

Andres Legarra

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

138
papers

6,411
citations

41
h-index

77
g-index

148
ext. papers

8,644
ext. citations

3.2
avg, IF

6.27
L-index

#	Paper	IF	Citations
138	Computing strategies for multi-population genomic evaluation.. <i>Genetics Selection Evolution</i> , 2022 , 54, 10	4.9	
137	Unfavorable genetic correlations between fecal egg count and milk production traits in the French blond-faced Manech dairy sheep breed.. <i>Genetics Selection Evolution</i> , 2022 , 54, 14	4.9	0
136	Multibreed genomic evaluation for production traits of dairy cattle in the United States using single-step genomic best linear unbiased predictor.. <i>Journal of Dairy Science</i> , 2022 ,	4	1
135	Dissecting genetic trends to understand breeding practices in livestock: a maternal pig line example. <i>Genetics Selection Evolution</i> , 2021 , 53, 89	4.9	0
134	Genomic and pedigree estimation of inbreeding depression for semen traits in the Basco-Bàrnaise dairy sheep breed. <i>Journal of Dairy Science</i> , 2021 , 104, 3221-3230	4	4
133	Genomic prediction of hybrid crops allows disentangling dominance and epistasis. <i>Genetics</i> , 2021 , 218,	4	6
132	Islands of runs of homozygosity indicate selection signatures in Ovis aries 6 (OAR6) of French dairy sheep. <i>JDS Communications</i> , 2021 , 2, 132-136	1.4	0
131	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	2.9	8
130	Selection and drift reduce genetic variation for milk yield in Manech Tête Rousse dairy sheep. <i>JDS Communications</i> , 2021 , 2, 31-34	1.4	2
129	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. <i>Genetics Selection Evolution</i> , 2021 , 53, 4	4.9	0
128	The correlation of substitution effects across populations and generations in the presence of nonadditive functional gene action. <i>Genetics</i> , 2021 , 219,	4	1
127	Genetic evaluation including intermediate omics features. <i>Genetics</i> , 2021 , 219,	4	2
126	Purebred and Crossbred Genomic Evaluation and Mate Allocation Strategies To Exploit Dominance in Pig Crossbreeding Schemes. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 2829-2841	3.2	8
125	Inbreeding, effective population size, and coancestry in the Latxa dairy sheep breed. <i>Journal of Dairy Science</i> , 2020 , 103, 5215-5226	4	3
124	GIBBSTHUR: Software for Estimating Variance Components and Predicting Breeding Values for Ranking Traits Based on a Thurstonian Model. <i>Animals</i> , 2020 , 10,	3.1	2
123	Effects of ignoring inbreeding in model-based accuracy for BLUP and SSGBLUP. <i>Journal of Animal Breeding and Genetics</i> , 2020 , 137, 356-364	2.9	9
122	Current status of genomic evaluation. <i>Journal of Animal Science</i> , 2020 , 98,	0.7	33

121	Short communication: Methods to compute genomic inbreeding for ungenotyped individuals. <i>Journal of Dairy Science</i> , 2020 , 103, 3363-3367	4	6
120	Exploring the inclusion of genomic information and metafounders in Latxa dairy sheep genetic evaluations. <i>Journal of Dairy Science</i> , 2020 , 103, 6346-6353	4	5
119	Behavior of the Linear Regression method to estimate bias and accuracies with correct and incorrect genetic evaluation models. <i>Journal of Dairy Science</i> , 2020 , 103, 529-544	4	7
118	Genome-wide association study for feed efficiency in collective cage-raised rabbits under full and restricted feeding. <i>Animal Genetics</i> , 2020 , 51, 799-810	2.5	2
117	Single-Step Genomic Evaluations from Theory to Practice: Using SNP Chips and Sequence Data in BLUPF90. <i>Genes</i> , 2020 , 11,	4.2	33
116	Theoretical and empirical comparisons of expected and realized relationships for the X-chromosome. <i>Genetics Selection Evolution</i> , 2020 , 52, 50	4.9	3
115	Bias and accuracy of dairy sheep evaluations using BLUP and SGBLUP with metafounders and unknown parent groups. <i>Genetics Selection Evolution</i> , 2020 , 52, 47	4.9	14
114	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	0.7	78
113	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	0.7	78
112	Dissecting total genetic variance into additive and dominance components of purebred and crossbred pig traits. <i>Animal</i> , 2019 , 13, 2429-2439	3.1	4
111	Inbreeding and effective population size in French dairy sheep: Comparison between genomic and pedigree estimates. <i>Journal of Dairy Science</i> , 2019 , 102, 4227-4237	4	13
110	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	4.9	39
109	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	4	18
108	Modeling missing pedigree in single-step genomic BLUP. <i>Journal of Dairy Science</i> , 2019 , 102, 2336-2346	4	17
107	Non-additive Effects in Genomic Selection. <i>Frontiers in Genetics</i> , 2018 , 9, 78	4.5	84
106	Genomic selection models for directional dominance: an example for litter size in pigs. <i>Genetics Selection Evolution</i> , 2018 , 50, 1	4.9	28
105	Genomic Model with Correlation Between Additive and Dominance Effects. <i>Genetics</i> , 2018 , 209, 711-723	4	12
104	Semi-parametric estimates of population accuracy and bias of predictions of breeding values and future phenotypes using the LR method. <i>Genetics Selection Evolution</i> , 2018 , 50, 53	4.9	52

