Andres Legarra

List of Publications by Year
in descending order

141 papers	9,615 citations	46918 47 h-index	42291 92 g-index
149 all docs	149 docs citations	149 times ranked	4030 citing authors

#	Article	IF	Citations
1	Hot topic: A unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. Journal of Dairy Science, 2010, 93, 743-752.	1.4	1,058
2	A relationship matrix including full pedigree and genomic information. Journal of Dairy Science, 2009, 92, 4656-4663.	1.4	723
3	Predicting Quantitative Traits With Regression Models for Dense Molecular Markers and Pedigree. Genetics, 2009, 182, 375-385.	1.2	514
4	Genome-wide association mapping including phenotypes from relatives without genotypes. Genetical Research, 2012, 94, 73-83.	0.3	453
5	Computing procedures for genetic evaluation including phenotypic, full pedigree, and genomic information. Journal of Dairy Science, 2009, 92, 4648-4655.	1.4	444
6	Performance of Genomic Selection in Mice. Genetics, 2008, 180, 611-618.	1.2	332
7	Bias in genomic predictions for populations under selection. Genetical Research, 2011, 93, 357-366.	0.3	285
8	Single Step, a general approach for genomic selection. Livestock Science, 2014, 166, 54-65.	0.6	260
9	On the Additive and Dominant Variance and Covariance of Individuals Within the Genomic Selection Scope. Genetics, 2013, 195, 1223-1230.	1.2	253
10	Genome-wide association mapping including phenotypes from relatives without genotypes in a single-step (ssGWAS) for 6-week body weight in broiler chickens. Frontiers in Genetics, 2014, 5, 134.	1.1	173
11	Using recursion to compute the inverse of the genomic relationship matrix. Journal of Dairy Science, 2014, 97, 3943-3952.	1.4	168
12	Non-additive Effects in Genomic Selection. Frontiers in Genetics, 2018, 9, 78.	1.1	157
13	Semi-parametric estimates of population accuracy and bias of predictions of breeding values and future phenotypes using the LR method. Genetics Selection Evolution, 2018, 50, 53.	1.2	146
14	Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus1. Journal of Animal Science, 2015, 93, 2653-2662.	0.2	139
15	Efficient computation of the genomic relationship matrix and other matrices used in single‐step evaluation. Journal of Animal Breeding and Genetics, 2011, 128, 422-428.	0.8	132
16	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
17	Sequence- vs. chip-assisted genomic selection: accurate biological information is advised. Genetics Selection Evolution, 2015, 47, 43.	1.2	130
18	Orthogonal Estimates of Variances for Additive, Dominance, and Epistatic Effects in Populations. Genetics, 2017, 206, 1297-1307.	1.2	125

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19	Ancestral Relationships Using Metafounders: Finite Ancestral Populations and Across Population Relationships. Genetics, 2015, 200, 455-468.	1.2	119
20	Improved Lasso for genomic selection. Genetical Research, 2011, 93, 77-87.	0.3	110
21	Genetic Variation in the Social Environment Contributes to Health and Disease. PLoS Genetics, 2017, 13, e1006498.	1.5	110
22	Effect of different genomic relationship matrices on accuracy and scale1. Journal of Animal Science, 2011, 89, 2673-2679.	0.2	100
23	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
24	Technical Note: Computing Strategies in Genome-Wide Selection. Journal of Dairy Science, 2008, 91, 360-366.	1.4	93
25	Joint genomic evaluation of French dairy cattle breeds using multiple-trait models. Genetics Selection Evolution, 2012, 44, 39.	1.2	93
26	Current status of genomic evaluation. Journal of Animal Science, 2020, 98, .	0.2	90
27	The Dimensionality of Genomic Information and Its Effect on Genomic Prediction. Genetics, 2016, 203, 573-581.	1.2	81
28	Comparing estimates of genetic variance across different relationship models. Theoretical Population Biology, 2016, 107, 26-30.	0.5	81
29	Unknownâ€parent groups in singleâ€step genomic evaluation. Journal of Animal Breeding and Genetics, 2013, 130, 252-258.	0.8	80
30	Single-Step Genomic Evaluations from Theory to Practice: Using SNP Chips and Sequence Data in BLUPF90. Genes, 2020, 11, 790.	1.0	77
31	Incorporation of causative quantitative trait nucleotides in single-step GBLUP. Genetics Selection Evolution, 2017, 49, 59.	1.2	73
32	Methods to approximate reliabilities in single-step genomic evaluation. Journal of Dairy Science, 2013, 96, 647-654.	1.4	72
33	Genomic evaluation by including dominance effects and inbreeding depression for purebred and crossbred performance with an application in pigs. Genetics Selection Evolution, 2016, 48, 92.	1.2	72
34	Genomic selection in the French Lacaune dairy sheep breed. Journal of Dairy Science, 2012, 95, 2723-2733.	1.4	70
35	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
36	Computational strategies for national integration of phenotypic, genomic, and pedigree data in a single-step best linear unbiased prediction. Journal of Dairy Science, 2012, 95, 4629-4645.	1.4	66

