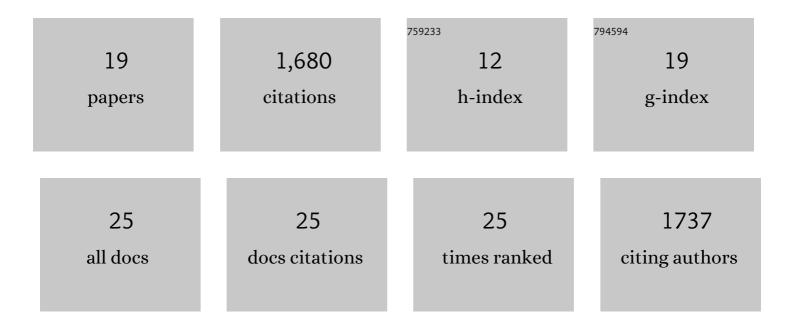
Amanda J Chamberlain

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6890830/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Recovery of mitogenomes from whole genome sequences to infer maternal diversity in 1883 modern taurine and indicine cattle. Scientific Reports, 2022, 12, 5582.	3.3	6
2	Bayesian genome-wide analysis of cattle traits using variants with functional and evolutionary significance. Animal Production Science, 2021, 61, 1818-1827.	1.3	6
3	Genome-wide fine-mapping identifies pleiotropic and functional variants that predict many traits across global cattle populations. Nature Communications, 2021, 12, 860.	12.8	60
4	Functional annotations of three domestic animal genomes provide vital resources for comparative and agricultural research. Nature Communications, 2021, 12, 1821.	12.8	105
5	Putative Causal Variants Are Enriched in Annotated Functional Regions From Six Bovine Tissues. Frontiers in Genetics, 2021, 12, 664379.	2.3	20
6	Evolution of tissue and developmental specificity of transcription start sites in Bos taurus indicus. Communications Biology, 2021, 4, 829.	4.4	2
7	Expression quantitative trait loci in sheep liver and muscle contribute to variations in meat traits. Genetics Selection Evolution, 2021, 53, 8.	3.0	12
8	Mutant alleles differentially shape fitness and other complex traits in cattle. Communications Biology, 2021, 4, 1353.	4.4	6
9	Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19398-19408.	7.1	99
10	Survey of allele specific expression in bovine muscle. Scientific Reports, 2019, 9, 4297.	3.3	15
11	Fine-mapping sequence mutations with a major effect on oligosaccharide content in bovine milk. Scientific Reports, 2019, 9, 2137.	3.3	13
12	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. Nature Genetics, 2018, 50, 362-367.	21.4	286
13	Putative bovine topological association domains and CTCF binding motifs can reduce the search space for causative regulatory variants of complex traits. BMC Genomics, 2018, 19, 395.	2.8	42
14	Genome variants associated with RNA splicing variations in bovine are extensively shared between tissues. BMC Genomics, 2018, 19, 521.	2.8	34
15	Genetic variability of the activity of bidirectional promoters: a pilot study in bovine muscle. DNA Research, 2017, 24, 221-233.	3.4	2
16	<scp>GO</scp> â€ <scp>FAANG</scp> meeting: a Gathering On Functional Annotation of <scp>An</scp> imal Genomes. Animal Genetics, 2016, 47, 528-533.	1.7	65
17	Extensive variation between tissues in allele specific expression in an outbred mammal. BMC Genomics, 2015, 16, 993.	2.8	86
18	Improved precision of QTL mapping using a nonlinear Bayesian method in a multi-breed population leads to greater accuracy of across-breed genomic predictions. Genetics Selection Evolution, 2015, 47, 29.	3.0	113

#	Article	IF	CITATIONS
19	Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle. Nature Genetics, 2014, 46, 858-865.	21.4	697