

Paul M Vanraden

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6761359/publications.pdf>

Version: 2024-02-01

14
papers

1,276
citations

840776

11
h-index

1058476

14
g-index

17
all docs

17
docs citations

17
times ranked

1561
citing authors

#	ARTICLE	IF	CITATIONS
1	Invited review: Unknown-parent groups and metafounders in single-step genomic BLUP. <i>Journal of Dairy Science</i> , 2022, 105, 923-939.	3.4	9
2	Comprehensive analyses of 723 transcriptomes enhance genetic and biological interpretations for complex traits in cattle. <i>Genome Research</i> , 2020, 30, 790-801.	5.5	97
3	GWAS and fine-mapping of livability and six disease traits in Holstein cattle. <i>BMC Genomics</i> , 2020, 21, 41.	2.8	66
4	Functional annotation and Bayesian fine-mapping reveals candidate genes for important agronomic traits in Holstein bulls. <i>Communications Biology</i> , 2019, 2, 212.	4.4	61
5	Genetic and epigenetic architecture of paternal origin contribute to gestation length in cattle. <i>Communications Biology</i> , 2019, 2, 100.	4.4	41
6	Ranking sires using genetic selection indices based on financial investment methods versus lifetime net merit. <i>Journal of Dairy Science</i> , 2019, 102, 9060-9075.	3.4	7
7	Dissection of additive, dominance, and imprinting effects for production and reproduction traits in Holstein cattle. <i>BMC Genomics</i> , 2017, 18, 425.	2.8	46
8	Selecting sequence variants to improve genomic predictions for dairy cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 32.	3.0	113
9	Changes in genetic selection differentials and generation intervals in US Holstein dairy cattle as a result of genomic selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3995-4004.	7.1	395
10	Fast imputation using medium or low-coverage sequence data. <i>BMC Genetics</i> , 2015, 16, 82.	2.7	86
11	Cattle Sex-Specific Recombination and Genetic Control from a Large Pedigree Analysis. <i>PLoS Genetics</i> , 2015, 11, e1005387.	3.5	168
12	Increasing Long-Term Response by Selecting for Favorable Minor Alleles. <i>PLoS ONE</i> , 2014, 9, e88510.	2.5	12
13	Bovine Exome Sequence Analysis and Targeted SNP Genotyping of Recessive Fertility Defects BH1, HH2, and HH3 Reveal a Putative Causative Mutation in SMC2 for HH3. <i>PLoS ONE</i> , 2014, 9, e92769.	2.5	69
14	Improvement of Prediction Ability for Genomic Selection of Dairy Cattle by Including Dominance Effects. <i>PLoS ONE</i> , 2014, 9, e103934.	2.5	74