

Emily L Clark

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

1,022
citations

687363

13
h-index

713466

21
g-index

32
all docs

32
docs citations

32
times ranked

981
citing authors

#	ARTICLE	IF	CITATIONS
1	A high resolution atlas of gene expression in the domestic sheep (<i>Ovis aries</i>). PLoS Genetics, 2017, 13, e1006997.	3.5	210
2	ADGRE1 (EMR1, F4/80) Is a Rapidly-Evolving Gene Expressed in Mammalian Monocyte-Macrophages. Frontiers in Immunology, 2018, 9, 2246.	4.8	149
3	Species-Specific Transcriptional Regulation of Genes Involved in Nitric Oxide Production and Arginine Metabolism in Macrophages. ImmunoHorizons, 2018, 2, 27-37.	1.8	124
4	From FAANG to fork: application of highly annotated genomes to improve farmed animal production. Genome Biology, 2020, 21, 285.	8.8	74
5	Cross-species inference of long non-coding RNAs greatly expands the ruminant transcriptome. Genetics Selection Evolution, 2018, 50, 20.	3.0	65
6	Comprehensive Transcriptional Profiling of the Gastrointestinal Tract of Ruminants from Birth to Adulthood Reveals Strong Developmental Stage Specific Gene Expression. G3: Genes, Genomes, Genetics, 2019, 9, 359-373.	1.8	48
7	Functional Annotation of the Transcriptome of the Pig, <i>Sus scrofa</i> , Based Upon Network Analysis of an RNAseq Transcriptional Atlas. Frontiers in Genetics, 2019, 10, 1355.	2.3	42
8	Integration of quantitated expression estimates from polyA-selected and rRNA-depleted RNA-seq libraries. BMC Bioinformatics, 2017, 18, 301.	2.6	40
9	Elimination of Reference Mapping Bias Reveals Robust Immune Related Allele-Specific Expression in Crossbred Sheep. Frontiers in Genetics, 2019, 10, 863.	2.3	38
10	Species-Specificity of Transcriptional Regulation and the Response to Lipopolysaccharide in Mammalian Macrophages. Frontiers in Cell and Developmental Biology, 2020, 8, 661.	3.7	29
11	A Mini-Atlas of Gene Expression for the Domestic Goat (<i>Capra hircus</i>). Frontiers in Genetics, 2019, 10, 1080.	2.3	24
12	Global Analysis of Transcription Start Sites in the New Ovine Reference Genome (<i>Oar rambouillet</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.3	21
13	Whole-Genome Sequence Data Suggest Environmental Adaptation of Ethiopian Sheep Populations. Genome Biology and Evolution, 2021, 13, .	2.5	20
14	VarGoats project: a dataset of 1159 whole-genome sequences to dissect <i>Capra hircus</i> global diversity. Genetics Selection Evolution, 2021, 53, 86.	3.0	16
15	Expression of mitochondrial protein genes encoded by nuclear and mitochondrial genomes correlate with energy metabolism in dairy cattle. BMC Genomics, 2020, 21, 720.	2.8	15
16	Profiling of open chromatin in developing pig (<i>Sus scrofa</i>) muscle to identify regulatory regions. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	13
17	Genetic and genomic analyses underpin the feasibility of concomitant genetic improvement of milk yield and mastitis resistance in dairy sheep. PLoS ONE, 2019, 14, e0214346.	2.5	12
18	Expression of Calcification and Extracellular Matrix Genes in the Cardiovascular System of the Healthy Domestic Sheep (<i>Ovis aries</i>). Frontiers in Genetics, 2020, 11, 919.	2.3	9

#	ARTICLE	IF	CITATIONS
19	KLB dysregulation mediates disrupted muscle development in intrauterine growth restriction. <i>Journal of Physiology</i> , 2022, 600, 1771-1790.	2.9	6
20	Genetic Diversity of Cameroon Cattle and a Putative Genomic Map for Resistance to Bovine Tuberculosis. <i>Frontiers in Genetics</i> , 2020, 11, 550215.	2.3	2
21	Use of quantitative real-time PCR to determine the local inflammatory response in the intestinal mucosa and <i>muscularis</i> of horses undergoing small intestinal resection. <i>Equine Veterinary Journal</i> , 2022, 54, 52-62.	1.7	2