

John C Mcewan

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

138 papers	7,756 citations	44 h-index	86 g-index
150 ext. papers	9,692 ext. citations	4.3 avg, IF	5.12 L-index

#	Paper	IF	Citations
138	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863
137	Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. <i>Science</i> , 2009 , 324, 528-32	33.3	612
136	Genome-wide analysis of the world's sheep breeds reveals high levels of historic mixture and strong recent selection. <i>PLoS Biology</i> , 2012 , 10, e1001258	9.7	488
135	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 cells. <i>Biology of Reproduction</i> , 2001 , 64, 1225-35	3.9	379
134	Understanding the relationship between the inbreeding coefficient and multilocus heterozygosity: theoretical expectations and empirical data. <i>Heredity</i> , 2004 , 93, 255-65	3.6	325
133	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014 , 344, 1168-1173	33.3	294
132	A genome wide survey of SNP variation reveals the genetic structure of sheep breeds. <i>PLoS ONE</i> , 2009 , 4, e4668	3.7	208
131	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. <i>Genome Research</i> , 2014 , 24, 1517-25	9.7	197
130	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015 , 16, 57	18.3	196
129	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, 18644-9	11.5	159
128	Genome-wide association mapping identifies the genetic basis of discrete and quantitative variation in sexual weaponry in a wild sheep population. <i>Molecular Ecology</i> , 2011 , 20, 2555-66	5.7	149
127	Two different bacterial community types are linked with the low-methane emission trait in sheep. <i>PLoS ONE</i> , 2014 , 9, e103171	3.7	145
126	Heritability estimates of methane emissions from sheep. <i>Animal</i> , 2013 , 7 Suppl 2, 316-21	3.1	133
125	Genomic scan of selective sweeps in thin and fat tail sheep breeds for identifying of candidate regions associated with fat deposition. <i>BMC Genetics</i> , 2012 , 13, 10	2.6	132
124	The sheep genome reference sequence: a work in progress. <i>Animal Genetics</i> , 2010 , 41, 449-53	2.5	128
123	Linkage disequilibrium in domestic sheep. <i>Genetics</i> , 2002 , 160, 1113-22	4	124
122	Design and characterization of a 52K SNP chip for goats. <i>PLoS ONE</i> , 2014 , 9, e86227	3.7	121

121	Evidence for the presence of a major gene influencing ovulation rate on the X chromosome of sheep. <i>Biology of Reproduction</i> , 1991 , 44, 620-4	3.9	103
120	Fatty acid synthase effects on bovine adipose fat and milk fat. <i>Mammalian Genome</i> , 2007 , 18, 64-74	3.2	102
119	Selection signatures in worldwide sheep populations. <i>PLoS ONE</i> , 2014 , 9, e103813	3.7	101
118	Microarray analysis of selection lines from outbred populations to identify genes involved with nematode parasite resistance in sheep. <i>Physiological Genomics</i> , 2005 , 21, 59-69	3.6	99
117	Breeding sheep in New Zealand that are less reliant on anthelmintics to maintain health and productivity. <i>New Zealand Veterinary Journal</i> , 2001 , 49, 236-46	1.7	94
116	Infertility due to bilateral ovarian hypoplasia in sheep homozygous (FecXI FecXI) for the Inverdale prolificacy gene located on the X chromosome. <i>Biology of Reproduction</i> , 1992 , 46, 636-40	3.9	91
115	Genome-wide association study for birth weight in Nellore cattle points to previously described orthologous genes affecting human and bovine height. <i>BMC Genetics</i> , 2013 , 14, 52	2.6	83
114	Animal board invited review: genetic possibilities to reduce enteric methane emissions from ruminants. <i>Animal</i> , 2015 , 9, 1431-40	3.1	77
113	Economic values for ewe prolificacy and lamb survival in New Zealand sheep. <i>Livestock Science</i> , 1999 , 58, 75-90		77
112	Construction of relatedness matrices using genotyping-by-sequencing data. <i>BMC Genomics</i> , 2015 , 16, 1047	4.5	74
111	Gene expression profiling of naïve sheep genetically resistant and susceptible to gastrointestinal nematodes. <i>BMC Genomics</i> , 2006 , 7, 42	4.5	71
110	A physical map of the bovine genome. <i>Genome Biology</i> , 2007 , 8, R165	18.3	67
109	Linkage disequilibrium over short physical distances measured in sheep using a high-density SNP chip. <i>Animal Genetics</i> , 2014 , 45, 754-7	2.5	65
108	Using comparative genomics to reorder the human genome sequence into a virtual sheep genome. <i>Genome Biology</i> , 2007 , 8, R152	18.3	65
107	Signatures of selection in sheep bred for resistance or susceptibility to gastrointestinal nematodes. <i>BMC Genomics</i> , 2014 , 15, 637	4.5	64
106	An examination of positive selection and changing effective population size in Angus and Holstein cattle populations (<i>Bos taurus</i>) using a high density SNP genotyping platform and the contribution of ancient polymorphism to genomic diversity in Domestic cattle. <i>BMC Genomics</i> , 2009 , 10, 181	4.5	64
105	SNPs for parentage testing and traceability in globally diverse breeds of sheep. <i>PLoS ONE</i> , 2014 , 9, e94851	3.7	62
104	Discovery of quantitative trait loci for resistance to parasitic nematode infection in sheep: I. Analysis of outcross pedigrees. <i>BMC Genomics</i> , 2006 , 7, 178	4.5	61

