Roberto Carvalheiro

List of Publications by Year
in descending order

113 papers	2,636 citations	185998 28 h-index	243296 44 g-index
118 all docs	118 docs citations	118 times ranked	1955 citing authors

#	Article	IF	Citations
1	Genomic Prediction Accuracy for Resistance Against *Piscirickettsia salmonis* in Farmed Rainbow Trout. G3: Genes, Genomes, Genetics, 2018, 8, 719-726.	0.8	122
2	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
3	Study of whole genome linkage disequilibrium in Nellore cattle. BMC Genomics, 2013, 14, 305.	1.2	106
4	Accuracy of genotype imputation in Nelore cattle. Genetics Selection Evolution, 2014, 46, 69.	1.2	86
5	Genome-Wide Association Study for Indicator Traits of Sexual Precocity in Nellore Cattle. PLoS ONE, 2016, 11, e0159502.	1.1	82
6	Accuracy of genomic predictions in Bos indicus (Nellore) cattle. Genetics Selection Evolution, 2014, 46, 17.	1.2	77
7	Genome-Wide Association Study of Meat Quality Traits in Nellore Cattle. PLoS ONE, 2016, 11, e0157845.	1.1	76
8	Single-step genomic evaluation improves accuracy of breeding value predictions for resistance to infectious pancreatic necrosis virus in rainbow trout. Genomics, 2019, 111, 127-132.	1.3	74
9	A comparison of statistical methods for genomic selection in a mice population. BMC Genetics, 2012, 13, 100.	2.7	72
10	Bayesian genome‐wide association analysis for body weight in farmed Atlantic salmon (*Salmo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5(	0.6	70
11	Linkage disequilibrium levels in Bos indicus and Bos taurus cattle using medium and high density SNP chip data and different minor allele frequency distributions. Livestock Science, 2014, 166, 121-132.	0.6	69
12	Assessment of autozygosity in Nellore cows (Bos indicus) through high-density SNP genotypes. Frontiers in Genetics, 2015, 6, 5.	1.1	69
13	Genome-wide CNV analysis reveals variants associated with growth traits in Bos indicus. BMC Genomics, 2016, 17, 419.	1.2	69
14	Genome-wide association between single nucleotide polymorphisms with beef fatty acid profile in Nellore cattle using the single step procedure. BMC Genomics, 2016, 17, 213.	1.2	66
15	Accuracy of genotype imputation and genomic predictions in a two-generation farmed Atlantic salmon population using high-density and low-density SNP panels. Aquaculture, 2018, 491, 147-154.	1.7	56
16	Accuracies of genomic prediction of feed efficiency traits using different prediction and validation methods in an experimental Nelore cattle population1. Journal of Animal Science, 2016, 94, 3613-3623.	0.2	55
17	Sliding window haplotype approaches overcome single SNP analysis limitations in identifying genes for meat tenderness in Nelore cattle. BMC Genetics, 2019, 20, 8.	2.7	53
18	Genomic prediction of breeding values for carcass traits in Nellore cattle. Genetics Selection Evolution, 2016, 48, 7.	1.2	48

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19	A PLAG1 mutation contributed to stature recovery in modern cattle. Scientific Reports, 2017, 7, 17140.	1.6	42
20	Population Genomic Structure and Genome-Wide Linkage Disequilibrium in Farmed Atlantic Salmon (Salmo salar L.) Using Dense SNP Genotypes. Frontiers in Genetics, 2018, 9, 649.	1.1	38
21	Genome-wide association study provides strong evidence of genes affecting the reproductive performance of Nellore beef cows. PLoS ONE, 2017, 12, e0178551.	1.1	36
22	Unraveling genetic sensitivity of beef cattle to environmental variation under tropical conditions. Genetics Selection Evolution, 2019, 51, 29.	1.2	35
23	Genome-Wide Mapping of Loci Explaining Variance in Scrotal Circumference in Nellore Cattle. PLoS ONE, 2014, 9, e88561.	1.1	33
24	Genome-wide association study of reproductive traits in Nellore heifers using Bayesian inference. Genetics Selection Evolution, 2015, 47, 67.	1.2	32
25	Accuracy of genomic predictions in Gyr (Bos indicus) dairy cattle. Journal of Dairy Science, 2017, 100, 5479-5490.	1.4	32
26	Genetic parameter estimates for carcass traits and visual scores including or not genomic information1. Journal of Animal Science, 2016, 94, 1821-1826.	0.2	31
27	Genome scan for postmortem carcass traits in Nellore cattle1. Journal of Animal Science, 2016, 94, 4087-4095.	0.2	31
28	Genetics and genomics of uniformity and resilience in livestock and aquaculture species: A review. Journal of Animal Breeding and Genetics, 2020, 137, 263-280.	0.8	30
29	Genome-wide scan highlights the role of candidate genes on phenotypic plasticity for age at first calving in Nellore heifers. Scientific Reports, 2020, 10, 6481.	1.6	30
30	Genotype Ã— environment interaction for age at first calving, scrotal circumference, and yearling weight in Nellore cattle using reaction norms in multitrait random regression models. Journal of Animal Science, 2015, 93, 1503-1510.	0.2	29
31	Strategies for single nucleotide polymorphism (SNP) genotyping to enhance genotype imputation in Gyr (Bos indicus) dairy cattle: Comparison of commercially available SNP chips. Journal of Dairy Science, 2015, 98, 4969-4989.	1.4	29
32	Low levels of taurine introgression in the current Brazilian Nelore and Gir indicine cattle populations. Genetics Selection Evolution, 2015, 47, 31.	1.2	29
33	Genetic variability of residual variance of production traits in Nellore beef cattle. Livestock Science, 2011, 142, 164-169.	0.6	25
34	Genetic control of temperament traits across species: association of autism spectrum disorder risk genes with cattle temperament. Genetics Selection Evolution, 2020, 52, 51.	1.2	25
35	Genetic and environmental heterogeneity of residual variance of weight traits in Nellore beef cattle. Genetics Selection Evolution, 2012, 44, 19.	1.2	23
36	Genome-wide association study for growth traits in Nelore cattle. Animal, 2018, 12, 1358-1362.	1.3	23

