

# Andres Legarra

## List of Publications by Year in descending order

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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	Removing data and using metafounders alleviates biases for all traits in Lacaune dairy sheep predictions. <i>Journal of Dairy Science</i> , 2022, 105, 2439-2452.	1.4	10
2	Computing strategies for multi-population genomic evaluation. <i>Genetics Selection Evolution</i> , 2022, 54, 10.	1.2	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> , 2022, 54, 14.	1.2	3
4	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, 105, 5141-5152.	1.4	14
5	Genomic evaluation and genome-wide association studies for total number of teats in a combined American and Danish Yorkshire pig populations selected in China. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	5
6	High genetic correlation for milk yield across Manech and Latxa dairy sheep from France and Spain. <i>JDS Communications</i> , 2022, 3, 260-264.	0.5	2
7	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
8	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
9	Selection and drift reduce genetic variation for milk yield in Manech Tête Rouse dairy sheep. <i>JDS Communications</i> , 2021, 2, 31-34.	0.5	9
10	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.	1.2	12
11	Genomic and pedigree estimation of inbreeding depression for semen traits in the Basco-Béarnaise dairy sheep breed. <i>Journal of Dairy Science</i> , 2021, 104, 3221-3230.	1.4	16
12	Genomic prediction of hybrid crops allows disentangling dominance and epistasis. <i>Genetics</i> , 2021, 218, .	1.2	20
13	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.	0.5	3
14	The correlation of substitution effects across populations and generations in the presence of nonadditive functional gene action. <i>Genetics</i> , 2021, 219, .	1.2	12
15	Genetic evaluation including intermediate omics features. <i>Genetics</i> , 2021, 219, .	1.2	32
16	Dissecting genetic trends to understand breeding practices in livestock: a maternal pig line example. <i>Genetics Selection Evolution</i> , 2021, 53, 89.	1.2	7
17	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.	1.4	33
18	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.	0.6	9

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19	Single-Step Genomic Evaluations from Theory to Practice: Using SNP Chips and Sequence Data in BLUPF90. <i>Genes</i> , 2020, 11, 790.	1.0	77
20	Theoretical and empirical comparisons of expected and realized relationships for the X-chromosome. <i>Genetics Selection Evolution</i> , 2020, 52, 50.	1.2	9
21	Bias and accuracy of dairy sheep evaluations using BLUP and SSGBLUP with metafounders and unknown parent groups. <i>Genetics Selection Evolution</i> , 2020, 52, 47.	1.2	43
22	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
23	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
24	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.	0.8	15
25	Inbreeding, effective population size, and coancestry in the Latxa dairy sheep breed. <i>Journal of Dairy Science</i> , 2020, 103, 5215-5226.	1.4	13
26	GIBBSTHUR: Software for Estimating Variance Components and Predicting Breeding Values for Ranking Traits Based on a Thurstonian Model. <i>Animals</i> , 2020, 10, 1001.	1.0	2
27	Association analysis of loci implied in buffering epistasis. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	2
28	Effects of ignoring inbreeding in model-based accuracy for BLUP and SSGBLUP. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 356-364.	0.8	26
29	Current status of genomic evaluation. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	90
30	Short communication: Methods to compute genomic inbreeding for ungenotyped individuals. <i>Journal of Dairy Science</i> , 2020, 103, 3363-3367.	1.4	12
31	Exploring the inclusion of genomic information and metafounders in Latxa dairy sheep genetic evaluations. <i>Journal of Dairy Science</i> , 2020, 103, 6346-6353.	1.4	9
32	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.	1.2	97
33	Dissecting total genetic variance into additive and dominance components of purebred and crossbred pig traits. <i>Animal</i> , 2019, 13, 2429-2439.	1.3	9
34	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.	1.4	35
35	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
36	Modeling missing pedigree in single-step genomic BLUP. <i>Journal of Dairy Science</i> , 2019, 102, 2336-2346.	1.4	32

