

# Pablo A S Fonseca

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

454  
citations

840585

11  
h-index

752573

20  
g-index

31  
all docs

31  
docs citations

31  
times ranked

503  
citing authors

#	ARTICLE	IF	CITATIONS
1	GALLO: An R package for genomic annotation and integration of multiple data sources in livestock for positional candidate loci. <i>GigaScience</i> , 2020, 9, .	3.3	86
2	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.	1.4	42
3	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.	1.1	33
4	Genetic mechanisms regulating the host response during mastitis. <i>Journal of Dairy Science</i> , 2019, 102, 9043-9059.	1.4	32
5	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.	0.7	31
6	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.	1.1	23
7	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.	1.4	19
8	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.	1.4	19
9	Biotinidase deficiency: Genotype-biochemical phenotype association in Brazilian patients. <i>PLoS ONE</i> , 2017, 12, e0177503.	1.1	19
10	Genetic mechanisms underlying spermatic and testicular traits within and among cattle breeds: systematic review and prioritization of GWAS results1. <i>Journal of Animal Science</i> , 2018, 96, 4978-4999.	0.2	17
11	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.	1.2	14
12	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, 543.	1.0	14
13	Retelling the recent evolution of genetic diversity for Guzerã: Inferences from LD decay, runs of homozygosity and Ne over the generations. <i>Livestock Science</i> , 2016, 193, 110-117.	0.6	13
14	Transcriptomic Profiles of Monocyte-Derived Macrophages in Response to <i>Escherichia coli</i> is Associated with the Host Genetics. <i>Scientific Reports</i> , 2020, 10, 271.	1.6	13
15	Detection and Visualization of Heterozygosity-Rich Regions and Runs of Homozygosity in Worldwide Sheep Populations. <i>Animals</i> , 2021, 11, 2696.	1.0	12
16	Genetic Diversity and Population Genetic Structure of a Guzerã ( <i>Bos indicus</i> ) Meta-Population. <i>Animals</i> , 2021, 11, 1125.	1.0	11
17	Genes underlying genetic correlation between growth, reproductive and parasite burden traits in beef cattle. <i>Livestock Science</i> , 2021, 244, 104332.	0.6	10
18	Genome-wide association study for beef fatty acid profile using haplotypes in Nellore cattle. <i>Livestock Science</i> , 2021, 245, 104396.	0.6	10

#	ARTICLE	IF	CITATIONS
19	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.	1.0	9
20	A new tetra-primer ARMS-PCR for genotyping bovine kappa-casein polymorphisms. <i>Genetics and Molecular Research</i> , 2013, 12, 6521-6526.	0.3	8
21	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.	2.7	5
22	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.	0.6	4
23	Putative Causal Variant on <i>Vlgr1</i> for the Epileptic Phenotype in the Model Wistar Audiogenic Rat. <i>Frontiers in Neurology</i> , 2021, 12, 647859.	1.1	4
24	Genome-wide association study using haplotype libraries and repeated-measures model to identify candidate genomic regions for stillbirth in Holstein cattle. <i>Journal of Dairy Science</i> , 2022, 105, 1314-1326.	1.4	4
25	Reducing cryptic relatedness in genomic data sets via a central node exclusion algorithm. <i>Molecular Ecology Resources</i> , 2018, 18, 435-447.	2.2	0
26	Genomic and phenotypic analyses of antral follicle count in Aberdeen Angus cows. <i>Livestock Science</i> , 2021, 249, 104534.	0.6	0
27	46 Endometrial transcriptome profiles associated with bovine preimplantation pregnancy outcome and parity. <i>Journal of Animal Science</i> , 2020, 98, 26-27.	0.2	0
28	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.	0.2	0
29	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.	0.2	0
30	Working memory and arithmetic impairments in children with FMR1 premutation and gray zone alleles. <i>Dementia E Neuropsychologia</i> , 2022, 16, 105-114.	0.3	0