

Irene van den Berg

List of Publications by Year in descending order

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Version: 2024-02-01

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

#	ARTICLE	IF	CITATIONS
19	QTL fine mapping with Bayes C($\hat{\epsilon}$): a simulation study. <i>Genetics Selection Evolution</i> , 2013, 45, 19.	3.0	27