

Laercio R Porto-Neto

List of Publications by Year in descending order

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Version: 2024-02-01

98
papers

3,650
citations

186209

28
h-index

149623

56
g-index

104
all docs

104
docs citations

104
times ranked

3234
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of Angus SteerSELECT: a genomic-based tool to identify performance differences of Australian Angus steers during feedlot finishing: Phase 1 validation. <i>Animal Production Science</i> , 2021, 61, 1884-1892.	0.6	7
2	ImmuneDEX: updated genomic estimates of genetic parameters and breeding values for Australian Angus cattle. <i>Animal Production Science</i> , 2021, 61, 1919-1924.	0.6	3
3	Genetic parameter estimates for male and female fertility traits using genomic data to improve fertility in Australian beef cattle. <i>Animal Production Science</i> , 2021, , .	0.6	7
4	Exploring genomic approaches to fast-track genetic gains in breechstrike resistance in Merino sheep. <i>Animal Production Science</i> , 2021, , .	0.6	0
5	Comparison of Genetic Merit for Weight and Meat Traits between the Polled and Horned Cattle in Multiple Beef Breeds. <i>Animals</i> , 2021, 11, 870.	1.0	6
6	ImmuneDEX: a strategy for the genetic improvement of immune competence in Australian Angus cattle. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	11
7	Network Analyses Predict Small RNAs That Might Modulate Gene Expression in the Testis and Epididymis of <i>Bos indicus</i> Bulls. <i>Frontiers in Genetics</i> , 2021, 12, 610116.	1.1	7
8	Meta-Analysis of Heifer Traits Identified Reproductive Pathways in <i>Bos indicus</i> Cattle. <i>Genes</i> , 2021, 12, 768.	1.0	27
9	Introgression, admixture, and selection facilitate genetic adaptation to high-altitude environments in cattle. <i>Genomics</i> , 2021, 113, 1491-1503.	1.3	10
10	Multiple Country and Breed Genomic Prediction of Tick Resistance in Beef Cattle. <i>Frontiers in Immunology</i> , 2021, 12, 620847.	2.2	14
11	Chromatin accessibility and regulatory vocabulary across indicine cattle tissues. <i>Genome Biology</i> , 2021, 22, 273.	3.8	21
12	Bias, dispersion, and accuracy of genomic predictions for feedlot and carcass traits in Australian Angus steers. <i>Genetics Selection Evolution</i> , 2021, 53, 77.	1.2	7
13	Associations between immune competence phenotype and feedlot health and productivity in Angus cattle. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	6
14	A low-density SNP genotyping panel for the accurate prediction of cattle breeds. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	10
15	Optimized Genetic Testing for Polledness in Multiple Breeds of Cattle. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 539-544.	0.8	12
16	Genome-Wide Co-Expression Distributions as a Metric to Prioritize Genes of Functional Importance. <i>Genes</i> , 2020, 11, 1231.	1.0	1
17	Genetic control of temperament traits across species: association of autism spectrum disorder risk genes with cattle temperament. <i>Genetics Selection Evolution</i> , 2020, 52, 51.	1.2	25
18	Exploring the Regulatory Potential of Long Non-Coding RNA in Feed Efficiency of Indicine Cattle. <i>Genes</i> , 2020, 11, 997.	1.0	11

