John C Mcewan

List of Publications by Year
in descending order

142 papers	10,745 citations	41344 49 h-index	33894 99 g-index
151 all docs	151 docs citations	151 times ranked	8930 citing authors

#	Article	IF	Citations
1	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	12.6	1,038
2	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. Science, 2009, 324, 528-532.	12.6	746
3	Genome-Wide Analysis of the World's Sheep Breeds Reveals High Levels of Historic Mixture and Strong Recent Selection. PLoS Biology, 2012, 10, e1001258.	5.6	719
4	Highly Prolific Booroola Sheep Have a Mutation in the Intracellular Kinase Domain of Bone Morphogenetic Protein IB Receptor (ALK-6) That Is Expressed in Both Oocytes and Granulosa Cells1. Biology of Reproduction, 2001, 64, 1225-1235.	2.7	475
5	The sheep genome illuminates biology of the rumen and lipid metabolism. Science, 2014, 344, 1168-1173.	12.6	436
6	Understanding the relationship between the inbreeding coefficient and multilocus heterozygosity: theoretical expectations and empirical data. Heredity, 2004, 93, 255-265.	2.6	360
7	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. Genome Research, 2014, 24, 1517-1525.	5.5	332
8	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. Genome Biology, 2015, 16, 57.	8.8	331
9	A Genome Wide Survey of SNP Variation Reveals the Genetic Structure of Sheep Breeds. PLoS ONE, 2009, 4, e4668.	2.5	269
10	Two Different Bacterial Community Types Are Linked with the Low-Methane Emission Trait in Sheep. PLoS ONE, 2014, 9, e103171.	2.5	246
11	Genomic scan of selective sweeps in thin and fat tail sheep breeds for identifying of candidate regions associated with fat deposition. BMC Genetics, 2012, 13, 10.	2.7	236
12	Design and Characterization of a 52K SNP Chip for Goats. PLoS ONE, 2014, 9, e86227.	2.5	220
13	Genome-wide association mapping identifies the genetic basis of discrete and quantitative variation in sexual weaponry in a wild sheep population. Molecular Ecology, 2011, 20, 2555-2566.	3.9	217
14	Heritability estimates of methane emissions from sheep. Animal, 2013, 7, 316-321.	3.3	209
15	Selection Signatures in Worldwide Sheep Populations. PLoS ONE, 2014, 9, e103813.	2.5	197
16	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18644-18649.	7.1	196
17	The sheep genome reference sequence: a work in progress. Animal Genetics, 2010, 41, 449-453.	1.7	173
18	Linkage Disequilibrium in Domestic Sheep. Genetics, 2002, 160, 1113-1122.	2.9	145

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19	Fatty acid synthase effects on bovine adipose fat and milk fat. Mammalian Genome, 2007, 18, 64-74.	2.2	123
20	Construction of relatedness matrices using genotyping-by-sequencing data. BMC Genomics, 2015, 16, 1047.	2.8	122
21	Animal board invited review: genetic possibilities to reduce enteric methane emissions from ruminants. Animal, 2015, 9, 1431-1440.	3.3	119
22	Evidence for the Presence of a Major Gene Influencing Ovulation Rate on the X Chromosome of Sheep. Biology of Reproduction, 1991, 44, 620-624.	2.7	116
23	Linkage disequilibrium over short physical distances measured in sheep using a high‐density <scp>SNP</scp> chip. Animal Genetics, 2014, 45, 754-757.	1.7	113
24	Genome-wide association study for birth weight in Nellore cattle points to previously described orthologous genes affecting human and bovine height. BMC Genetics, 2013, 14, 52.	2.7	111
25	Infertility Due to Bilateral Ovarian Hypoplasia in Sheep Homozygous (FecX1 FecX1) for the Inverdale Prolificacy Gene Located on the X Chromosome. Biology of Reproduction, 1992, 46, 636-640.	2.7	110
26	Signatures of selection in sheep bred for resistance or susceptibility to gastrointestinal nematodes. BMC Genomics, 2014, 15, 637.	2.8	109