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37	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
38	Single‐Step Genomic and Pedigree Genotype Ã— Environment Interaction Models for Predicting Wheat Lines in International Environments. Plant Genome, 2017, 10, plantgenome2016.09.0089.	1.6	66
39	Analysis of Fertility and Dystocia in Holsteins Using Recursive Models to Handle Censored and Categorical Data. Journal of Dairy Science, 2007, 90, 2012-2024.	1.4	64
40	Genetic Parameters of Udder Traits, Somatic Cell Score, and Milk Yield in Latxa Sheep. Journal of Dairy Science, 2005, 88, 2238-2245.	1.4	63
41	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
42	Genomic analysis of dominance effects on milk production and conformation traits in Fleckvieh cattle. Genetics Selection Evolution, 2014, 46, 40.	1.2	59
43	Assessment of accuracy of genomic prediction for French Lacaune dairy sheep. Journal of Dairy Science, 2014, 97, 1107-1116.	1.4	58
44	A note on the rationale for estimating genealogical coancestry from molecular markers. Genetics Selection Evolution, 2011, 43, 1-10.	1.2	57
45	A genome scan for QTL affecting resistance to Haemonchus contortus in sheep1. Journal of Animal Science, 2012, 90, 4690-4705.	0.2	57
46	Genomic selection models for directional dominance: an example for litter size in pigs. Genetics Selection Evolution, 2018, 50, 1.	1.2	56
47	Metafounders are related to F st fixation indices and reduce bias in single-step genomic evaluations. Genetics Selection Evolution, 2017, 49, 34.	1.2	55
48	Application of Bayesian least absolute shrinkage and selection operator (LASSO) and BayesCÏ€ methods for genomic selection in French Holstein and MontbÃ©liarde breeds. Journal of Dairy Science, 2013, 96, 575-591.	1.4	49
49	Application of single-step genomic evaluation for crossbred performance in pig1. Journal of Animal Science, 2016, 94, 936-948.	0.2	48
50	Within- and across-breed genomic predictions and genomic relationships for Western Pyrenees dairy sheep breeds Latxa, Manech, and Basco-BÃ©arnaise. Journal of Dairy Science, 2014, 97, 3200-3212.	1.4	47
51	Dominance and epistatic genetic variances for litter size in pigs using genomic models. Genetics Selection Evolution, 2018, 50, 71.	1.2	45
52	Bias and accuracy of dairy sheep evaluations using BLUP and SSGBLUP with metafounders and unknown parent groups. Genetics Selection Evolution, 2020, 52, 47.	1.2	43
53	A comparison of partial least squares (PLS) and sparse PLS regressions in genomic selection in French dairy cattle. Journal of Dairy Science, 2012, 95, 2120-2131.	1.4	41
54	Multi‐breed genetic evaluation in a Gelbvieh population. Journal of Animal Breeding and Genetics, 2007, 124, 286-295.	0.8	40

