

Ricardo Pong-Wong

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

3,771
citations

236925

25
h-index

138484

58
g-index

59
all docs

59
docs citations

59
times ranked

4700
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-Genome Regression and Prediction Methods Applied to Plant and Animal Breeding. <i>Genetics</i> , 2013, 193, 327-345.	2.9	732
2	The Impact of Genetic Architecture on Genome-Wide Evaluation Methods. <i>Genetics</i> , 2010, 185, 1021-1031.	2.9	639
3	Genomic Prediction in Animals and Plants: Simulation of Data, Validation, Reporting, and Benchmarking. <i>Genetics</i> , 2013, 193, 347-365.	2.9	370
4	Application of high-dimensional feature selection: evaluation for genomic prediction in man. <i>Scientific Reports</i> , 2015, 5, 10312.	3.3	233
5	Genomic prediction of host resistance to sea lice in farmed Atlantic salmon populations. <i>Genetics Selection Evolution</i> , 2016, 48, 47.	3.0	203
6	Homozygosity for a single base-pair mutation in the oocyte-specific GDF9 gene results in sterility in Thoka sheep. <i>Reproduction</i> , 2009, 138, 921-933.	2.6	141
7	Localising Loci underlying Complex Trait Variation Using Regional Genomic Relationship Mapping. <i>PLoS ONE</i> , 2012, 7, e46501.	2.5	111
8	A simple and rapid method for calculating identity-by-descent matrices using multiple markers. <i>Genetics Selection Evolution</i> , 2001, 33, 453-71.	3.0	106
9	Evaluating the contribution of genetics and familial shared environment to common disease using the UK Biobank. <i>Nature Genetics</i> , 2016, 48, 980-983.	21.4	105
10	Genome-wide association study identifies novel loci associated with resistance to bovine tuberculosis. <i>Heredity</i> , 2014, 112, 543-551.	2.6	92
11	Genome-wide association and regional heritability mapping to identify loci underlying variation in nematode resistance and body weight in Scottish Blackface lambs. <i>Heredity</i> , 2013, 110, 420-429.	2.6	90
12	Genome-wide association reveals QTL for growth, bone and in vivo carcass traits as assessed by computed tomography in Scottish Blackface lambs. <i>Genetics Selection Evolution</i> , 2016, 48, 11.	3.0	58
13	Genome wide analysis reveals single nucleotide polymorphisms associated with fatness and putative novel copy number variants in three pig breeds. <i>BMC Genomics</i> , 2013, 14, 784.	2.8	54
14	Application of Selection Mapping to Identify Genomic Regions Associated with Dairy Production in Sheep. <i>PLoS ONE</i> , 2014, 9, e94623.	2.5	45
15	Genomic Prediction for Tuberculosis Resistance in Dairy Cattle. <i>PLoS ONE</i> , 2014, 9, e96728.	2.5	42
16	Optimisation of contribution of candidate parents to maximise genetic gain and restricting inbreeding using semidefinite programming (Open Access publication). <i>Genetics Selection Evolution</i> , 2007, 39, 3-25.	3.0	41
17	Quantitative trait loci mapping for canine hip dysplasia and its related traits in UK Labrador Retrievers. <i>BMC Genomics</i> , 2014, 15, 833.	2.8	41
18	Correlations in refractive errors between siblings in the Singapore Cohort Study of Risk factors for Myopia. <i>British Journal of Ophthalmology</i> , 2007, 91, 781-784.	3.9	37

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19	Cow genotyping strategies for genomic selection in a small dairy cattle population. <i>Journal of Dairy Science</i> , 2017, 100, 439-452.	3.4	37
20	The power of regional heritability analysis for rare and common variant detection: simulations and application to eye biometrical traits. <i>Frontiers in Genetics</i> , 2013, 4, 232.	2.3	36
21	A joint analysis to identify loci underlying variation in nematode resistance in three European sheep populations. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 426-436.	2.0	33
22	Genetic factors controlling wool shedding in a composite Ascare sheep flock. <i>Animal Genetics</i> , 2013, 44, 742-749.	1.7	32
23	Balancing selection at a premature stop mutation in the myostatin gene underlies a recessive leg weakness syndrome in pigs. <i>PLoS Genetics</i> , 2019, 15, e1007759.	3.5	31
24	The value of genomic relationship matrices to estimate levels of inbreeding. <i>Genetics Selection Evolution</i> , 2021, 53, 42.	3.0	31
25	Genetic Control of Canine Leishmaniasis: Genome-Wide Association Study and Genomic Selection Analysis. <i>PLoS ONE</i> , 2012, 7, e35349.	2.5	31
26	Genomic prediction of traits related to canine hip dysplasia. <i>Frontiers in Genetics</i> , 2015, 6, 97.	2.3	28
27	Regional heritability mapping method helps explain missing heritability of blood lipid traits in isolated populations. <i>Heredity</i> , 2016, 116, 333-338.	2.6	26
28	The use of genomic coancestry matrices in the optimisation of contributions to maintain genetic diversity at specific regions of the genome. <i>Genetics Selection Evolution</i> , 2016, 48, 2.	3.0	25
29	Genomic prediction of complex human traits: relatedness, trait architecture and predictive meta-models. <i>Human Molecular Genetics</i> , 2015, 24, 4167-4182.	2.9	24
30	Genome-wide analysis of mitral valve disease in Cavalier King Charles Spaniels. <i>Veterinary Journal</i> , 2012, 193, 283-286.	1.7	23
31	Detecting parent of origin and dominant QTL in a two-generation commercial poultry pedigree using variance component methodology. <i>Genetics Selection Evolution</i> , 2009, 41, 6.	3.0	19
32	Genetic dissection of complex behaviour traits in German Shepherd dogs. <i>Heredity</i> , 2019, 123, 746-758.	2.6	19
33	QTL analysis and genomic selection using RADseq derived markers in Sitka spruce: the potential utility of within family data. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	17
34	<i>Lawsonia intracellularis</i> infection of intestinal crypt cells is associated with specific depletion of secreted MUC2 in goblet cells. <i>Veterinary Immunology and Immunopathology</i> , 2015, 168, 61-67.	1.2	16
35	Haplotype Heritability Mapping Method Uncovers Missing Heritability of Complex Traits. <i>Scientific Reports</i> , 2018, 8, 4982.	3.3	14
36	Genome-wide association studies for milk production traits in Valle del Belice sheep using repeated measures. <i>Animal Genetics</i> , 2019, 50, 311-314.	1.7	14