27	Breeding sheep in New Zealand that are less reliant on anthelmintics to maintain health and productivity. New Zealand Veterinary Journal, 2001, 49, 236-246.	0.9	103
28	Microarray analysis of selection lines from outbred populations to identify genes involved with nematode parasite resistance in sheep. Physiological Genomics, 2005, 21, 59-69.	2.3	103
29	SNPs for Parentage Testing and Traceability in Globally Diverse Breeds of Sheep. PLoS ONE, 2014, 9, e94851.	2.5	88
30	Genomic application in sheep and goat breeding. Animal Frontiers, 2016, 6, 39-44.	1.7	87
31	Economic values for ewe prolificacy and lamb survival in New Zealand sheep. Livestock Science, 1999, 58, 75-90.	1.2	86
32	Accuracy of genotype imputation in Nelore cattle. Genetics Selection Evolution, 2014, 46, 69.	3.0	86
33	Gene expression profiling of Naïve sheep genetically resistant and susceptible to gastrointestinal nematodes. BMC Genomics, 2006, 7, 42.	2.8	78
34	Using comparative genomics to reorder the human genome sequence into a virtual sheep genome. Genome Biology, 2007, 8, R152.	9.6	77
35	Accuracy of genomic predictions in Bos indicus (Nellore) cattle. Genetics Selection Evolution, 2014, 46, 17.	3.0	77
36	Early stages of myogenesis in a large mammal: Formation of successive generations of myotubes in sheep tibialis cranialis muscle. Journal of Muscle Research and Cell Motility, 1992, 13, 534-550.	2.0	76

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37	A physical map of the bovine genome. Genome Biology, 2007, 8, R165.	9.6	73
38	An examination of positive selection and changing effective population size in Angus and Holstein cattle populations (Bos taurus) using a high density SNP genotyping platform and the contribution of ancient polymorphism to genomic diversity in Domestic cattle. BMC Genomics, 2009, 10, 181.	2.8	72
39	Gene network analysis identifies rumen epithelial cell proliferation, differentiation and metabolic pathways perturbed by diet and correlated with methane production. Scientific Reports, 2016, 6, 39022.	3.3	68
40	Discovery of quantitative trait loci for resistance to parasitic nematode infection in sheep: I. Analysis of outcross pedigrees. BMC Genomics, 2006, 7, 178.	2.8	67
41	Myosin heavy chain composition of single fibres and their origins and distribution in developing fascicles of sheep tibialis cranialis muscles. Journal of Muscle Research and Cell Motility, 1992, 13, 551-572.	2.0	64
42	Repeatability of methane emissions from sheep. Animal Feed Science and Technology, 2011, 166-167, 210-218.	2.2	62
43	Exclusion probabilities for pedigree testing farm animals. Theoretical and Applied Genetics, 1996, 92, 966-975.	3.6	61
44	Phenotypic markers for selection of nematode-resistant sheep. International Journal for Parasitology, 1996, 26, 899-911.	3.1	60
45	On the origin of European sheep as revealed by the diversity of the Balkan breeds and by optimizing population-genetic analysis tools. Genetics Selection Evolution, 2020, 52, 25.	3.0	58
46	Consistent divergence times and allele sharing measured from cross€species application of <scp>SNP</scp> chips developed for three domestic species. Molecular Ecology Resources, 2012, 12, 1145-1150.	4.8	56
47	A High Throughput Single Nucleotide Polymorphism Multiplex Assay for Parentage Assignment in New Zealand Sheep. PLoS ONE, 2014, 9, e93392.	2.5	55
48	Genetic parameters of methane emissions determined using portable accumulation chambers in lambs and ewes grazing pasture and genetic correlations with emissions determined in respiration chambers1. Journal of Animal Science, 2018, 96, 3031-3042.	0.5	55
49	Phylogenetic reconstruction and the identification of ancient polymorphism in the Bovini tribe (Bovidae, Bovinae). BMC Genomics, 2009, 10, 177.	2.8	54
