

# Andres Legarra

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/1865732/andres-legarra-publications-by-citations.pdf>

**Version:** 2024-04-29

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	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> , <b>2010</b> , 93, 743-52	4	708
137	A relationship matrix including full pedigree and genomic information. <i>Journal of Dairy Science</i> , <b>2009</b> , 92, 4656-63	4	493
136	Predicting quantitative traits with regression models for dense molecular markers and pedigree. <i>Genetics</i> , <b>2009</b> , 182, 375-85	4	392
135	Computing procedures for genetic evaluation including phenotypic, full pedigree, and genomic information. <i>Journal of Dairy Science</i> , <b>2009</b> , 92, 4648-55	4	322
134	Genome-wide association mapping including phenotypes from relatives without genotypes. <i>Genetical Research</i> , <b>2012</b> , 94, 73-83	1.1	278
133	Performance of genomic selection in mice. <i>Genetics</i> , <b>2008</b> , 180, 611-8	4	257
132	Bias in genomic predictions for populations under selection. <i>Genetical Research</i> , <b>2011</b> , 93, 357-66	1.1	205
131	Single Step, a general approach for genomic selection. <i>Livestock Science</i> , <b>2014</b> , 166, 54-65	1.7	172
130	On the additive and dominant variance and covariance of individuals within the genomic selection scope. <i>Genetics</i> , <b>2013</b> , 195, 1223-30	4	169
129	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> , <b>2014</b> , 5, 134	4.5	117
128	Efficient computation of the genomic relationship matrix and other matrices used in single-step evaluation. <i>Journal of Animal Breeding and Genetics</i> , <b>2011</b> , 128, 422-8	2.9	101
127	Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus. <i>Journal of Animal Science</i> , <b>2015</b> , 93, 2653-62	0.7	94
126	Sequence- vs. chip-assisted genomic selection: accurate biological information is advised. <i>Genetics Selection Evolution</i> , <b>2015</b> , 47, 43	4.9	86
125	Improved Lasso for genomic selection. <i>Genetical Research</i> , <b>2011</b> , 93, 77-87	1.1	85
124	Non-additive Effects in Genomic Selection. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 78	4.5	84
123	Using recursion to compute the inverse of the genomic relationship matrix. <i>Journal of Dairy Science</i> , <b>2014</b> , 97, 3943-52	4	82
122	Technical note: Computing strategies in genome-wide selection. <i>Journal of Dairy Science</i> , <b>2008</b> , 91, 360-64		82

121	Weighting Strategies for Single-Step Genomic BLUP: An Iterative Approach for Accurate Calculation of GEBV and GWAS. <i>Frontiers in Genetics</i> , <b>2016</b> , 7, 151	4.5	80
120	Effect of different genomic relationship matrices on accuracy and scale. <i>Journal of Animal Science</i> , <b>2011</b> , 89, 2673-9	0.7	78
119	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> , <b>2020</b> , 98, 6-7	0.7	78
118	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> , <b>2020</b> , 98, 246-247	0.7	78
117	Joint genomic evaluation of French dairy cattle breeds using multiple-trait models. <i>Genetics Selection Evolution</i> , <b>2012</b> , 44, 39	4.9	76
116	Orthogonal Estimates of Variances for Additive, Dominance, and Epistatic Effects in Populations. <i>Genetics</i> , <b>2017</b> , 206, 1297-1307	4	69
115	Ancestral Relationships Using Metafounders: Finite Ancestral Populations and Across Population Relationships. <i>Genetics</i> , <b>2015</b> , 200, 455-68	4	61
114	Genomic selection in the French Lacaune dairy sheep breed. <i>Journal of Dairy Science</i> , <b>2012</b> , 95, 2723-33	4	60
113	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> , <b>2012</b> , 95, 4629-45	4	58
112	Genetic Variation in the Social Environment Contributes to Health and Disease. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006498	6	53
111	Unknown-parent groups in single-step genomic evaluation. <i>Journal of Animal Breeding and Genetics</i> , <b>2013</b> , 130, 252-8	2.9	53
110	Accuracy of estimated breeding values with genomic information on males, females, or both: an example on broiler chicken. <i>Genetics Selection Evolution</i> , <b>2015</b> , 47, 56	4.9	52
109	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> , <b>2018</b> , 50, 53	4.9	52
108	Analysis of fertility and dystocia in Holsteins using recursive models to handle censored and categorical data. <i>Journal of Dairy Science</i> , <b>2007</b> , 90, 2012-24	4	51
107	Genomic analysis of dominance effects on milk production and conformation traits in Fleckvieh cattle. <i>Genetics Selection Evolution</i> , <b>2014</b> , 46, 40	4.9	48
106	A genome scan for QTL affecting resistance to <i>Haemonchus contortus</i> in sheep. <i>Journal of Animal Science</i> , <b>2012</b> , 90, 4690-705	0.7	48
105	Single-Step Genomic and Pedigree Genotype $\times$ Environment Interaction Models for Predicting Wheat Lines in International Environments. <i>Plant Genome</i> , <b>2017</b> , 10, plantgenome2016.09.0089	4.4	47
104	Methods to approximate reliabilities in single-step genomic evaluation. <i>Journal of Dairy Science</i> , <b>2013</b> , 96, 647-54	4	44

