## Robert John Tempelman

List of Publications by Year in descending order

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47 papers

1,200 citations

257101 24 h-index 395343 33 g-index

48 all docs 48 docs citations

48 times ranked

1469 citing authors

#	Article	IF	CITATIONS
1	Limitations in use of ovarian reserve biomarkers to predict the superovulation response in small ovarian reserve heifers. Theriogenology, 2022, 182, 53-62.	0.9	1
2	The use of milk Fourier-transform mid-infrared spectroscopy to diagnose pregnancy and determine spectral regional associations with pregnancy in US dairy cows. Journal of Dairy Science, 2022, 105, 3209-3221.	1.4	3
3	Estimates of genetic parameters for feeding behavior traits and their associations with feed efficiency in Holstein cows. Journal of Dairy Science, 2022, 105, 7564-7574.	1.4	11
4	Negative impact of high doses of follicle-stimulating hormone during superovulation on the ovulatory follicle function in small ovarian reserve dairy heifers. Biology of Reproduction, 2021, 104, 695-705.	1.2	17
5	Knockdown of Death-Associated Protein Expression Induces Global Transcriptome Changes in Proliferating and Differentiating Muscle Satellite Cells. Frontiers in Physiology, 2020, 11, 1036.	1.3	O
6	Diagnosing pregnancy status using infrared spectra and milk composition in dairy cows. Journal of Dairy Science, 2018, 101, 2496-2505.	1.4	35
7	Genome-Wide Association Analyses Based on Broadly Different Specifications for Prior Distributions, Genomic Windows, and Estimation Methods. Genetics, 2017, 206, 1791-1806.	1.2	31
8	Aflatoxin levels in sunflower seeds and cakes collected from micro- and small-scale sunflower oil processors in Tanzania. PLoS ONE, 2017, 12, e0175801.	1.1	29
9	Genotype by environment interaction for tick resistance of Hereford and Braford beef cattle using reaction norm models. Genetics Selection Evolution, 2016, 48, 3.	1.2	18
10	Short communication: On recognizing the proper experimental unit in animal studies in the dairy sciences. Journal of Dairy Science, 2016, 99, 8871-8879.	1.4	41
11	Genomic Prediction Accounting for Residual Heteroskedasticity. G3: Genes, Genomes, Genetics, 2016, 6, 1-13.	0.8	8
12	Guest Editors' Introduction to the Special Issue on "Statistical Genomics and Transcriptomics in Agriculture― Journal of Agricultural, Biological, and Environmental Statistics, 2015, 20, 439-441.	0.7	0
13	Improving the computational efficiency of fully Bayes inference and assessing the effect of misspecification of hyperparameters in whole-genome prediction models. Genetics Selection Evolution, 2015, 47, 13.	1.2	12
14	Statistical and Computational Challenges in Whole Genome Prediction and Genome-Wide Association Analyses for Plant and Animal Breeding. Journal of Agricultural, Biological, and Environmental Statistics, 2015, 20, 442-466.	0.7	10
15	Inhibition of Listeria monocytogenes in Full- and Low-Sodium Frankfurters at 4, 7, or 10°C Using Spray-Dried Mixtures of Organic Acid Salts. Journal of Food Protection, 2013, 76, 1557-1567.	0.8	6
16	A Bayesian Antedependence Model for Whole Genome Prediction. Genetics, 2012, 190, 1491-1501.	1.2	62
17	Passage of Campylobacter jejuni through the chicken reservoir or mice promotes phase variation in contingency genes Cj0045 and Cj0170 that strongly associates with colonization and disease in a mouse model. Microbiology (United Kingdom), 2012, 158, 1304-1316.	0.7	36
18	Hierarchical Bayesian modeling of heterogeneous cluster―and subject―evel associations between continuous and binary outcomes in dairy production. Biometrical Journal, 2012, 54, 230-248.	0.6	9