50	Investigations into the GDF8 g+6723G-A polymorphism in New Zealand Texel sheep1. Journal of Animal Science, 2009, 87, 1856-1864.	0.5	52
51	A directed search in the region of GDF8 for quantitative trait loci affecting carcass traits in Texel sheep1. Journal of Animal Science, 2005, 83, 1988-2000.	0.5	49
52	Carcass composition and meat quality differences between pasture-reared ewe and ram lambs. Meat Science, 2005, 71, 383-391.	5.5	49
53	Assessing accuracy of imputation using different SNP panel densities in a multi-breed sheep population. Genetics Selection Evolution, 2016, 48, 71.	3.0	48
54	Prediction of genomic breeding values for growth, carcass and meat quality traits in a multi-breed sheep population using a HD SNP chip. BMC Genetics, 2017, 18, 7.	2.7	48

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55	Neural control of the sequence of expression of myosin heavy chain isoforms in foetal mammalian muscles. Development (Cambridge), 1989, 107, 751-69.	2.5	48
56	Genetic diversity of a New Zealand multi-breed sheep population and composite breeds' history revealed by a high-density SNP chip. BMC Genetics, 2017, 18, 25.	2.7	47
57	Genetic parameters for predicted methane production and laser methane detector measurements1. Journal of Animal Science, 2015, 93, 11-20.	0.5	44
58	Large animal models of rare genetic disorders: sheep as phenotypically relevant models of human genetic disease. Orphanet Journal of Rare Diseases, 2015, 10, 107.	2.7	43
59	Estimation of linkage disequilibrium and effective population size in New Zealand sheep using three different methods to create genetic maps. BMC Genetics, 2017, 18, 68.	2.7	43
60	Bone density in sheep: genetic variation and quantitative trait loci localisation. Bone, 2003, 33, 540-548.	2.9	37
61	Genome-Wide DNA Methylation Patterns and Transcription Analysis in Sheep Muscle. PLoS ONE, 2014, 9, e101853.	2.5	37
62	Genetic parameters for various growth, carcass and meat quality traits in a New Zealand sheep population. Small Ruminant Research, 2017, 154, 81-91.	1.2	37
63	Molecular evolution of the Bovini tribe (Bovidae, Bovinae): Is there evidence of rapid evolution or reduced selective constraint in Domestic cattle?. BMC Genomics, 2009, 10, 179.	2.8	33
64	Genomic prediction of breeding values in the New Zealand sheep industry using a 50K SNP chip1. Journal of Animal Science, 2014, 92, 4375-4389.	0.5	33
65	Genome-Wide Mapping of Loci Explaining Variance in Scrotal Circumference in Nellore Cattle. PLoS ONE, 2014, 9, e88561.	2.5	33
66	Genetic parameters for production traits in New Zealand dual-purpose sheep, with an emphasis on dagginess1. Journal of Animal Science, 2012, 90, 1411-1420.	0.5	31
67	Meat quality traits were unaffected by a quantitative trait locus affecting leg composition traits in Texel sheep1. Journal of Animal Science, 2005, 83, 2729-2735.	0.5	30
68	Selection for high or low backfat depth in Coopworth sheep: juvenile traits. Animal Science, 1997, 65, 93-103.	1.3	29
69	Transcriptional profiling of Ovis aries identifies Ovar-DQA1 allele frequency differences between nematode-resistant and susceptible selection lines. Physiological Genomics, 2007, 30, 253-261.	2.3	29
70	Imputation of microsatellite alleles from dense SNP genotypes for parentage verification across multiple Bos taurus and Bos indicus breeds. Frontiers in Genetics, 2013, 4, 176.	2.3	29
71	Copy number variants in the sheep genome detected using multiple approaches. BMC Genomics, 2016, 17, 441.	2.8	27
72	Genetically resistant sheep avoid parasites to a greater extent than do susceptible sheep. Proceedings of the Royal Society B: Biological Sciences, 2007, 274, 1839-1844.	2.6	26