103	Assessment of accuracy of genomic prediction for French Lacaune dairy sheep. <i>Journal of Dairy Science</i> , <b>2014</b> , 97, 1107-16	4	44
102	A note on the rationale for estimating genealogical coancestry from molecular markers. <i>Genetics Selection Evolution</i> , <b>2011</b> , 43, 1-10	4.9	43
101	Genomic evaluation by including dominance effects and inbreeding depression for purebred and crossbred performance with an application in pigs. <i>Genetics Selection Evolution</i> , <b>2016</b> , 48, 92	4.9	42
100	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> , <b>2016</b> , 99, 1968-1974	4	42
99	The Dimensionality of Genomic Information and Its Effect on Genomic Prediction. <i>Genetics</i> , <b>2016</b> , 203, 573-81	4	42
98	Genetic parameters of udder traits, somatic cell score, and milk yield in Latxa sheep. <i>Journal of Dairy Science</i> , <b>2005</b> , 88, 2238-45	4	42
97	Comparing estimates of genetic variance across different relationship models. <i>Theoretical Population Biology</i> , <b>2016</b> , 107, 26-30	1.2	41
96	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> , <b>2013</b> , 96, 575-91	4	40
95	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> , <b>2015</b> , 98, 4090-4	4	39
94	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> , <b>2019</b> , 51, 28	4.9	39
93	Incorporation of causative quantitative trait nucleotides in single-step GBLUP. <i>Genetics Selection Evolution</i> , <b>2017</b> , 49, 59	4.9	38
92	Genomic BLUP including additive and dominant variation in purebreds and F1 crossbreds, with an application in pigs. <i>Genetics Selection Evolution</i> , <b>2016</b> , 48, 6	4.9	34
91	Metafounders are related to F fixation indices and reduce bias in single-step genomic evaluations. <i>Genetics Selection Evolution</i> , <b>2017</b> , 49, 34	4.9	34
90	Constructing covariance functions for random regression models for growth in Gelbvieh beef cattle. <i>Journal of Animal Science</i> , <b>2004</b> , 82, 1564-71	0.7	34
89	Current status of genomic evaluation. <i>Journal of Animal Science</i> , <b>2020</b> , 98,	0.7	33
88	Single-Step Genomic Evaluations from Theory to Practice: Using SNP Chips and Sequence Data in BLUPF90. <i>Genes</i> , <b>2020</b> , 11,	4.2	33
87	Application of single-step genomic evaluation for crossbred performance in pig. <i>Journal of Animal Science</i> , <b>2016</b> , 94, 936-48	0.7	33
86	Multi-breed genetic evaluation in a Gelbvieh population. <i>Journal of Animal Breeding and Genetics</i> , <b>2007</b> , 124, 286-95	2.9	32

