

Lars RÅĳnnegÅŸrd

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

1,391
citations

430874

18
h-index

377865

34
g-index

55
all docs

55
docs citations

55
times ranked

2068
citing authors

#	ARTICLE	IF	CITATIONS
1	Capturing indirect genetic effects on phenotypic variability: Competition meets canalization. <i>Evolutionary Applications</i> , 2022, 15, 694-705.	3.1	6
2	Proportional Cerebellum Size Predicts Fear Habituation in Chickens. <i>Frontiers in Physiology</i> , 2022, 13, 826178.	2.8	1
3	Where do we find missing data in a commercial real-time location system? Evidence from 2 dairy farms. <i>JDS Communications</i> , 2021, 2, 345-350.	1.5	7
4	Homogeneity density scores of quarter milk in automatic milking systems. <i>Journal of Dairy Science</i> , 2021, 104, 10121-10130.	3.4	2
5	Detecting and predicting changes in milk homogeneity using data from automatic milking systems. <i>Journal of Dairy Science</i> , 2021, 104, 11009-11017.	3.4	3
6	Probabilistic inference of the genetic architecture underlying functional enrichment of complex traits. <i>Nature Communications</i> , 2021, 12, 6972.	12.8	14
7	Investigating Stochastic Differential Equations Modelling for Levodopa Infusion in Patients with Parkinson's Disease. <i>European Journal of Drug Metabolism and Pharmacokinetics</i> , 2020, 45, 41-49.	1.6	5
8	Comparison of methods for predicting cow composite somatic cell counts. <i>Journal of Dairy Science</i> , 2020, 103, 8433-8442.	3.4	19
9	The evolution of peer-reviewed papers. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 77-78.	2.0	0
10	Genomic Prediction Including SNP-Specific Variance Predictors. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3333-3343.	1.8	5
11	Genomic Selection. <i>Population Genomics</i> , 2018, , 427-480.	0.5	4
12	Modelling the co-evolution of indirect genetic effects and inherited variability. <i>Heredity</i> , 2018, 121, 631-647.	2.6	17
13	Artificial Selection Response due to Polygenic Adaptation from a Multilocus, Multiallelic Genetic Architecture. <i>Molecular Biology and Evolution</i> , 2017, 34, 2678-2689.	8.9	27
14	Genetics of Interactive Behavior in Silver Foxes (<i>Vulpes vulpes</i>). <i>Behavior Genetics</i> , 2017, 47, 88-101.	2.1	15
15	To What Extent do Neighbouring Populations Affect Local Population Growth Over Time?. <i>Population, Space and Place</i> , 2016, 22, 68-83.	2.3	3
16	Reindeer habitat selection under the risk of brown bear predation during calving season. <i>Ecosphere</i> , 2016, 7, e01583.	2.2	10
17	Increasing the power of genome wide association studies in natural populations using repeated measures " evaluation and implementation. <i>Methods in Ecology and Evolution</i> , 2016, 7, 792-799.	5.2	55
18	Wind farm construction impacts reindeer migration and movement corridors. <i>Landscape Ecology</i> , 2015, 30, 1527-1540.	4.2	50