103	Dominance and epistatic genetic variances for litter size in pigs using genomic models. <i>Genetics Selection Evolution</i> , 2018 , 50, 71	4.9	19
102	GWAS by GBLUP: Single and Multimarker EMMAX and Bayes Factors, with an Example in Detection of a Major Gene for Horse Gait. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 2301-2308	3.2	13
101	Invited review: efficient computation strategies in genomic selection. <i>Animal</i> , 2017 , 11, 731-736	3.1	25
100	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. <i>Journal of Animal Science</i> , 2017 , 95, 49-52	0.7	5
99	Orthogonal Estimates of Variances for Additive, Dominance, and Epistatic Effects in Populations. <i>Genetics</i> , 2017 , 206, 1297-1307	4	69
98	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. <i>Journal of Animal Breeding and Genetics</i> , 2017 , 134, 184-195	2.9	10
97	Evaluating Sequence-Based Genomic Prediction with an Efficient New Simulator. <i>Genetics</i> , 2017 , 205, 939-953	4	20
96	Genetic Variation in the Social Environment Contributes to Health and Disease. <i>PLoS Genetics</i> , 2017 , 13, e1006498	6	53
95	A fast indirect method to compute functions of genomic relationships concerning genotyped and ungenotyped individuals, for diversity management. <i>Genetics Selection Evolution</i> , 2017 , 49, 87	4.9	9
94	Technical note: Genomic evaluation for crossbred performance in a single-step approach with metafounders. <i>Journal of Animal Science</i> , 2017 , 95, 1472-1480	0.7	21
93	Role of inbreeding depression, non-inbred dominance deviations and random year-season effect in genetic trends for prolificacy in closed rabbit lines. <i>Journal of Animal Breeding and Genetics</i> , 2017 , 134, 441-452	2.9	8
92	Single-Step Genomic and Pedigree Genotype \times Environment Interaction Models for Predicting Wheat Lines in International Environments. <i>Plant Genome</i> , 2017 , 10, plantgenome2016.09.0089	4.4	47
91	Metafounders are related to F fixation indices and reduce bias in single-step genomic evaluations. <i>Genetics Selection Evolution</i> , 2017 , 49, 34	4.9	34
90	Estimates of the actual relationship between half-sibs in a pig population. <i>Journal of Animal Breeding and Genetics</i> , 2017 , 134, 109-118	2.9	3
89	Incorporation of causative quantitative trait nucleotides in single-step GBLUP. <i>Genetics Selection Evolution</i> , 2017 , 49, 59	4.9	38
88	Influence of epistasis on response to genomic selection using complete sequence data. <i>Genetics Selection Evolution</i> , 2017 , 49, 66	4.9	15
87	Technical note: Genomic evaluation for crossbred performance in a single-step approach with metafounders. <i>Journal of Animal Science</i> , 2017 , 95, 1472	0.7	17
86	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. <i>Journal of Animal Science</i> , 2017 , 95, 49	0.7	8