103	Accuracy of genomic predictions in Bos indicus (Nellore) cattle. <i>Genetics Selection Evolution</i> , 2014 , 46, 17	4.9	60
102	Early stages of myogenesis in a large mammal: formation of successive generations of myotubes in sheep tibialis cranialis muscle. <i>Journal of Muscle Research and Cell Motility</i> , 1992 , 13, 534-50	3.5	57
101	Exclusion probabilities for pedigree testing farm animals. <i>Theoretical and Applied Genetics</i> , 1996 , 92, 966-75	6	53
100	Accuracy of genotype imputation in Nelore cattle. <i>Genetics Selection Evolution</i> , 2014 , 46, 69	4.9	51
99	Phenotypic markers for selection of nematode-resistant sheep. <i>International Journal for Parasitology</i> , 1996 , 26, 899-911	4.3	51
98	Myosin heavy chain composition of single fibres and their origins and distribution in developing fascicles of sheep tibialis cranialis muscles. <i>Journal of Muscle Research and Cell Motility</i> , 1992 , 13, 551-72	3.5	51
97	Repeatability of methane emissions from sheep. <i>Animal Feed Science and Technology</i> , 2011 , 166-167, 210-218	3	49
96	Neural control of the sequence of expression of myosin heavy chain isoforms in foetal mammalian muscles. <i>Development (Cambridge)</i> , 1989 , 107, 751-69	6.6	48
95	Phylogenetic reconstruction and the identification of ancient polymorphism in the Bovini tribe (Bovidae, Bovinae). <i>BMC Genomics</i> , 2009 , 10, 177	4.5	45
94	A high throughput single nucleotide polymorphism multiplex assay for parentage assignment in New Zealand sheep. <i>PLoS ONE</i> , 2014 , 9, e93392	3.7	43
93	Investigations into the GDF8 g+6723G-A polymorphism in New Zealand Texel sheep. <i>Journal of Animal Science</i> , 2009 , 87, 1856-64	0.7	39
92	Genomic application in sheep and goat breeding. <i>Animal Frontiers</i> , 2016 , 6, 39-44	5.5	39
91	Consistent divergence times and allele sharing measured from cross-species application of SNP chips developed for three domestic species. <i>Molecular Ecology Resources</i> , 2012 , 12, 1145-50	8.4	38
90	Carcass composition and meat quality differences between pasture-reared ewe and ram lambs. <i>Meat Science</i> , 2005 , 71, 383-91	6.4	38
89	A directed search in the region of GDF8 for quantitative trait loci affecting carcass traits in Texel sheep. <i>Journal of Animal Science</i> , 2005 , 83, 1988-2000	0.7	36
88	Genetic parameters for predicted methane production and laser methane detector measurements. <i>Journal of Animal Science</i> , 2015 , 93, 11-20	0.7	32
87	Genome-wide DNA methylation patterns and transcription analysis in sheep muscle. <i>PLoS ONE</i> , 2014 , 9, e101853	3.7	31
86	Bone density in sheep: genetic variation and quantitative trait loci localisation. <i>Bone</i> , 2003 , 33, 540-8	4.7	31