85	Genomic selection models for directional dominance: an example for litter size in pigs. <i>Genetics Selection Evolution</i> , <b>2018</b> , 50, 1	4.9	28
84	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> , <b>2014</b> , 97, 3200-12	4	28
83	A comparison of partial least squares (PLS) and sparse PLS regressions in genomic selection in French dairy cattle. <i>Journal of Dairy Science</i> , <b>2012</b> , 95, 2120-31	4	28
82	A comparison of methods for whole-genome QTL mapping using dense markers in four livestock species. <i>Genetics Selection Evolution</i> , <b>2015</b> , 47, 6	4.9	26
81	Invited review: efficient computation strategies in genomic selection. <i>Animal</i> , <b>2017</b> , 11, 731-736	3.1	25
80	Linear models for joint association and linkage QTL mapping. <i>Genetics Selection Evolution</i> , <b>2009</b> , 41, 43	4.9	25
79	Economic weights of fertility, prolificacy, milk yield and longevity in dairy sheep. <i>Animal</i> , <b>2007</b> , 1, 193-203.	3.1	24
78	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> , <b>2015</b> , 16, 816	4.5	23
77	Technical note: Genomic evaluation for crossbred performance in a single-step approach with metafounders. <i>Journal of Animal Science</i> , <b>2017</b> , 95, 1472-1480	0.7	21
76	Pedigree and genomic evaluation of pigs using a terminal-cross model. <i>Genetics Selection Evolution</i> , <b>2016</b> , 48, 32	4.9	21
75	Evaluating Sequence-Based Genomic Prediction with an Efficient New Simulator. <i>Genetics</i> , <b>2017</b> , 205, 939-953	4	20
74	Genetic evaluation for three-way crossbreeding. <i>Genetics Selection Evolution</i> , <b>2015</b> , 47, 98	4.9	20
73	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> , <b>2015</b> , 47, 89	4.9	19
72	Quality control of genotypes using heritability estimates of gene content at the marker. <i>Genetics</i> , <b>2015</b> , 199, 675-81	4	19
71	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> , <b>2011</b> , 128, 386-93	2.9	19
70	Dominance and epistatic genetic variances for litter size in pigs using genomic models. <i>Genetics Selection Evolution</i> , <b>2018</b> , 50, 71	4.9	19
69	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> , <b>2014</b> , 46, 13	4.9	18
68	Genetic parameters of product quality and hepatic metabolism in fattened mule ducks. <i>Journal of Animal Science</i> , <b>2011</b> , 89, 669-79	0.7	18

67	Economic weights of somatic cell score in dairy sheep. <i>Animal</i> , <b>2007</b> , 1, 205-12	3.1	18
66	Genetic parameters of milk traits in Latxa dairy sheep. <i>Animal Science</i> , <b>2001</b> , 73, 407-412		18
65	Test day models and genetic parameters in Latxa and Manchega dairy ewes. <i>Livestock Science</i> , <b>2001</b> , 67, 253-264		18
64	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> , <b>2019</b> , 102, 10012-10019	4	18
63	Multivariate genomic model improves analysis of oil palm ( <i>Elaeis guineensis</i> Jacq.) progeny tests. <i>Molecular Breeding</i> , <b>2016</b> , 36, 1	3.4	17
62	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> , <b>2013</b> , 91, 1076-85	0.7	17
61	Fine tuning genomic evaluations in dairy cattle through SNP pre-selection with the Elastic-Net algorithm. <i>Genetical Research</i> , <b>2011</b> , 93, 409-17	1.1	17
60	Technical note: Genomic evaluation for crossbred performance in a single-step approach with metafounders. <i>Journal of Animal Science</i> , <b>2017</b> , 95, 1472	0.7	17
59	Modeling missing pedigree in single-step genomic BLUP. <i>Journal of Dairy Science</i> , <b>2019</b> , 102, 2336-2346	4	17
58	The effects of selective breeding against scrapie susceptibility on the genetic variability of the Latxa Black-Faced sheep breed. <i>Genetics Selection Evolution</i> , <b>2006</b> , 38, 495-511	4.9	16
57	Influence of epistasis on response to genomic selection using complete sequence data. <i>Genetics Selection Evolution</i> , <b>2017</b> , 49, 66	4.9	15
56	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> , <b>2011</b> , 90, 731-6	3.9	14
55	Using the product threshold model for estimating separately the effect of temperature on male and female fertility. <i>Journal of Animal Science</i> , <b>2011</b> , 89, 3983-95	0.7	14
54	Bias and accuracy of dairy sheep evaluations using BLUP and SSGBLUP with metafounders and unknown parent groups. <i>Genetics Selection Evolution</i> , <b>2020</b> , 52, 47	4.9	14
53	Inbreeding and effective population size in French dairy sheep: Comparison between genomic and pedigree estimates. <i>Journal of Dairy Science</i> , <b>2019</b> , 102, 4227-4237	4	13
52	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> , <b>2018</b> , 8, 2301-2308	3.2	13
51	Genomic Model with Correlation Between Additive and Dominance Effects. <i>Genetics</i> , <b>2018</b> , 209, 711-723	4	12
50	Bayesian model selection of contemporary groups for BLUP genetic evaluation in Latxa dairy sheep. <i>Livestock Science</i> , <b>2005</b> , 93, 205-212		12