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55	Genomic BLUP including additive and dominant variation in purebreds and F1 crossbreds, with an application in pigs. Genetics Selection Evolution, 2016, 48, 6.	1.2	39
56	Evaluating Sequence-Based Genomic Prediction with an Efficient New Simulator. Genetics, 2017, 205, 939-953.	1.2	39
57	Constructing covariance functions for random regression models for growth in Gelbvieh beef cattle. Journal of Animal Science, 2004, 82, 1564-1571.	0.2	38
58	Invited review: efficient computation strategies in genomic selection. Animal, 2017, 11, 731-736.	1.3	37
59	Alternative SNP weighting for single-step genomic best linear unbiased predictor evaluation of stature in US Holsteins in the presence of selected sequence variants. Journal of Dairy Science, 2019, 102, 10012-10019.	1.4	37
60	Economic weights of fertility, prolificacy, milk yield and longevity in dairy sheep. Animal, 2007, 1, 193-203.	1.3	35
61	GWAS by GBLUP: Single and Multimarker EMMAX and Bayes Factors, with an Example in Detection of a Major Gene for Horse Gait. G3: Genes, Genomes, Genetics, 2018, 8, 2301-2308.	0.8	35
62	Inbreeding and effective population size in French dairy sheep: Comparison between genomic and pedigree estimates. Journal of Dairy Science, 2019, 102, 4227-4237.	1.4	35
63	Fine mapping of QTL and genomic prediction using allele-specific expression SNPs demonstrates that the complex trait of genetic resistance to Marek's disease is predominantly determined by transcriptional regulation. BMC Genomics, 2015, 16, 816.	1.2	33
64	Behavior of the Linear Regression method to estimate bias and accuracies with correct and incorrect genetic evaluation models. Journal of Dairy Science, 2020, 103, 529-544.	1.4	33
65	Genetic evaluation for three-way crossbreeding. Genetics Selection Evolution, 2015, 47, 98.	1.2	32
66	Pedigree and genomic evaluation of pigs using a terminal-cross model. Genetics Selection Evolution, 2016, 48, 32.	1.2	32
67	Modeling missing pedigree in single-step genomic BLUP. Journal of Dairy Science, 2019, 102, 2336-2346.	1.4	32
68	Genetic evaluation including intermediate omics features. Genetics, 2021, 219, .	1.2	32
69	Technical note: Genomic evaluation for crossbred performance in a single-step approach with metafounders1. Journal of Animal Science, 2017, 95, 1472-1480.	0.2	30
70	Genomic Model with Correlation Between Additive and Dominance Effects. Genetics, 2018, 209, 711-723.	1.2	29
71	Linear models for joint association and linkage QTL mapping. Genetics Selection Evolution, 2009, 41, 43.	1.2	28
72	Evaluation of the utility of diagonal elements of the genomic relationship matrix as a diagnostic tool to detect mislabelled genotyped animals in a broiler chicken population. Journal of Animal Breeding and Genetics, 2011, 128, 386-393.	0.8	28

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73	Genetic parameters for growth and faecal worm egg count following Haemonchus contortus experimental infestations using pedigree and molecular information. Genetics Selection Evolution, 2014, 46, 13.	1.2	28
74	A comparison of methods for whole-genome QTL mapping using dense markers in four livestock species. Genetics Selection Evolution, 2015, 47, 6.	1.2	28
75	Validation of single‐step GBLUP genomic predictions from threshold models using the linear regression method: An application in chicken mortality. Journal of Animal Breeding and Genetics, 2021, 138, 4-13.	0.8	28
76	Multivariate genomic model improves analysis of oil palm (Elaeis guineensis Jacq.) progeny tests. Molecular Breeding, 2016, 36, 1.	1.0	27
77	Use of a reduced set of single nucleotide polymorphisms for genetic evaluation of resistance to Salmonella carrier state in laying hens. Poultry Science, 2011, 90, 731-736.	1.5	26
78	Quality Control of Genotypes Using Heritability Estimates of Gene Content at the Marker. Genetics, 2015, 199, 675-681.	1.2	26
79	Effects of ignoring inbreeding in model‐based accuracy for BLUP and SSGBLUP. Journal of Animal Breeding and Genetics, 2020, 137, 356-364.	0.8	26
80	Technical note: Genomic evaluation for crossbred performance in a single-step approach with metafounders. Journal of Animal Science, 2017, 95, 1472.	0.2	26
81	Genetic parameters of product quality and hepatic metabolism in fattened mule ducks1. Journal of Animal Science, 2011, 89, 669-679.	0.2	25
82	Genetic evaluation with major genes and polygenic inheritance when some animals are not genotyped using gene content multiple-trait BLUP. Genetics Selection Evolution, 2015, 47, 89.	1.2	24
83	Fine tuning genomic evaluations in dairy cattle through SNP pre-selection with the Elastic-Net algorithm. Genetical Research, 2011, 93, 409-417.	0.3	23
84	Influence of epistasis on response to genomic selection using complete sequence data. Genetics Selection Evolution, 2017, 49, 66.	1.2	23
85	Test day models and genetic parameters in Latxa and Manchega dairy ewes. Livestock Science, 2001, 67, 253-264.	1.2	21
86	Genetic parameters of milk traits in Latxa dairy sheep. Animal Science, 2001, 73, 407-412.	1.3	20
87	Computation of deregressed proofs for genomic selection when own phenotypes exist with an application in French show-jumping horses1. Journal of Animal Science, 2013, 91, 1076-1085.	0.2	20
88	Genomic prediction of hybrid crops allows disentangling dominance and epistasis. Genetics, 2021, 218, .	1.2	20
89	The effects of selective breeding against scrapie susceptibility on the genetic variability of the Latxa Black-Faced sheep breed. Genetics Selection Evolution, 2006, 38, 495.	1.2	19
90	Economic weights of somatic cell score in dairy sheep. Animal, 2007, 1, 205-212.	1.3	19

