## Denis Laloë

## List of Publications by Year in descending order

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186265 133252 3,966 77 28 59 citations h-index g-index papers 81 81 81 6157 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. Briefings in Bioinformatics, 2013, 14, 671-683.	6.5	1,064
2	Maximizing the Reliability of Genomic Selection by Optimizing the Calibration Set of Reference Individuals: Comparison of Methods in Two Diverse Groups of Maize Inbreds ( <i>Zea mays</i> L.). Genetics, 2012, 192, 715-728.	2.9	258
3	A whole genome Bayesian scan for adaptive genetic divergence in West African cattle. BMC Genomics, 2009, 10, 550.	2.8	186
4	Pangenomic Classification of Pituitary Neuroendocrine Tumors. Cancer Cell, 2020, 37, 123-134.e5.	16.8	186
5	Insights into the Genetic History of French Cattle from Dense SNP Data on 47 Worldwide Breeds. PLoS ONE, 2010, 5, e13038.	2.5	167
6	Genetic diversity measures of local European beef cattle breeds for conservation purposes. Genetics Selection Evolution, 2001, 33, 311-32.	3.0	146
7	Molecular fingerprinting of the podocyte reveals novel gene and protein regulatory networks. Kidney International, 2013, 83, 1052-1064.	5.2	130
8	Analysis of genetic relationships between 10 cattle breeds with 17 microsatellites. Animal Genetics, 1997, 28, 338-345.	1.7	86
9	Immunity Traits in Pigs: Substantial Genetic Variation and Limited Covariation. PLoS ONE, 2011, 6, e22717.	2.5	86
10	Genetic Characterization of Southwestern European Bovine Breeds: A Historical and Biogeographical Reassessment With a Set of 16 Microsatellites., 2003, 94, 243-250.		78
11	Precision and information in linear models of genetic evaluation. Genetics Selection Evolution, 1993, 25, 1.	3.0	76
12	Out of America: tracing the genetic footprints of the global diffusion of maize. Theoretical and Applied Genetics, 2013, 126, 2671-2682.	3.6	72
13	Using molecular markers and multivariate methods to study the genetic diversity of local European and Asian chicken breeds. Animal Genetics, 2008, 39, 121-129.	1.7	65
14	Contribution of mammary epithelial cells to the immune response during early stages of a bacterial infection to Staphylococcus aureus. Veterinary Research, 2014, 45, 16.	3.0	65
15	Genetic parameters for birth and weaning traits in French specialized beef cattle breeds. Livestock Science, 2004, 89, 121-128.	1.2	61
16	Characterisation and Comparison of Lactating Mouse and Bovine Mammary Gland miRNomes. PLoS ONE, 2014, 9, e91938.	2.5	61
17	The impact of genomic selection on genetic diversity and genetic gain in three French dairy cattle breeds. Genetics Selection Evolution, 2019, 51, 52.	3.0	61
18	Microsatellite-based phylogeny of Indian domestic goats. BMC Genetics, 2008, 9, 11.	2.7	58

