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**Deregressing estimated breeding values and weighting information for genomic regression analyses**

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#	Paper	IF	Citations
463	Genomic Selection in Aquaculture: Methods and Practical Considerations. <b>2010</b> , 165-183		1
462	International genomic evaluation methods for dairy cattle. <i>Genetics Selection Evolution</i> , <b>2010</b> , 42, 7	4.9	50
461	Comparison between genomic predictions using daughter yield deviation and conventional estimated breeding value as response variables. <b>2010</b> , 127, 423-32		52
460	A whole-genome association analysis of noncompensatory fertility in Holstein bulls. <i>Journal of Dairy Science</i> , <b>2011</b> , 94, 4695-9	4	36
459	Reliabilities of genomic prediction using combined reference data of the Nordic Red dairy cattle populations. <i>Journal of Dairy Science</i> , <b>2011</b> , 94, 4700-7	4	72
458	Short Communication: Associations of BoLA alleles DRB3.2*16 and DRB3.2*23 with health-related traits in Holstein bulls. <b>2011</b> , 91, 597-600		1
457	Accuracy and Training Population Design for Genomic Selection on Quantitative Traits in Elite North American Oats. <b>2011</b> , 4,		171
456	Dimension reduction and variable selection for genomic selection: application to predicting milk yield in Holsteins. <b>2011</b> , 128, 247-57		32
455	A genome-wide association study of direct gestation length in US Holstein and Italian Brown populations. <i>Animal Genetics</i> , <b>2011</b> , 42, 585-91	2.5	18
454	Developing marker-assisted models for evaluating growth traits in Canadian beef cattle genetic improvement. <i>Livestock Science</i> , <b>2011</b> , 138, 62-68	1.7	10
453	Whole-genome SNP association analysis of reproduction traits in the Finnish Landrace pig breed. <i>Genetics Selection Evolution</i> , <b>2011</b> , 43, 42	4.9	26
452	The nature, scope and impact of genomic prediction in beef cattle in the United States. <i>Genetics Selection Evolution</i> , <b>2011</b> , 43, 17	4.9	66
451	Deregressed EBV as the response variable yield more reliable genomic predictions than traditional EBV in pure-bred pigs. <i>Genetics Selection Evolution</i> , <b>2011</b> , 43, 38	4.9	82
450	Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. <i>Genetics Selection Evolution</i> , <b>2011</b> , 43, 40	4.9	153
449	Breeding value prediction for production traits in layer chickens using pedigree or genomic relationships in a reduced animal model. <i>Genetics Selection Evolution</i> , <b>2011</b> , 43, 5	4.9	104
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447	Bias in genomic predictions for populations under selection. <b>2011</b> , 93, 357-66		205

446	Physiology and Endocrinology Symposium: How single nucleotide polymorphism chips will advance our knowledge of factors controlling puberty and aid in selecting replacement beef females. <b>2012</b> , 90, 1152-65		36
445	A common dataset for genomic analysis of livestock populations. <i>G3: Genes, Genomes, Genetics</i> , <b>2012</b> , 2, 429-35	3.2	59
444	Accuracy of genomic breeding values in multibreed beef cattle populations derived from deregressed breeding values and phenotypes. <b>2012</b> , 90, 4177-90		47
443	Evaluation of Genomic Prediction Methods for Fusarium Head Blight Resistance in Wheat. <b>2012</b> , 5, 51-61		166
442	Genome-wide association mapping including phenotypes from relatives without genotypes. <b>2012</b> , 94, 73-83		278
441	Bayesian models with dominance effects for genomic evaluation of quantitative traits. <b>2012</b> , 94, 21-37		60
440	Single-step methods for genomic evaluation in pigs. <i>Animal</i> , <b>2012</b> , 6, 1565-71	3.1	184
439	Genome-wide association mapping of milk production traits in Braunvieh cattle. <i>Journal of Dairy Science</i> , <b>2012</b> , 95, 5357-5364	4	21
438	Genomic prediction for Nordic Red Cattle using one-step and selection index blending. <i>Journal of Dairy Science</i> , <b>2012</b> , 95, 909-17	4	87
437	Different methods to calculate genomic predictions--comparisons of BLUP at the single nucleotide polymorphism level (SNP-BLUP), BLUP at the individual level (G-BLUP), and the one-step approach (H-BLUP). <i>Journal of Dairy Science</i> , <b>2012</b> , 95, 4065-73	4	34
436	Invited review: Genomic analysis of data from physiological studies. <i>Journal of Dairy Science</i> , <b>2012</b> , 95, 499-507	4	2
435	Genome-wide association study to identify chromosomal regions associated with antibody response to <i>Mycobacterium avium</i> subspecies paratuberculosis in milk of Dutch Holstein-Friesians. <i>Journal of Dairy Science</i> , <b>2012</b> , 95, 2740-8	4	27
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432	A stage-wise approach for the analysis of multi-environment trials. <b>2012</b> , 54, 844-60		98
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428	Estimates of marker effects for measures of milk flow in the Italian brown Swiss dairy cattle population. <b>2012</b> , 8, 199		3
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426	A novel analytical method, Birth Date Selection Mapping, detects response of the Angus ( <i>Bos taurus</i> ) genome to selection on complex traits. <b>2012</b> , 13, 606		29
425	Genomic selection for fruit quality traits in apple ( <i>Malus domestica</i> Borkh.). <b>2012</b> , 7, e36674		154
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421	Genomic selection for growth and wood quality in Eucalyptus: capturing the missing heritability and accelerating breeding for complex traits in forest trees. <b>2012</b> , 194, 116-128		228
420	Genome-wide association analysis and genetic architecture of egg weight and egg uniformity in layer chickens. <i>Animal Genetics</i> , <b>2012</b> , 43 Suppl 1, 87-96	2.5	76
419	L1 insertion within SPEF2 gene is associated with increased litter size in the Finnish Yorkshire population. <b>2012</b> , 129, 92-7		18
418	Whole-genome regression and prediction methods applied to plant and animal breeding. <b>2013</b> , 193, 327-45		544
417	Genome-wide association study for birth weight in Nellore cattle points to previously described orthologous genes affecting human and bovine height. <b>2013</b> , 14, 52		83
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415	Predicting expected progeny difference for marbling score in Angus cattle using artificial neural networks and Bayesian regression models. <i>Genetics Selection Evolution</i> , <b>2013</b> , 45, 34	4.9	35
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413	Genomic selection using low density marker panels with application to a sire line in pigs. <i>Genetics Selection Evolution</i> , <b>2013</b> , 45, 28	4.9	42
412	Accuracy of genomic prediction for milk production traits in the Chinese Holstein population using a reference population consisting of cows. <i>Journal of Dairy Science</i> , <b>2013</b> , 96, 5315-23	4	38
411	Accuracy of genomic prediction using different models and response variables in the Nordic Red cattle population. <b>2013</b> , 130, 333-40		21

