

Ole Fredslund Christensen

List of Publications by Year in descending order

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33
papers

1,935
citations

471477

17
h-index

361001

35
g-index

38
all docs

38
docs citations

38
times ranked

1437
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic prediction when some animals are not genotyped. <i>Genetics Selection Evolution</i> , 2010, 42, 2.	3.0	639
2	Estimating Additive and Non-Additive Genetic Variances and Predicting Genetic Merits Using Genome-Wide Dense Single Nucleotide Polymorphism Markers. <i>PLoS ONE</i> , 2012, 7, e45293.	2.5	261
3	Single Step, a general approach for genomic selection. <i>Livestock Science</i> , 2014, 166, 54-65.	1.6	260
4	Ancestral Relationships Using Metafounders: Finite Ancestral Populations and Across Population Relationships. <i>Genetics</i> , 2015, 200, 455-468.	2.9	119
5	Compatibility of pedigree-based and marker-based relationship matrices for single-step genetic evaluation. <i>Genetics Selection Evolution</i> , 2012, 44, 37.	3.0	82
6	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.	3.0	72
7	Genomic evaluation of both purebred and crossbred performances. <i>Genetics Selection Evolution</i> , 2014, 46, 23.	3.0	67
8	Metafounders are related to F_{st} fixation indices and reduce bias in single-step genomic evaluations. <i>Genetics Selection Evolution</i> , 2017, 49, 34.	3.0	55
9	Genome-wide association study for conformation traits in three Danish pig breeds. <i>Genetics Selection Evolution</i> , 2017, 49, 12.	3.0	45
10	Genetic evaluation for three-way crossbreeding. <i>Genetics Selection Evolution</i> , 2015, 47, 98.	3.0	32
11	Genome-wide association analyses using a Bayesian approach for litter size and piglet mortality in Danish Landrace and Yorkshire pigs. <i>BMC Genomics</i> , 2016, 17, 468.	2.8	32
12	Genetic evaluation including intermediate omics features. <i>Genetics</i> , 2021, 219, .	2.9	32
13	Genomic prediction of crossbred performance based on purebred Landrace and Yorkshire data using a dominance model. <i>Genetics Selection Evolution</i> , 2016, 48, 40.	3.0	29
14	Genomic Model with Correlation Between Additive and Dominance Effects. <i>Genetics</i> , 2018, 209, 711-723.	2.9	29
15	Genomic prediction using models with dominance and imprinting effects for backfat thickness and average daily gain in Danish Duroc pigs. <i>Genetics Selection Evolution</i> , 2016, 48, 67.	3.0	21
16	Statistical model and testing designs to increase response to selection with constrained inbreeding in genomic breeding programs for pigs affected by social genetic effects. <i>Genetics Selection Evolution</i> , 2021, 53, 1.	3.0	20
17	Sparse single-step method for genomic evaluation in pigs. <i>Genetics Selection Evolution</i> , 2016, 48, 48.	3.0	19
18	A bivariate genomic model with additive, dominance and inbreeding depression effects for sire line and three-way crossbred pigs. <i>Genetics Selection Evolution</i> , 2019, 51, 45.	3.0	18

#	ARTICLE	IF	CITATIONS
19	Imputation of genotypes in Danish purebred and two-way crossbred pigs using low-density panels. <i>Genetics Selection Evolution</i> , 2015, 47, 54.	3.0	13
20	Estimation of variance components and prediction of breeding values based on group records from varying group sizes. <i>Genetics Selection Evolution</i> , 2018, 50, 42.	3.0	11
21	Use of genomic models to study genetic control of environmental variance. <i>Genetical Research</i> , 2011, 93, 125-138.	0.9	10
22	Breed of origin of alleles and genomic predictions for crossbred dairy cows. <i>Genetics Selection Evolution</i> , 2021, 53, 84.	3.0	10
23	Genomic diversity revealed by whole-genome sequencing in three Danish commercial pig breeds. <i>Journal of Animal Science</i> , 2020, 98, .	0.5	9
24	Large-scale association study on daily weight gain in pigs reveals overlap of genetic factors for growth in humans. <i>BMC Genomics</i> , 2022, 23, 133.	2.8	8
25	Genetic associations between stayability and longevity in commercial crossbred sows, and stayability in multiplier sows. <i>Journal of Animal Science</i> , 2020, 98, .	0.5	6
26	Prediction of breeding values for group-recorded traits including genomic information and an individually recorded correlated trait. <i>Heredity</i> , 2021, 126, 206-217.	2.6	6
27	Predictive performances of animal models using different multibreed relationship matrices in systems with rotational crossbreeding. <i>Genetics Selection Evolution</i> , 2022, 54, 25.	3.0	6
28	Single-step genomic evaluation with metafounders for feed conversion ratio and average daily gain in Danish Landrace and Yorkshire pigs. <i>Genetics Selection Evolution</i> , 2021, 53, 79.	3.0	5
29	Models with indirect genetic effects depending on group sizes: a simulation study assessing the precision of the estimates of the dilution parameter. <i>Genetics Selection Evolution</i> , 2019, 51, 24.	3.0	4
30	Genomic predictions for crossbred dairy cows by combining solutions from purebred evaluation based on breed origin of alleles. <i>Journal of Dairy Science</i> , 2022, 105, 5178-5191.	3.4	4
31	Use of Repeated Group Measurements with Drop Out Animals for Variance Component Estimation and Genetic Evaluation: A Simulation Study. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2935-2940.	1.8	3
32	Selection for social genetic effects in purebreds increases growth in crossbreds. <i>Genetics Selection Evolution</i> , 2021, 53, 15.	3.0	3
33	Genetic parameters and genomic prediction for feed intake recorded at the group and individual level in different production systems for growing pigs. <i>Genetics Selection Evolution</i> , 2021, 53, 33.	3.0	3