

# Lars RÅĳnnegÅŸrd

## List of Publications by Year in descending order

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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	hglm: A Package for Fitting Hierarchical Generalized Linear Models. R Journal, 2010, 2, 20.	1.8	133
2	Inheritance Beyond Plain Heritability: Variance-Controlling Genes in Arabidopsis thaliana. PLoS Genetics, 2012, 8, e1002839.	3.5	130
3	Detecting Major Genetic Loci Controlling Phenotypic Variability in Experimental Crosses. Genetics, 2011, 188, 435-447.	2.9	129
4	Recent developments in statistical methods for detecting genetic loci affecting phenotypic variability. BMC Genetics, 2012, 13, 63.	2.7	105
5	Genetic heterogeneity of residual variance - estimation of variance components using double hierarchical generalized linear models. Genetics Selection Evolution, 2010, 42, 8.	3.0	85
6	A Novel Generalized Ridge Regression Method for Quantitative Genetics. Genetics, 2013, 193, 1255-1268.	2.9	68
7	Evaluation of four methods used to estimate population density of moose Alces alces. Wildlife Biology, 2008, 14, 358-371.	1.4	63
8	Increasing the power of genome wide association studies in natural populations using repeated measures " evaluation and implementation. Methods in Ecology and Evolution, 2016, 7, 792-799.	5.2	55
9	Estimation of genetic variance for macro- and micro-environmental sensitivity using double hierarchical generalized linear models. Genetics Selection Evolution, 2013, 45, 23.	3.0	51
10	Wind farm construction impacts reindeer migration and movement corridors. Landscape Ecology, 2015, 30, 1527-1540.	4.2	50
11	Genome-wide association mapping in a wild avian population identifies a link between genetic and phenotypic variation in a life-history trait. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20150156.	2.6	45
12	Fine mapping and replication of QTL in outbred chicken advanced intercross lines. Genetics Selection Evolution, 2011, 43, 3.	3.0	44
13	Genetic heterogeneity of within-family variance of body weight in Atlantic salmon (Salmo salar). Genetics Selection Evolution, 2013, 45, 41.	3.0	35
14	Separation of base allele and sampling term effects gives new insights in variance component QTL analysis. BMC Genetics, 2007, 8, 1.	2.7	32
15	Artificial Selection Response due to Polygenic Adaptation from a Multilocus, Multiallelic Genetic Architecture. Molecular Biology and Evolution, 2017, 34, 2678-2689.	8.9	27
16	Fitting Conditional and Simultaneous Autoregressive Spatial Models in hglm. R Journal, 2015, 7, 5.	1.8	27
17	An Improved Method for Quantitative Trait Loci Detection and Identification of Within-Line Segregation in F2 Intercross Designs. Genetics, 2008, 178, 2315-2326.	2.9	24
18	Lifetime patterns in adult female mass, reproduction, and offspring mass in semidomestic reindeer (Rangifer tarandus tarandus). Canadian Journal of Zoology, 2002, 80, 2047-2055.	1.0	21

#	ARTICLE	IF	CITATIONS
19	Comparison of methods for predicting cow composite somatic cell counts. <i>Journal of Dairy Science</i> , 2020, 103, 8433-8442.	3.4	19
20	Modelling the co-evolution of indirect genetic effects and inherited variability. <i>Heredity</i> , 2018, 121, 631-647.	2.6	17
21	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
22	Genetics of Interactive Behavior in Silver Foxes ( <i>Vulpes vulpes</i> ). <i>Behavior Genetics</i> , 2017, 47, 88-101.	2.1	15
23	Probabilistic inference of the genetic architecture underlying functional enrichment of complex traits. <i>Nature Communications</i> , 2021, 12, 6972.	12.8	14
24	High Female Mortality Resulting in Herd Collapse in Free-Ranging Domesticated Reindeer ( <i>Rangifer</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.5	13
25	Issues with data transformation in genome-wide association studies for phenotypic variability. <i>F1000Research</i> , 2013, 2, 200.	1.6	12
26	Defining the Assumptions Underlying Modeling of Epistatic QTL Using Variance Component Methods. <i>Journal of Heredity</i> , 2008, 99, 421-425.	2.4	11
27	Reindeer habitat selection under the risk of brown bear predation during calving season. <i>Ecosphere</i> , 2016, 7, e01583.	2.2	10
28	Genetic response to selection on reindeer calf weights. <i>Rangifer</i> , 2003, 23, 13.	0.6	9
29	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
30	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
31	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
32	MAPfastR: Quantitative Trait Loci Mapping in Outbred Line Crosses. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2147-2149.	1.8	7
33	Application of a genomic model for high-dimensional chemometric analysis. <i>Journal of Chemometrics</i> , 2014, 28, 548-557.	1.3	7
34	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
35	Breeding schemes in reindeer husbandry. <i>Rangifer</i> , 2003, 23, 45.	0.6	7
36	Capturing indirect genetic effects on phenotypic variability: Competition meets canalization. <i>Evolutionary Applications</i> , 2022, 15, 694-705.	3.1	6

#	ARTICLE	IF	CITATIONS
37	Is Firm Interdependence Within Industries Important for Portfolio Credit Risk?. SSRN Electronic Journal, 2006, , .	0.4	5
38	Genomic Prediction Including SNP-Specific Variance Predictors. G3: Genes, Genomes, Genetics, 2019, 9, 3333-3343.	1.8	5
39	Investigating Stochastic Differential Equations Modelling for Levodopa Infusion in Patients with Parkinson's Disease. European Journal of Drug Metabolism and Pharmacokinetics, 2020, 45, 41-49.	1.6	5
40	Assessing a multiple QTL search using the variance component model. Computational Biology and Chemistry, 2010, 34, 34-41.	2.3	4
41	Exploring the potential of hierarchical generalized linear models in animal breeding and genetics. Journal of Animal Breeding and Genetics, 2013, 130, 415-416.	2.0	4
42	Genomic Selection. Population Genomics, 2018, , 427-480.	0.5	4
43	Newton-type methods for REML estimation in genetic analysis of quantitative traits. Journal of Computational Methods in Sciences and Engineering, 2008, 8, 53-67.	0.2	3
44	To What Extent do Neighbouring Populations Affect Local Population Growth Over Time?. Population, Space and Place, 2016, 22, 68-83.	2.3	3
45	Detecting and predicting changes in milk homogeneity using data from automatic milking systems. Journal of Dairy Science, 2021, 104, 11009-11017.	3.4	3
46	Interpolation Methods to Improve Data Quality of Indoor Positioning Data for Dairy Cattle. Frontiers in Animal Science, 0, 3, .	1.9	3
47	How to deal with genotype uncertainty in variance component quantitative trait loci analyses. Genetical Research, 2011, 93, 333-342.	0.9	2
48	Homogeneity density scores of quarter milk in automatic milking systems. Journal of Dairy Science, 2021, 104, 10121-10130.	3.4	2
49	Modelling dominance in a flexible intercross analysis. BMC Genetics, 2009, 10, 30.	2.7	1
50	Proportional Cerebellum Size Predicts Fear Habituation in Chickens. Frontiers in Physiology, 2022, 13, 826178.	2.8	1
51	Non-iterative variance component estimation in QTL analysis. Journal of Animal Breeding and Genetics, 2009, 126, 110-116.	2.0	0
52	The evolution of peer-reviewed papers. Journal of Animal Breeding and Genetics, 2019, 136, 77-78.	2.0	0