49	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> , <b>2014</b> , 131, 445-51	2.9	11
48	Different ways to model biological relationships between fertility and pH of the semen in rabbits. <i>Journal of Animal Science</i> , <b>2011</b> , 89, 1294-303	0.7	11
47	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> , <b>2017</b> , 134, 184-195	2.9	10
46	Genetic basis of semen traits and their relationship with growth rate in rabbits. <i>Journal of Animal Science</i> , <b>2012</b> , 90, 1385-97	0.7	10
45	Validation of models for analysis of ranks in horse breeding evaluation. <i>Genetics Selection Evolution</i> , <b>2010</b> , 42, 3	4.9	10
44	Effects of ignoring inbreeding in model-based accuracy for BLUP and SGBLUP. <i>Journal of Animal Breeding and Genetics</i> , <b>2020</b> , 137, 356-364	2.9	9
43	A fast indirect method to compute functions of genomic relationships concerning genotyped and ungenotyped individuals, for diversity management. <i>Genetics Selection Evolution</i> , <b>2017</b> , 49, 87	4.9	9
42	Imputation of genotypes in Danish purebred and two-way crossbred pigs using low-density panels. <i>Genetics Selection Evolution</i> , <b>2015</b> , 47, 54	4.9	9
41	A comparison of methods to estimate genomic relationships using pedigree and markers in livestock populations. <i>Journal of Animal Breeding and Genetics</i> , <b>2016</b> , 133, 452-462	2.9	9
40	Purebred and Crossbred Genomic Evaluation and Mate Allocation Strategies To Exploit Dominance in Pig Crossbreeding Schemes. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 2829-2841	3.2	8
39	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> , <b>2017</b> , 134, 441-452	2.9	8
38	Variance and covariance of actual relationships between relatives at one locus. <i>PLoS ONE</i> , <b>2013</b> , 8, e57003	3.7	8
37	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> , <b>2017</b> , 95, 49	0.7	8
36	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> , <b>2021</b> , 138, 4-13	2.9	8
35	Economic weights for major milk constituents of Manchega dairy ewes. <i>Journal of Dairy Science</i> , <b>2010</b> , 93, 3303-9	4	7
34	Behavior of the Linear Regression method to estimate bias and accuracies with correct and incorrect genetic evaluation models. <i>Journal of Dairy Science</i> , <b>2020</b> , 103, 529-544	4	7
33	Genomic selection for carrier-state resistance in chicken commercial lines. <i>BMC Proceedings</i> , <b>2011</b> , 5 Suppl 4, S24	2.3	6
32	Short communication: Methods to compute genomic inbreeding for ungenotyped individuals. <i>Journal of Dairy Science</i> , <b>2020</b> , 103, 3363-3367	4	6