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37	A two-step approach combining the Gompertz growth model with genomic selection for longitudinal data. BMC Proceedings, 2010, 4, S4.	1.6	13
38	Effect of the prior distribution of SNP effects on the estimation of total breeding value. BMC Proceedings, 2012, 6, S6.	1.6	13
39	Regional Heritability Mapping to identify loci underlying genetic variation of complex traits. BMC Proceedings, 2014, 8, S3.	1.6	13
40	Phenotypic and genetic parameter estimates of cheese-making traits and their relationships with milk production, composition and functional traits in Spanish Assaf sheep. Livestock Science, 2019, 228, 76-83.	1.6	13
41	Genome-Wide Analysis in Swine Associates Corneal Graft Rejection with Donor-Recipient Mismatches in Three Novel Histocompatibility Regions and One Locus Homologous to the Mouse H-3 Locus. PLoS ONE, 2016, 11, e0152155.	2.5	12
42	Defining the Assumptions Underlying Modeling of Epistatic QTL Using Variance Component Methods. Journal of Heredity, 2008, 99, 421-425.	2.4	11
43	A Regression-Based Approach to Selection Mapping. Journal of Heredity, 2011, 102, 294-305.	2.4	11
44	An analysis of effects of heterozygosity in dairy cattle for bovine tuberculosis resistance. Animal Genetics, 2018, 49, 103-109.	1.7	10
45	Evaluating different genomic coancestry matrices for managing genetic variability in turbot. Aquaculture, 2020, 520, 734985.	3.5	10
46	Use of haplotypes to identify regions harbouring lethal recessive variants in pigs. Genetics Selection Evolution, 2017, 49, 57.	3.0	8
47	Efficiency of genomic prediction for boar taint reduction in Danish Landrace pigs. Animal Genetics, 2015, 46, 607-616.	1.7	7
48	Genomic-Based Optimum Contribution in Conservation and Genetic Improvement Programs with Antagonistic Fitness and Productivity Traits. Frontiers in Genetics, 2016, 7, 25.	2.3	7
49	Selective advantage of implementing optimal contributions selection and timescales for the convergence of long-term genetic contributions. Genetics Selection Evolution, 2018, 50, 24.	3.0	7
50	Detection of multiple quantitative trait loci and their pleiotropic effects in outbred pig populations. Genetics Selection Evolution, 2009, 41, 44.	3.0	6
51	Detection of genomic regions underlying milk production traits in Valle del Belice dairy sheep using regional heritability mapping. Journal of Animal Breeding and Genetics, 2021, 138, 552-561.	2.0	6
52	Mapping of quantitative trait loci affecting classical scrapie incubation time in a population comprising several generations of scrapie-infected sheep. Journal of General Virology, 2010, 91, 575-579.	2.9	5
53	Changes in Allele Frequencies When Different Genomic Coancestry Matrices Are Used for Maintaining Genetic Diversity. Genes, 2021, 12, 673.	2.4	5
54	Applying different genomic evaluation approaches on QTLMAS2010 dataset. BMC Proceedings, 2011, 5, S9.	1.6	4

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55	Antagonistic genetic correlations for milking traits within the genome of dairy cattle. PLoS ONE, 2017, 12, e0175105.	2.5	4
56	Optimisation of contribution of candidate parents to maximise genetic gain and restricting inbreeding using semidefinite programming (Open Access publication). Genetics Selection Evolution, 2007, 39, 3-25.	3.0	4
57	Estimation of genomic breeding values using the Horseshoe prior. BMC Proceedings, 2014, 8, S6.	1.6	3
58	Effect of genotyping strategies on the sustained benefit of single-step genomic BLUP over multiple generations. Genetics Selection Evolution, 2022, 54, 23.	3.0	2