410	Accuracy of genomic prediction using an evenly spaced, low-density single nucleotide polymorphism panel in broiler chickens. <b>2013</b> , 92, 1712-23		21
409	Association genetics of oleoresin flow in loblolly pine: discovering genes and predicting phenotype for improved resistance to bark beetles and bioenergy potential. <b>2013</b> , 199, 89-100		45
408	Implementing a QTL detection study (GWAS) using genomic prediction methodology. <b>2013</b> , 1019, 275-98		72
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406	Accuracy of prediction of genomic breeding values for residual feed intake and carcass and meat quality traits in <i>Bos taurus</i> , <i>Bos indicus</i> , and composite beef cattle. <b>2013</b> , 91, 3088-104		111
405	Genomic estimated breeding values using genomic relationship matrices in a cloned population of loblolly pine. <i>G3: Genes, Genomes, Genetics</i> , <b>2013</b> , 3, 909-16	3.2	58
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384	Reliability of molecular breeding values for Warner-Bratzler shear force and carcass traits of beef cattle - an independent validation study. <b>2014</b> , 92, 2896-904		17
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381	Kernel-based variance component estimation and whole-genome prediction of pre-corrected phenotypes and progeny tests for dairy cow health traits. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 56	4.5	21
380	A genome-wide association study reveals a novel candidate gene for sperm motility in pigs. <b>2014</b> , 151, 201-7		22
379	Accuracy of genomic predictions in <i>Bos indicus</i> (Nellore) cattle. <i>Genetics Selection Evolution</i> , <b>2014</b> , 46, 17	4.9	60
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341	Genome-wide association study reveals novel loci for litter size and its variability in a Large White pig population. <b>2015</b> , 16, 1049		48
340	Including different groups of genotyped females for genomic prediction in a Nordic Jersey population. <i>Journal of Dairy Science</i> , <b>2015</b> , 98, 9051-9	4	14
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337	Comparison of iterated single-step and Bayesian regressions on genomic evaluations for age at 100 kg in swine. <b>2015</b> , 93, 4675-83		
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335	Can multi-subpopulation reference sets improve the genomic predictive ability for pigs?. <b>2015</b> , 93, 5618-30		3
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333	Genetic analysis and genomic selection of stayability and productive life in New Zealand ewes. <b>2015</b> , 93, 3268-77		6
332	Accuracy of genomic prediction using deregressed breeding values estimated from purebred and crossbred offspring phenotypes in pigs. <b>2015</b> , 93, 3313-21		9
331	Genomic prediction of disease occurrence using producer-recorded health data: a comparison of methods. <i>Genetics Selection Evolution</i> , <b>2015</b> , 47, 41	4.9	3
330	Artificial selection on introduced Asian haplotypes shaped the genetic architecture in European commercial pigs. <b>2015</b> , 282, 20152019		18
329	Discovering candidate genes that regulate resin canal number in <i>Pinus taeda</i> stems by integrating genetic analysis across environments, ages, and populations. <b>2015</b> , 205, 627-41		35
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318	Genomic selection prediction accuracy in a perennial crop: case study of oil palm ( <i>Elaeis guineensis</i> Jacq.). <b>2015</b> , 128, 397-410		57
317	Development and implementation of genomic predictions in beef cattle. <b>2016</b> , 6, 32-38		32
316	Marker-Based Estimates Reveal Significant Nonadditive Effects in Clonally Propagated Cassava (): Implications for the Prediction of Total Genetic Value and the Selection of Varieties. <i>G3: Genes, Genomes, Genetics</i> , <b>2016</b> , 6, 3497-3506	3.2	21
315	Genomic selection in commercial pig breeding. <b>2016</b> , 6, 15-22		56
314	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
313	Quantitative analysis of short- and long-distance racing performance in young and adult horses and association analysis with functional candidate genes in Spanish Trotter horses. <b>2016</b> , 133, 347-56		7
312	Accuracy of genomic prediction of purebreds for cross bred performance in pigs. <b>2016</b> , 133, 443-451		13
311	Performance of genomic prediction within and across generations in maritime pine. <b>2016</b> , 17, 604		58
310	Genomic selection in the German Landrace population of the Bavarian herdbook. <b>2016</b> , 94, 4549-4557		
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306	Genomic heritabilities and genomic estimated breeding values for methane traits in Angus cattle. <b>2016</b> , 94, 902-8		27
305	Genomic selection for tolerance to heat stress in Australian dairy cattle. <i>Journal of Dairy Science</i> , <b>2016</b> , 99, 2849-2862	4	85
304	Validation of simultaneous deregression of cow and bull breeding values and derivation of appropriate weights. <i>Journal of Dairy Science</i> , <b>2016</b> , 99, 6403-6419	4	17
303	Lessons for livestock genomics from genome and transcriptome sequencing in cattle and other mammals. <i>Genetics Selection Evolution</i> , <b>2016</b> , 48, 59	4.9	18

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300	Advantages of continuous genotype values over genotype classes for GWAS in higher polyploids: a comparative study in hexaploid chrysanthemum. <b>2016</b> , 17, 672		15
299	Detection of quantitative trait loci for maternal traits using high-density genotypes of Blonde d'Aquitaine beef cattle. <b>2016</b> , 17, 88		23
298	Maximum difference analysis: a new empirical method for genome-wide association studies. <b>2016</b> , 15, 396-406		1
297	A 0.5-Mbp deletion on bovine chromosome 23 is a strong candidate for stillbirth in Nordic Red cattle. <i>Genetics Selection Evolution</i> , <b>2016</b> , 48, 35	4.9	13
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295	Genomic prediction of breeding values for carcass traits in Nellore cattle. <i>Genetics Selection Evolution</i> , <b>2016</b> , 48, 7	4.9	40
294	A genome-wide association study for genetic susceptibility to Mycobacterium bovis infection in dairy cattle identifies a susceptibility QTL on chromosome 23. <i>Genetics Selection Evolution</i> , <b>2016</b> , 48, 19	4.9	37
293	Exploiting biological priors and sequence variants enhances QTL discovery and genomic prediction of complex traits. <b>2016</b> , 17, 144		158
292	Genomic Prediction Accounting for Residual Heteroskedasticity. <i>G3: Genes, Genomes, Genetics</i> , <b>2015</b> , 6, 1-13	3.2	5
291	Differentially Expressed Genes in Endometrium and Corpus Luteum of Holstein Cows Selected for High and Low Fertility Are Enriched for Sequence Variants Associated with Fertility. <b>2016</b> , 94, 19		35
290	Accuracy of Genomic Prediction in Switchgrass ( <i>Panicum virgatum</i> L.) Improved by Accounting for Linkage Disequilibrium. <i>G3: Genes, Genomes, Genetics</i> , <b>2016</b> , 6, 1049-62	3.2	24
289	Genome-wide association study of growth and body composition traits in Brangus beef cattle. <i>Livestock Science</i> , <b>2016</b> , 183, 4-11	1.7	18
288	Genomic selection in a commercial winter wheat population. <b>2016</b> , 129, 641-51		99
287	An Equation to Predict the Accuracy of Genomic Values by Combining Data from Multiple Traits, Populations, or Environments. <b>2016</b> , 202, 799-823		45
286	Targeted imputation of sequence variants and gene expression profiling identifies twelve candidate genes associated with lactation volume, composition and calving interval in dairy cattle. <b>2016</b> , 27, 81-97		39
285	Genomic selection in maritime pine. <b>2016</b> , 242, 108-119		65