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73	Linkage Disequilibrium Estimation in Low Coverage High-Throughput Sequencing Data. Genetics, 2018, 209, 389-400.	2.9	26
74	Expression of Genes for Appetite-Regulating Peptides in the Hypothalamus of Genetically Selected Lean and Fat Sheep. Neuroendocrinology, 2010, 91, 223-238.	2.5	24
75	Genomic prediction and genome-wide association study for dagginess and host internal parasite resistance in New Zealand sheep. BMC Genomics, 2015, 16, 958.	2.8	24
76	Growth hormone and ghrelin receptor genes are differentially expressed between genetically lean and fat selection lines of sheep. Journal of Animal Science, 2006, 84, 324-331.	0.5	23
77	Expansion of the Bactericidal/Permeability Increasing-like (BPI-like) protein locus in cattle. BMC Genomics, 2007, 8, 75.	2.8	23
78	A restriction enzyme reduced representation sequencing approach for low-cost, high-throughput metagenome profiling. PLoS ONE, 2020, 15, e0219882.	2.5	23
79	Characterization of an X-chromosomal non-mosaic monosomy (59, X0) dairy heifer detected using routinely available single nucleotide polymorphism genotype data1. Journal of Animal Science, 2017, 95, 1042-1049.	0.5	22
80	Establishment of a pipeline to analyse non-synonymous SNPs in Bos taurus. BMC Genomics, 2006, 7, 298.	2.8	21
81	Genomics detects population structure within and between ocean basins in a circumpolar seabird: The white‑chinned petrel. Molecular Ecology, 2019, 28, 4552-4572.	3.9	21
82	Integration of molecular and quantitative information in sheep and goat industry breeding programmes. Small Ruminant Research, 2007, 70, 32-41.	1.2	20
83	Genomic breed prediction in New Zealand sheep. BMC Genetics, 2014, 15, 92.	2.7	20
84	Genetic characterisation of protective vaccine responses in sheep using multi-valent Dichelobacter nodosus vaccines. Veterinary Immunology and Immunopathology, 1999, 72, 219-229.	1.2	19
85	Economic benefits in selection for weight and composition of lamb cuts predicted by computer tomography. Livestock Science, 2004, 90, 123-133.	1.2	17
86	Liveweight, fleece weight and prolificacy of Romney ewes carrying the Inverdale prolificacy gene (FecXI) located on the X-chromosome. Livestock Science, 1993, 34, 83-91.	1.2	16
87	Genetic relationships between dagginess, breech bareness, and wool traits in New Zealand dual-purpose sheep1. Journal of Animal Science, 2013, 91, 4578-4588.	0.5	16
88	Genetic parameters of plasma and ruminal volatile fatty acids in sheep fed alfalfa pellets and genetic correlations with enteric methane emissions1. Journal of Animal Science, 2019, 97, 2711-2724.	0.5	16
89	Genomic signatures of inbreeding in a critically endangered parrot, the kākāpō. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	16
90	Catalase gene is associated with facial eczema disease resistance in sheep. Animal Genetics, 1999, 30, 286-295.	1.7	15

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91	Selection for high or low backfat depth in Coopworth sheep: breeding-ewe traits. Animal Science, 2001, 73, 241-252.	1.3	15
92	An ovine hepatorenal fibrocystic model of a Meckel-like syndrome associated with dysmorphic primary cilia and TMEM67 mutations. Scientific Reports, 2017, 7, 1601.	3.3	15
93	Estimates of genetic parameters for breech strike and potential indirect indicators in sheep. New Zealand Veterinary Journal, 2015, 63, 98-103.	0.9	14
94	Towards genomic selection for facial eczema disease tolerance in the New Zealand sheep industry. Animal Genetics, 2014, 45, 559-564.	1.7	13
95	Across-Experiment Transcriptomics of Sheep Rumen Identifies Expression of Lipid/Oxo-Acid Metabolism and Muscle Cell Junction Genes Associated With Variation in Methane-Related Phenotypes. Frontiers in Genetics, 2018, 9, 330.	2.3	13