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37	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.	1.2	146
38	Dominance and epistatic genetic variances for litter size in pigs using genomic models. <i>Genetics Selection Evolution</i> , 2018, 50, 71.	1.2	45
39	CWAS 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.	0.8	35
40	Non-additive Effects in Genomic Selection. <i>Frontiers in Genetics</i> , 2018, 9, 78.	1.1	157
41	Genomic selection models for directional dominance: an example for litter size in pigs. <i>Genetics Selection Evolution</i> , 2018, 50, 1.	1.2	56
42	Genomic Model with Correlation Between Additive and Dominance Effects. <i>Genetics</i> , 2018, 209, 711-723.	1.2	29
43	Invited review: efficient computation strategies in genomic selection. <i>Animal</i> , 2017, 11, 731-736.	1.3	37
44	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
45	Orthogonal Estimates of Variances for Additive, Dominance, and Epistatic Effects in Populations. <i>Genetics</i> , 2017, 206, 1297-1307.	1.2	125
46	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.	0.8	13
47	Evaluating Sequence-Based Genomic Prediction with an Efficient New Simulator. <i>Genetics</i> , 2017, 205, 939-953.	1.2	39
48	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.	0.8	10
49	Single-Step Genomic and Pedigree Genotype × Environment Interaction Models for Predicting Wheat Lines in International Environments. <i>Plant Genome</i> , 2017, 10, plantgenome2016.09.0089.	1.6	66
50	Metafounders are related to F <sub>st</sub> fixation indices and reduce bias in single-step genomic evaluations. <i>Genetics Selection Evolution</i> , 2017, 49, 34.	1.2	55
51	Estimates of the actual relationship between half-sibs in a pig population. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 109-118.	0.8	7
52	Incorporation of causative quantitative trait nucleotides in single-step GBLUP. <i>Genetics Selection Evolution</i> , 2017, 49, 59.	1.2	73
53	Influence of epistasis on response to genomic selection using complete sequence data. <i>Genetics Selection Evolution</i> , 2017, 49, 66.	1.2	23
54	193 Including causative variants into single step genomic BLUP. <i>Journal of Animal Science</i> , 2017, 95, 95-96.	0.2	1

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55	Genetic Variation in the Social Environment Contributes to Health and Disease. <i>PLoS Genetics</i> , 2017, 13, e1006498.	1.5	110
56	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.	1.2	12
57	Technical note: Genomic evaluation for crossbred performance in a single-step approach with metafounders1. <i>Journal of Animal Science</i> , 2017, 95, 1472-1480.	0.2	30
58	Technical note: Genomic evaluation for crossbred performance in a single-step approach with metafounders. <i>Journal of Animal Science</i> , 2017, 95, 1472.	0.2	26
59	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.	0.2	11
60	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.	1.1	131
61	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.	0.8	15
62	Application of single-step genomic evaluation for crossbred performance in pig1. <i>Journal of Animal Science</i> , 2016, 94, 936-948.	0.2	48
63	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.	1.2	72
64	Pedigree and genomic evaluation of pigs using a terminal-cross model. <i>Genetics Selection Evolution</i> , 2016, 48, 32.	1.2	32
65	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.	1.2	39
66	A combined coalescence geneâ€dropping tool for evaluating genomic selection in complex scenarios (ms2gs). <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 85-91.	0.8	3
67	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.	1.4	66
68	Multivariate genomic model improves analysis of oil palm ( <i>Elaeis guineensis</i> Jacq.) progeny tests. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	27
69	The Dimensionality of Genomic Information and Its Effect on Genomic Prediction. <i>Genetics</i> , 2016, 203, 573-581.	1.2	81
70	Comparing estimates of genetic variance across different relationship models. <i>Theoretical Population Biology</i> , 2016, 107, 26-30.	0.5	81
71	0292 Dimensionality of genomic information and APY inverse of genomic relationship matrix. <i>Journal of Animal Science</i> , 2016, 94, 138-139.	0.2	0
72	Genetic evaluation for three-way crossbreeding. <i>Genetics Selection Evolution</i> , 2015, 47, 98.	1.2	32

