

Sandrine Lagarrigue

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

802
citations

686830

13
h-index

713013

21
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25
all docs

25
docs citations

25
times ranked

1329
citing authors

#	ARTICLE	IF	CITATIONS
1	A transcriptome multi-tissue analysis identifies biological pathways and genes associated with variations in feed efficiency of growing pigs. <i>BMC Genomics</i> , 2017, 18, 244.	1.2	113
2	Multi-species annotation of transcriptome and chromatin structure in domesticated animals. <i>BMC Biology</i> , 2019, 17, 108.	1.7	109
3	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	0.6	97
4	Long noncoding RNAs in lipid metabolism: literature review and conservation analysis across species. <i>BMC Genomics</i> , 2019, 20, 882.	1.2	63
5	Transcriptome-wide investigation of genomic imprinting in chicken. <i>Nucleic Acids Research</i> , 2014, 42, 3768-3782.	6.5	59
6	Long noncoding RNA repertoire in chicken liver and adipose tissue. <i>Genetics Selection Evolution</i> , 2017, 49, 6.	1.2	59
7	Mapping quantitative trait loci affecting fatness and breast muscle weight in meat-type chicken lines divergently selected on abdominal fatness. <i>Genetics Selection Evolution</i> , 2006, 38, 85.	1.2	50
8	Analysis of Allele-Specific Expression in Mouse Liver by RNA-Seq: A Comparison With <i>Cis</i> -eQTL Identified Using Genetic Linkage. <i>Genetics</i> , 2013, 195, 1157-1166.	1.2	43
9	Detection of a <i>Cis</i> eQTL Controlling <i>BMCO1</i> Gene Expression Leads to the Identification of a QTG for Chicken Breast Meat Color. <i>PLoS ONE</i> , 2011, 6, e14825.	1.1	35
10	RNA-Seq Data for Reliable SNP Detection and Genotype Calling: Interest for Coding Variant Characterization and <i>Cis</i> -Regulation Analysis by Allele-Specific Expression in Livestock Species. <i>Frontiers in Genetics</i> , 2021, 12, 655707.	1.1	30
11	Limited RNA Editing in Exons of Mouse Liver and Adipose. <i>Genetics</i> , 2013, 193, 1107-1115.	1.2	24
12	An integrative atlas of chicken long non-coding genes and their annotations across 25 tissues. <i>Scientific Reports</i> , 2020, 10, 20457.	1.6	20
13	Combined QTL and Selective Sweep Mappings with Coding SNP Annotation and <i>cis</i> -eQTL Analysis Revealed <i>PARK2</i> and <i>JAG2</i> as New Candidate Genes for Adiposity Regulation. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 517-529.	0.8	17
14	Molecular alterations induced by a high-fat high-fiber diet in porcine adipose tissues: variations according to the anatomical fat location. <i>BMC Genomics</i> , 2016, 17, 120.	1.2	16
15	Genome-Wide Characterization of RNA Editing in Chicken Embryos Reveals Common Features among Vertebrates. <i>PLoS ONE</i> , 2015, 10, e0126776.	1.1	15
16	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 <i>COG3</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 321-335.	0.8	13
17	LncRNAs in domesticated animals: from dog to livestock species. <i>Mammalian Genome</i> , 2022, 33, 248-270.	1.0	10
18	Chicken adaptive response to low energy diet: main role of the hypothalamic lipid metabolism revealed by a phenotypic and multi-tissue transcriptomic approach. <i>BMC Genomics</i> , 2019, 20, 1033.	1.2	7

#	ARTICLE	IF	CITATIONS
19	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
20	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