96	Liveweight, ovulation rate, and wool growth responses of light and heavy ewes to differential feeding. New Zealand Journal of Crop and Horticultural Science, 1983, 11, 219-224.	0.2	11
97	The effect of liveweight and liveweight change on ewe ovulation rate at 3 successive oestrous cycles. New Zealand Journal of Agricultural Research, 1985, 28, 457-462.	1.6	11
98	Autoradiographic localisation of [3H]-SCH23390 and [3H]-spiperone binding sites in honey bee brain. , 1998, 394, 29-37.		11
99	Exclusion and Genomic Relatedness Methods for Assignment of Parentage Using Genotyping-by-Sequencing Data. G3: Genes, Genomes, Genetics, 2019, 9, 3239-3247.	1.8	11
100	CYTOLOGICAL MONITORING OF NICKEL SINTER PLANT WORKERS. Annals of the New York Academy of Sciences, 1976, 271, 365-369.	3.8	10
101	Finding disease resistance QTL in sheep. Animal Biotechnology, 1997, 8, 13-22.	1.5	10
102	Application of Low Coverage Genotyping by Sequencing in Selectively Bred Arctic Charr (<i>Salvelinus) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.8	10
103	GBS Data Identify Pigmentation-Specific Genes of Potential Role in Skin-Photosensitization in Two Tunisian Sheep Breeds. Animals, 2020, 10, 5.	2.3	9
104	Exclusion probabilities for pedigree testing farm animals. Theoretical and Applied Genetics, 1996, 92, 966-975.	3.6	9
105	Future perspectives for the implementation of genetic markers for parasite resistance in sheep. Tropical Biomedicine, 2008, 25, 18-33.	0.7	9
106	Genetic analysis and genomic selection of stayability and productive life in New Zealand ewes1. Journal of Animal Science, 2015, 93, 3268-3277.	0.5	8
107	Characterization of an X-chromosomal non-mosaic monosomy (59, X0) dairy heifer detected using routinely available single nucleotide polymorphism genotype data. Journal of Animal Science, 2017, 95, 1042.	0.5	8
108	Testing the neutral theory of molecular evolution using genomic data: a comparison of the human and bovine transcriptome. Genetics Selection Evolution, 2006, 38, 321.	3.0	7

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109	Inference of transcriptional regulation using gene expression data from the bovine and human genomes. BMC Genomics, 2007, 8, 265.	2.8	7
110	Individual-level correlations of rumen volatile fatty acids with enteric methane emissions for ranking methane yield in sheep fed fresh pasture. Animal Production Science, 2021, 61, 300.	1.3	7
111	Across‐country genomic predictions in Norwegian and New Zealand Composite sheep populations with similar development history. Journal of Animal Breeding and Genetics, 2022, 139, 1-12.	2.0	7
112	Natural variation in methane emission of sheep fed on a lucerne pellet diet is unrelated to rumen ciliate community type. Microbiology (United Kingdom), 2016, 162, 459-465.	1.8	7
113	Sheep from low-methane-yield selection lines created on alfalfa pellets also have lower methane yield under pastoral farming conditions1,2. Journal of Animal Science, 2017, 95, 3905-3913.	0.5	7
114	The physiological effects of natural variation in growth hormone gene copy number in ram lambs. Domestic Animal Endocrinology, 1997, 14, 381-390.	1.6	6
115	Distribution of prion protein genotypes in breeds of sheep in New Zealand. New Zealand Veterinary Journal, 2007, 55, 222-227.	0.9	6
116	A QTL study of growth and body shape in the inter-species hybrid of PÃ¨re David's deer (Elaphurus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.7	6
117	Population Connectivity and Traces of Mitochondrial Introgression in New Zealand Black-Billed Gulls (Larus bulleri). Genes, 2018, 9, 544.	2.4	6
118	Heritability of ram mating success in multi-sire breeding situations. Animal, 2019, 13, 917-923.	3.3	6