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19	X chromosome variants are associated with male fertility traits in two bovine populations. <i>Genetics Selection Evolution</i> , 2020, 52, 46.	1.2	16
20	Uncovering Sub-Structure and Genomic Profiles in Across-Countries Subpopulations of Angus Cattle. <i>Scientific Reports</i> , 2020, 10, 8770.	1.6	6
21	In silico validation of pooled genotyping strategies for genomic evaluation in Angus cattle. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	3
22	Selection signatures in tropical cattle are enriched for promoter and coding regions and reveal missense mutations in the damage response gene HELB. <i>Genetics Selection Evolution</i> , 2020, 52, 27.	1.2	17
23	Gene Networks Driving Genetic Variation in Milk and Cheese-Making Traits of Spanish Assaf Sheep. <i>Genes</i> , 2020, 11, 715.	1.0	15
24	Association analysis of loci implied in buffering epistasis. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	2
25	272 Proposing a combination of heritable fertility traits for bull selection. <i>Journal of Animal Science</i> , 2020, 98, 83-84.	0.2	0
26	Across-sex genomic-assisted genetic correlations for sex-influenced traits in Brahman cattle. <i>Genetics Selection Evolution</i> , 2019, 51, 41.	1.2	6
27	Genomic clues of the evolutionary history of <i>Bos indicus</i> cattle. <i>Animal Genetics</i> , 2019, 50, 557-568.	0.6	59
28	Pooled genotyping strategies for the rapid construction of genomic reference populations1. <i>Journal of Animal Science</i> , 2019, 97, 4761-4769.	0.2	14
29	Systems Biology Reveals NR2F6 and TGFB1 as Key Regulators of Feed Efficiency in Beef Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 230.	1.1	41
30	DNA Testing and Genetic Evaluation for Poll Breeding in Tropically Adapted Beef Cattle. <i>Proceedings (mdpi)</i> , 2019, 36, 98.	0.2	0
31	Neuropeptidome of the Hypothalamus and Pituitary Gland of Indicine $\tilde{\text{A}}$ —Taurine Heifers: Evidence of Differential Neuropeptide Processing in the Pituitary Gland before and after Puberty. <i>Journal of Proteome Research</i> , 2018, 17, 1852-1865.	1.8	13
32	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. <i>Nature Communications</i> , 2018, 9, 859.	5.8	126
33	Mammalian genomic regulatory regions predicted by utilizing human genomics, transcriptomics, and epigenetics data. <i>GigaScience</i> , 2018, 7, 1-17.	3.3	27
34	Weighting genomic and genealogical information for genetic parameter estimation and breeding value prediction in tropical beef cattle. <i>Journal of Animal Science</i> , 2018, 96, 612-617.	0.2	5
35	Candidate mutations used to aid the prediction of genetic merit for female reproductive traits in tropical beef cattle. <i>Revista Brasileira De Zootecnia</i> , 2018, 47, .	0.3	4
36	Accuracy of genomic selection predictions for hip height in Brahman cattle using different relationship matrices. <i>Pesquisa Agropecuaria Brasileira</i> , 2018, 53, 717-726.	0.9	3

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37	Combining multi-OMICs information to identify key-regulator genes for pleiotropic effect on fertility and production traits in beef cattle. PLoS ONE, 2018, 13, e0205295.	1.1	33
38	Pre- and post-puberty expression of genes and proteins in the uterus of <i>Bos indicus</i> heifers: the luteal phase effect post-puberty. Animal Genetics, 2018, 49, 539-549.	0.6	20
39	Convergent Evolution of Slick Coat in Cattle through Truncation Mutations in the Prolactin Receptor. Frontiers in Genetics, 2018, 9, 57.	1.1	45
40	Evaluation of nonadditive effects in yearling weight of tropical beef cattle. Journal of Animal Science, 2018, 96, 4028-4034.	0.2	13
41	RAPID COMMUNICATION: A haplotype information theory method reveals genes of evolutionary interest in European vs. Asian pigs. Journal of Animal Science, 2018, 96, 3064-3069.	0.2	3
42	Genetic diversity and signatures of selection in various goat breeds revealed by genome-wide SNP markers. BMC Genomics, 2017, 18, 229.	1.2	141
43	Estimating the genetic merit of sires by using pooled DNA from progeny of undetermined pedigree. Genetics Selection Evolution, 2017, 49, 28.	1.2	19
44	The <i>Bos taurus</i> – <i>Bos indicus</i> balance in fertility and milk related genes. PLoS ONE, 2017, 12, e0181930.	1.1	33
45	Global differential gene expression in the pituitary gland and the ovaries of pre- and postpubertal Brahman heifers. Journal of Animal Science, 2017, 95, 599.	0.2	14
46	Genomic inbreeding depression for climatic adaptation of tropical beef cattle. Journal of Animal Science, 2017, 95, 3809.	0.2	21
47	Candidate Gene Expression in <i>Bos indicus</i> Ovarian Tissues: Prepubertal and Postpubertal Heifers in Diestrus. Frontiers in Veterinary Science, 2016, 3, 94.	0.9	7
48	Transcriptome analyses identify five transcription factors differentially expressed in the hypothalamus of post- versus prepubertal Brahman heifers. Journal of Animal Science, 2016, 94, 3693-3702.	0.2	27
49	Genomic structure and marker-derived gene networks for growth and meat quality traits of Brazilian Nelore beef cattle. BMC Genomics, 2016, 17, 235.	1.2	31
50	Genomic analyses of tropical beef cattle fertility based on genotyping pools of Brahman cows with unknown pedigree. Journal of Animal Science, 2016, 94, 4096-4108.	0.2	29
51	Polymorphisms and genes associated with puberty in heifers. Theriogenology, 2016, 86, 333-339.	0.9	12
52	Prioritization for conservation of Iranian native cattle breeds based on genome-wide SNP data. Conservation Genetics, 2016, 17, 77-89.	0.8	16
53	Identification of Gene Networks for Residual Feed Intake in Angus Cattle Using Genomic Prediction and RNA-seq. PLoS ONE, 2016, 11, e0152274.	1.1	106
54	Genome-wide association for the outcome of fixed-time artificial insemination of Brahman heifers in northern Australia. Journal of Animal Science, 2015, 93, 5119-5127.	0.2	12