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37	Association of Copy Number Variation at Intron 3 of HMGA2 With Navel Length in Bos indicus. Frontiers in Genetics, 2018, 9, 627.	1.1	23
38	Genomic selection for meat quality traits in Nelore cattle. Meat Science, 2019, 148, 32-37.	2.7	23
39	Pleiotropic Genes Affecting Carcass Traits in Bos indicus (Nellore) Cattle Are Modulators of Growth. PLoS ONE, 2016, 11, e0158165.	1.1	23
40	Principal component analysis of breeding values for growth and reproductive traits and genetic association with adult size in beef cattle1. Journal of Animal Science, 2016, 94, 5014-5022.	0.2	21
41	Reaction norm for yearling weight in beef cattle using single-step genomic evaluation1. Journal of Animal Science, 2018, 96, 27-34.	0.2	21
42	Multitrait meta-analysis identified genomic regions associated with sexual precocity in tropical beef cattle1. Journal of Animal Science, 2018, 96, 4087-4099.	0.2	21
43	Assessing the value of phenotypic information from non-genotyped animals for QTL mapping of complex traits in real and simulated populations. BMC Genetics, 2016, 17, 89.	2.7	20
44	Comparative Genomic Analysis of Three Salmonid Species Identifies Functional Candidate Genes Involved in Resistance to the Intracellular Bacterium Piscirickettsia salmonis. Frontiers in Genetics, 2019, 10, 665.	1.1	20
45	Whole-genome sequencing provides new insights into genetic mechanisms of tropical adaptation in Nellore (Bos primigenius indicus). Scientific Reports, 2020, 10, 9412.	1.6	20
46	Genetic control of residual variance of yearling weight in Nellore beef cattle. Journal of Animal Science, 2017, 95, 1425-1433.	0.2	18
47	Unravelling biological biotypes for growth, visual score and reproductive traits in Nellore cattle via principal component analysis. Livestock Science, 2018, 217, 37-43.	0.6	18
48	Genomic predictions combining SNP markers and copy number variations in Nellore cattle. BMC Genomics, 2018, 19, 441.	1.2	18
49	Strategies for genotype imputation in composite beef cattle. BMC Genetics, 2015, 16, 99.	2.7	17
50	Imputation accuracy to whole-genome sequence in Nellore cattle. Genetics Selection Evolution, 2021, 53, 27.	1.2	17
51	Optimum contribution selection using differential evolution. Revista Brasileira De Zootecnia, 2010, 39, 1429-1436.	0.3	16
52	Evaluation of mature cow weight: Genetic correlations with traits used in selection indices, correlated responses, and genetic trends in Nelore cattle. Journal of Animal Science, 2013, 91, 20-28.	0.2	15
53	Genetic parameter estimates for temperament, heifer rebreeding, and stayability in Nellore cattle. Livestock Science, 2017, 206, 45-50.	0.6	15
54	Prediction of meat quality traits in Nelore cattle by near-infrared reflectance spectroscopy1. Journal of Animal Science, 2018, 96, 4229-4237.	0.2	15