85	Comparing estimates of genetic variance across different relationship models. <i>Theoretical Population Biology</i> , 2016 , 107, 26-30	1.2	41
84	Genomic evaluation by including dominance effects and inbreeding depression for purebred and crossbred performance with an application in pigs. <i>Genetics Selection Evolution</i> , 2016 , 48, 92	4.9	42
83	Pedigree and genomic evaluation of pigs using a terminal-cross model. <i>Genetics Selection Evolution</i> , 2016 , 48, 32	4.9	21
82	Genomic BLUP including additive and dominant variation in purebreds and F1 crossbreds, with an application in pigs. <i>Genetics Selection Evolution</i> , 2016 , 48, 6	4.9	34
81	A combined coalescence gene-dropping tool for evaluating genomic selection in complex scenarios (ms2gs). <i>Journal of Animal Breeding and Genetics</i> , 2016 , 133, 85-91	2.9	3
80	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	4	42
79	Multivariate genomic model improves analysis of oil palm (<i>Elaeis guineensis</i> Jacq.) progeny tests. <i>Molecular Breeding</i> , 2016 , 36, 1	3.4	17
78	The Dimensionality of Genomic Information and Its Effect on Genomic Prediction. <i>Genetics</i> , 2016 , 203, 573-81	4	42
77	0292 Dimensionality of genomic information and APY inverse of genomic relationship matrix. <i>Journal of Animal Science</i> , 2016 , 94, 138-139	0.7	
76	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	4.5	80
75	A comparison of methods to estimate genomic relationships using pedigree and markers in livestock populations. <i>Journal of Animal Breeding and Genetics</i> , 2016 , 133, 452-462	2.9	9
74	Application of single-step genomic evaluation for crossbred performance in pig. <i>Journal of Animal Science</i> , 2016 , 94, 936-48	0.7	33
73	Ancestral Relationships Using Metafounders: Finite Ancestral Populations and Across Population Relationships. <i>Genetics</i> , 2015 , 200, 455-68	4	61
72	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	4.9	52
71	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, 4090-4	4	39
70	A comparison of methods for whole-genome QTL mapping using dense markers in four livestock species. <i>Genetics Selection Evolution</i> , 2015 , 47, 6	4.9	26
69	Genetic evaluation for three-way crossbreeding. <i>Genetics Selection Evolution</i> , 2015 , 47, 98	4.9	20
68	Sequence- vs. chip-assisted genomic selection: accurate biological information is advised. <i>Genetics Selection Evolution</i> , 2015 , 47, 43	4.9	86

67	Imputation of genotypes in Danish purebred and two-way crossbred pigs using low-density panels. <i>Genetics Selection Evolution</i> , 2015 , 47, 54	4.9	9
66	Genetic evaluation with major genes and polygenic inheritance when some animals are not genotyped using gene content multiple-trait BLUP. <i>Genetics Selection Evolution</i> , 2015 , 47, 89	4.9	19
65	Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus. <i>Journal of Animal Science</i> , 2015 , 93, 2653-62	0.7	94
64	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. <i>BMC Genomics</i> , 2015 , 16, 816	4.5	23
63	Quality control of genotypes using heritability estimates of gene content at the marker. <i>Genetics</i> , 2015 , 199, 675-81	4	19
62	Single-marker and multi-marker mixed models for polygenic score analysis in family-based data. <i>BMC Proceedings</i> , 2014 , 8, S63	2.3	1
61	Genetic parameters for growth and faecal worm egg count following <i>Haemonchus contortus</i> experimental infestations using pedigree and molecular information. <i>Genetics Selection Evolution</i> , 2014 , 46, 13	4.9	18
60	Differences between genomic-based and pedigree-based relationships in a chicken population, as a function of quality control and pedigree links among individuals. <i>Journal of Animal Breeding and Genetics</i> , 2014 , 131, 445-51	2.9	11
59	Using recursion to compute the inverse of the genomic relationship matrix. <i>Journal of Dairy Science</i> , 2014 , 97, 3943-52	4	82
58	Genome-wide association mapping including phenotypes from relatives without genotypes in a single-step (ssGWAS) for 6-week body weight in broiler chickens. <i>Frontiers in Genetics</i> , 2014 , 5, 134	4.5	117
57	The coefficient of dominance is not (always) estimable with biallelic markers. <i>Journal of Animal Breeding and Genetics</i> , 2014 , 131, 97-104	2.9	3
56	Genomic analysis of dominance effects on milk production and conformation traits in Fleckvieh cattle. <i>Genetics Selection Evolution</i> , 2014 , 46, 40	4.9	48
55	Within- and across-breed genomic predictions and genomic relationships for Western Pyrenees dairy sheep breeds Latxa, Manech, and Basco-Bàrnaise. <i>Journal of Dairy Science</i> , 2014 , 97, 3200-12	4	28
54	Single Step, a general approach for genomic selection. <i>Livestock Science</i> , 2014 , 166, 54-65	1.7	172
53	Assessment of accuracy of genomic prediction for French Lacaune dairy sheep. <i>Journal of Dairy Science</i> , 2014 , 97, 1107-16	4	44
52	Unknown-parent groups in single-step genomic evaluation. <i>Journal of Animal Breeding and Genetics</i> , 2013 , 130, 252-8	2.9	53
51	On the additive and dominant variance and covariance of individuals within the genomic selection scope. <i>Genetics</i> , 2013 , 195, 1223-30	4	169
50	Short communication: Accounting for new mutations in genomic prediction models. <i>Journal of Dairy Science</i> , 2013 , 96, 5398-402	4	3