#	Article	IF	CITATIONS
19	WIDDE: a Web-Interfaced next generation database for genetic diversity exploration, with a first application in cattle. BMC Genomics, 2015, 16, 940.	2.8	56
20	Overexpression of miR-30b in the Developing Mouse Mammary Gland Causes a Lactation Defect and Delays Involution. PLoS ONE, 2012, 7, e45727.	2.5	55
21	Evaluation models and genetic parameters for calving difficulty in beef cattle. Journal of Animal Science, 2003, 81, 933-938.	0.5	50
22	Genetic structure of eighteen local south European beef cattle breeds by comparative F-statistics analysis. Journal of Animal Breeding and Genetics, 2003, 120, 73-87.	2.0	46
23	A genomic map of climate adaptation in Mediterranean cattle breeds. Molecular Ecology, 2019, 28, 1009-1029.	3.9	46
24	DNA Methylation and Transcription in a Distal Region Upstream from the Bovine AlphaS1 Casein Gene after Once or Twice Daily Milking. PLoS ONE, 2014, 9, e111556.	2.5	39
25	Considerations on measures of precision and connectedness in mixed linear models of genetic evaluation. Genetics Selection Evolution, 1996, 28, 1.	3.0	38
26	Chondrocytes Play a Major Role in the Stimulation of Bone Growth by Thyroid Hormone. Endocrinology, 2014, 155, 3123-3135.	2.8	34
27	Next-generation sequencing identifies equine cartilage and subchondral bone miRNAs and suggests their involvement in osteochondrosis physiopathology. BMC Genomics, 2014, 15, 798.	2.8	31
28	Stable Methylation at Promoters Distinguishes Epiblast Stem Cells from Embryonic Stem Cells and the In Vivo Epiblasts. Stem Cells and Development, 2014, 23, 2014-2029.	2.1	31
29	Food Deprivation Affects the miRNome in the Lactating Goat Mammary Gland. PLoS ONE, 2015, 10, e0140111.	2.5	31
30	Is a Multivariate Consensus Representation of Genetic Relationships Among Populations Always Meaningful?. Genetics, 2002, 162, 473-484.	2.9	30
31	Caractérisation de la race bovine Somba à l'aide de marqueurs moléculaires. Revue D'Elevage Et De Medecine Veterinaire Des Pays Tropicaux, 2001, 54, 129.	0.5	28
32	Epithelial response to a high-protein diet in rat colon. BMC Genomics, 2017, 18, 116.	2.8	27
33	Genomics for Ruminants in Developing Countries: From Principles to Practice. Frontiers in Genetics, 2018, 9, 251.	2.3	25
34	Genetic structure of the European Charolais and Limousin cattle metapopulations using pedigree analyses. Journal of Animal Science, 2011, 89, 1719-1730.	0.5	23
35	Spatial Trends of Genetic Variation of Domestic Ruminants in Europe. Diversity, 2010, 2, 932-945.	1.7	22
36	A molecular analysis of the patterns of genetic diversity in local chickens from western Algeria in comparison with commercial lines and wild jungle fowls. Journal of Animal Breeding and Genetics, 2016, 133, 59-70.	2.0	21

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37	Assessment of trade-offs between feed efficiency, growth-related traits, and immune activity in experimental lines of layer chickens. Genetics Selection Evolution, 2021, 53, 44.	3.0	21
38	Sunflower oil supplementation affects the expression of miR-20a-5p and miR-142-5p in the lactating bovine mammary gland. PLoS ONE, 2017, 12, e0185511.	2.5	20
39	A proposal of criteria of robustness analysis in genetic evaluation. Livestock Science, 2003, 80, 241-256.	1.2	18
40	Consensus genetic structuring and typological value of markers using multiple co-inertia analysis. Genetics Selection Evolution, 2007, 39, 545.	3.0	18
41	Which Individuals To Choose To Update the Reference Population? Minimizing the Loss of Genetic Diversity in Animal Genomic Selection Programs. G3: Genes, Genomes, Genetics, 2018, 8, 113-121.	1.8	18
42	Characterization of Holstein and Normande whole milk miRNomes highlights breed specificities. Scientific Reports, 2019, 9, 20345.	3.3	18
43	Use of structured antedependence models for the genetic analysis of growth curves1. Journal of Animal Science, 2004, 82, 3465-3473.	0.5	17
44	Revealing fine scale subpopulation structure in the Vietnamese H'mong cattle breed for conservation purposes. BMC Genetics, 2010, 11, 45.	2.7	17
45	Genetic and transcriptomic analyses provide new insights on the early antiviral response to VHSV in resistant and susceptible rainbow trout. BMC Genomics, 2018, 19, 482.	2.8	17
46	Should genetic groups be fitted in BLUP evaluation? Practical answer for the French AI beef sire evaluation. Genetics Selection Evolution, 2004, 36, 325-45.	3.0	16
47	Domestic Fowl Breed Variation in Egg White Protein Expression: Application of Proteomics and Transcriptomics. Journal of Agricultural and Food Chemistry, 2018, 66, 11854-11863.	5.2	16
48	Impact of strong selection for the PrP major gene on genetic variability of four French sheep breeds(Open Access publication). Genetics Selection Evolution, 2008, 40, 663-680.	3.0	16
49	Estimation of genetic parameters of preweaning performance in the French Limousin cattle breed. Genetics Selection Evolution, 1993, 25, 1.	3.0	14
50	Fine-tuned adaptation of embryo–endometrium pairs at implantation revealed by transcriptome analyses in Bos taurus. PLoS Biology, 2019, 17, e3000046.	5.6	14
51	Characterization of Casein Gene Complex and Genetic Diversity Analysis in Indian Goats. Animal Biotechnology, 2010, 21, 122-134.	1.5	13
52	Molecular signatures of muscle growth and composition deciphered by the meta-analysis of age-related public transcriptomics data. Physiological Genomics, 2020, 52, 322-332.	2.3	13
53	Measuring connectedness among herds in mixed linear models: From theory to practice in large-sized genetic evaluations. Genetics Selection Evolution, 2008, 40, 145-159.	3.0	13
54	A sampling method for estimating the accuracy of predicted breeding values in genetic evaluation. Genetics Selection Evolution, 2001, 33, 473-86.	3.0	12