284	Genome-wide association analysis and pathways enrichment for lactation persistency in Canadian Holstein cattle. <i>Journal of Dairy Science</i> , <b>2017</b> , 100, 1955-1970	4	43
283	Case-control association mapping by proxy using family history of disease. <b>2017</b> , 49, 325-331		121
282	Genomic prediction of reproduction traits for Merino sheep. <i>Animal Genetics</i> , <b>2017</b> , 48, 338-348	2.5	4
281	Whole-genome association analysis of pork meat pH revealed three significant regions and several potential genes in Finnish Yorkshire pigs. <b>2017</b> , 18, 13		11
280	Application of Whole-Genome Prediction Methods for Genome-Wide Association Studies: A Bayesian Approach. <b>2017</b> , 22, 172-193		36
279	Accuracy of genomic predictions in Gyr ( <i>Bos indicus</i> ) dairy cattle. <i>Journal of Dairy Science</i> , <b>2017</b> , 100, 5472-5490	19	
278	Interleukin 8 haplotypes drive divergent responses in uterine endometrial cells and are associated with somatic cell score in Holstein-Friesian cattle. <b>2017</b> , 184, 18-28		5
277	Incorporating the single-step strategy into a random regression model to enhance genomic prediction of longitudinal traits. <b>2017</b> , 119, 459-467		15
276	Detecting Familial Aggregation. <b>2017</b> , 1666, 133-169		1
275	Genomic Relationships and GBLUP. <b>2017</b> , 311-354		2
274	Genomic Selection. <b>2017</b> , 355-384		
273	Functional validation of GPIHBP1 and identification of a functional mutation in GPIHBP1 for milk fat traits in dairy cattle. <i>Scientific Reports</i> , <b>2017</b> , 7, 8546	4.9	13
272	Association of candidate gene polymorphisms with milk technological traits, yield, composition, and somatic cell score in Italian Holstein-Friesian sires. <i>Journal of Dairy Science</i> , <b>2017</b> , 100, 7271-7281	4	21
271	Performance Gains in Genome-Wide Association Studies for Longitudinal Traits via Modeling Time-varied effects. <i>Scientific Reports</i> , <b>2017</b> , 7, 590	4.9	21
270	Genomic Prediction in a Large African Maize Population. <b>2017</b> , 57, 2361-2371		17
269	A PLAG1 mutation contributed to stature recovery in modern cattle. <i>Scientific Reports</i> , <b>2017</b> , 7, 17140	4.9	32
268	Whole-genome sequence-based genomic prediction in laying chickens with different genomic relationship matrices to account for genetic architecture. <i>Genetics Selection Evolution</i> , <b>2017</b> , 49, 8	4.9	33
267	Tag SNP selection for prediction of tick resistance in Brazilian Braford and Hereford cattle breeds using Bayesian methods. <i>Genetics Selection Evolution</i> , <b>2017</b> , 49, 49	4.9	21

266	Genomic regions underlying susceptibility to bovine tuberculosis in Holstein-Friesian cattle. <b>2017</b> , 18, 27		14
265	Cow genotyping strategies for genomic selection in a small dairy cattle population. <i>Journal of Dairy Science</i> , <b>2017</b> , 100, 439-452	4	27
264	Genetic and genomic analysis of hyperthelia in Brown Swiss cattle. <i>Journal of Dairy Science</i> , <b>2017</b> , 100, 402-411	4	6
263	Genome-wide association study for semen traits of the bulls in Chinese Holstein. <i>Animal Genetics</i> , <b>2017</b> , 48, 80-84	2.5	15
262	Novel harmful recessive haplotypes for reproductive traits in pigs. <b>2017</b> , 134, 129-135		11
261	Incorporation of causative quantitative trait nucleotides in single-step GBLUP. <i>Genetics Selection Evolution</i> , <b>2017</b> , 49, 59	4.9	38
260	Multi-breed genomic prediction using Bayes R with sequence data and dropping variants with a small effect. <i>Genetics Selection Evolution</i> , <b>2017</b> , 49, 70	4.9	16
259	A heuristic method to identify runs of homozygosity associated with reduced performance in livestock. <b>2017</b> , 95, 4318-4332		10
258	Application of a Bayesian non-linear model hybrid scheme to sequence data for genomic prediction and QTL mapping. <b>2017</b> , 18, 618		9
257	The impact of training strategies on the accuracy of genomic predictors in United States Red Angus cattle. <b>2017</b> , 95, 3406-3414		6
256	A major gene for host response to porcine reproductive and respiratory syndrome is not unfavorably associated with overall performance under nonchallenging conditions in commercial pig lines. <b>2017</b> , 95, 2838-2847		6
255	Genomic prediction accuracies in space and time for height and wood density of Douglas-fir using exome capture as the genotyping platform. <b>2017</b> , 18, 930		38
254	Genomic Selection for Yield and Seed Protein Content in Soybean: A Study of Breeding Program Data and Assessment of Prediction Accuracy. <b>2017</b> , 57, 1325-1337		40
253	Empirical comparison between different methods for genomic prediction of number of piglets born alive in moderate sized breeding populations. <b>2017</b> , 95, 1434-1443		4
252	Contribution of rare and low-frequency whole-genome sequence variants to complex traits variation in dairy cattle. <i>Genetics Selection Evolution</i> , <b>2017</b> , 49, 60	4.9	6
251	Genetic effects of PDGFRB and MARCH1 identified in GWAS revealing strong associations with semen production traits in Chinese Holstein bulls. <b>2017</b> , 18, 63		17
250	Prospects for Genomic Selection in Cassava Breeding. <b>2017</b> , 10, plantgenome2017.03.0015		63
249	Genome-wide association studies of fertility and calving traits in Brown Swiss cattle using imputed whole-genome sequences. <b>2017</b> , 18, 910		26