49	Application of Bayesian least absolute shrinkage and selection operator (LASSO) and BayesC methods for genomic selection in French Holstein and Montblier breeds. <i>Journal of Dairy Science</i> , 2013 , 96, 575-91	4	40
48	Methods to approximate reliabilities in single-step genomic evaluation. <i>Journal of Dairy Science</i> , 2013 , 96, 647-54	4	44
47	Computation of deregressed proofs for genomic selection when own phenotypes exist with an application in French show-jumping horses. <i>Journal of Animal Science</i> , 2013 , 91, 1076-85	0.7	17
46	Variance and covariance of actual relationships between relatives at one locus. <i>PLoS ONE</i> , 2013 , 8, e57003	0.7	8
45	LDSO: a program to simulate pedigrees and molecular information under various evolutionary forces. <i>Journal of Animal Breeding and Genetics</i> , 2012 , 129, 417-21	2.9	4
44	A comparison of partial least squares (PLS) and sparse PLS regressions in genomic selection in French dairy cattle. <i>Journal of Dairy Science</i> , 2012 , 95, 2120-31	4	28
43	Genomic selection in the French Lacaune dairy sheep breed. <i>Journal of Dairy Science</i> , 2012 , 95, 2723-33	4	60
42	Computational strategies for national integration of phenotypic, genomic, and pedigree data in a single-step best linear unbiased prediction. <i>Journal of Dairy Science</i> , 2012 , 95, 4629-45	4	58
41	Joint genomic evaluation of French dairy cattle breeds using multiple-trait models. <i>Genetics Selection Evolution</i> , 2012 , 44, 39	4.9	76
40	A genome scan for QTL affecting resistance to <i>Haemonchus contortus</i> in sheep. <i>Journal of Animal Science</i> , 2012 , 90, 4690-705	0.7	48
39	Genetic basis of semen traits and their relationship with growth rate in rabbits. <i>Journal of Animal Science</i> , 2012 , 90, 1385-97	0.7	10
38	Fine-mapping quantitative trait loci with a medium density marker panel: efficiency of population structures and comparison of linkage disequilibrium linkage analysis models. <i>Genetical Research</i> , 2012 , 94, 223-34	1.1	4
37	Genome-wide association mapping including phenotypes from relatives without genotypes. <i>Genetical Research</i> , 2012 , 94, 73-83	1.1	278
36	Improved Lasso for genomic selection. <i>Genetical Research</i> , 2011 , 93, 77-87	1.1	85
35	Genomic selection for carrier-state resistance in chicken commercial lines. <i>BMC Proceedings</i> , 2011 , 5 Suppl 4, S24	2.3	6
34	Genetic parameters of product quality and hepatic metabolism in fattened mule ducks. <i>Journal of Animal Science</i> , 2011 , 89, 669-79	0.7	18
33	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. <i>Journal of Animal Breeding and Genetics</i> , 2011 , 128, 386-93	2.9	19
32	Efficient computation of the genomic relationship matrix and other matrices used in single-step evaluation. <i>Journal of Animal Breeding and Genetics</i> , 2011 , 128, 422-8	2.9	101