85	Genome-wide mapping of loci explaining variance in scrotal circumference in Nellore cattle. <i>PLoS ONE</i> , 2014 , 9, e88561	3.7	29
84	Prediction of genomic breeding values for growth, carcass and meat quality traits in a multi-breed sheep population using a HD SNP chip. <i>BMC Genetics</i> , 2017 , 18, 7	2.6	28
83	Selection for high or low backfat depth in Coopworth sheep: juvenile traits. <i>Animal Science</i> , 1997 , 65, 93-103		28
82	Assessing accuracy of imputation using different SNP panel densities in a multi-breed sheep population. <i>Genetics Selection Evolution</i> , 2016 , 48, 71	4.9	27
81	Large animal models of rare genetic disorders: sheep as phenotypically relevant models of human genetic disease. <i>Orphanet Journal of Rare Diseases</i> , 2015 , 10, 107	4.2	27
80	Genomic prediction of breeding values in the New Zealand sheep industry using a 50K SNP chip. <i>Journal of Animal Science</i> , 2014 , 92, 4375-89	0.7	26
79	On the origin of European sheep as revealed by the diversity of the Balkan breeds and by optimizing population-genetic analysis tools. <i>Genetics Selection Evolution</i> , 2020 , 52, 25	4.9	25
78	Transcriptional profiling of Ovis aries identifies Ovar-DQA1 allele frequency differences between nematode-resistant and susceptible selection lines. <i>Physiological Genomics</i> , 2007 , 30, 253-61	3.6	25
77	Meat quality traits were unaffected by a quantitative trait locus affecting leg composition traits in Texel sheep. <i>Journal of Animal Science</i> , 2005 , 83, 2729-35	0.7	25
76	Molecular evolution of the Bovini tribe (Bovidae, Bovinae): is there evidence of rapid evolution or reduced selective constraint in Domestic cattle?. <i>BMC Genomics</i> , 2009 , 10, 179	4.5	24
75	Genetic parameters of methane emissions determined using portable accumulation chambers in lambs and ewes grazing pasture and genetic correlations with emissions determined in respiration chambers. <i>Journal of Animal Science</i> , 2018 , 96, 3031-3042	0.7	22
74	Genetic parameters for production traits in New Zealand dual-purpose sheep, with an emphasis on dagginess. <i>Journal of Animal Science</i> , 2012 , 90, 1411-20	0.7	22
73	Genetic parameters for various growth, carcass and meat quality traits in a New Zealand sheep population. <i>Small Ruminant Research</i> , 2017 , 154, 81-91	1.7	21
72	Expression of genes for appetite-regulating peptides in the hypothalamus of genetically selected lean and fat sheep. <i>Neuroendocrinology</i> , 2010 , 91, 223-38	5.6	21
71	Expansion of the Bactericidal/Permeability Increasing-like (BPI-like) protein locus in cattle. <i>BMC Genomics</i> , 2007 , 8, 75	4.5	21
70	Genetically resistant sheep avoid parasites to a greater extent than do susceptible sheep. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007 , 274, 1839-44	4.4	21
69	Linkage Disequilibrium Estimation in Low Coverage High-Throughput Sequencing Data. <i>Genetics</i> , 2018 , 209, 389-400	4	19
68	Genetic diversity of a New Zealand multi-breed sheep population and composite breeds history revealed by a high-density SNP chip. <i>BMC Genetics</i> , 2017 , 18, 25	2.6	19

