Irene van den Berg

List of Publications by Year
in descending order

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19
papers

545
citations

687363
13
h-index

794594
19
g-index

20
all docs

20
docs citations

20
times ranked

520
citing authors

#	Article	IF	Citations
1	Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19398-19408.	7.1	99
2	Using Sequence Variants in Linkage Disequilibrium with Causative Mutations to Improve Across-Breed Prediction in Dairy Cattle: A Simulation Study. G3: Genes, Genomes, Genetics, 2016, 6, 2553-2561.	1.8	53
3	Sequence variants selected from a multi-breed GWAS can improve the reliability of genomic predictions in dairy cattle. Genetics Selection Evolution, 2016, 48, 83.	3.0	52
4	Meta-analysis for milk fat and protein percentage using imputed sequence variant genotypes in 94,321 cattle from eight cattle breeds. Genetics Selection Evolution, 2020, 52, 37.	3.0	41
5	Comparing power and precision of within-breed and multibreed genome-wide association studies of production traits using whole-genome sequence data for 5 French and Danish dairy cattle breeds. Journal of Dairy Science, 2016, 99, 8932-8945.	3.4	40
6	Multi-breed genomic prediction using Bayes R with sequence data and dropping variants with a small effect. Genetics Selection Evolution, 2017, 49, 70.	3.0	29
7	Predicting the effect of reference population on the accuracy of within, across, and multibreed genomic prediction. Journal of Dairy Science, 2019, 102, 3155-3174.	3.4	29
8	Genetic parameters for methane emission traits in Australian dairy cows. Journal of Dairy Science, 2021, 104, 539-549.	3.4	29
9	QTL fine mapping with Bayes C(Ï€): a simulation study. Genetics Selection Evolution, 2013, 45, 19.	3.0	27
10	Overlap between eQTL and QTL associated with production traits and fertility in dairy cattle. BMC Genomics, 2019, 20, 291.	2.8	25
11	Effect direction meta-analysis of GWAS identifies extreme, prevalent and shared pleiotropy in a large mammal. Communications Biology, 2020, 3, 88.	4.4	25
12	On the use of whole-genome sequence data for across-breed genomic prediction and fine-scale mapping of QTL. Genetics Selection Evolution, 2021, 53, 19.	3.0	22
13	Optimizing genomic prediction for Australian Red dairy cattle. Journal of Dairy Science, 2020, 103, 6276-6298.	3.4	21
14	The use of milk mid-infrared spectroscopy to improve genomic prediction accuracy of serum biomarkers. Journal of Dairy Science, 2021, 104, 2008-2017.	3.4	13
15	Concordance analysis for QTL detection in dairy cattle: a case study of leg morphology. Genetics Selection Evolution, 2014, 46, 31.	3.0	12
16	Estimating methane coefficients to predict the environmental impact of traits in the Australian dairy breeding program. Journal of Dairy Science, 2021, 104, 10979-10990.	3.4	10
17	GWAS and genomic prediction of milk urea nitrogen in Australian and New Zealand dairy cattle. Genetics Selection Evolution, 2022, 54, 15.	3.0	9
18	Genetic parameters of blood urea nitrogen and milk urea nitrogen concentration in dairy cattle managed in pasture-based production systems of New Zealand and Australia. Animal Production Science, 2021, 61, 1801-1810.	1.3	7

#	ARTICLE	IF	CITATIONS
19	Using mid-infrared spectroscopy to increase GWAS power to detect QTL associated with blood urea nitrogen. Genetics Selection Evolution, 2022, 54, 27.	3.0	2