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55	Use of ridge regression for the prediction of early growth performance in crossbred calves. Genetics and Molecular Biology, 2007, 30, 536-544.	0.6	14
56	Mate selection in aquaculture breeding using differential evolution algorithm. Aquaculture Research, 2017, 48, 5490-5497.	0.9	13
57	Genome-wide association study using haplotype alleles for the evaluation of reproductive traits in Nelore cattle. PLoS ONE, 2018, 13, e0201876.	1.1	13
58	RAPID COMMUNICATION: Multi-breed validation study unraveled genomic regions associated with puberty traits segregating across tropically adapted breeds1. Journal of Animal Science, 2019, 97, 3027-3033.	0.2	13
59	Genome Association Study for Visual Scores in Nellore Cattle Measured at Weaning. BMC Genomics, 2019, 20, 150.	1.2	13
60	Genome-wide prediction for complex traits under the presence of dominance effects in simulated populations using GBLUP and machine learning methods. Journal of Animal Science, 2020, 98, .	0.2	13
61	Comparison of selection criteria for pre-weaning growth traits of Nelore cattle. Livestock Science, 2004, 86, 163-167.	1.2	12
62	Genetic effects on preweaning weight gain of Nelore-Hereford calves according to different models and estimation methods1. Journal of Animal Science, 2006, 84, 2925-2933.	0.2	12
63	Genetic relationship among reproductive traits in Nellore cattle. Animal, 2015, 9, 760-765.	1.3	11
64	Comparison of models for the genetic evaluation of reproductive traits with censored data in Nellore cattle1. Journal of Animal Science, 2016, 94, 2297-2306.	0.2	11
65	Genomic regions underlying uniformity of yearling weight in Nellore cattle evaluated under different response variables. BMC Genomics, 2018, 19, 619.	1.2	11
66	Genomic analysis of stayability in Nellore cattle. PLoS ONE, 2017, 12, e0179076.	1.1	11
67	Estimativas de efeitos genéticos em bezerros cruzados por diferentes modelos e métodos de estimação. Revista Brasileira De Zootecnia, 2006, 35, 1020-1027.	0.3	11
68	Sustainable Intensification of Beef Production in the Tropics: The Role of Genetically Improving Sexual Precocity of Heifers. Animals, 2022, 12, 174.	1.0	11
69	Genomics applied to livestock and aquaculture breeding. Evolutionary Applications, 2022, 15, 517-522.	1.5	11
70	Imputation of non-genotyped individuals using genotyped progeny in Nellore, a Bos indicus cattle breed. Livestock Science, 2014, 166, 176-189.	0.6	10
71	Body condition score of Nellore beef cows: a heritable measure to improve the selection of reproductive and maternal traits. Animal, 2015, 9, 1278-1284.	1.3	10
72	Efeitos da Heterogeneidade de Variância Residual entre Grupos de Contemporâneos na Avaliação Genética de Bovinos de Corte. Revista Brasileira De Zootecnia, 2002, 31, 1680-1688.	0.3	10

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73	Genome-wide association study and functional analysis of feet and leg conformation traits in Nellore cattle. Journal of Animal Science, 2018, 96, 1617-1627.	0.2	9
74	Genetic and genomic analyses of testicular hypoplasia in Nellore cattle. PLoS ONE, 2019, 14, e0211159.	1.1	9
75	Mate selection allows changing the genetic variability of the progeny while optimizing genetic response and controlling inbreeding. Aquaculture, 2018, 495, 409-414.	1.7	8
76	Prediction of genomic breeding values for reproductive traits in Nellore heifers. Theriogenology, 2019, 125, 12-17.	0.9	8
77	Development of a SNP linkage map and genome-wide association study for resistance to Aeromonas hydrophila in pacu (Piaractus mesopotamicus). BMC Genomics, 2020, 21, 672.	1.2	8
78	Genotype by environment interaction and genetic parameters for growth traits in the Neotropical fish pacu (Piaractus mesopotamicus). Aquaculture, 2021, 530, 735933.	1.7	8
79	Signatures of selection in Nelore cattle revealed by whole-genome sequencing data. Genomics, 2022, 114, 110304.	1.3	8
80	Genetic parameters for an alternative criterion to improve productive longevity of Nellore cows1. Journal of Animal Science, 2012, 90, 4209-4216.	0.2	7
81	Meta-analysis across Nellore cattle populations identifies common metabolic mechanisms that regulate feed efficiency-related traits. BMC Genomics, 2022, 23, .	1.2	7
82	Uncovering Sub-Structure and Genomic Profiles in Across-Countries Subpopulations of Angus Cattle. Scientific Reports, 2020, 10, 8770.	1.6	6
83	Application of a novel 50K SNP genotyping array to assess the genetic diversity and linkage disequilibrium in a farmed Pacific white shrimp (Litopenaeus vannamei) population. Aquaculture Reports, 2021, 20, 100691.	0.7	6
84	Accuracy of genotype imputation to whole genome sequencing level using different populations of Nile tilapia. Aquaculture, 2022, 551, 737947.	1.7	6
85	Influence of X-chromosome markers on reproductive traits of beef cattle. Livestock Science, 2019, 220, 152-157.	0.6	5
86	Accounting for population structure in selective cow genotyping strategies. Journal of Animal Breeding and Genetics, 2019, 136, 23-39.	0.8	5
87	Herd-of-origin effect on the post-weaning performance of centrally tested Nellore beef cattle. Tropical Animal Health and Production, 2014, 46, 1235-1241.	0.5	4
88	Genetic analysis of the temperament of Nellore cattle using linear and threshold models. Animal, 2015, 9, 388-394.	1.3	4
89	Genetic analysis of feet and leg conformation traits in Nelore cattle1. Journal of Animal Science, 2017, 95, 2379-2384.	0.2	4
90	Genomic regions associated with principal components for growth, visual score and reproductive traits in Nellore cattle. Livestock Science, 2020, 233, 103936.	0.6	4

