

# Ricardo Pong-Wong

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2302534/publications.pdf>

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	Effect of genotyping strategies on the sustained benefit of single-step genomic BLUP over multiple generations. <i>Genetics Selection Evolution</i> , 2022, 54, 23.	3.0	2
2	Changes in Allele Frequencies When Different Genomic Coancestry Matrices Are Used for Maintaining Genetic Diversity. <i>Genes</i> , 2021, 12, 673.	2.4	5
3	Detection of genomic regions underlying milk production traits in Valle del Belice dairy sheep using regional heritability mapping. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 552-561.	2.0	6
4	The value of genomic relationship matrices to estimate levels of inbreeding. <i>Genetics Selection Evolution</i> , 2021, 53, 42.	3.0	31
5	Evaluating different genomic coancestry matrices for managing genetic variability in turbot. <i>Aquaculture</i> , 2020, 520, 734985.	3.5	10
6	Phenotypic and genetic parameter estimates of cheese-making traits and their relationships with milk production, composition and functional traits in Spanish Assaf sheep. <i>Livestock Science</i> , 2019, 228, 76-83.	1.6	13
7	Genetic dissection of complex behaviour traits in German Shepherd dogs. <i>Heredity</i> , 2019, 123, 746-758.	2.6	19
8	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
9	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
10	An analysis of effects of heterozygosity in dairy cattle for bovine tuberculosis resistance. <i>Animal Genetics</i> , 2018, 49, 103-109.	1.7	10
11	Haplotype Heritability Mapping Method Uncovers Missing Heritability of Complex Traits. <i>Scientific Reports</i> , 2018, 8, 4982.	3.3	14
12	Selective advantage of implementing optimal contributions selection and timescales for the convergence of long-term genetic contributions. <i>Genetics Selection Evolution</i> , 2018, 50, 24.	3.0	7
13	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
14	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
15	Use of haplotypes to identify regions harbouring lethal recessive variants in pigs. <i>Genetics Selection Evolution</i> , 2017, 49, 57.	3.0	8
16	Antagonistic genetic correlations for milking traits within the genome of dairy cattle. <i>PLoS ONE</i> , 2017, 12, e0175105.	2.5	4
17	Genomic-Based Optimum Contribution in Conservation and Genetic Improvement Programs with Antagonistic Fitness and Productivity Traits. <i>Frontiers in Genetics</i> , 2016, 7, 25.	2.3	7
18	Genomic prediction of host resistance to sea lice in farmed Atlantic salmon populations. <i>Genetics Selection Evolution</i> , 2016, 48, 47.	3.0	203

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	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
22	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
23	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. <i>PLoS ONE</i> , 2016, 11, e0152155.	2.5	12
24	Efficiency of genomic prediction for boar taint reduction in Danish Landrace pigs. <i>Animal Genetics</i> , 2015, 46, 607-616.	1.7	7
25	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
26	Application of high-dimensional feature selection: evaluation for genomic prediction in man. <i>Scientific Reports</i> , 2015, 5, 10312.	3.3	233
27	Genomic prediction of traits related to canine hip dysplasia. <i>Frontiers in Genetics</i> , 2015, 6, 97.	2.3	28
28	<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
29	Genomic Prediction for Tuberculosis Resistance in Dairy Cattle. <i>PLoS ONE</i> , 2014, 9, e96728.	2.5	42
30	Estimation of genomic breeding values using the Horseshoe prior. <i>BMC Proceedings</i> , 2014, 8, S6.	1.6	3
31	Genome-wide association study identifies novel loci associated with resistance to bovine tuberculosis. <i>Heredity</i> , 2014, 112, 543-551.	2.6	92
32	Regional Heritability Mapping to identify loci underlying genetic variation of complex traits. <i>BMC Proceedings</i> , 2014, 8, S3.	1.6	13
33	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
34	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
35	Application of Selection Mapping to Identify Genomic Regions Associated with Dairy Production in Sheep. <i>PLoS ONE</i> , 2014, 9, e94623.	2.5	45
36	Whole-Genome Regression and Prediction Methods Applied to Plant and Animal Breeding. <i>Genetics</i> , 2013, 193, 327-345.	2.9	732

#	ARTICLE	IF	CITATIONS
37	Genetic factors controlling wool shedding in a composite <i>E</i> asycare sheep flock. <i>Animal Genetics</i> , 2013, 44, 742-749.	1.7	32
38	Genomic Prediction in Animals and Plants: Simulation of Data, Validation, Reporting, and Benchmarking. <i>Genetics</i> , 2013, 193, 347-365.	2.9	370
39	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
40	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
41	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
42	Localising Loci underlying Complex Trait Variation Using Regional Genomic Relationship Mapping. <i>PLoS ONE</i> , 2012, 7, e46501.	2.5	111
43	Genome-wide analysis of mitral valve disease in Cavalier King Charles Spaniels. <i>Veterinary Journal</i> , 2012, 193, 283-286.	1.7	23
44	Effect of the prior distribution of SNP effects on the estimation of total breeding value. <i>BMC Proceedings</i> , 2012, 6, S6.	1.6	13
45	Genetic Control of Canine Leishmaniasis: Genome-Wide Association Study and Genomic Selection Analysis. <i>PLoS ONE</i> , 2012, 7, e35349.	2.5	31
46	Applying different genomic evaluation approaches on QTLMAS2010 dataset. <i>BMC Proceedings</i> , 2011, 5, S9.	1.6	4
47	A Regression-Based Approach to Selection Mapping. <i>Journal of Heredity</i> , 2011, 102, 294-305.	2.4	11
48	A two-step approach combining the Gompertz growth model with genomic selection for longitudinal data. <i>BMC Proceedings</i> , 2010, 4, S4.	1.6	13
49	Mapping of quantitative trait loci affecting classical scrapie incubation time in a population comprising several generations of scrapie-infected sheep. <i>Journal of General Virology</i> , 2010, 91, 575-579.	2.9	5
50	The Impact of Genetic Architecture on Genome-Wide Evaluation Methods. <i>Genetics</i> , 2010, 185, 1021-1031.	2.9	639
51	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
52	Detection of multiple quantitative trait loci and their pleiotropic effects in outbred pig populations. <i>Genetics Selection Evolution</i> , 2009, 41, 44.	3.0	6
53	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
54	Defining the Assumptions Underlying Modeling of Epistatic QTL Using Variance Component Methods. <i>Journal of Heredity</i> , 2008, 99, 421-425.	2.4	11

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	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	4
58	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