248	Genome-wide association study of Stayability and Heifer Pregnancy in Red Angus cattle. <b>2018</b> , 96, 846-853		5
247	Prospecting genes associated with navel length, coat and scrotal circumference traits in Canchim cattle. <i>Livestock Science</i> , <b>2018</b> , 210, 33-38	1.7	4
246	Comparing deregression methods for genomic prediction of test-day traits in dairy cattle. <b>2018</b> , 135, 97-106		14
245	Considering dominance in reduced single-step genomic evaluations. <b>2018</b> , 135, 151-158		4
244	Genomic breeding values, SNP effects and gene identification for disease traits in cow training sets. <i>Animal Genetics</i> , <b>2018</b> , 49, 178-192	2.5	15
243	Genomic Selection. <b>2018</b> , 427-480		4
242	Genome-wide association mapping and genomic prediction for CBSD resistance in <i>Manihot esculenta</i> . <i>Scientific Reports</i> , <b>2018</b> , 8, 1549	4.9	45
241	Accuracy of genomic selection to predict maize single-crosses obtained through different mating designs. <b>2018</b> , 131, 1153-1162		34
240	Improving accuracy of genomic prediction in Brangus cattle by adding animals with imputed low-density SNP genotypes. <b>2018</b> , 135, 14-27		10
239	Genome-wide association study of conformation and milk yield in mixed-breed dairy goats. <i>Journal of Dairy Science</i> , <b>2018</b> , 101, 2213-2225	4	23
238	Genotype imputation from various low-density SNP panels and its impact on accuracy of genomic breeding values in pigs. <i>Animal</i> , <b>2018</b> , 12, 2235-2245	3.1	9
237	Candidate gene association analyses for ketosis resistance in Holsteins. <i>Journal of Dairy Science</i> , <b>2018</b> , 101, 5240-5249	4	8
236	Benchmarking Bayesian genome enabled-prediction models for age at first calving in Nellore cows. <i>Livestock Science</i> , <b>2018</b> , 211, 75-79	1.7	4
235	A Simple Test Identifies Selection on Complex Traits. <b>2018</b> , 209, 321-333		12
234	Genome-wide association analysis of salmon lice ( <i>Lepeophtheirus salmonis</i> ) resistance in a North American Atlantic salmon population. <b>2018</b> , 49, 1329-1338		9
233	Accuracy and bias of genomic prediction with different de-regression methods. <i>Animal</i> , <b>2018</b> , 12, 1111-1117	1.7	5
232	Short communication: Genomic prediction using imputed whole-genome sequence variants in Brown Swiss Cattle. <i>Journal of Dairy Science</i> , <b>2018</b> , 101, 1292-1296	4	13
231	Genome-wide association studies to identify quantitative trait loci affecting milk production traits in water buffalo. <i>Journal of Dairy Science</i> , <b>2018</b> , 101, 433-444	4	40

230	Association of Copy Number Variation at Intron 3 of With Navel Length in. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 627	4.5	9
229	Expected benefit of genomic selection over forward selection in conifer breeding and deployment. <b>2018</b> , 13, e0208232		20
228	Genome-wide association study using haplotype alleles for the evaluation of reproductive traits in Nelore cattle. <b>2018</b> , 13, e0201876		6
227	Potential of Genome-Wide Studies in Unrelated Plus Trees of a Coniferous Species, (Japanese Cedar). <b>2018</b> , 9, 1322		10
226	Short communication: Single-step genomic evaluation of milk production traits using multiple-trait random regression model in Chinese Holsteins. <i>Journal of Dairy Science</i> , <b>2018</b> , 101, 11143-11149	4	10
225	PIBLUP: High-Performance Software for Large-Scale Genetic Evaluation of Animals and Plants. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 226	4.5	2
224	Effect of Hidden Relatedness on Single-Step Genetic Evaluation in an Advanced Open-Pollinated Breeding Program. <b>2018</b> , 109, 802-810		19
223	Genomic prediction ability for beef fatty acid profile in Nelore cattle using different pseudo-phenotypes. <b>2018</b> , 59, 493-501		1
222	Genomic regions underlying uniformity of yearling weight in Nelore cattle evaluated under different response variables. <b>2018</b> , 19, 619		5
221	Training Population Optimization for Prediction of Cassava Brown Streak Disease Resistance in West African Clones. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 3903-3913	3.2	17
220	Balancing selection on a recessive lethal deletion with pleiotropic effects on two neighboring genes in the porcine genome. <b>2018</b> , 14, e1007661		14
219	Genomic Selection in Preliminary Yield Trials in a Winter Wheat Breeding Program. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 2735-2747	3.2	43
218	Novel genetic polymorphisms associated with carcass traits in grazing Texel sheep. <b>2018</b> , 145, 202-208		19
217	Comparison of genomic predictions for lowly heritable traits using multi-step and single-step genomic best linear unbiased predictor in Holstein cattle. <i>Journal of Dairy Science</i> , <b>2018</b> , 101, 8076-8086 <sup>4</sup>		16
216	Genomic predictions combining SNP markers and copy number variations in Nelore cattle. <b>2018</b> , 19, 441		8
215	Genome-wide copy number variant analysis reveals variants associated with 10 diverse production traits in Holstein cattle. <b>2018</b> , 19, 314		25
214	Genomic Prediction Using Individual-Level Data and Summary Statistics from Multiple Populations. <b>2018</b> , 210, 53-69		6
213	Utility of whole-genome sequence data for across-breed genomic prediction. <i>Genetics Selection Evolution</i> , <b>2018</b> , 50, 27	4.9	32