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73	Sequence- vs. chip-assisted genomic selection: accurate biological information is advised. <i>Genetics Selection Evolution</i> , 2015, 47, 43.	1.2	130
74	Imputation of genotypes in Danish purebred and two-way crossbred pigs using low-density panels. <i>Genetics Selection Evolution</i> , 2015, 47, 54.	1.2	13
75	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.	1.2	24
76	Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus1. <i>Journal of Animal Science</i> , 2015, 93, 2653-2662.	0.2	139
77	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.	1.2	33
78	Quality Control of Genotypes Using Heritability Estimates of Gene Content at the Marker. <i>Genetics</i> , 2015, 199, 675-681.	1.2	26
79	Ancestral Relationships Using Metafounders: Finite Ancestral Populations and Across Population Relationships. <i>Genetics</i> , 2015, 200, 455-468.	1.2	119
80	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.	1.2	69
81	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.	1.4	60
82	A comparison of methods for whole-genome QTL mapping using dense markers in four livestock species. <i>Genetics Selection Evolution</i> , 2015, 47, 6.	1.2	28
83	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.	1.1	173
84	The coefficient of dominance is not (always) estimable with biallelic markers. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 97-104.	0.8	3
85	Genomic analysis of dominance effects on milk production and conformation traits in Fleckvieh cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 40.	1.2	59
86	Within- and across-breed genomic predictions and genomic relationships for Western Pyrenees dairy sheep breeds Latxa, Manech, and Basco-Barnaise. <i>Journal of Dairy Science</i> , 2014, 97, 3200-3212.	1.4	47
87	Single Step, a general approach for genomic selection. <i>Livestock Science</i> , 2014, 166, 54-65.	0.6	260
88	Assessment of accuracy of genomic prediction for French Lacaune dairy sheep. <i>Journal of Dairy Science</i> , 2014, 97, 1107-1116.	1.4	58
89	Single-marker and multi-marker mixed models for polygenic score analysis in family-based data. <i>BMC Proceedings</i> , 2014, 8, S63.	1.8	1
90	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.	1.2	28

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91	Differences between genomicâ€based and pedigreeâ€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
92	Using recursion to compute the inverse of the genomic relationship matrix. Journal of Dairy Science, 2014, 97, 3943-3952.	1.4	168
93	Unknownâ€parent groups in singleâ€step genomic evaluation. Journal of Animal Breeding and Genetics, 2013, 130, 252-258.	0.8	80
94	On the Additive and Dominant Variance and Covariance of Individuals Within the Genomic Selection Scope. Genetics, 2013, 195, 1223-1230.	1.2	253
95	Short communication: Accounting for new mutations in genomic prediction models. Journal of Dairy Science, 2013, 96, 5398-5402.	1.4	3
96	Application of Bayesian least absolute shrinkage and selection operator (LASSO) and BayesCâ€ methods for genomic selection in French Holstein and MontbÃ©liarde breeds. Journal of Dairy Science, 2013, 96, 575-591.	1.4	49
97	Methods to approximate reliabilities in single-step genomic evaluation. Journal of Dairy Science, 2013, 96, 647-654.	1.4	72
98	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
99	Variance and Covariance of Actual Relationships between Relatives at One Locus. PLoS ONE, 2013, 8, e57003.	1.1	10
100	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
101	Genome-wide association mapping including phenotypes from relatives without genotypes. Genetical Research, 2012, 94, 73-83.	0.3	453
102	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
103	Genomic selection in the French Lacaune dairy sheep breed. Journal of Dairy Science, 2012, 95, 2723-2733.	1.4	70
104	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
105	Joint genomic evaluation of French dairy cattle breeds using multiple-trait models. Genetics Selection Evolution, 2012, 44, 39.	1.2	93
106	A genome scan for QTL affecting resistance to Haemonchus contortus in sheep1. Journal of Animal Science, 2012, 90, 4690-4705.	0.2	57
107	Genetic basis of semen traits and their relationship with growth rate in rabbits1. Journal of Animal Science, 2012, 90, 1385-1397.	0.2	12
108	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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109	Improved Lasso for genomic selection. <i>Genetical Research</i> , 2011, 93, 77-87.	0.3	110
110	Genomic selection for carrier-state resistance in chicken commercial lines. <i>BMC Proceedings</i> , 2011, 5, S24.	1.8	10
111	Genetic parameters of product quality and hepatic metabolism in fattened mule ducks <sup>1</sup> . <i>Journal of Animal Science</i> , 2011, 89, 669-679.	0.2	25
112	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, 386-393.	0.8	28
113	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, 422-428.	0.8	132
114	A note on the rationale for estimating genealogical coancestry from molecular markers. <i>Genetics Selection Evolution</i> , 2011, 43, 1-10.	1.2	57
115	Use of a reduced set of single nucleotide polymorphisms for genetic evaluation of resistance to <i>Salmonella</i> carrier state in laying hens. <i>Poultry Science</i> , 2011, 90, 731-736.	1.5	26
116	Bias in genomic predictions for populations under selection. <i>Genetical Research</i> , 2011, 93, 357-366.	0.3	285
117	Fine tuning genomic evaluations in dairy cattle through SNP pre-selection with the Elastic-Net algorithm. <i>Genetical Research</i> , 2011, 93, 409-417.	0.3	23
118	Different ways to model biological relationships between fertility and pH of the semen in rabbits <sup>1</sup> . <i>Journal of Animal Science</i> , 2011, 89, 1294-1303.	0.2	12
119	Effect of different genomic relationship matrices on accuracy and scale <sup>1</sup> . <i>Journal of Animal Science</i> , 2011, 89, 2673-2679.	0.2	100
120	Using the product threshold model for estimating separately the effect of temperature on male and female fertility <sup>1</sup> . <i>Journal of Animal Science</i> , 2011, 89, 3983-3995.	0.2	19
121	Does probabilistic modelling of linkage disequilibrium evolution improve the accuracy of QTL location in animal pedigree?. <i>Genetics Selection Evolution</i> , 2010, 42, 38.	1.2	2
122	Validation of models for analysis of ranks in horse breeding evaluation. <i>Genetics Selection Evolution</i> , 2010, 42, 3.	1.2	15
123	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, 743-752.	1.4	1,058
124	Economic weights for major milk constituents of Manchega dairy ewes. <i>Journal of Dairy Science</i> , 2010, 93, 3303-3309.	1.4	7
125	Product versus additive threshold models for analysis of reproduction outcomes in animal genetics <sup>1</sup> . <i>Journal of Animal Science</i> , 2009, 87, 2510-2518.	0.2	8
126	Linear models for joint association and linkage QTL mapping. <i>Genetics Selection Evolution</i> , 2009, 41, 43.	1.2	28



