Sandrine Lagarrigue

List of Publications by Year in descending order

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686830 713013 20 802 13 21 citations g-index h-index papers 25 25 25 1329 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	LncRNAs in domesticated animals: from dog to livestock species. Mammalian Genome, 2022, 33, 248-270.	1.0	10
2	RNA-Seq Data for Reliable SNP Detection and Genotype Calling: Interest for Coding Variant Characterization and Cis-Regulation Analysis by Allele-Specific Expression in Livestock Species. Frontiers in Genetics, 2021, 12, 655707.	1.1	30
3	Watch Out for a Second SNP: Focus on Multi-Nucleotide Variants in Coding Regions and Rescued Stop-Gained. Frontiers in Genetics, 2021, 12, 659287.	1.1	2
4	An integrative atlas of chicken long non-coding genes and their annotations across 25 tissues. Scientific Reports, 2020, 10, 20457.	1.6	20
5	Chicken adaptive response to low energy diet: main role of the hypothalamic lipid metabolism revealed by a phenotypic and multi-tissue transcriptomic approach. BMC Genomics, 2019, 20, 1033.	1.2	7
6	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. BMC Biology, 2019, 17, 108.	1.7	109
7	Long noncoding RNAs in lipid metabolism: literature review and conservation analysis across species. BMC Genomics, 2019, 20, 882.	1.2	63
8	Long noncoding RNA repertoire in chicken liver and adipose tissue. Genetics Selection Evolution, 2017, 49, 6.	1.2	59
9	A transcriptome multi-tissue analysis identifies biological pathways and genes associated with variations in feed efficiency of growing pigs. BMC Genomics, 2017, 18, 244.	1.2	113
10	Molecular alterations induced by a high-fat high-fiber diet in porcine adipose tissues: variations according to the anatomical fat location. BMC Genomics, 2016, 17, 120.	1.2	16
11	The Extent of mRNA Editing Is Limited in Chicken Liver and Adipose, but Impacted by Tissular Context, Genotype, Age, and Feeding as Exemplified with a Conserved Edited Site in COG3. G3: Genes, Genomes, Genetics, 2016, 6, 321-335.	0.8	13
12	Combined QTL and Selective Sweep Mappings with Coding SNP Annotation and <i>cis </i> -eQTL Analysis Revealed <i>PARK2 </i> and <i>JAG2 </i> sas New Candidate Genes for Adiposity Regulation. G3: Genes, Genomes, Genetics, 2015, 5, 517-529.	0.8	17
13	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	0.6	97
14	Genome-Wide Characterization of RNA Editing in Chicken Embryos Reveals Common Features among Vertebrates. PLoS ONE, 2015, 10, e0126776.	1.1	15
15	Transcriptome-wide investigation of genomic imprinting in chicken. Nucleic Acids Research, 2014, 42, 3768-3782.	6.5	59
16	Using a large-scale knowledge database on reactions and regulations to propose key upstream regulators of various sets of molecules participating in cell metabolism. BMC Systems Biology, 2014, 8, 32.	3.0	5
17	Limited RNA Editing in Exons of Mouse Liver and Adipose. Genetics, 2013, 193, 1107-1115.	1.2	24
18	Analysis of Allele-Specific Expression in Mouse Liver by RNA-Seq: A Comparison With <i>Cis</i> eQTL Identified Using Genetic Linkage. Genetics, 2013, 195, 1157-1166.	1,2	43

#	Article	IF	CITATIONS
19	Detection of a Cis eQTL Controlling BMCO1 Gene Expression Leads to the Identification of a QTG for Chicken Breast Meat Color. PLoS ONE, 2011, 6, e14825.	1.1	35
20	Mapping quantitative trait loci affecting fatness and breast muscle weight in meat-type chicken lines divergently selected on abdominal fatness. Genetics Selection Evolution, 2006, 38, 85.	1.2	50