

Pablo A S Fonseca

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5706394/pablo-a-s-fonseca-publications-by-citations.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	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
27	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
26	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
25	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
24	Genetic mechanisms regulating the host response during mastitis. <i>Journal of Dairy Science</i> , 2019 , 102, 9043-9059	4	13
23	Biotinidase deficiency: Genotype-biochemical phenotype association in Brazilian patients. <i>PLoS ONE</i> , 2017 , 12, e0177503	3.7	12
22	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
21	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	4.9	9
20	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
19	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
18	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
17	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
16	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
15	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
14	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
13	Genome-wide association study for beef fatty acid profile using haplotypes in Nellore cattle. <i>Livestock Science</i> , 2021 , 245, 104396	1.7	3
12	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

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	Genetic Diversity and Population Genetic Structure of a Guzerú Meta-Population. <i>Animals</i> , 2021 , 11,	3.1	2
9	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
8	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
7	Genes underlying genetic correlation between growth, reproductive and parasite burden traits in beef cattle. <i>Livestock Science</i> , 2021 , 244, 104332	1.7	1
6	Reducing cryptic relatedness in genomic data sets via a central node exclusion algorithm. <i>Molecular Ecology Resources</i> , 2018 , 18, 435-447	8.4	
5	46 Endometrial transcriptome profiles associated with bovine preimplantation pregnancy outcome and parity. <i>Journal of Animal Science</i> , 2020 , 98, 26-27	0.7	
4	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	
3	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	
2	Genomic and phenotypic analyses of antral follicle count in Aberdeen Angus cows. <i>Livestock Science</i> , 2021 , 249, 104534	1.7	
1	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	