

Christopher M Seabury

List of Publications by Year in descending order

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35
papers

2,004
citations

331538

21
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377752

34
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docs citations

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times ranked

2833
citing authors

#	ARTICLE	IF	CITATIONS
1	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004254.	1.5	391
2	Production of hornless dairy cattle from genome-edited cell lines. <i>Nature Biotechnology</i> , 2016, 34, 479-481.	9.4	267
3	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18644-18649.	3.3	196
4	Genome-wide association study for feed efficiency and growth traits in U.S. beef cattle. <i>BMC Genomics</i> , 2017, 18, 386.	1.2	159
5	QTLs associated with dry matter intake, metabolic mid-test weight, growth and feed efficiency have little overlap across 4 beef cattle studies. <i>BMC Genomics</i> , 2014, 15, 1004.	1.2	97
6	Susceptibility loci revealed for bovine respiratory disease complex in pre-weaned holstein calves. <i>BMC Genomics</i> , 2014, 15, 1164.	1.2	85
7	Diversity and evolution of 11 innate immune genes in <i>Bos taurus taurus</i> and <i>Bos taurus indicus</i> cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 151-156.	3.3	81
8	Quantum dots trigger immunomodulation of the NF κ B pathway in human skin cells. <i>Molecular Immunology</i> , 2011, 48, 1349-1359.	1.0	57
9	Immunological Response to Single Pathogen Challenge with Agents of the Bovine Respiratory Disease Complex: An RNA-Sequence Analysis of the Bronchial Lymph Node Transcriptome. <i>PLoS ONE</i> , 2015, 10, e0131459.	1.1	51
10	A Multi-Platform Draft de novo Genome Assembly and Comparative Analysis for the Scarlet Macaw (<i>Ara macao</i>). <i>PLoS ONE</i> , 2013, 8, e62415.	1.1	51
11	Prion protein gene (PRNP) variants and evidence for strong purifying selection in functionally important regions of bovine exon 3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15142-15147.	3.3	50
12	Mechanisms Underlying Mammalian Hybrid Sterility in Two Feline Interspecies Models. <i>Molecular Biology and Evolution</i> , 2015, 32, 2534-2546.	3.5	48
13	Evolution of the Bovine TLR Gene Family and Member Associations with <i>Mycobacterium avium</i> Subspecies Paratuberculosis Infection. <i>PLoS ONE</i> , 2011, 6, e27744.	1.1	48
14	Comparative PRNP genotyping of U.S. cattle sires for potential association with BSE. <i>Mammalian Genome</i> , 2004, 15, 828-833.	1.0	46
15	Genome-Wide Polymorphism and Comparative Analyses in the White-Tailed Deer (<i>Odocoileus</i>) Tj ETQq1 1 0.784314 _{1.1} rgBT /Overlock 10 ₄₁	1.1	41
16	Genome-wide association and genotype by environment interactions for growth traits in U.S. Gelbvieh cattle. <i>BMC Genomics</i> , 2019, 20, 926.	1.2	37
17	A Draft De Novo Genome Assembly for the Northern Bobwhite (<i>Colinus virginianus</i>) Reveals Evidence for a Rapid Decline in Effective Population Size Beginning in the Late Pleistocene. <i>PLoS ONE</i> , 2014, 9, e90240.	1.1	34
18	Tissue Tropism in Host Transcriptional Response to Members of the Bovine Respiratory Disease Complex. <i>Scientific Reports</i> , 2017, 7, 17938.	1.6	28

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19	Frequencies of polymorphisms associated with BSE resistance differ significantly between <i>Bos taurus</i> , <i>Bos indicus</i> , and composite cattle. <i>BMC Veterinary Research</i> , 2008, 4, 36.	0.7	25
20	Innate immune gene variation and differential susceptibility to uterine diseases in Holstein cows. <i>Theriogenology</i> , 2013, 80, 384-390.	0.9	24
21	Analysis of sequence variability and protein domain architectures for bovine peptidoglycan recognition protein 1 and Toll-like receptors 2 and 6. <i>Genomics</i> , 2008, 92, 235-245.	1.3	23
22	Powerful detection of polygenic selection and evidence of environmental adaptation in US beef cattle. <i>PLoS Genetics</i> , 2021, 17, e1009652.	1.5	23
23	Validation of 46 loci associated with female fertility traits in cattle. <i>BMC Genomics</i> , 2019, 20, 576.	1.2	22
24	Identification of Loci and Pathways Associated with Heifer Conception Rate in U.S. Holsteins. <i>Genes</i> , 2020, 11, 767.	1.0	21
25	Annotated Draft Genome Assemblies for the Northern Bobwhite (<i>Colinus virginianus</i>) and the Scaled Quail (<i>Callipepla squamata</i>) Reveal Disparate Estimates of Modern Genome Diversity and Historic Effective Population Size. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3047-3058.	0.8	20
26	Accurate Genomic Predictions for Chronic Wasting Disease in U.S. White-Tailed Deer. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1433-1441.	0.8	17
27	Sequence Analysis and Polymorphism Discovery in 4 Members of the Bovine Cathelicidin Gene Family. <i>Journal of Heredity</i> , 2009, 100, 241-245.	1.0	11
28	Genome-wide association and genotype by environment interactions for growth traits in U.S. Red Angus cattle. <i>BMC Genomics</i> , 2022, 23, .	1.2	11
29	Results of the BRD CAP project: progress toward identifying genetic markers associated with BRD susceptibility. <i>Animal Health Research Reviews</i> , 2014, 15, 157-160.	1.4	8
30	Rapid Macrosatellite Evolution Promotes X-Linked Hybrid Male Sterility in a Feline Interspecies Cross. <i>Molecular Biology and Evolution</i> , 2021, 38, 5588-5609.	3.5	8
31	QTL-mapping and genomic prediction for bovine respiratory disease in U.S. Holsteins using sequence imputation and feature selection. <i>BMC Genomics</i> , 2019, 20, 555.	1.2	6
32	Northern Bobwhite (<i>Colinus virginianus</i>) Mitochondrial Population Genomics Reveals Structure, Divergence, and Evidence for Heteroplasmy. <i>PLoS ONE</i> , 2015, 10, e0144913.	1.1	5
33	Molecular Characterization of the Rocky Mountain Elk (<i>Cervus elaphus nelsoni</i>) PRNP Putative Promoter. <i>Journal of Heredity</i> , 2007, 98, 678-686.	1.0	4
34	Genotype by Environment Interactions for Chronic Wasting Disease in Farmed U.S. White-tailed Deer. <i>G3: Genes, Genomes, Genetics</i> , 2022, , .	0.8	2
35	Disparate Modes of Evolution Shaped Modern Prion (PRNP) and Prion-Related Doppel (PRND) Variation in Domestic Cattle. <i>PLoS ONE</i> , 2016, 11, e0155924.	1.1	0