31	A note on the rationale for estimating genealogical coancestry from molecular markers. <i>Genetics Selection Evolution</i> , 2011 , 43, 1-10	4.9	43
30	Use of a reduced set of single nucleotide polymorphisms for genetic evaluation of resistance to Salmonella carrier state in laying hens. <i>Poultry Science</i> , 2011 , 90, 731-6	3.9	14
29	Bias in genomic predictions for populations under selection. <i>Genetical Research</i> , 2011 , 93, 357-66	1.1	205
28	Fine tuning genomic evaluations in dairy cattle through SNP pre-selection with the Elastic-Net algorithm. <i>Genetical Research</i> , 2011 , 93, 409-17	1.1	17
27	Different ways to model biological relationships between fertility and pH of the semen in rabbits. <i>Journal of Animal Science</i> , 2011 , 89, 1294-303	0.7	11
26	Effect of different genomic relationship matrices on accuracy and scale. <i>Journal of Animal Science</i> , 2011 , 89, 2673-9	0.7	78
25	Using the product threshold model for estimating separately the effect of temperature on male and female fertility. <i>Journal of Animal Science</i> , 2011 , 89, 3983-95	0.7	14
24	Hot topic: a unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. <i>Journal of Dairy Science</i> , 2010 , 93, 743-52	4	708
23	Economic weights for major milk constituents of Manchega dairy ewes. <i>Journal of Dairy Science</i> , 2010 , 93, 3303-9	4	7
22	Does probabilistic modelling of linkage disequilibrium evolution improve the accuracy of QTL location in animal pedigree?. <i>Genetics Selection Evolution</i> , 2010 , 42, 38	4.9	2
21	Validation of models for analysis of ranks in horse breeding evaluation. <i>Genetics Selection Evolution</i> , 2010 , 42, 3	4.9	10
20	Product versus additive threshold models for analysis of reproduction outcomes in animal genetics. <i>Journal of Animal Science</i> , 2009 , 87, 2510-8	0.7	5
19	Linear models for joint association and linkage QTL mapping. <i>Genetics Selection Evolution</i> , 2009 , 41, 43	4.9	25
18	Predicting quantitative traits with regression models for dense molecular markers and pedigree. <i>Genetics</i> , 2009 , 182, 375-85	4	392
17	A relationship matrix including full pedigree and genomic information. <i>Journal of Dairy Science</i> , 2009 , 92, 4656-63	4	493
16	Computing procedures for genetic evaluation including phenotypic, full pedigree, and genomic information. <i>Journal of Dairy Science</i> , 2009 , 92, 4648-55	4	322
15	Technical note: Computing strategies in genome-wide selection. <i>Journal of Dairy Science</i> , 2008 , 91, 360-64		82
14	Performance of genomic selection in mice. <i>Genetics</i> , 2008 , 180, 611-8	4	257

13	Multi-breed genetic evaluation in a Gelbvieh population. <i>Journal of Animal Breeding and Genetics</i> , 2007 , 124, 286-95	2.9	32
12	Economic weights of fertility, prolificacy, milk yield and longevity in dairy sheep. <i>Animal</i> , 2007 , 1, 193-203.	3.1	24
11	Economic weights of somatic cell score in dairy sheep. <i>Animal</i> , 2007 , 1, 205-12	3.1	18
10	Analysis of fertility and dystocia in Holsteins using recursive models to handle censored and categorical data. <i>Journal of Dairy Science</i> , 2007 , 90, 2012-24	4	51
9	The effects of selective breeding against scrapie susceptibility on the genetic variability of the Latxa Black-Faced sheep breed. <i>Genetics Selection Evolution</i> , 2006 , 38, 495-511	4.9	16
8	Genetic parameters of udder traits, somatic cell score, and milk yield in Latxa sheep. <i>Journal of Dairy Science</i> , 2005 , 88, 2238-45	4	42
7	Bayesian model selection of contemporary groups for BLUP genetic evaluation in Latxa dairy sheep. <i>Livestock Science</i> , 2005 , 93, 205-212		12
6	Constructing covariance functions for random regression models for growth in Gelbvieh beef cattle. <i>Journal of Animal Science</i> , 2004 , 82, 1564-71	0.7	34
5	Genetic parameters of milk traits in Latxa dairy sheep. <i>Animal Science</i> , 2001 , 73, 407-412		18
4	Test day models and genetic parameters in Latxa and Manchega dairy ewes. <i>Livestock Science</i> , 2001 , 67, 253-264		18
3	The Correlation of Substitution Effects Across Populations and Generations in the Presence of Non-Additive Functional Gene Action		2
2	Exact p-values for large-scale single step genome-wide association, with an application for birth weight in American Angus		2
1	Association analysis of loci implied in Buffering Epistasis		1