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55	Prospecting major genes in dairy buffaloes. <i>BMC Genomics</i> , 2015, 16, 872.	1.2	97
56	Compression distance can discriminate animals by genetic profile, build relationship matrices and estimate breeding values. <i>Genetics Selection Evolution</i> , 2015, 47, 78.	1.2	7
57	Genomic correlation: harnessing the benefit of combining two unrelated populations for genomic selection. <i>Genetics Selection Evolution</i> , 2015, 47, 84.	1.2	35
58	Towards breed formation by island model divergence in Korean cattle. <i>BMC Evolutionary Biology</i> , 2015, 15, 284.	3.2	11
59	Low frequency of Y anomaly detected in Australian Brahman cow-herds. <i>Meta Gene</i> , 2015, 3, 59-61.	0.3	2
60	Non-synonymous mutations mapped to chromosome X associated with andrological and growth traits in beef cattle. <i>BMC Genomics</i> , 2015, 16, 384.	1.2	34
61	Characterization of linkage disequilibrium, consistency of gametic phase and admixture in Australian and Canadian goats. <i>BMC Genetics</i> , 2015, 16, 67.	2.7	91
62	Multi-Tissue Omics Analyses Reveal Molecular Regulatory Networks for Puberty in Composite Beef Cattle. <i>PLoS ONE</i> , 2014, 9, e102551.	1.1	125
63	The Genetic Architecture of Climatic Adaptation of Tropical Cattle. <i>PLoS ONE</i> , 2014, 9, e113284.	1.1	128
64	Genome-wide detection of signatures of selection in Korean Hanwoo cattle. <i>Animal Genetics</i> , 2014, 45, 180-190.	0.6	40
65	Speed Index in the Racing Quarter Horse: A Genome-wide Association Study. <i>Journal of Equine Veterinary Science</i> , 2014, 34, 1263-1268.	0.4	10
66	Linkage disequilibrium over short physical distances measured in sheep using a high-density SNP chip. <i>Animal Genetics</i> , 2014, 45, 754-757.	0.6	113
67	Variation in genes involved in epigenetic processes offers insights into tropically adapted cattle diversity. <i>Frontiers in Genetics</i> , 2014, 5, 89.	1.1	1
68	Performance of different SNP panels for parentage testing in two East Asian cattle breeds. <i>Animal Genetics</i> , 2014, 45, 572-575.	0.6	27
69	Post-partum anoestrus in tropical beef cattle: A systems approach combining gene expression and genome-wide association results. <i>Livestock Science</i> , 2014, 166, 158-166.	0.6	11
70	The extent of linkage disequilibrium in beef cattle breeds using high-density SNP genotypes. <i>Genetics Selection Evolution</i> , 2014, 46, 22.	1.2	113
71	Information compression exploits patterns of genome composition to discriminate populations and highlight regions of evolutionary interest. <i>BMC Bioinformatics</i> , 2014, 15, 66.	1.2	15
72	A marker-derived gene network reveals the regulatory role of PPARGC1A, HNF4G, and FOXP3 in intramuscular fat deposition of beef cattle. <i>Journal of Animal Science</i> , 2014, 92, 2832-2845.	0.2	77

