99, 1968-1974.	3.4	66
11	Hot topic: Use of genomic recursions in single-step genomic best linear unbiased predictor (BLUP) with a large number of genotypes. <i>Journal of Dairy Science</i> , 2015, 98, 4090-4094.	3.4	60
12	Methods for genomic evaluation of a relatively small genotyped dairy population and effect of genotyped cow information in multiparity analyses. <i>Journal of Dairy Science</i> , 2014, 97, 1742-1752.	3.4	57
13	Dimensionality of genomic information and performance of the Algorithm for Proven and Young for different livestock species. <i>Genetics Selection Evolution</i> , 2016, 48, 82.	3.0	56
14	Accuracies of genomic prediction of feed efficiency traits using different prediction and validation methods in an experimental Nelore cattle population1. <i>Journal of Animal Science</i> , 2016, 94, 3613-3623.	0.5	55
15	Development of genomic predictions for harvest and carcass weight in channel catfish. <i>Genetics Selection Evolution</i> , 2018, 50, 66.	3.0	54
16	Are evaluations on young genotyped animals benefiting from the past generations?. <i>Journal of Dairy Science</i> , 2014, 97, 3930-3942.	3.4	53
17	Implications of <scp>SNP</scp> weighting on single-step genomic predictions for different reference population sizes. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 463-471.	2.0	47
18	Invited review: Advances and applications of random regression models: From quantitative genetics to genomics. <i>Journal of Dairy Science</i> , 2019, 102, 7664-7683.	3.4	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.	3.4	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.	0.5	44
21	Genetics and genomics of reproductive disorders in Canadian Holstein cattle. <i>Journal of Dairy Science</i> , 2019, 102, 1341-1353.	3.4	44
22	Controlling bias in genomic breeding values for young genotyped bulls. <i>Journal of Dairy Science</i> , 2019, 102, 9956-9970.	3.4	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.	3.4	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.	2.3	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.	3.0	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.	3.4	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.	3.4	36
28	Genome-wide identification of loci associated with growth in rainbow trout. <i>BMC Genomics</i> , 2020, 21, 209.	2.8	34
29	Genetic evaluations for growth heat tolerance in Angus cattle1. <i>Journal of Animal Science</i> , 2016, 94, 4143-4150.	0.5	33
30	Changes in genetic parameters for fitness and growth traits in pigs under genomic selection. <i>Journal of Animal Science</i> , 2020, 98, .	0.5	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.	0.5	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.	3.4	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.	2.3	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.	2.0	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.	2.0	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.	3.0	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.	3.4	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.	0.5	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.	0.5	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.	2.0	21
41	Sexual dimorphism in livestock species selected for economically important traits1. <i>Journal of Animal Science</i> , 2016, 94, 3684-3692.	0.5	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.	3.4	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.	0.5	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.	3.4	20
45	Genomic investigation of milk production in Italian buffalo. <i>Italian Journal of Animal Science</i> , 2021, 20, 539-547.	1.9	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.	3.5	18
47	Genomic predictions for fillet yield and firmness in rainbow trout using reduced-density SNP panels. <i>BMC Genomics</i> , 2021, 22, 92.	2.8	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.	3.4	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, .	0.5	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.	0.5	15
51	Genomic predictions in purebreds with a multibreed genomic relationship matrix1. <i>Journal of Animal Science</i> , 2019, 97, 4418-4427.	0.5	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, .	0.5	14
53	Emerging issues in genomic selection. <i>Journal of Animal Science</i> , 2021, 99, .	0.5	14
54	Application of single step genomic BLUP under different uncertain paternity scenarios using simulated data. <i>PLoS ONE</i> , 2017, 12, e0181752.	2.5	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.	3.4	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, .	0.5	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.	2.0	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.	3.4	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.	3.4	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.	0.5	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, .	0.5	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.	3.4	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.	2.3	11
65	Investigating the persistence of accuracy of genomic predictions over time in broilers. <i>Journal of Animal Science</i> , 2021, 99, .	0.5	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.	0.5	10
67	Applying the Metafounders Approach for Genomic Evaluation in a Multibreed Beef Cattle Population. <i>Frontiers in Genetics</i> , 2020, 11, 556399.	2.3	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.	2.8	9
69	Reducing computational cost of large-scale genomic evaluation by using indirect genomic prediction. <i>JDS Communications</i> , 2021, 2, 356-360.	1.5	9
70	Invited review: Unknown-parent groups and metafounders in single-step genomic BLUP. <i>Journal of Dairy Science</i> , 2022, 105, 923-939.	3.4	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.	3.4	8
72	Regional and seasonal analyses of weights in growing Angus cattle1. <i>Journal of Animal Science</i> , 2016, 94, 4369-4375.	0.5	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, .	0.5	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, .	0.5	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.	0.5	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.	2.8	6
77	Changes in genomic predictions when new information is added. <i>Journal of Animal Science</i> , 2021, 99, .	0.5	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.	2.3	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.	2.0	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, .	3.0	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, .	3.0	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.	2.0	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, .	0.5	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.	1.7	4
86	Past, present, and future developments in single-step genomic models. <i>Italian Journal of Animal Science</i> , 2022, 21, 673-685.	1.9	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.	0.5	3
88	Indirect genomic predictions for milk yield in crossbred Holstein-Jersey dairy cattle. <i>Journal of Dairy Science</i> , 2021, 104, 5728-5737.	3.4	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, .	0.5	3
90	International bull evaluations by genomic BLUP with a prediction population. <i>Journal of Dairy Science</i> , 2019, 102, 2330-2335.	3.4	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.	0.5	2
92	193 Including causative variants into single step genomic BLUP. <i>Journal of Animal Science</i> , 2017, 95, 95-96.	0.5	1
93	Impact of embryo transfer phenotypic records on large-scale beef cattle genetic evaluations. <i>Revista Brasileira De Zootecnia</i> , 2018, 47, .	0.8	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.	0.5	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.	0.5	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.	2.4	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.	0.5	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.	1.4	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, .	0.5	1
100	335 Genomic predictions with a multi-breed genomic relationship matrix. <i>Journal of Animal Science</i> , 2019, 97, 49-50.	0.5	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.	0.5	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.	0.5	1
103	Development of genomic predictions for Angus cattle in Brazil incorporating genotypes from related American sires. <i>Journal of Animal Science</i> , 2022, , .	0.5	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.	0.5	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.	0.5	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, .	1.5	0
107	PSVIII-38 Genomic prediction for tick resistance in Angus cattle. <i>Journal of Animal Science</i> , 2019, 97, 263-263.	0.5	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.	0.5	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.	0.5	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.	0.5	0
111	Introduction: ADSA and Interbull Joint Breeding and Genetics Symposia. <i>Journal of Dairy Science</i> , 2020, 103, 5275-5277.	3.4	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.	0.5	0
114	384 Genetic and Genomic Analysis in Livestock with Increasing Datasets. <i>Journal of Animal Science</i> , 2020, 98, 137-138.	0.5	0
115	31 Changes in genomic predictions when new data is included. <i>Journal of Animal Science</i> , 2020, 98, 7-8.	0.5	0