212	Genetic Selection to Enhance Animal Welfare Using Meat Inspection Data from Slaughter Plants. <i>Animals</i> , <b>2018</b> , 8,	3.1	8
211	Short communication: Association analysis of diacylglycerol acyltransferase (DGAT1) mutation on chromosome 14 for milk yield and composition traits, somatic cell score, and coagulation properties in Holstein bulls. <i>Journal of Dairy Science</i> , <b>2018</b> , 101, 8087-8091	4	7
210	Including gene networks to predict calving difficulty in Holstein, Brown Swiss and Jersey cattle. <b>2018</b> , 19, 20		4
209	Genomic prediction using different estimation methodology, blending and cross-validation techniques for growth traits and visual scores in Hereford and Braford cattle. <b>2018</b> , 96, 2579-2595		4
208	A multi-trait Bayesian method for mapping QTL and genomic prediction. <i>Genetics Selection Evolution</i> , <b>2018</b> , 50, 10	4.9	17
207	Weighted single-step GWAS and gene network analysis reveal new candidate genes for semen traits in pigs. <i>Genetics Selection Evolution</i> , <b>2018</b> , 50, 40	4.9	29
206	The impact of selective genotyping on the response to selection using single-step genomic best linear unbiased prediction. <b>2018</b> , 96, 4532-4542		5
205	Comparing SNP panels and statistical methods for estimating genomic breed composition of individual animals in ten cattle breeds. <b>2018</b> , 19, 56		10
204	Accuracy of Genomic Prediction for Foliar Terpene Traits in. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 2573-2583	3.5	14
203	Impact of Phenotypic Correction Method and Missing Phenotypic Data on Genomic Prediction of Maize Hybrids. <b>2018</b> , 58, 1481-1491		9
202	Genomic Prediction of Grain Yield and Drought-Adaptation Capacity in Sorghum Is Enhanced by Multi-Trait Analysis. <b>2019</b> , 10, 997		26
201	Use of a single-step approach for integrating foreign information into national genomic evaluation in Holstein cattle. <i>Journal of Dairy Science</i> , <b>2019</b> , 102, 8175-8183	4	5
200	QTL-mapping and genomic prediction for bovine respiratory disease in U.S. Holsteins using sequence imputation and feature selection. <b>2019</b> , 20, 555		3
199	Genome-wide association analysis for Hydroxybutyrate concentration in Milk in Holstein dairy cattle. <b>2019</b> , 20, 58		16
198	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
197	Invited review: Advances and applications of random regression models: From quantitative genetics to genomics. <i>Journal of Dairy Science</i> , <b>2019</b> , 102, 7664-7683	4	18
196	Multi-breed genome-wide association studies across countries for electronically recorded behavior traits in local dual-purpose cows. <b>2019</b> , 14, e0221973		3
195	Alternative selection methods and explicit or implied economic-worth functions for different traits in tree breeding. <b>2019</b> , 15, 1		5



194	Cassava yield traits predicted by genomic selection methods. <b>2019</b> , 14, e0224920		14
193	Weighted Single-Step Genome-Wide Association Study of Semen Traits in Holstein Bulls of China. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 1053	4.5	6
192	Detection of a Frameshift Deletion in the Gene Leads to Prevention of Severe Myopathy and Postnatal Mortality in Pigs. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 1226	4.5	4
191	Increasing the accuracy of genomic prediction in pure-bred Limousin beef cattle by including cross-bred Limousin data and accounting for an F94L variant in MSTN. <i>Animal Genetics</i> , <b>2019</b> , 50, 621-633 <sup>2.5</sup>		6
190	Non-Destructive Evaluation Techniques and What They Tell Us about Wood Property Variation. <b>2019</b> , 10, 728		37
189	<i>Bos taurus-indicus</i> hybridization correlates with intralocus sexual-conflict effects of PRDM9 on male and female fertility in Holstein cattle. <b>2019</b> , 20, 71		2
188	Reaffirmation of known major genes and the identification of novel candidate genes associated with carcass-related metrics based on whole genome sequence within a large multi-breed cattle population. <b>2019</b> , 20, 720		26
187	Genome-wide association for milk production traits and somatic cell score in different lactation stages of Ayrshire, Holstein, and Jersey dairy cattle. <i>Journal of Dairy Science</i> , <b>2019</b> , 102, 8159-8174	4	21
186	A novel mutation in the promoter region of RPL8 regulates milk fat traits in dairy cattle by binding transcription factor Pax6. <b>2019</b> , 1864, 158528		2
185	Genetic Parameter Estimation and Genomic Prediction of Duroc Boars' Sperm Morphology Abnormalities. <i>Animals</i> , <b>2019</b> , 9,	3.1	2
184	A targeted genotyping approach to enhance the identification of variants for lactation persistency in dairy cows. <b>2019</b> , 97, 4066-4075		2
183	Efficient genetic value prediction using incomplete omics data. <b>2019</b> , 132, 1211-1222		7
182	Genetic Variation and Trait Correlations in an East African Cassava Breeding Population for Genomic Selection. <b>2019</b> , 59, 460-473		9
181	Predicting Genetic Variance from Genomewide Marker Effects Estimated from a Diverse Panel of Maize Inbreds. <b>2019</b> , 59, 583-590		4
180	Genetic and genomic analyses of testicular hypoplasia in Nellore cattle. <b>2019</b> , 14, e0211159		6
179	Short communication: Replication of genome-wide association studies for milk production traits in Chinese Holstein by an efficient rotated linear mixed model. <i>Journal of Dairy Science</i> , <b>2019</b> , 102, 2378-2383	4	9
178	Functional annotation and Bayesian fine-mapping reveals candidate genes for important agronomic traits in Holstein bulls. <b>2019</b> , 2, 212		28
177	Impact of including information from bulls and their daughters in the training population of multiple-step genomic evaluations in dairy cattle: A simulation study. <b>2019</b> , 136, 441-452		3

