Brenda M Murdoch

List of Publications by Year
in descending order

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63 papers	3,509 citations	249298 26 h-index	162838 57 g-index
64 all docs	64 docs citations	64 times ranked	4023 citing authors

#	Article	IF	Citations
1	The Agricultural Genome to Phenome Initiative (AG2PI): creating a shared vision across crop and livestock research communities. Genome Biology, 2022, 23, 3.	3.8	5
2	An improved ovine reference genome assembly to facilitate in-depth functional annotation of the sheep genome. GigaScience, 2022, 11, .	3.3	24
3	Variants Within Genes EDIL3 and ADGRB3 are Associated With Divergent Fecal Egg Counts in Katahdin Sheep at Weaning. Frontiers in Genetics, 2022, 13, 817319.	1.1	6
4	Ten simple rules to ruin a collaborative environment. PLoS Computational Biology, 2022, 18, e1009957.	1.5	1
5	A high-density genome-wide association with absolute blood monocyte count in domestic sheep identifies novel loci. PLoS ONE, 2022, 17, e0266748.	1.1	0
6	Response of Rambouillet Lambs to an Artificial Gastrointestinal Nematode Infection. Animals, 2022, 12, 1199.	1.0	4
7	Single Nucleotide Polymorphism Effects on Lamb Fecal Egg Count Estimated Breeding Values in Progeny-Tested Katahdin Sires. Frontiers in Genetics, 2022, 13, 866176.	1.1	2
8	Genome-Wide Association Analyses of Fertility Traits in Beef Heifers. Genes, 2021, 12, 217.	1.0	10
9	Characterizing Genetic Regulatory Elements in Ovine Tissues. Frontiers in Genetics, 2021, 12, 628849.	1.1	8
10	Evolution of the sheep industry and genetic research in the United States: opportunities for convergence in the twentyâ€first century. Animal Genetics, 2021, 52, 395-408.	0.6	24
11	Key genetic variants associated with variation of milk oligosaccharides from diverse human populations. Genomics, 2021, 113, 1867-1875.	1.3	24
12	Variation in type two taste receptor genes is associated with bitter tasting phenylthiocarbamide consumption in mature Targhee and Rambouillet rams. Translational Animal Science, 2021, 5, txab142.	0.4	1
13	Genes involved in immune, gene translation and chromatin organization pathways associated with Mycoplasma ovipneumoniae presence in nasal secretions of domestic sheep. PLoS ONE, 2021, 16, e0247209.	1.1	8
14	Identifying genetic variants affecting cattle grazing behavior experiencing mild heat load. Translational Animal Science, 2021, 5, S61-S66.	0.4	1
15	Examining the extent of environmental contributions toward DNA methylation and phenotypic variation. Animal Frontiers, 2021, 11, 83-89.	0.8	5
16	A novel understanding of global DNA methylation in bobcat (<i>Lynx rufus</i>). Genome, 2020, 63, 125-130.	0.9	4
17	Genomeâ€wide association study to identify genetic loci associated with gastrointestinal nematode resistance in Katahdin sheep. Animal Genetics, 2020, 51, 330-335.	0.6	20
18	Global Analysis of Transcription Start Sites in the New Ovine Reference Genome (Oar rambouillet) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	21

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19	Genetic structure and admixture in sheep from terminal breeds in the United States. Animal Genetics, 2020, 51, 284-291.	0.6	21
20	De novo assembly of the cattle reference genome with single-molecule sequencing. GigaScience, 2020, 9, .	3.3	380
21	28 The functional annotation of the sheep genome project. Journal of Animal Science, 2019, 97, 16-16.	0.2	17
22	Global DNA Methylation in the Limbic System of Cattle. Epigenomes, 2019, 3, 8.	0.8	8
23	A Vision for Development and Utilization of High-Throughput Phenotyping and Big Data Analytics in Livestock. Frontiers in Genetics, 2019, 10, 1197.	1.1	64
24	Genomic testing of female Holsteins: a resource for selection and improvement1. Translational Animal Science, 2018, 2, S149-S154.	0.4	2
25	Meiotic Recombination Differences in Rams from Three Breeds of Sheep in the US. Cytogenetic and Genome Research, 2018, 156, 106-116.	0.6	3
26	Germ Cellâ€“Specific Retinoic Acid Receptor Î± Functions in Germ Cell Organization, Meiotic Integrity, and Spermatogonia. Endocrinology, 2018, 159, 3403-3420.	1.4	18
27	Complete Mitochondrial Genome Sequence of Bighorn Sheep. Genome Announcements, 2018, 6, .	0.8	2
28	A SNP resource for studying North American moose. F1000Research, 2018, 7, 40.	0.8	7
29	Nutritional Influence on Epigenetic Marks and Effect on Livestock Production. Frontiers in Genetics, 2016, 7, 182.	1.1	42
30	Genetics of Prion Disease in Cattle. Bioinformatics and Biology Insights, 2015, 9S4, BBI.S29678.	1.0	12
31	Oncorhynchus mykiss pax7 sequence variations with comparative analyses against other teleost species. SpringerPlus, 2015, 4, 263.	1.2	2
32	Germline mosaicism does not explain the maternal age effect on trisomy. American Journal of Medical Genetics, Part A, 2013, 161, 2495-2503.	0.7	13
33	Altered Cohesin Gene Dosage Affects Mammalian Meiotic Chromosome Structure and Behavior. PLoS Genetics, 2013, 9, e1003241.	1.5	42
34	Bisphenol A alters early oogenesis and follicle formation in the fetal ovary of the rhesus monkey. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17525-17530.	3.3	186
35	Gene Expression in the Fetal Mouse Ovary Is Altered by Exposure to Low Doses of Bisphenol A1. Biology of Reproduction, 2011, 84, 79-86.	1.2	82
36	Genome-Wide Scan Identifies Loci Associated with Classical BSE Occurrence. PLoS ONE, 2011, 6, e26819.	1.1	9