67	Integration of molecular and quantitative information in sheep and goat industry breeding programmes. <i>Small Ruminant Research</i> , 2007 , 70, 32-41	1.7	19
66	Establishment of a pipeline to analyse non-synonymous SNPs in <i>Bos taurus</i> . <i>BMC Genomics</i> , 2006 , 7, 298	4.5	18
65	Growth hormone and ghrelin receptor genes are differentially expressed between genetically lean and fat selection lines of sheep. <i>Journal of Animal Science</i> , 2006 , 84, 324-31	0.7	18
64	Copy number variants in the sheep genome detected using multiple approaches. <i>BMC Genomics</i> , 2016 , 17, 441	4.5	18
63	Estimation of linkage disequilibrium and effective population size in New Zealand sheep using three different methods to create genetic maps. <i>BMC Genetics</i> , 2017 , 18, 68	2.6	17
62	Economic benefits in selection for weight and composition of lamb cuts predicted by computer tomography. <i>Livestock Science</i> , 2004 , 90, 123-133		15
61	Genetic characterisation of protective vaccine responses in sheep using multi-valent <i>Dichelobacter nodosus</i> vaccines. <i>Veterinary Immunology and Immunopathology</i> , 1999 , 72, 219-29	2	15
60	Gene network analysis identifies rumen epithelial cell proliferation, differentiation and metabolic pathways perturbed by diet and correlated with methane production. <i>Scientific Reports</i> , 2016 , 6, 39022	4.9	15
59	Genomic prediction and genome-wide association study for dagginess and host internal parasite resistance in New Zealand sheep. <i>BMC Genomics</i> , 2015 , 16, 958	4.5	14
58	Utilization of high throughput genome sequencing technology for large scale single nucleotide polymorphism discovery in red deer and Canadian elk		14
57	Genomic breed prediction in New Zealand sheep. <i>BMC Genetics</i> , 2014 , 15, 92	2.6	13
56	Genetic relationships between dagginess, breech bareness, and wool traits in New Zealand dual-purpose sheep. <i>Journal of Animal Science</i> , 2013 , 91, 4578-88	0.7	12
55	Imputation of microsatellite alleles from dense SNP genotypes for parentage verification across multiple <i>Bos taurus</i> and <i>Bos indicus</i> breeds. <i>Frontiers in Genetics</i> , 2013 , 4, 176	4.5	12
54	Selection for high or low backfat depth in Coopworth sheep: breeding-ewe traits. <i>Animal Science</i> , 2001 , 73, 241-252		12
53	Catalase gene is associated with facial eczema disease resistance in sheep. <i>Animal Genetics</i> , 1999 , 30, 286-95	2.5	12
52	Liveweight, fleece weight and prolificacy of Romney ewes carrying the Inverdale prolificacy gene (<i>FecXI</i>) located on the X-chromosome. <i>Livestock Science</i> , 1993 , 34, 83-91		12
51	Characterization of an X-chromosomal non-mosaic monosomy (59, X0) dairy heifer detected using routinely available single nucleotide polymorphism genotype data. <i>Journal of Animal Science</i> , 2017 , 95, 1042-1049	0.7	11
50	Autoradiographic localisation of [3H]-SCH23390 and [3H]-spiperone binding sites in honey bee brain. <i>Journal of Comparative Neurology</i> , 1998 , 394, 29-37	3.4	11