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73	<sc>snpqc</sc> â€“ an R pipeline for quality control of <sc>l</sc>llumina <sc>SNP</sc> genotyping array data. Animal Genetics, 2014, 45, 758-761.	0.6	25
74	Genome-Wide Mapping of Loci Explaining Variance in Scrotal Circumference in Nellore Cattle. PLoS ONE, 2014, 9, e88561.	1.1	33
75	Genome-wide association study for birth weight in Nellore cattle points to previously described orthologous genes affecting human and bovine height. BMC Genetics, 2013, 14, 52.	2.7	111
76	Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. BMC Genomics, 2013, 14, 876.	1.2	142
77	R for Genome-Wide Association Studies. Methods in Molecular Biology, 2013, 1019, 1-17.	0.4	9
78	Quality Control for Genome-Wide Association Studies. Methods in Molecular Biology, 2013, 1019, 129-147.	0.4	10
79	Detection of Signatures of Selection Using F ST. Methods in Molecular Biology, 2013, 1019, 423-436.	0.4	34
80	Genome-Wide Analysis of the World's Sheep Breeds Reveals High Levels of Historic Mixture and Strong Recent Selection. PLoS Biology, 2012, 10, e1001258.	2.6	719
81	Tracking the Emergence of a New Breed Using 49,034 SNP in Sheep. PLoS ONE, 2012, 7, e41508.	1.1	9
82	The RIPK2 gene: a positional candidate for tick burden supported by genetic associations in cattle and immunological response of knockout mouse. Immunogenetics, 2012, 64, 379-388.	1.2	9
83	Variation in the <sc><i>XKR4</i></sc> gene was significantly associated with subcutaneous rump fat thickness in indicine and composite cattle. Animal Genetics, 2012, 43, 785-789.	0.6	46
84	DNA variation in the gene ELTD1 is associated with tick burden in cattle. Animal Genetics, 2011, 42, 50-55.	0.6	21
85	Molecular genetic approaches for identifying the basis of variation in resistance to tick infestation in cattle. Veterinary Parasitology, 2011, 180, 165-172.	0.7	58
86	A genome-wide association study of meat and carcass traits in Australian cattle1. Journal of Animal Science, 2011, 89, 2297-2309.	0.2	112
87	Effect of SNP origin on analyses of genetic diversity in cattle. Animal Production Science, 2010, 50, 792.	0.6	15
88	Haplotypes that include the integrin alpha 11 gene are associated with tick burden in cattle. BMC Genetics, 2010, 11, 55.	2.7	24
89	A genome-wide association study of tick burden and milk composition in cattle. Animal Production Science, 2010, 50, 235.	0.6	37
90	Myostatin (GDF8) single nucleotide polymorphisms in Nellore cattle. Genetics and Molecular Research, 2009, 8, 822-830.	0.3	36

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91	Germicide capacity of macrophages ($M\ddot{u}1/2$) in the Antarctic fish <i>Notothenia coriiceps</i> (Richardson, 1844) at $0\ddot{u}1/2$ C. <i>Polar Biology</i> , 2005, 28, 326-328.	0.5	13
92	Microscopical study of experimental wound healing in <i>Notothenia coriiceps</i> (CabeĂšsuda) at $0\ddot{u}$ C. <i>Cell and Tissue Research</i> , 2005, 321, 401-410.	1.5	14
93	Satellyptus: analysis and database of microsatellites from ESTs of <i>Eucalyptus</i> . <i>Genetics and Molecular Biology</i> , 2005, 28, 589-600.	0.6	22
94	Kinetics of induced wound repair at $0\ddot{u}$ C in the Antarctic fish (CabeĂšsuda) <i>Notothenia coriiceps</i> . <i>Polar Biology</i> , 2004, 27, 458-465.	0.5	11
95	New perspectives on the dispersal mechanisms of the Antarctic brooding bivalve <i>Mysella charcoti</i> (Lamy, 1906). <i>Polar Biology</i> , 2002, 25, 538-541.	0.5	19
96	Phagocytosis in vitro and in vivo in the Antarctic sea urchin <i>Sterechinus neumayeri</i> at $0\ddot{u}$ C. <i>Polar Biology</i> , 2002, 25, 891-897.	0.5	22
97	Phagocytosis and giant cell formation at 0 o C by macrophage (MO) of <i>Notothenia coriiceps</i> . <i>Journal of Fish Biology</i> , 2002, 60, 466-478.	0.7	16
98	Comparative Study of in Vivo and in Vitro Phagocytosis Including Germicidal Capacity in <i>Odontaster validus</i> (Koehler, 1906) at $0\ddot{u}$ C. <i>Journal of Invertebrate Pathology</i> , 2001, 77, 180-185.	1.5	16