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91	Investigating potential causal relationships among carcass and meat quality traits using structural equation model in Nellore cattle. Meat Science, 2022, 187, 108771.	2.7	4
92	Current applications and perspectives of genomic selection in Bos indicus (Nellore) cattle. Livestock Science, 2022, 263, 105001.	0.6	4
93	Dois critérios de seleção na pré- desmama em bovinos da raça Gir. 2. Efeito na classificação dos animais. Revista Brasileira De Zootecnia, 2005, 34, 816-826.	0.3	3
94	Comparação de critérios de seleção para precocidade de crescimento em bovinos da raça Guzerá. Revista Brasileira De Zootecnia, 2009, 38, 284-291.	0.3	3
95	Acasalamento dirigido para aumentar a produção de animais geneticamente superiores e reduzir a variabilidade da progênie em bovinos. Revista Brasileira De Zootecnia, 2009, 38, 1201-1204.	0.3	3
96	Analysis of genetic correlations of hip height with selection indices and mature weight in Nelore cattle. Journal of Applied Genetics, 2013, 54, 89-95.	1.0	3
97	Contribuição genética ótima aplicada à seleção de ovinos Santa Inês. Pesquisa Agropecuaria Brasileira, 2016, 51, 745-750.	0.9	3
98	Evaluation of longevity modeling censored records in Nellore. Animal, 2017, 11, 2113-2119.	1.3	3
99	Reproductive performance of cows and genetic correlation with weight gains and principal components of traits used in selection of Nelore cattle. Livestock Science, 2019, 229, 77-84.	0.6	3
100	Mate selection provides similar genetic progress and average inbreeding than optimum contribution selection in the long-term. Aquaculture, 2020, 526, 735376.	1.7	3
101	Dois critérios de seleção na pré-desmama em bovinos da raça Gir. 1. Estimativas de parâmetros genéticos. Revista Brasileira De Zootecnia, 2005, 34, 807-815.	0.3	3
102	Trait-specific long-term consequences of genomic selection in beef cattle. Genetica, 2018, 146, 85-99.	0.5	2
103	Across‐breed validation study confirms and identifies new loci associated with sexual precocity in Brahman and Nellore cattle. Journal of Animal Breeding and Genetics, 2020, 137, 139-154.	0.8	2
104	Comparison of GWA statistical methods for traits under different genetic structures: A simulation study. Livestock Science, 2020, 241, 104213.	0.6	2
105	Effect of harvest weight and its uniformity on survival in Litopenaeus vannamei reared in different systems. Aquaculture, 2021, 531, 735891.	1.7	1
106	Comparison of methods for predicting genomic breeding values for growth traits in Nellore cattle. Tropical Animal Health and Production, 2021, 53, 349.	0.5	1
107	Association Mapping for Sugarcane Quality Traits at Three Harvest Times. Sugar Tech, 0, , 1.	0.9	1
108	Effect of quality control, density and allele frequency of markers on the accuracy of genomic prediction for complex traits in Nellore cattle. Animal Production Science, 2019, 59, 48.	0.6	1

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109	Uso combinado de sêmen sexado e acasalamento dirigido sobre uma população de bovinos de corte submetida a seleção: estudo de simulação. Revista Brasileira De Zootecnia, 2009, 38, 2368-2374.	0.3	1
110	How Bioinformatics Enables Livestock Applied Sciences in the Genomic Era. Lecture Notes in Computer Science, 2012, , 192-201.	1.0	1
111	Alternative adjustment of scrotal circumference for growth traits in Nellore cattle. Revista Brasileira De Zootecnia, 2020, 49, .	0.3	1
112	Development of genomic predictions for Angus cattle in Brazil incorporating genotypes from related American sires. Journal of Animal Science, 2022, , .	0.2	1
113	A Random Forest-Based Genome-Wide Scan Reveals Fertility-Related Candidate Genes and Potential Inter-Chromosomal Epistatic Regions Associated With Age at First Calving in Nellore Cattle. Frontiers in Genetics, 2022, 13, .	1.1	1