49	An ovine hepatorenal fibrocystic model of a Meckel-like syndrome associated with dysmorphic primary cilia and TMEM67 mutations. <i>Scientific Reports</i> , 2017 , 7, 1601	4.9	10
48	The effect of liveweight and liveweight change on ewe ovulation rate at 3 successive oestrous cycles. <i>New Zealand Journal of Agricultural Research</i> , 1985 , 28, 457-462	1.9	10
47	Estimates of genetic parameters for breech strike and potential indirect indicators in sheep. <i>New Zealand Veterinary Journal</i> , 2015 , 63, 98-103	1.7	9
46	Finding disease resistance QTL in sheep. <i>Animal Biotechnology</i> , 1997 , 8, 13-22	1.4	9
45	Future perspectives for the implementation of genetic markers for parasite resistance in sheep. <i>Tropical Biomedicine</i> , 2008 , 25, 18-33	0.5	9
44	Towards genomic selection for facial eczema disease tolerance in the New Zealand sheep industry. <i>Animal Genetics</i> , 2014 , 45, 559-64	2.5	8
43	Cytological monitoring of nickel sinter plant workers. <i>Annals of the New York Academy of Sciences</i> , 1976 , 271, 365-9	6.5	8
42	Testing the neutral theory of molecular evolution using genomic data: a comparison of the human and bovine transcriptome. <i>Genetics Selection Evolution</i> , 2006 , 38, 321-41	4.9	7
41	Natural variation in methane emission of sheep fed on a lucerne pellet diet is unrelated to rumen ciliate community type. <i>Microbiology (United Kingdom)</i> , 2016 , 162, 459-465	2.9	7
40	Characterization of an X-chromosomal non-mosaic monosomy (59, X0) dairy heifer detected using routinely available single nucleotide polymorphism genotype data. <i>Journal of Animal Science</i> , 2017 , 95, 1042	0.7	7
39	A restriction enzyme reduced representation sequencing approach for low-cost, high-throughput metagenome profiling. <i>PLoS ONE</i> , 2020 , 15, e0219882	3.7	6
38	Genomics detects population structure within and between ocean basins in a circumpolar seabird: The white-chinned petrel. <i>Molecular Ecology</i> , 2019 , 28, 4552-4572	5.7	6
37	Genetic analysis and genomic selection of stayability and productive life in New Zealand ewes. <i>Journal of Animal Science</i> , 2015 , 93, 3268-77	0.7	6
36	Inference of transcriptional regulation using gene expression data from the bovine and human genomes. <i>BMC Genomics</i> , 2007 , 8, 265	4.5	6
35	Application of Low Coverage Genotyping by Sequencing in Selectively Bred Arctic Charr (). <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 2069-2078	3.2	5
34	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. <i>Frontiers in Genetics</i> , 2018 , 9, 330	4.5	5
33	A QTL study of growth and body shape in the inter-species hybrid of Père David's deer (<i>Elaphurus davidianus</i>) and red deer (<i>Cervus elaphus</i>). <i>Animal Genetics</i> , 2007 , 38, 270-6	2.5	5
32	Distribution of prion protein genotypes in breeds of sheep in New Zealand. <i>New Zealand Veterinary Journal</i> , 2007 , 55, 222-7	1.7	5