176	Genome-wide association study and genomic predictions for exterior traits in Yorkshire pigs1. <b>2019</b> , 97, 2793-2802		4
175	A genome-wide single nucleotide polymorphism and copy number variation analysis for number of piglets born alive. <b>2019</b> , 20, 321		17
174	Genomic prediction of bovine leukosis incidence in a US Holstein population. <i>Livestock Science</i> , <b>2019</b> , 225, 73-77	1.7	1
173	Genome-wide association study of endo-parasite phenotypes using imputed whole-genome sequence data in dairy and beef cattle. <i>Genetics Selection Evolution</i> , <b>2019</b> , 51, 15	4.9	20
172	Bayes Factor-Based Regulatory Gene Network Analysis of Genome-Wide Association Study of Economic Traits in a Purebred Swine Population. <b>2019</b> , 10,		4
171	Genome-wide association study between CNVs and milk production traits in Valle del Belice sheep. <b>2019</b> , 14, e0215204		18
170	Identification of recombination hotspots and quantitative trait loci for recombination rate in layer chickens. <b>2019</b> , 10, 20		6
169	Candidate genes associated with the heritable humoral response to <i>Mycobacterium avium</i> ssp. paratuberculosis in dairy cows have factors in common with gastrointestinal diseases in humans. <i>Journal of Dairy Science</i> , <b>2019</b> , 102, 4249-4263	4	15
168	Genome Association Study for Visual Scores in Nellore Cattle Measured at Weaning. <b>2019</b> , 20, 150		4
167	The impact of clustering methods for cross-validation, choice of phenotypes, and genotyping strategies on the accuracy of genomic predictions. <b>2019</b> , 97, 1534-1549		1
166	Scanning the genomes of parents for imprinted loci acting in their un-genotyped progeny. <i>Scientific Reports</i> , <b>2019</b> , 9, 654	4.9	1
165	Genome-wide associations and detection of potential candidate genes for direct genetic and maternal genetic effects influencing dairy cattle body weight at different ages. <i>Genetics Selection Evolution</i> , <b>2019</b> , 51, 4	4.9	17
164	Variance components for bovine tuberculosis infection and multi-breed genome-wide association analysis using imputed whole genome sequence data. <b>2019</b> , 14, e0212067		18
163	Efficient Estimation of Marker Effects in Plant Breeding. <i>G3: Genes, Genomes, Genetics</i> , <b>2019</b> , 9, 3855-3866		6
162	Historical Introgressions from a Wild Relative of Modern Cassava Improved Important Traits and May Be Under Balancing Selection. <b>2019</b> , 213, 1237-1253		16
161	Genetic Correlation, Genome-Wide Association and Genomic Prediction of Portable NIRS Predicted Carotenoids in Cassava Roots. <b>2019</b> , 10, 1570		12
160	Genomic Regions Associated With Gestation Length Detected Using Whole-Genome Sequence Data Differ Between Dairy and Beef Cattle. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 1068	4.5	8
159	Single-Step Methodology for Genomic Evaluation in Turkeys (). <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 1248	4.5	10

158	Accounting for population structure in selective cow genotyping strategies. <b>2019</b> , 136, 23-39		3
157	Genomic prediction of lactation curves for milk, fat, protein, and somatic cell score in Holstein cattle. <i>Journal of Dairy Science</i> , <b>2019</b> , 102, 452-463	4	12
156	Genomic selection of juvenile height across a single-generational gap in Douglas-fir. <b>2019</b> , 122, 848-863		17
155	Genetic evaluation of gestation length and its use in managing calving patterns. <i>Journal of Dairy Science</i> , <b>2019</b> , 102, 476-487	4	7
154	Genomic index selection provides a pragmatic framework for setting and refining multi-objective breeding targets in Miscanthus. <b>2019</b> , 124, 521-530		7
153	Prediction of genomic breeding values for reproductive traits in Nellore heifers. <b>2019</b> , 125, 12-17		7
152	Tag-SNP selection using Bayesian genomewide association study for growth traits in Hereford and Braford cattle. <b>2020</b> , 137, 449-467		4
151	Novel strategies for genomic prediction of untested single-cross maize hybrids using unbalanced historical data. <b>2020</b> , 133, 443-455		10
150	Value of sharing cow reference population between countries on reliability of genomic prediction for milk yield traits. <i>Journal of Dairy Science</i> , <b>2020</b> , 103, 1711-1728	4	5
149	Aerial high-throughput phenotyping enables indirect selection for grain yield at the early generation, seed-limited stages in breeding programs. <b>2020</b> , 60, 3096-3114		14
148	GWAS-Based Identification of New Loci for Milk Yield, Fat, and Protein in Holstein Cattle. <i>Animals</i> , <b>2020</b> , 10,	3.1	10
147	Genomic Predictive Ability for Foliar Nutritive Traits in Perennial Ryegrass. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 695-708	3.2	14
146	Genomic Tools for the Conservation and Genetic Improvement of a Highly Fragmented Breed-The Ramo Grande Cattle from the Azores. <i>Animals</i> , <b>2020</b> , 10,	3.1	4
145	Genomic Prediction and Selection for Fruit Traits in Winter Squash. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 3601-3610	3.2	5
144	Combining Random Forests and a Signal Detection Method Leads to the Robust Detection of Genotype-Phenotype Associations. <b>2020</b> , 11,		4
143	Identification of wild barley derived alleles associated with plant development in an Australian environment. <b>2020</b> , 216, 1		4
142	Improving Genomic Prediction of Crossbred and Purebred Dairy Cattle. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 598580	4.5	3
141	Estimation of Variance Components and Genomic Prediction for Individual Birth Weight Using Three Different Genome-Wide SNP Platforms in Yorkshire Pigs. <i>Animals</i> , <b>2020</b> , 10,	3.1	0

140	Breed- and trait-specific associations define the genetic architecture of calving performance traits in cattle. <b>2020</b> , 98,		5
139	Effect of trait's expression level on single-step genomic evaluation of resistance to <i>Dothistroma</i> needle blight. <b>2020</b> , 20, 205		11
138	The value of early-stage phenotyping for wheat breeding in the age of genomic selection. <b>2020</b> , 133, 2499-2520		5
137	Improving root characterisation for genomic prediction in cassava. <i>Scientific Reports</i> , <b>2020</b> , 10, 8003	4.9	8
136	Evaluation of Selection Methods for Resistance to a Specialist Insect Pest of Squash ( <i>Cucurbita pepo</i> ). <b>2020</b> , 10, 847		5
135	Gene Networks Driving Genetic Variation in Milk and Cheese-Making Traits of Spanish Assaf Sheep. <b>2020</b> , 11,		6
134	Pedigree relatedness and pseudo-phenotypes as a first approach to assess and maintain genetic diversity of the Walloon PiErain pig population. <i>Livestock Science</i> , <b>2020</b> , 233, 103950	1.7	0
133	Genomic Analysis Using Bayesian Methods under Different Genotyping Platforms in Korean Duroc Pigs. <i>Animals</i> , <b>2020</b> , 10,	3.1	1
132	Identification of Age-Specific and Common Key Regulatory Mechanisms Governing Eggshell Strength in Chicken Using Random Forests. <b>2020</b> , 11,		6
131	Selective efficiency of genome-wide selection in <i>Coffea canephora</i> breeding. <b>2020</b> , 16, 1		10
130	Current status of genomic evaluation. <b>2020</b> , 98,		33
129	Quantitative Genomic Dissection of Soybean Yield Components. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 665-675	3.2	11
128	Modeling spatial trends and enhancing genetic selection: An approach to soybean seed composition breeding. <b>2021</b> , 61, 976-988		4
127	GENOME-WIDE ASSOCIATION STUDY FOR GROWTH TRAITS IN BLANCO OREJINERO (BON) CATTLE FROM COLOMBIA. <i>Livestock Science</i> , <b>2021</b> , 243, 104366	1.7	2
126	Weighted Single-Step GWAS Identified Candidate Genes Associated with Growth Traits in a Duroc Pig Population. <b>2021</b> , 12,		3
125	Major quantitative trait loci influencing milk production and conformation traits in Guernsey dairy cattle detected on <i>Bos taurus</i> autosome 19. <i>Journal of Dairy Science</i> , <b>2021</b> , 104, 550-560	4	4
124	Development of Angus SteerSELECT: a genomic-based tool to identify performance differences of Australian Angus steers during feedlot finishing: Phase 1 validation. <i>Animal Production Science</i> , <b>2021</b> ,	1.4	3
123	Genomic prediction ability for feed efficiency traits using different models and pseudo-phenotypes under several validation strategies in Nelore cattle. <i>Animal</i> , <b>2021</b> , 15, 100085	3.1	0