119	Hitchhiking Mapping of Candidate Regions Associated with Fat Deposition in Iranian Thin and Fat Tail Sheep Breeds Suggests New Insights into Molecular Aspects of Fat Tail Selection. Animals, 2022, 12, 1423.	2.3	6
120	Effect of Cimaterol implants on lamb growth and carcass traits. New Zealand Journal of Agricultural Research, 1990, 33, 413-427.	1.6	5
121	Development of an in situ procedure to evaluate the reticulo-rumen morphology of sheep selected for divergent methane emissions. Animal, 2019, 13, 542-548.	3.3	5
122	Using genotyping‐by‐sequencing to predict gender in animals. Animal Genetics, 2019, 50, 307-310.	1.7	5
123	Genome-wide selection of discriminant SNP markers for breed assignment in indigenous sheep breeds. Annals of Animal Science, 2021, 21, 807-831.	1.6	5
124	Geographical contrasts of Y‐chromosomal haplogroups from wild and domestic goats reveal ancient migrations and recent introgressions. Molecular Ecology, 2022, 31, 4364-4380.	3.9	5
125	Physical mapping of thestearoyl-CoA desaturase(SCD) locus in sheep. Animal Genetics, 2004, 35, 163-163.	1.7	4
126	A multiway analysis for identifying high integrity bovine BACs. BMC Genomics, 2009, 10, 46.	2.8	4

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127	Excreta emissions in progeny of low and high enteric methane yield selection line sheep fed pasture of different qualities. Animal Feed Science and Technology, 2019, 257, 114289.	2.2	4
128	Molecular and bioinformatic strategies for gene discovery for meat traits: a reverse genetics approach. Australian Journal of Experimental Agriculture, 2005, 45, 801.	1.0	3
129	Genome-wide DNA methylation analysis: no evidence for stable hemimethylation in the sheep muscle genome. Animal Genetics, 2015, 46, 185-189.	1.7	3
130	Ovine rumen papillae biopsy via oral endoscopy; a rapid and repeatable method for serial sampling. New Zealand Veterinary Journal, 2016, 64, 174-178.	0.9	3
131	Ovine keratome: identification, localisation and genomic organisation of keratin and keratinâ€associated proteins. Animal Genetics, 2018, 49, 361-370.	1.7	3
132	Brown adipose tissue in lean and fat selection lines of sheep identified by immunodetection of uncoupling protein in western blots of tissue homogenates. Comparative Biochemistry and Physiology Part B: Comparative Biochemistry, 1989, 94, 493-498.	0.2	2
133	Breeding Low Emitting Ruminants: Predicting Methane from Microbes. Proceedings (mdpi), 2020, 36, .	0.2	2
134	Generation of a preliminary bovine gene atlas, using expression clustering to annotate gene function. Genetics and Molecular Research, 2009, 8, 1013-1027.	0.2	2
135	Low-cost sample preservation methods for high-throughput processing of rumen microbiomes. Animal Microbiome, 2022, 4, .	3.8	2
136	Comparative mapping of sheep chromosome 2q. Cytogenetic and Genome Research, 2007, 116, 85-92.	1.1	1
137	An entropy-reducing data representation approach for bioinformatic data. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	1
138	Testing the neutral theory of molecular evolution using genomic data: a comparison of the human and bovine transcriptome. Genetics Selection Evolution, 2006, 38, 321-341.	3.0	1
139	Genetic variation in skin traits in New Zealand lambs. Journal of the Science of Food and Agriculture, 2022, , .	3.5	1
140	Expression of NPY and POMC in the hypothalamic arcuate nucleus of genetically lean and fat sheep. Frontiers in Neuroendocrinology, 2006, 27, 8-9.	5.2	0
141	P3048 Gene network analysis identifies rumen epithelial processes perturbed by diet and correlated with methane production and yield. Journal of Animal Science, 2016, 94, 76-77.	0.5	0
142	Genomic Tools for the Identification of Loci Associated with Facial Eczema in New Zealand Sheep. Genes, 2021, 12, 1560.	2.4	0