31	Liveweight, ovulation rate, and wool growth responses of light and heavy ewes to differential feeding. <i>New Zealand Journal of Crop and Horticultural Science</i> , 1983 , 11, 219-224		5
30	Exclusion and Genomic Relatedness Methods for Assignment of Parentage Using Genotyping-by-Sequencing Data. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 3239-3247	3.2	5
29	Using genotyping-by-sequencing to predict gender in animals. <i>Animal Genetics</i> , 2019 , 50, 307-310	2.5	4
28	The physiological effects of natural variation in growth hormone gene copy number in ram lambs. <i>Domestic Animal Endocrinology</i> , 1997 , 14, 381-90	2.3	4
27	Exclusion probabilities for pedigree testing farm animals 1996 , 92, 966		4
26	Sheep from low-methane-yield selection lines created on alfalfa pellets also have lower methane yield under pastoral farming conditions ^{1,2} . <i>Journal of Animal Science</i> , 2017 , 95, 3905-3913	0.7	4
25	Excreta emissions in progeny of low and high enteric methane yield selection line sheep fed pasture of different qualities. <i>Animal Feed Science and Technology</i> , 2019 , 257, 114289	3	3
24	Genetic parameters of plasma and ruminal volatile fatty acids in sheep fed alfalfa pellets and genetic correlations with enteric methane emissions ¹ . <i>Journal of Animal Science</i> , 2019 , 97, 2711-2724	0.7	3
23	Ovine rumen papillae biopsy via oral endoscopy; a rapid and repeatable method for serial sampling. <i>New Zealand Veterinary Journal</i> , 2016 , 64, 174-8	1.7	3
22	Physical mapping of the stearoyl-CoA desaturase (SCD) locus in sheep. <i>Animal Genetics</i> , 2004 , 35, 163	2.5	3
21	Effect of Cimaterol implants on lamb growth and carcass traits. <i>New Zealand Journal of Agricultural Research</i> , 1990 , 33, 413-427	1.9	3
20	GBS Data Identify Pigmentation-Specific Genes of Potential Role in Skin-Photosensitization in Two Tunisian Sheep Breeds. <i>Animals</i> , 2019 , 10,	3.1	3
19	Heritability of ram mating success in multi-sire breeding situations. <i>Animal</i> , 2019 , 13, 917-923	3.1	3
18	Genomic signatures of inbreeding in a critically endangered parrot, the kākāpō <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	3
17	Genome-wide DNA methylation analysis: no evidence for stable hemimethylation in the sheep muscle genome. <i>Animal Genetics</i> , 2015 , 46, 185-9	2.5	2
16	Ovine keratome: identification, localisation and genomic organisation of keratin and keratin-associated proteins. <i>Animal Genetics</i> , 2018 , 49, 361-370	2.5	2
15	A multiway analysis for identifying high integrity bovine BACs. <i>BMC Genomics</i> , 2009 , 10, 46	4.5	2
14	Molecular and bioinformatic strategies for gene discovery for meat traits: a reverse genetics approach. <i>Australian Journal of Experimental Agriculture</i> , 2005 , 45, 801		2

13	Brown adipose tissue in lean and fat selection lines of sheep identified by immunodetection of uncoupling protein in western blots of tissue homogenates. <i>Comparative Biochemistry and Physiology Part B: Comparative Biochemistry</i> , 1989 , 94, 493-8		2
12	Generation of a preliminary bovine gene atlas, using expression clustering to annotate gene function. <i>Genetics and Molecular Research</i> , 2009 , 8, 1013-27	1.2	2
11	Construction of relatedness matrices using genotyping-by-sequencing data		2
10	Comparative mapping of sheep chromosome 2q. <i>Cytogenetic and Genome Research</i> , 2007 , 116, 85-92	1.9	1
9	Linkage Disequilibrium Estimation in Low Coverage High-Throughput Sequencing Data		1
8	Population Connectivity and Traces of Mitochondrial Introgression in New Zealand Black-Billed Gulls (). <i>Genes</i> , 2018 , 9,	4.2	1
7	An entropy-reducing data representation approach for bioinformatic data. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	1
6	Development of an in situ procedure to evaluate the reticulo-rumen morphology of sheep selected for divergent methane emissions. <i>Animal</i> , 2019 , 13, 542-548	3.1	0
5	Breeding Low Emitting Ruminants: Predicting Methane from Microbes. <i>Proceedings (mdpi)</i> , 2019 , 36, 177	0.3	0
4	Individual-level correlations of rumen volatile fatty acids with enteric methane emissions for ranking methane yield in sheep fed fresh pasture. <i>Animal Production Science</i> , 2021 , 61, 300	1.4	0
3	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. <i>Animals</i> , 2022 , 12, 1423	3.1	0
2	Expression of NPY and POMC in the hypothalamic arcuate nucleus of genetically lean and fat sheep. <i>Frontiers in Neuroendocrinology</i> , 2006 , 27, 8-9	8.9	
1	P3048 Gene network analysis identifies rumen epithelial processes perturbed by diet and correlated with methane production and yield. <i>Journal of Animal Science</i> , 2016 , 94, 76-77	0.7	