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91	Using the product threshold model for estimating separately the effect of temperature on male and female fertility1. Journal of Animal Science, 2011, 89, 3983-3995.	0.2	19
92	Differences between genomic‐based and pedigree‐based relationships in a chicken population, as a function of quality control and pedigree links among individuals. Journal of Animal Breeding and Genetics, 2014, 131, 445-451.	0.8	19
93	Genomic and pedigree estimation of inbreeding depression for semen traits in the Basco-Béarnaise dairy sheep breed. Journal of Dairy Science, 2021, 104, 3221-3230.	1.4	16
94	Bayesian model selection of contemporary groups for BLUP genetic evaluation in Latxa dairy sheep. Livestock Science, 2005, 93, 205-212.	1.2	15
95	Validation of models for analysis of ranks in horse breeding evaluation. Genetics Selection Evolution, 2010, 42, 3.	1.2	15
96	A comparison of methods to estimate genomic relationships using pedigree and markers in livestock populations. Journal of Animal Breeding and Genetics, 2016, 133, 452-462.	0.8	15
97	Purebred and Crossbred Genomic Evaluation and Mate Allocation Strategies To Exploit Dominance in Pig Crossbreeding Schemes. G3: Genes, Genomes, Genetics, 2020, 10, 2829-2841.	0.8	15
98	Multibreed genomic evaluation for production traits of dairy cattle in the United States using single-step genomic best linear unbiased predictor. Journal of Dairy Science, 2022, 105, 5141-5152.	1.4	14
99	Imputation of genotypes in Danish purebred and two-way crossbred pigs using low-density panels. Genetics Selection Evolution, 2015, 47, 54.	1.2	13
100	Pedigree‐based estimation of covariance between dominance deviations and additive genetic effects in closed rabbit lines considering inbreeding and using a computationally simpler equivalent model. Journal of Animal Breeding and Genetics, 2017, 134, 184-195.	0.8	13
101	Inbreeding, effective population size, and coancestry in the Latxa dairy sheep breed. Journal of Dairy Science, 2020, 103, 5215-5226.	1.4	13
102	Different ways to model biological relationships between fertility and pH of the semen in rabbits1. Journal of Animal Science, 2011, 89, 1294-1303.	0.2	12
103	Genetic basis of semen traits and their relationship with growth rate in rabbits1. Journal of Animal Science, 2012, 90, 1385-1397.	0.2	12
104	A fast indirect method to compute functions of genomic relationships concerning genotyped and ungenotyped individuals, for diversity management. Genetics Selection Evolution, 2017, 49, 87.	1.2	12
105	Detection of unrecorded environmental challenges in high-frequency recorded traits, and genetic determinism of resilience to challenge, with an application on feed intake in lambs. Genetics Selection Evolution, 2021, 53, 4.	1.2	12
106	The correlation of substitution effects across populations and generations in the presence of nonadditive functional gene action. Genetics, 2021, 219, .	1.2	12
107	Short communication: Methods to compute genomic inbreeding for ungenotyped individuals. Journal of Dairy Science, 2020, 103, 3363-3367.	1.4	12
108	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 gradient. Journal of Animal Science, 2017, 95, 49.	0.2	11