122	Emerging issues in genomic selection. <b>2021</b> , 99,		2
121	Genome-Wide Association Study Identifies New Candidate Markers for Somatic Cells Score in a Local Dairy Sheep. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 643531	4.5	5
120	Genetic analysis of wheat ( <i>Triticum aestivum</i> ) adaptation to heat stress. <b>2021</b> , 134, 1387-1407		4
119	Genomic prediction ability for carcass composition indicator traits in Nellore cattle. <i>Livestock Science</i> , <b>2021</b> , 245, 104421	1.7	1
118	EEF1D facilitates milk lipid synthesis by regulation of PI3K-Akt signaling in mammals. <b>2021</b> , 35, e21455		2
117	Genome-wide association and transcriptome studies identify candidate genes and pathways for feed conversion ratio in pigs. <b>2021</b> , 22, 294		2
116	Genomic prediction for growth using a low-density SNP panel in dromedary camels. <i>Scientific Reports</i> , <b>2021</b> , 11, 7675	4.9	3
115	Prediction of genomic breeding values of milk traits in Brazilian Saanen goats. <b>2021</b> , 138, 541-551		1
114	Genome-Wide Identification of Candidate Genes for Milk Production Traits in Korean Holstein Cattle. <i>Animals</i> , <b>2021</b> , 11,	3.1	3
113	Effectiveness of genomic selection for improving provitamin A carotenoid content and associated traits in cassava. <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> , 11,	3.2	2
112	Leveraging breeding programs and genomic data in Norway spruce ( <i>Picea abies</i> L. Karst) for GWAS analysis. <b>2021</b> , 22, 179		10
111	Genomic Prediction of Average Daily Gain, Back-Fat Thickness, and Loin Muscle Depth Using Different Genomic Tools in Canadian Swine Populations. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 665344	4.5	0
110	Identification of new semen trait-related candidate genes in Duroc boars through genome-wide association and weighted gene co-expression network analyses. <b>2021</b> , 99,		2
109	Genomic prediction for fusiform rust disease incidence in a large cloned population of <i>Pinus taeda</i> . <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> , 11,	3.2	2
108	A major QTL at the LHCGR/FSHR locus for multiple birth in Holstein cattle. <i>Genetics Selection Evolution</i> , <b>2021</b> , 53, 57	4.9	1
107	A combined GWAS approach reveals key loci for socially-affected traits in Yorkshire pigs. <b>2021</b> , 4, 891		0
106	Host Genetics of Response to Porcine Reproductive and Respiratory Syndrome in Sows: Reproductive Performance. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 707870	4.5	1
105	Genome-wide association study and functional analyses for clinical and subclinical ketosis in Holstein cattle. <i>Journal of Dairy Science</i> , <b>2021</b> , 104, 10076-10089	4	2

104	Non-additive QTL mapping of lactation traits in 124,000 sequence-imputed cattle reveals novel recessive loci.		
103	Genome-Wide Association Studies for Milk Somatic Cell Score in Romanian Dairy Cattle. <b>2021</b> , 12,		2
102	Genome-wide association and genomic prediction for scrotal circumference in Hereford and Braford bulls. <b>2021</b> , 172, 268-280		0
101	Genotype-by-environment interactions at the trait level and total merit index level for milk production and functional traits in Brown Swiss cattle. <i>Animal</i> , <b>2021</b> , 15, 100052	3.1	2
100	Efficient weighting methods for genomic best linear-unbiased prediction (BLUP) adapted to the genetic architectures of quantitative traits. <b>2021</b> , 126, 320-334		3
99	Comparison of one-stage and two-stage genome-wide association studies.		2
98	Prospects for genomic selection in cassava breeding.		2
97	Leveraging Transcriptomics Data for Genomic Prediction Models in Cassava.		4
96	Fast Bayesian fine-mapping of 35 production, reproduction and body conformation traits in dairy cattle.		6
95	GWAS and fine-mapping of livability and six disease traits in Holstein cattle. <b>2020</b> , 21, 41		26
94	A genome-wide association study reveals loci influencing height and other conformation traits in horses. <b>2012</b> , 7, e37282		101
93	Genome-wide association study reveals genetic architecture of eating behavior in pigs and its implications for humans obesity by comparative mapping. <b>2013</b> , 8, e71509		52
92	Genome-wide mapping of loci explaining variance in scrotal circumference in Nellore cattle. <b>2014</b> , 9, e88561		29
91	Pleiotropic Genes Affecting Carcass Traits in <i>Bos indicus</i> (Nellore) Cattle Are Modulators of Growth. <b>2016</b> , 11, e0158165		16
90	Optimizing genomic prediction for Australian Red dairy cattle. <i>Journal of Dairy Science</i> , <b>2020</b> , 103, 6276-6298		9
89	Survival analyses in Holstein cows considering direct disease diagnoses and specific SNP marker effects. <i>Journal of Dairy Science</i> , <b>2020</b> , 103, 8257-8273	4	3
88	A Genome Wide Association Study for Longevity in Cattle. <b>2014</b> , 04, 46-55		13
87	Comparison of genome-wide association and genomic prediction methods for milk production traits in Korean Holstein cattle. <b>2019</b> , 32, 913-921		6