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55	Comparison of sow farrowing characteristics between a Chinese breed and three French breeds. Livestock Science, 2009, 125, 132-140.	1.6	12
56	Genetic and morphometric characterization of a local Vietnamese Swamp Buffalo population. Journal of Animal Breeding and Genetics, 2010, 127, 74-84.	2.0	12
57	Measuring connectedness among herds in mixed linear models: From theory to practice in large-sized genetic evaluations. Genetics Selection Evolution, 2008, 40, 145.	3.0	11
58	Detection of new pathways involved in the acceptance and the utilisation of a plant-based diet in isogenic lines of rainbow trout fry. PLoS ONE, 2018, 13, e0201462.	2.5	11
59	Genetic diversity and relationships among six local cattle populations in semi-arid areas assessed by a bovine medium-density single nucleotide polymorphism data. Animal, 2019, 13, 8-14.	3.3	11
60	The Prion-like protein Shadoo is involved in mouse embryonic and mammary development and differentiation. Scientific Reports, 2020, 10, 6765.	3.3	10
61	Etude du statut phylogénétique du bovin Kouri du lac Tchad à l'aide de marqueurs moléculaires. Revue D'Elevage Et De Medecine Veterinaire Des Pays Tropicaux, 1999, 52, 155-162.	0.5	9
62	Milk from dams fed an obesogenic diet combined with a high-fat/high-sugar diet induces long-term abnormal mammary gland development in the rabbit1. Journal of Animal Science, 2015, 93, 1641-1655.	0.5	8
63	Genetic improvement of canine hip dysplasia through sire selection across countries. Veterinary Journal, 2019, 248, 18-24.	1.7	7
64	Relations génétiques entre populations de taurins ou zébus d'Afrique de l'Ouest et taurins européens. Genetics Selection Evolution, 1998, 30, 1.	3.0	5
65	Breeding policies and management of pedigree dogs in 15 national kennel clubs. Veterinary Journal, 2018, 234, 130-135.	1.7	5
66	A unified framework for the integration of multiple hierarchical clusterings or networks from multi-source data. BMC Bioinformatics, 2021, 22, 392.	2.6	5
67	Impact of strong selection for the PrP major gene on genetic variability of four French sheep breeds (Open Access publication). Genetics Selection Evolution, 2008, 40, 663-80.	3.0	4
68	Trends of the genetic connectedness measures among Nelore beef cattle herds. Journal of Animal Breeding and Genetics, 2012, 129, 20-29.	2.0	4
69	Differences during the first lactation between cows cloned by somatic cell nuclear transfer and noncloned cows. Journal of Dairy Science, 2016, 99, 4778-4794.	3.4	4
70	Different pre-implantation phenotypes of bovine blastocysts produced in vitro. Reproduction, 2019, 157, 163-178.	2.6	4
71	Individualized multi-omic pathway deviation scores using multiple factor analysis. Biostatistics, 2020,	1.5	3
72	Consensus genetic structuring and typological value of markers using multiple co-inertia analysis. Genetics Selection Evolution, 2007, 39, 545-567.	3.0	3

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73	Landscape and bioclimatic diversity of milk protein variability in tropical goats. Small Ruminant Research, 2022, 207, 106614.	1.2	3
74	PiQSARS: A pipeline for quantitative and statistical analyses of ratiometric fluorescent biosensors. MethodsX, 2020, 7, 101034.	1.6	2
75	Intensified Use of Reproductive Technologies and Reduced Dimensions of Breeding Schemes Put Genetic Diversity at Risk in Dairy Cattle Breeds. Animals, 2020, 10, 1903.	2.3	2
76	Potential genetic robustness of Prnp and Sprn double knockout mouse embryos towards ShRNA-lentiviral inoculation. Veterinary Research, 2022, 53, .	3.0	1
77	Use of relationship matrix in the evaluation of natural service Limousin bulls. Genetics Selection Evolution, 1992, 24, 1.	3.0	0