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127	Predicting Quantitative Traits With Regression Models for Dense Molecular Markers and Pedigree. <i>Genetics</i> , 2009, 182, 375-385.	1.2	514
128	A relationship matrix including full pedigree and genomic information. <i>Journal of Dairy Science</i> , 2009, 92, 4656-4663.	1.4	723
129	Computing procedures for genetic evaluation including phenotypic, full pedigree, and genomic information. <i>Journal of Dairy Science</i> , 2009, 92, 4648-4655.	1.4	444
130	Technical Note: Computing Strategies in Genome-Wide Selection. <i>Journal of Dairy Science</i> , 2008, 91, 360-366.	1.4	93
131	Performance of Genomic Selection in Mice. <i>Genetics</i> , 2008, 180, 611-618.	1.2	332
132	Economic weights of fertility, prolificacy, milk yield and longevity in dairy sheep. <i>Animal</i> , 2007, 1, 193-203.	1.3	35
133	Economic weights of somatic cell score in dairy sheep. <i>Animal</i> , 2007, 1, 205-212.	1.3	19
134	Analysis of Fertility and Dystocia in Holsteins Using Recursive Models to Handle Censored and Categorical Data. <i>Journal of Dairy Science</i> , 2007, 90, 2012-2024.	1.4	64
135	Multi-breed genetic evaluation in a Gelbvieh population. <i>Journal of Animal Breeding and Genetics</i> , 2007, 124, 286-295.	0.8	40
136	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.	1.2	19
137	Bayesian model selection of contemporary groups for BLUP genetic evaluation in Latxa dairy sheep. <i>Livestock Science</i> , 2005, 93, 205-212.	1.2	15
138	Genetic Parameters of Udder Traits, Somatic Cell Score, and Milk Yield in Latxa Sheep. <i>Journal of Dairy Science</i> , 2005, 88, 2238-2245.	1.4	63
139	Constructing covariance functions for random regression models for growth in Gelbvieh beef cattle. <i>Journal of Animal Science</i> , 2004, 82, 1564-1571.	0.2	38
140	Genetic parameters of milk traits in Latxa dairy sheep. <i>Animal Science</i> , 2001, 73, 407-412.	1.3	20
141	Test day models and genetic parameters in Latxa and Manchega dairy ewes. <i>Livestock Science</i> , 2001, 67, 253-264.	1.2	21