

Amanda J Chamberlain

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6890830/publications.pdf>

Version: 2024-02-01

19
papers

1,680
citations

759233

12
h-index

794594

19
g-index

25
all docs

25
docs citations

25
times ranked

1737
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle. <i>Nature Genetics</i> , 2014, 46, 858-865.	21.4	697
2	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. <i>Nature Genetics</i> , 2018, 50, 362-367.	21.4	286
3	Improved precision of QTL mapping using a nonlinear Bayesian method in a multi-breed population leads to greater accuracy of across-breed genomic predictions. <i>Genetics Selection Evolution</i> , 2015, 47, 29.	3.0	113
4	Functional annotations of three domestic animal genomes provide vital resources for comparative and agricultural research. <i>Nature Communications</i> , 2021, 12, 1821.	12.8	105
5	Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19398-19408.	7.1	99
6	Extensive variation between tissues in allele specific expression in an outbred mammal. <i>BMC Genomics</i> , 2015, 16, 993.	2.8	86
7	<scp>GO</scp>â€œ<scp>FAANG</scp> meeting: a Gathering On Functional Annotation of <scp>An</scp>imal Genomes. <i>Animal Genetics</i> , 2016, 47, 528-533.	1.7	65
8	Genome-wide fine-mapping identifies pleiotropic and functional variants that predict many traits across global cattle populations. <i>Nature Communications</i> , 2021, 12, 860.	12.8	60
9	Putative bovine topological association domains and CTCF binding motifs can reduce the search space for causative regulatory variants of complex traits. <i>BMC Genomics</i> , 2018, 19, 395.	2.8	42
10	Genome variants associated with RNA splicing variations in bovine are extensively shared between tissues. <i>BMC Genomics</i> , 2018, 19, 521.	2.8	34
11	Putative Causal Variants Are Enriched in Annotated Functional Regions From Six Bovine Tissues. <i>Frontiers in Genetics</i> , 2021, 12, 664379.	2.3	20
12	Survey of allele specific expression in bovine muscle. <i>Scientific Reports</i> , 2019, 9, 4297.	3.3	15
13	Fine-mapping sequence mutations with a major effect on oligosaccharide content in bovine milk. <i>Scientific Reports</i> , 2019, 9, 2137.	3.3	13
14	Expression quantitative trait loci in sheep liver and muscle contribute to variations in meat traits. <i>Genetics Selection Evolution</i> , 2021, 53, 8.	3.0	12
15	Bayesian genome-wide analysis of cattle traits using variants with functional and evolutionary significance. <i>Animal Production Science</i> , 2021, 61, 1818-1827.	1.3	6
16	Mutant alleles differentially shape fitness and other complex traits in cattle. <i>Communications Biology</i> , 2021, 4, 1353.	4.4	6
17	Recovery of mitogenomes from whole genome sequences to infer maternal diversity in 1883 modern taurine and indicine cattle. <i>Scientific Reports</i> , 2022, 12, 5582.	3.3	6
18	Genetic variability of the activity of bidirectional promoters: a pilot study in bovine muscle. <i>DNA Research</i> , 2017, 24, 221-233.	3.4	2

#	ARTICLE	IF	CITATIONS
19	Evolution of tissue and developmental specificity of transcription start sites in <i>Bos taurus indicus</i> . Communications Biology, 2021, 4, 829.	4.4	2