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37	Multiple loci contribute to genome-wide recombination levels in male mice. Mammalian Genome, 2010, 21, 550-555.	1.0	24
38	A 2cM genome-wide scan of European Holstein cattle affected by classical BSE. BMC Genetics, 2010, 11, 20.	2.7	22
39	Use of SNP genotyping to determine pedigree and breed composition of dairy cattle in Kenya. Journal of Animal Breeding and Genetics, 2010, 127, 348-351.	0.8	28
40	PRNP Haplotype Associated with Classical BSE Incidence in European Holstein Cattle. PLoS ONE, 2010, 5, e12786.	1.1	20
41	Fine mapping quantitative trait loci for feed intake and feed efficiency in beef cattle1. Journal of Animal Science, 2009, 87, 37-45.	0.2	68
42	A whole genome scan to map QTL for milk production traits and somatic cell score in Canadian Holstein bulls. Journal of Animal Breeding and Genetics, 2009, 126, 216-227.	0.8	86
43	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. Science, 2009, 324, 528-532.	6.0	746
44	An assessment of population structure in eight breeds of cattle using a whole genome SNP panel. BMC Genetics, 2008, 9, 37.	2.7	95
45	Identification of polymorphisms influencing feed intake and efficiency in beef cattle. Animal Genetics, 2008, 39, 225-231.	0.6	42
46	Linkage disequilibrium and signatures of selection on chromosomes 19 and 29 in beef and dairy cattle. Animal Genetics, 2008, 39, 597-605.	0.6	42
47	A Whole-Genome Scan to Map Quantitative Trait Loci for Conformation and Functional Traits in Canadian Holstein Bulls. Journal of Dairy Science, 2008, 91, 2844-2856.	1.4	61
48	Polymorphisms and haplotypes in the bovine neuropeptide Y, growth hormone receptor, ghrelin, insulin-like growth factor 2, and uncoupling proteins 2 and 3 genes and their associations with measures of growth, performance, feed efficiency, and carcass merit in beef cattle1. Journal of Animal Science, 2008, 86, 1-16.	0.2	172
49	A physical map of the bovine genome. Genome Biology, 2007, 8, R165.	13.9	73
50	Primary genome scan to identify putative quantitative trait loci for feedlot growth rate, feed intake, and feed efficiency of beef cattle1. Journal of Animal Science, 2007, 85, 3170-3181.	0.2	109
51	Whole genome linkage disequilibrium maps in cattle. BMC Genetics, 2007, 8, 74.	2.7	201
52	Construction of bovine whole-genome radiation hybrid and linkage maps using high-throughput genotyping. Animal Genetics, 2007, 38, 120-125.	0.6	36
53	A high resolution radiation hybrid map of bovine chromosome 14 identifies scaffold rearrangement in the latest bovine assembly. BMC Genomics, 2007, 8, 254.	1.2	19
54	High resolution radiation hybrid maps of bovine chromosomes 19 and 29: comparison with the bovine genome sequence assembly. BMC Genomics, 2007, 8, 310.	1.2	16

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55	Genetic analysis of flowering and maturity time in high latitude spring wheat. Euphytica, 2007, 154, 207-218.	0.6	55
56	Identification and fine mapping of quantitative trait loci for growth traits on bovine chromosomes 2, 6, 14, 19, 21, and 23 within one commercial line of Bos taurus1. Journal of Animal Science, 2004, 82, 3405-3414.	0.2	76
57	Assignment of theSIAT4Agene to bovine chromosome 14 by linkage mapping of an associated microsatellite. Animal Genetics, 2004, 35, 146-147.	0.6	0
58	Identification of three microsatellite loci on bovine chromosome 19. Animal Genetics, 2004, 35, 145-146.	0.6	1
59	Association of a single nucleotide polymorphism in the bovine leptin gene with feed intake, feed efficiency, growth, feeding behaviour, carcass quality and body composition. Canadian Journal of Animal Science, 2004, 84, 211-219.	0.7	69
60	Different measures of energetic efficiency and their phenotypic relationships with growth, feed intake, and ultrasound and carcass merit in hybrid cattle1. Journal of Animal Science, 2004, 82, 2451-2459.	0.2	148
61	Assessment of positional candidate genes myf5 and igf1 for growth on bovine chromosome 5 in commercial lines of Bos taurus1. Journal of Animal Science, 2004, 82, 1-7.	0.2	92
62	Fine mapping of quantitative trait loci and assessment of positional candidate genes for backfat on bovine chromosome 14 in a commercial line of Bos taurus1. Journal of Animal Science, 2003, 81, 1919-1925.	0.2	71
63	The identification of common haplotypes on bovine chromosome 5 within commercial lines of Bos taurus and their associations with growth traits1. Journal of Animal Science, 2002, 80, 1187-1194.	0.2	43