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19	Genome-wide association mapping in a wild avian population identifies a link between genetic and phenotypic variation in a life-history trait. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20150156.	2.6	45
20	Fitting Conditional and Simultaneous Autoregressive Spatial Models in hglm. <i>R Journal</i> , 2015, 7, 5.	1.8	27
21	High Female Mortality Resulting in Herd Collapse in Free-Ranging Domesticated Reindeer (<i>Rangifer</i>) Tj ETQq1 1 0.784314 rgBT /Overlaid	2.5	13
22	Application of a genomic model for high-dimensional chemometric analysis. <i>Journal of Chemometrics</i> , 2014, 28, 548-557.	1.3	7
23	Estimation of genetic variance for macro- and micro-environmental sensitivity using double hierarchical generalized linear models. <i>Genetics Selection Evolution</i> , 2013, 45, 23.	3.0	51
24	A Novel Generalized Ridge Regression Method for Quantitative Genetics. <i>Genetics</i> , 2013, 193, 1255-1268.	2.9	68
25	Exploring the potential of hierarchical generalized linear models in animal breeding and genetics. <i>Journal of Animal Breeding and Genetics</i> , 2013, 130, 415-416.	2.0	4
26	MAPfastR: Quantitative Trait Loci Mapping in Outbred Line Crosses. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2147-2149.	1.8	7
27	Genetic heterogeneity of within-family variance of body weight in Atlantic salmon (<i>Salmo salar</i>). <i>Genetics Selection Evolution</i> , 2013, 45, 41.	3.0	35
28	Issues with data transformation in genome-wide association studies for phenotypic variability. <i>F1000Research</i> , 2013, 2, 200.	1.6	12
29	Inheritance Beyond Plain Heritability: Variance-Controlling Genes in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2012, 8, e1002839.	3.5	130
30	Recent developments in statistical methods for detecting genetic loci affecting phenotypic variability. <i>BMC Genetics</i> , 2012, 13, 63.	2.7	105
31	Estimation and Interpretation of Genetic Effects with Epistasis Using the NOIA Model. <i>Methods in Molecular Biology</i> , 2012, 871, 191-204.	0.9	8
32	Hierarchical likelihood opens a new way of estimating genetic values using genome-wide dense marker maps. <i>BMC Proceedings</i> , 2011, 5, S14.	1.6	7
33	Fine mapping and replication of QTL in outbred chicken advanced intercross lines. <i>Genetics Selection Evolution</i> , 2011, 43, 3.	3.0	44
34	Detecting Major Genetic Loci Controlling Phenotypic Variability in Experimental Crosses. <i>Genetics</i> , 2011, 188, 435-447.	2.9	129
35	How to deal with genotype uncertainty in variance component quantitative trait loci analyses. <i>Genetical Research</i> , 2011, 93, 333-342.	0.9	2
36	Genetic heterogeneity of residual variance - estimation of variance components using double hierarchical generalized linear models. <i>Genetics Selection Evolution</i> , 2010, 42, 8.	3.0	85

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37	Assessing a multiple QTL search using the variance component model. <i>Computational Biology and Chemistry</i> , 2010, 34, 34-41.	2.3	4
38	hglm: A Package for Fitting Hierarchical Generalized Linear Models. <i>R Journal</i> , 2010, 2, 20.	1.8	133
39	Modelling dominance in a flexible intercross analysis. <i>BMC Genetics</i> , 2009, 10, 30.	2.7	1
40	Non-iterative variance component estimation in QTL analysis. <i>Journal of Animal Breeding and Genetics</i> , 2009, 126, 110-116.	2.0	0
41	An Improved Method for Quantitative Trait Loci Detection and Identification of Within-Line Segregation in F2 Intercross Designs. <i>Genetics</i> , 2008, 178, 2315-2326.	2.9	24
42	Defining the Assumptions Underlying Modeling of Epistatic QTL Using Variance Component Methods. <i>Journal of Heredity</i> , 2008, 99, 421-425.	2.4	11
43	Evaluation of four methods used to estimate population density of moose <i>Alces alces</i> . <i>Wildlife Biology</i> , 2008, 14, 358-371.	1.4	63
44	Newton-type methods for REML estimation in genetic analysis of quantitative traits. <i>Journal of Computational Methods in Sciences and Engineering</i> , 2008, 8, 53-67.	0.2	3
45	Increasing the Efficiency of Variance Component Quantitative Trait Loci Analysis by Using Reduced-Rank Identity-by-Descent Matrices. <i>Genetics</i> , 2007, 176, 1935-1938.	2.9	8
46	Separation of base allele and sampling term effects gives new insights in variance component QTL analysis. <i>BMC Genetics</i> , 2007, 8, 1.	2.7	32
47	Is Firm Interdependence Within Industries Important for Portfolio Credit Risk?. <i>SSRN Electronic Journal</i> , 2006, , .	0.4	5
48	Quality control of waste to incineration - waste composition analysis in Lidköping, Sweden. <i>Waste Management and Research</i> , 2005, 23, 527-533.	3.9	15
49	Genetic response to selection on reindeer calf weights. <i>Rangifer</i> , 2003, 23, 13.	0.6	9
50	Breeding schemes in reindeer husbandry. <i>Rangifer</i> , 2003, 23, 45.	0.6	7
51	Lifetime patterns in adult female mass, reproduction, and offspring mass in semidomestic reindeer (<i>Rangifer tarandus tarandus</i>). <i>Canadian Journal of Zoology</i> , 2002, 80, 2047-2055.	1.0	21
52	Interpolation Methods to Improve Data Quality of Indoor Positioning Data for Dairy Cattle. <i>Frontiers in Animal Science</i> , 0, 3, .	1.9	3