31	Genomic prediction of hybrid crops allows disentangling dominance and epistasis. <i>Genetics</i> , <b>2021</b> , 218,	4	6
30	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> , <b>2017</b> , 95, 49-52	0.7	5
29	Product versus additive threshold models for analysis of reproduction outcomes in animal genetics. <i>Journal of Animal Science</i> , <b>2009</b> , 87, 2510-8	0.7	5
28	Exploring the inclusion of genomic information and metafounders in Latxa dairy sheep genetic evaluations. <i>Journal of Dairy Science</i> , <b>2020</b> , 103, 6346-6353	4	5
27	Dissecting total genetic variance into additive and dominance components of purebred and crossbred pig traits. <i>Animal</i> , <b>2019</b> , 13, 2429-2439	3.1	4
26	LDSO: a program to simulate pedigrees and molecular information under various evolutionary forces. <i>Journal of Animal Breeding and Genetics</i> , <b>2012</b> , 129, 417-21	2.9	4
25	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> , <b>2012</b> , 94, 223-34	1.1	4
24	Genomic and pedigree estimation of inbreeding depression for semen traits in the Basco-Bàrnaise dairy sheep breed. <i>Journal of Dairy Science</i> , <b>2021</b> , 104, 3221-3230	4	4
23	Inbreeding, effective population size, and coancestry in the Latxa dairy sheep breed. <i>Journal of Dairy Science</i> , <b>2020</b> , 103, 5215-5226	4	3
22	A combined coalescence gene-dropping tool for evaluating genomic selection in complex scenarios (ms2gs). <i>Journal of Animal Breeding and Genetics</i> , <b>2016</b> , 133, 85-91	2.9	3
21	Short communication: Accounting for new mutations in genomic prediction models. <i>Journal of Dairy Science</i> , <b>2013</b> , 96, 5398-402	4	3
20	Estimates of the actual relationship between half-sibs in a pig population. <i>Journal of Animal Breeding and Genetics</i> , <b>2017</b> , 134, 109-118	2.9	3
19	The coefficient of dominance is not (always) estimable with biallelic markers. <i>Journal of Animal Breeding and Genetics</i> , <b>2014</b> , 131, 97-104	2.9	3
18	Theoretical and empirical comparisons of expected and realized relationships for the X-chromosome. <i>Genetics Selection Evolution</i> , <b>2020</b> , 52, 50	4.9	3
17	GIBBSTHUR: Software for Estimating Variance Components and Predicting Breeding Values for Ranking Traits Based on a Thurstonian Model. <i>Animals</i> , <b>2020</b> , 10,	3.1	2
16	Does probabilistic modelling of linkage disequilibrium evolution improve the accuracy of QTL location in animal pedigree?. <i>Genetics Selection Evolution</i> , <b>2010</b> , 42, 38	4.9	2
15	The Correlation of Substitution Effects Across Populations and Generations in the Presence of Non-Additive Functional Gene Action		2
14	Exact p-values for large-scale single step genome-wide association, with an application for birth weight in American Angus		2



13	Genome-wide association study for feed efficiency in collective cage-raised rabbits under full and restricted feeding. <i>Animal Genetics</i> , <b>2020</b> , 51, 799-810	2.5	2
12	Selection and drift reduce genetic variation for milk yield in Manech Tête Rousse dairy sheep. <i>JDS Communications</i> , <b>2021</b> , 2, 31-34	1.4	2
11	Genetic evaluation including intermediate omics features. <i>Genetics</i> , <b>2021</b> , 219,	4	2
10	Single-marker and multi-marker mixed models for polygenic score analysis in family-based data. <i>BMC Proceedings</i> , <b>2014</b> , 8, S63	2.3	1
9	Association analysis of loci implied in BufferingEpistasis		1
8	The correlation of substitution effects across populations and generations in the presence of nonadditive functional gene action. <i>Genetics</i> , <b>2021</b> , 219,	4	1
7	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> , <b>2022</b> ,	4	1
6	Dissecting genetic trends to understand breeding practices in livestock: a maternal pig line example. <i>Genetics Selection Evolution</i> , <b>2021</b> , 53, 89	4.9	0
5	Islands of runs of homozygosity indicate selection signatures in Ovis aries 6 (OAR6) of French dairy sheep. <i>JDS Communications</i> , <b>2021</b> , 2, 132-136	1.4	0
4	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> , <b>2021</b> , 53, 4	4.9	0
3	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> , <b>2022</b> , 54, 14	4.9	0
2	Computing strategies for multi-population genomic evaluation.. <i>Genetics Selection Evolution</i> , <b>2022</b> , 54, 10	4.9	
1	0292 Dimensionality of genomic information and APY inverse of genomic relationship matrix. <i>Journal of Animal Science</i> , <b>2016</b> , 94, 138-139	0.7	