86	Genome-wide association study for milk production traits in an economically important local dairy sheep breed. <b>2021</b> , 20, 1500-1505		
85	Genome-wide association study of resistance/susceptibility to infectious bovine keratoconjunctivitis in Brazilian Hereford cattle. <i>Animal Genetics</i> , <b>2021</b> , 52, 881-886	2.5	1
84	Genome-wide association analyses of carcass traits using copy number variants and raw intensity values of single nucleotide polymorphisms in cattle. <b>2021</b> , 22, 757		1
83	Representative methods for genomic prediction and current status of the approaches using biological knowledge. <b>2013</b> , 41, 93-99		
82	Application of MACE Proofs for Reliability Improvement of Dairy Sire Selection. <b>2014</b> , 48, 165-171		
81	Validation of diacylglycerol O-acyltransferase1 gene effect on milk yield using Bayesian regression. <b>2015</b> , 26, 1249-1258		1
80	A heuristic method to identify runs of homozygosity associated with reduced performance in livestock.		
79	Genome-wide association mapping and genomic prediction unravels CBD resistance in a <i>Manihot esculenta</i> breeding population.		1
78	A simple test identifies selection on complex traits in breeding and experimentally-evolved populations.		
77	Genomic prediction using individual-level data and summary statistics from multiple populations.		
76	Effects of preselection of genotyped animals on reliability and bias of genomic prediction in dairy cattle. <b>2019</b> , 32, 159-169		
75	Combining case-control status and family history of disease increases association power.		1
74	GWAS and Fine-Mapping of Livability and Six Disease Traits in Holstein Cattle.		
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72	Evaluaciones genéticas usando el mejor predictor lineal insesgado genético en una etapa en bovinos. <b>2020</b> , 21, 1-13		
71	Aerial High-Throughput Phenotyping Enabling Indirect Selection for Grain Yield at the Early-generation Seed-limited Stages in Breeding Programs.		
70	Invited review: A quarter of a century-International genetic evaluation of dairy sires using MACE methodology. <i>Journal of Dairy Science</i> , <b>2021</b> ,	4	0
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67	Non-additive QTL mapping of lactation traits in 124,000 cattle reveals novel recessive loci.. <i>Genetics Selection Evolution</i> , <b>2022</b> , 54, 5	4.9	0
66	Performance of Swedish Warmblood fragile foal syndrome carriers and breeding prospects.. <i>Genetics Selection Evolution</i> , <b>2022</b> , 54, 4	4.9	0
65	Genome-wide associations for heat stress response suggest potential candidate genes underlying milk fatty acid composition in dairy cattle.. <i>Journal of Dairy Science</i> , <b>2022</b> ,	4	1
64	Evaluation of the phenotypic and genomic background of variability based on litter size of Large White pigs.. <i>Genetics Selection Evolution</i> , <b>2022</b> , 54, 1	4.9	1
63	Genetic evaluation to design a reference cow population for the Holstein breed in Tunisia: a first step toward genomic selection. <i>Animal Production Science</i> , <b>2022</b> ,	1.4	0
62	Genome-wide association study with imputed whole-genome sequence variants including large deletions for female fertility in 3 Nordic dairy cattle breeds.. <i>Journal of Dairy Science</i> , <b>2021</b> ,	4	1
61	A Random Regression Model Based on a Single-Step Method for Improving the Genomic Prediction Accuracy of Residual Feed Intake in Pigs.. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 769849	4.5	
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59	Fine-Scale Analysis of Runs of Homozygosity Islands Affecting Fertility in Mares.. <i>Frontiers in Veterinary Science</i> , <b>2022</b> , 9, 754028	3.1	3
58	Functionally prioritised whole-genome sequence variants improve the accuracy of genomic prediction for heat tolerance.. <i>Genetics Selection Evolution</i> , <b>2022</b> , 54, 17	4.9	0
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56	Genome-wide association analysis for susceptibility to infection by <i>Mycobacterium avium</i> ssp. paratuberculosis in US Holsteins.. <i>Journal of Dairy Science</i> , <b>2022</b> ,	4	1
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52	Selection for seed size has uneven effects on specialized metabolite abundance in oat ( <i>Avena sativa</i> L). <i>G3: Genes, Genomes, Genetics</i> , <b>2021</b> ,	3.2	1
51	Image_1.tiff. <b>2019</b> ,		



50 Image\_2.tiff. **2019**,

49 Image\_3.tiff. **2019**,

48 Image\_4.tiff. **2019**,

47 Image\_5.tiff. **2019**,

46 Table\_1.xlsx. **2019**,

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43 Image\_1.png. **2019**,

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32	Direct genetic effects, maternal genetic effects, and maternal genetic sensitivity on prenatal heat stress for calf diseases and corresponding genomic loci in German Holsteins. <i>Journal of Dairy Science</i> , <b>2022</b> ,	4	○
31	Associated regions for multiple birth in Brown Swiss and Original Braunvieh cattle on chromosomes 15 and 11. <i>Animal Genetics</i> ,	2.5	
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27	Genome-Wide Association Analysis and Genetic Parameters for Feed Efficiency and Related Traits in Yorkshire and Duroc Pigs. <i>Animals</i> , <b>2022</b> , 12, 1902	3.1	
26	Genome-wide association study for carcass traits in Hanwoo cattle using additional relatives' information of non-genotyped animals.		
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24	An Integrative Genomic Prediction Approach for Predicting Buffalo Milk Traits by Incorporating Related Cattle QTLs. <b>2022</b> , 13, 1430		
23	Genome-Wide Association Study Reveals Additive and Non-Additive Effects on Growth Traits in Duroc Pigs. <b>2022</b> , 13, 1454		1
22	Genomic Selection in Chinese Holsteins Using Regularized Regression Models for Feature Selection of Whole Genome Sequencing Data. <b>2022</b> , 12, 2419		○
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19	Genetic variability and genotype by environment interaction of two major cassava processed products in multi-environments. 13,		○
18	Quantitative trait loci related to growth and wood quality traits in <i>Eucalyptus grandis</i> W. Hill identified through single- and multi-trait genome-wide association studies. <b>2022</b> , 18,		○
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14	Comparison of two multi-trait association testing methods and sequence-based fine mapping of six QTL in Swiss Large White pigs.	○
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9	Investigating Genetic Characteristics of Chinese Holstein Cow's Milk Somatic Cell Score by Genetic Parameter Estimation and Genome-Wide Association. <b>2023</b> , 13, 267	○
8	Genetic Evaluation of Body Weight of American Simmental Beef Cattle using Single-Step GBLUP Approaches. <b>2021</b> , 12, 139-150	○
7	Comparison of two multi-trait association testing methods and sequence-based fine mapping of six QTL in Swiss Large White pigs.	○
6	391. Detecting QTL for two lowly correlated traits using multi-trait and meta-analysis approaches in Swiss Large White pigs. <b>2022</b> ,	○
5	175. Making the most of genetic relationships between Iberian dairy sheep breeds: exploring multi-breed genomic evaluation. <b>2022</b> ,	○
4	655. Integration of beef cattle international estimated breeding values in the Italian evaluation. <b>2022</b> ,	○
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