

Aroa Surez Vega

List of Publications by Citations

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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.

38
papers

507
citations

13
h-index

21
g-index

51
ext. papers

792
ext. citations

3.2
avg, IF

3.91
L-index

#	Paper	IF	Citations
38	PSI-30 Identifying key regulator genes associated with parasite resistance and their link with climate conditions in sheep.. <i>Journal of Animal Science</i> , 2018 , 96, 187-188	0.7	78
37	322 Evaluation of the biological function of genes linked to regions with distortion of Mendelian segregation and their relation to reproductive traits in dairy cattle.. <i>Journal of Animal Science</i> , 2018 , 96, 122-122	0.7	78
36	Characterization and Comparative Analysis of the Milk Transcriptome in Two Dairy Sheep Breeds using RNA Sequencing. <i>Scientific Reports</i> , 2015 , 5, 18399	4.9	49
35	Comprehensive RNA-Seq profiling to evaluate lactating sheep mammary gland transcriptome. <i>Scientific Data</i> , 2016 , 3, 160051	8.2	34
34	Variant discovery in the sheep milk transcriptome using RNA sequencing. <i>BMC Genomics</i> , 2017 , 18, 170	4.5	28
33	Estimations of linkage disequilibrium, effective population size and ROH-based inbreeding coefficients in Spanish Churra sheep using imputed high-density SNP genotypes. <i>Animal Genetics</i> , 2017 , 48, 436-446	2.5	20
32	Transcriptome expression analysis of candidate milk genes affecting cheese-related traits in 2 sheep breeds. <i>Journal of Dairy Science</i> , 2016 , 99, 6381-6390	4	19
31	Isolation of RNA from milk somatic cells as an alternative to biopsies of mammary tissue for nutrigenomic studies in dairy ewes. <i>Journal of Dairy Science</i> , 2016 , 99, 8461-8471	4	16
30	Identification of quantitative trait loci underlying milk traits in Spanish dairy sheep using linkage plus combined linkage disequilibrium and linkage analysis approaches. <i>Journal of Dairy Science</i> , 2013 , 96, 6059-69	4	16
29	High-resolution analysis of selection sweeps identified between fine-wool Merino and coarse-wool Churra sheep breeds. <i>Genetics Selection Evolution</i> , 2017 , 49, 81	4.9	16
28	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
27	Elucidating fish oil-induced milk fat depression in dairy sheep: Milk somatic cell transcriptome analysis. <i>Scientific Reports</i> , 2017 , 7, 45905	4.9	13
26	Genetic mechanisms regulating the host response during mastitis. <i>Journal of Dairy Science</i> , 2019 , 102, 9043-9059	4	13
25	Exploring the mechanisms of resistance to <i>Teladorsagia circumcincta</i> infection in sheep through transcriptome analysis of abomasal mucosa and abomasal lymph nodes. <i>Veterinary Research</i> , 2018 , 49, 39	3.8	11
24	Combining GWAS and RNA-Seq Approaches for Detection of the Causal Mutation for Hereditary Junctional Epidermolysis Bullosa in Sheep. <i>PLoS ONE</i> , 2015 , 10, e0126416	3.7	10
23	Genetic mechanisms underlying spermatid 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
22	Identification of a 31-bp deletion in the RELN gene causing lissencephaly with cerebellar hypoplasia in sheep. <i>PLoS ONE</i> , 2013 , 8, e81072	3.7	9

21	Detection of quantitative trait loci and putative causal variants affecting somatic cell score in dairy sheep by using a 50K SNP chip and whole-genome sequencing. <i>Journal of Dairy Science</i> , 2018 , 101, 9072-9088	4.9	8
20	Genome-wide association study to identify genomic regions and positional candidate genes associated with male fertility in beef cattle. <i>Scientific Reports</i> , 2020 , 10, 20102	4.9	8
19	Conjugated linoleic acid (CLA)-induced milk fat depression: application of RNA-Seq technology to elucidate mammary gene regulation in dairy ewes. <i>Scientific Reports</i> , 2019 , 9, 4473	4.9	6
18	Gene Networks Driving Genetic Variation in Milk and Cheese-Making Traits of Spanish Assaf Sheep. <i>Genes</i> , 2020 , 11,	4.2	6
17	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
16	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
15	Identification of potential functional variants underlying ovine resistance to gastrointestinal nematode infection by using RNA-Seq. <i>Animal Genetics</i> , 2020 , 51, 266-277	2.5	5
14	Early adipose deposits in sheep: comparative analysis of the perirenal fat transcriptome of Assaf and Churra suckling lambs. <i>Animal Genetics</i> , 2018 , 49, 605-617	2.5	5
13	Hereditary lissencephaly and cerebellar hypoplasia in Churra lambs. <i>BMC Veterinary Research</i> , 2013 , 9, 156	2.7	4
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,	4.2	3
11	Generalized severe junctional epidermolysis bullosa with congenital absence of skin in churra lambs. <i>Veterinary Dermatology</i> , 2015 , 26, 367-73, e82-3	1.8	3
10	Genome-wide association studies (GWAS) and post-GWAS analyses for technological traits in Assaf and Churra dairy breeds. <i>Journal of Dairy Science</i> , 2021 , 104, 11850-11866	4	2
9	Analysis of Whole Genome Resequencing Datasets from a Worldwide Sample of Sheep Breeds to Identify Potential Causal Mutations Influencing Milk Composition Traits. <i>Animals</i> , 2020 , 10,	3.1	2
8	The Milk Microbiota of the Spanish Churra Sheep Breed: New Insights into the Complexity of the Milk Microbiome of Dairy Species. <i>Animals</i> , 2020 , 10,	3.1	2
7	Characterization of novel muscle expression profiles associated with meat quality in beef cattle.. <i>Evolutionary Applications</i> , 2022 , 15, 706-718	4.8	2
6	PSXVII-4 A comparison of weighted gene co-expression networks in high- and low-feed efficiency dairy cattle.. <i>Journal of Animal Science</i> , 2018 , 96, 146-147	0.7	1
5	PSXIV-18 Genome-wide association study to identify genomic regions and single nucleotide polymorphisms functionally associated with bull fertility.. <i>Journal of Animal Science</i> , 2018 , 96, 138-139	0.7	1
4	Study on the concordance between different SNP-genotyping platforms in sheep. <i>Animal Genetics</i> , 2021 , 52, 868-880	2.5	1

3	Genome-wide identification and characterization of <i>Fusarium circinatum</i> -responsive lncRNAs in <i>Pinus radiata</i> . <i>BMC Genomics</i> , 2022 , 23, 194	4.5	o
2	PSIII-8 Difference between two fecal egg count methods and estimation of genetic parameters for gastrointestinal parasite resistance traits in sheep. <i>Journal of Animal Science</i> , 2020 , 98, 232-233	0.7	
1	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	