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19	Inferring Upon Heterogeneous Associations in Dairy Cattle Performance Using a Bivariate Hierarchical Model. Journal of Agricultural, Biological, and Environmental Statistics, 2012, 17, 142-161.	0.7	5
20	Genome-Wide Linkage Analysis of Global Gene Expression in Loin Muscle Tissue Identifies Candidate Genes in Pigs. PLoS ONE, 2011, 6, e16766.	1.1	45
21	Transcriptional profiling identifies differentially expressed genes in developing turkey skeletal muscle. BMC Genomics, 2011, 12, 143.	1.2	41
22	Hierarchical Bayesian modeling of random and residual variance–covariance matrices in bivariate mixed effects models. Biometrical Journal, 2010, 52, 297-313.	0.6	19
23	Addressing scope of inference for global genetic evaluation of livestock. Revista Brasileira De Zootecnia, 2010, 39, 261-267.	0.3	4
24	A large-scale study of differential gene expression in monocyte-derived macrophages infected with several strains of Mycobacterium avium subspecies paratuberculosis. Briefings in Functional Genomics, 2010, 9, 220-237.	1.3	51
25	Modelos hierárquicos bayesianos para estimação robusta e análise de dados censurados em melhoramento animal. Revista Brasileira De Zootecnia, 2009, 38, 72-80.	0.3	4
26	Development of an Adjuvant-Free Cashew Nut Allergy Mouse Model. International Archives of Allergy and Immunology, 2009, 149, 299-304.	0.9	41
27	Sexual differentiation of the zebra finch song system: potential roles for sex chromosome genes. BMC Neuroscience, 2009, 10, 24.	0.8	55
28	Optimizing design of two-stage experiments for transcriptional profiling. Computational Statistics and Data Analysis, 2009, 53, 1639-1649.	0.7	5
29	Gene expression profiling in hepatic tissue of newly weaned pigs fed pharmacological zinc and phytase supplemented diets. BMC Genomics, 2008, 9, 421.	1.2	34
30	Selective Transcriptional Profiling and Data Analysis Strategies for Expression Quantitative Trait Loci Mapping in Outbred F2 Populations. Genetics, 2008, 180, 1679-1690.	1.2	11
31	Statistical Analysis of Efficient Unbalanced Factorial Designs for Two-Color Microarray Experiments. International Journal of Plant Genomics, 2008, 2008, 1-16.	2.2	9
32	Gene expression profiling of peripheral mononuclear cells in lame dairy cows with foot lesions. Veterinary Immunology and Immunopathology, 2007, 120, 234-245.	0.5	34
33	A novel method for testing social recognition in young pigs and the modulating effects of relocation. Applied Animal Behaviour Science, 2006, 99, 77-87.	0.8	17
34	A general approach to mixed effects modeling of residual variances in generalized linear mixed models. Genetics Selection Evolution, 2005, 37, 31-56.	1.2	46
35	Enhanced gene expression in the forebrain of hatchling and juvenile male zebra finches. Journal of Neurobiology, 2005, 64, 224-238.	3.7	29
36	Reassessing Design and Analysis of two-Colour Microarray Experiments Using Mixed Effects Models. Comparative and Functional Genomics, 2005, 6, 123-131.	2.0	58

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37	Assessing statistical precision, power, and robustness of alternative experimental designs for two color microarray platforms based on mixed effects models. Veterinary Immunology and Immunopathology, 2005, 105, 175-186.	0.5	44
38	Genetic evaluation of beef cattle accounting for uncertain paternity. Livestock Science, 2004, 89, 109-120.	1.2	12
39	A cDNA microarray from the telencephalon of juvenile male and female zebra finches. Journal of Neuroscience Methods, 2004, 138, 199-206.	1.3	42
40	Pharmacological Zinc and Phytase Supplementation Enhance Metallothionein mRNA Abundance and Protein Concentration in Newly Weaned Pigs. Journal of Nutrition, 2004, 134, 538-544.	1.3	46
41	Cumulative t-link threshold models for the genetic analysis of calving ease scores. Genetics Selection Evolution, 2003, 35, 489-512.	1.2	31
42	Bayesian inference on genetic merit under uncertain paternity. Genetics Selection Evolution, 2003, 35, 469-87.	1.2	24
43	Bovine mammary gene expression profiling using a cDNA microarray enhanced for mammary-specific transcripts. Physiological Genomics, 2003, 16, 8-18.	1.0	66
44	Parents' predicted transmitting abilities are not associated with culling prior to second lactation of Michigan, USA dairy cows. Preventive Veterinary Medicine, 2000, 43, 91-102.	0.7	3
45	Genetic Analysis of Fertility in Dairy Cattle Using Negative Binomial Mixed Models. Journal of Dairy Science, 1999, 82, 1834-1847.	1.4	20
46	Generalized Linear Mixed Models in Dairy Cattle Breeding. Journal of Dairy Science, 1998, 81, 1428-1444.	1.4	44
47	A Mixed Effects Model for Overdispersed Count Data in Animal Breeding. Biometrics, 1996, 52, 265.	0.8	31