

Pablo A S Fonseca

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

28
papers

173
citations

8
h-index

12
g-index

31
ext. papers

319
ext. citations

3.1
avg. IF

2.97
L-index

#	Paper	IF	Citations
28	Genome-wide association study for meat tenderness in beef cattle identifies patterns of the genetic contribution in different post-mortem stages.. <i>Meat Science</i> , 2022 , 186, 108733	6.4	1
27	Working memory and arithmetic impairments in children with FMR1 premutation and gray zone alleles. <i>Dementia E Neuropsychologia</i> , 2022 , 16, 105-114	2.1	
26	Genome-wide association study for beef fatty acid profile using haplotypes in Nellore cattle. <i>Livestock Science</i> , 2021 , 245, 104396	1.7	3
25	Genetic Diversity and Population Genetic Structure of a Guzerá() Meta-Population. <i>Animals</i> , 2021 , 11,	3.1	2
24	Putative Causal Variant on for the Epileptic Phenotype in the Model Wistar Audiogenic Rat. <i>Frontiers in Neurology</i> , 2021 , 12, 647859	4.1	1
23	Genomic and phenotypic analyses of antral follicle count in Aberdeen Angus cows. <i>Livestock Science</i> , 2021 , 249, 104534	1.7	
22	Genes underlying genetic correlation between growth, reproductive and parasite burden traits in beef cattle. <i>Livestock Science</i> , 2021 , 244, 104332	1.7	1
21	Identification of functional candidate variants and genes for feed efficiency in Holstein and Jersey cattle breeds using RNA-sequencing. <i>Journal of Dairy Science</i> , 2021 , 104, 1928-1950	4	6
20	Genetic mechanisms underlying feed utilization and implementation of genomic selection for improved feed efficiency in dairy cattle. <i>Canadian Journal of Animal Science</i> , 2020 , 100, 587-604	0.9	7
19	Weighted Gene Correlation Network Meta-Analysis Reveals Functional Candidate Genes Associated with High- and Sub-Fertile Reproductive Performance in Beef Cattle. <i>Genes</i> , 2020 , 11,	4.2	3
18	A comprehensive comparison of high-density SNP panels and an alternative ultra-high-density panel for genomic analyses in Nellore cattle. <i>Animal Production Science</i> , 2020 , 60, 333	1.4	2
17	Transcriptomic Profiles of Monocyte-Derived Macrophages in Response to Escherichia coli is Associated with the Host Genetics. <i>Scientific Reports</i> , 2020 , 10, 271	4.9	9
16	46 Endometrial transcriptome profiles associated with bovine preimplantation pregnancy outcome and parity. <i>Journal of Animal Science</i> , 2020 , 98, 26-27	0.7	
15	11 Genome-wide association study using repeated measures model for stillbirth in Holstein dairy cattle. <i>Journal of Animal Science</i> , 2020 , 98, 15-16	0.7	
14	352 Awardee Talk: Identification of novel haplotypes with recessive and allelic inheritance patterns affecting embryonic development processes, gestation losses and post-natal lethality in cattle. <i>Journal of Animal Science</i> , 2020 , 98, 83-83	0.7	
13	GALLO: An R package for genomic annotation and integration of multiple data sources in livestock for positional candidate loci. <i>GigaScience</i> , 2020 , 9,	7.6	15
12	Development and comparison of RNA-sequencing pipelines for more accurate SNP identification: practical example of functional SNP detection associated with feed efficiency in Nellore beef cattle. <i>BMC Genomics</i> , 2020 , 21, 703	4.5	6

11	Identifying functionally relevant candidate genes for inflexible ethanol intake in mice and humans using a guilt-by-association approach. <i>Brain and Behavior</i> , 2020 , 10, e01879	3.4	2
10	Genome-wide association for milk production traits and somatic cell score in different lactation stages of Ayrshire, Holstein, and Jersey dairy cattle. <i>Journal of Dairy Science</i> , 2019 , 102, 8159-8174	4	21
9	Implementation of Bayesian methods to identify SNP and haplotype regions with transmission ratio distortion across the whole genome: TRDscan v.1.0. <i>Journal of Dairy Science</i> , 2019 , 102, 3175-3188	4	7
8	Genetic mechanisms regulating the host response during mastitis. <i>Journal of Dairy Science</i> , 2019 , 102, 9043-9059	4	13
7	Reducing cryptic relatedness in genomic data sets via a central node exclusion algorithm. <i>Molecular Ecology Resources</i> , 2018 , 18, 435-447	8.4	
6	Genetic mechanisms underlying spermatic and testicular traits within and among cattle breeds: systematic review and prioritization of GWAS results. <i>Journal of Animal Science</i> , 2018 , 96, 4978-4999	0.7	10
5	Combining multi-OMICS information to identify key-regulator genes for pleiotropic effect on fertility and production traits in beef cattle. <i>PLoS ONE</i> , 2018 , 13, e0205295	3.7	22
4	Identification of Candidate Genes for Reactivity in Guzerat (<i>Bos indicus</i>) Cattle: A Genome-Wide Association Study. <i>PLoS ONE</i> , 2017 , 12, e0169163	3.7	16
3	Biotinidase deficiency: Genotype-biochemical phenotype association in Brazilian patients. <i>PLoS ONE</i> , 2017 , 12, e0177503	3.7	12
2	Retelling the recent evolution of genetic diversity for Guzerat: Inferences from LD decay, runs of homozygosity and Ne over the generations. <i>Livestock Science</i> , 2016 , 193, 110-117	1.7	7
1	A new tetra-primer ARMS-PCR for genotyping bovine kappa-casein polymorphisms. <i>Genetics and Molecular Research</i> , 2013 , 12, 6521-6	1.2	6