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109	Genomic selection for carrier-state resistance in chicken commercial lines. BMC Proceedings, 2011, 5, S24.	1.8	10
110	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. Journal of Animal Science, 2017, 95, 49-52.	0.2	10
111	Role of inbreeding depression, non‐inbred dominance deviations and random year‐season effect in genetic trends for prolificacy in closed rabbit lines. Journal of Animal Breeding and Genetics, 2017, 134, 441-452.	0.8	10
112	Variance and Covariance of Actual Relationships between Relatives at One Locus. PLoS ONE, 2013, 8, e57003.	1.1	10
113	Removing data and using metafounders alleviates biases for all traits in Lacaune dairy sheep predictions. Journal of Dairy Science, 2022, 105, 2439-2452.	1.4	10
114	Dissecting total genetic variance into additive and dominance components of purebred and crossbred pig traits. Animal, 2019, 13, 2429-2439.	1.3	9
115	Genome‐wide association study for feed efficiency in collective cage‐raised rabbits under full and restricted feeding. Animal Genetics, 2020, 51, 799-810.	0.6	9
116	Theoretical and empirical comparisons of expected and realized relationships for the X-chromosome. Genetics Selection Evolution, 2020, 52, 50.	1.2	9
117	Selection and drift reduce genetic variation for milk yield in Manech Tête Rousse dairy sheep. JDS Communications, 2021, 2, 31-34.	0.5	9
118	Exploring the inclusion of genomic information and metafounders in Latxa dairy sheep genetic evaluations. Journal of Dairy Science, 2020, 103, 6346-6353.	1.4	9
119	Product versus additive threshold models for analysis of reproduction outcomes in animal genetics1. Journal of Animal Science, 2009, 87, 2510-2518.	0.2	8
120	Economic weights for major milk constituents of Manchega dairy ewes. Journal of Dairy Science, 2010, 93, 3303-3309.	1.4	7
121	Estimates of the actual relationship between half‐sibs in a pig population. Journal of Animal Breeding and Genetics, 2017, 134, 109-118.	0.8	7
122	Dissecting genetic trends to understand breeding practices in livestock: a maternal pig line example. Genetics Selection Evolution, 2021, 53, 89.	1.2	7
123	Genomic evaluation and genome-wide association studies for total number of teats in a combined American and Danish Yorkshire pig populations selected in China. Journal of Animal Science, 2022, 100, .	0.2	5
124	On the equivalence between marker effect models and breeding value models and direct genomic values with the Algorithm for Proven and Young. Genetics Selection Evolution, 2022, 54, .	1.2	5
125	Fine-mapping quantitative trait loci with a medium density marker panel: efficiency of population structures and comparison of linkage disequilibrium linkage analysis models. Genetical Research, 2012, 94, 223-234.	0.3	4
126	LDSO: a program to simulate pedigrees and molecular information under various evolutionary forces. Journal of Animal Breeding and Genetics, 2012, 129, 417-421.	0.8	4

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127	Short communication: Accounting for new mutations in genomic prediction models. Journal of Dairy Science, 2013, 96, 5398-5402.	1.4	3
128	The coefficient of dominance is not (always) estimable with biallelic markers. Journal of Animal Breeding and Genetics, 2014, 131, 97-104.	0.8	3
129	A combined coalescence gene‑dropping tool for evaluating genomic selection in complex scenarios (ms2gs). Journal of Animal Breeding and Genetics, 2016, 133, 85-91.	0.8	3
130	Islands of runs of homozygosity indicate selection signatures in Ovis aries 6 (OAR6) of French dairy sheep. JDS Communications, 2021, 2, 132-136.	0.5	3
131	Unfavorable genetic correlations between fecal egg count and milk production traits in the French blond-faced Manech dairy sheep breed. Genetics Selection Evolution, 2022, 54, 14.	1.2	3
132	Does probabilistic modelling of linkage disequilibrium evolution improve the accuracy of QTL location in animal pedigree?. Genetics Selection Evolution, 2010, 42, 38.	1.2	2
133	GIBBSTHUR: Software for Estimating Variance Components and Predicting Breeding Values for Ranking Traits Based on a Thurstonian Model. Animals, 2020, 10, 1001.	1.0	2
134	Association analysis of loci implied in "buffering" epistasis. Journal of Animal Science, 2020, 98, .	0.2	2
135	High genetic correlation for milk yield across Manech and Latxa dairy sheep from France and Spain. JDS Communications, 2022, 3, 260-264.	0.5	2
136	Single-marker and multi-marker mixed models for polygenic score analysis in family-based data. BMC Proceedings, 2014, 8, S63.	1.8	1
137	193 Including causative variants into single step genomic BLUP. Journal of Animal Science, 2017, 95, 95-96.	0.2	1
138	PSXII-37 Validation of single-step GBLUP genomic predictions from threshold models using the linear regression method: an application in chicken mortality. Journal of Animal Science, 2020, 98, 246-247.	0.2	1
139	22 Accuracy of indirect predictions for large datasets based on prediction error covariance of SNP effects from single-step GBLUP. Journal of Animal Science, 2020, 98, 6-7.	0.2	0
140	0292 Dimensionality of genomic information and APY inverse of genomic relationship matrix. Journal of Animal Science, 2016, 94, 138-139.	0.2	0
141	Computing strategies for multi-population genomic evaluation. Genetics Selection Evolution, 2022, 54, 10.	1.2	0