

John C Mcewan

List of Publications by Year in Descending Order

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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	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
137	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
136	Genomic signatures of inbreeding in a critically endangered parrot, the kākāpō. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	3
135	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
134	A restriction enzyme reduced representation sequencing approach for low-cost, high-throughput metagenome profiling. <i>PLoS ONE</i> , 2020 , 15, e0219882	3.7	6
133	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
132	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
131	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
130	Using genotyping-by-sequencing to predict gender in animals. <i>Animal Genetics</i> , 2019 , 50, 307-310	2.5	4
129	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
128	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
127	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
126	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
125	Breeding Low Emitting Ruminants: Predicting Methane from Microbes. <i>Proceedings (mdpi)</i> , 2019 , 36, 177	0.3	0
124	Heritability of ram mating success in multi-sire breeding situations. <i>Animal</i> , 2019 , 13, 917-923	3.1	3
123	Linkage Disequilibrium Estimation in Low Coverage High-Throughput Sequencing Data. <i>Genetics</i> , 2018 , 209, 389-400	4	19
122	Ovine keratome: identification, localisation and genomic organisation of keratin and keratin-associated proteins. <i>Animal Genetics</i> , 2018 , 49, 361-370	2.5	2

121	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
120	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
119	Population Connectivity and Traces of Mitochondrial Introgression in New Zealand Black-Billed Gulls (). <i>Genes</i> , 2018 , 9,	4.2	1
118	An entropy-reducing data representation approach for bioinformatic data. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	1
117	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
116	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
115	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
114	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
113	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
112	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
111	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
110	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
109	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
108	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
107	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
106	Copy number variants in the sheep genome detected using multiple approaches. <i>BMC Genomics</i> , 2016 , 17, 441	4.5	18
105	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	
104	Genomic application in sheep and goat breeding. <i>Animal Frontiers</i> , 2016 , 6, 39-44	5.5	39

103	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
102	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
101	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
100	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
99	Animal board invited review: genetic possibilities to reduce enteric methane emissions from ruminants. <i>Animal</i> , 2015 , 9, 1431-40	3.1	77
98	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
97	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
96	Construction of relatedness matrices using genotyping-by-sequencing data. <i>BMC Genomics</i> , 2015 , 16, 1047	4.5	74
95	Genetic parameters for predicted methane production and laser methane detector measurements. <i>Journal of Animal Science</i> , 2015 , 93, 11-20	0.7	32
94	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
93	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
92	Signatures of selection in sheep bred for resistance or susceptibility to gastrointestinal nematodes. <i>BMC Genomics</i> , 2014 , 15, 637	4.5	64
91	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014 , 344, 1168-1173	33.3	294
90	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. <i>Genome Research</i> , 2014 , 24, 1517-25	9.7	197
89	Design and characterization of a 52K SNP chip for goats. <i>PLoS ONE</i> , 2014 , 9, e86227	3.7	121
88	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
87	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
86	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

85	Accuracy of genotype imputation in Nelore cattle. <i>Genetics Selection Evolution</i> , 2014 , 46, 69	4.9	51
84	Genome-wide DNA methylation patterns and transcription analysis in sheep muscle. <i>PLoS ONE</i> , 2014 , 9, e101853	3.7	31
83	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
82	Accuracy of genomic predictions in Bos indicus (Nelore) cattle. <i>Genetics Selection Evolution</i> , 2014 , 46, 17	4.9	60
81	Genomic breed prediction in New Zealand sheep. <i>BMC Genetics</i> , 2014 , 15, 92	2.6	13
80	Selection signatures in worldwide sheep populations. <i>PLoS ONE</i> , 2014 , 9, e103813	3.7	101
79	Genome-wide mapping of loci explaining variance in scrotal circumference in Nelore cattle. <i>PLoS ONE</i> , 2014 , 9, e88561	3.7	29
78	SNPs for parentage testing and traceability in globally diverse breeds of sheep. <i>PLoS ONE</i> , 2014 , 9, e94851	3.7	62
77	Genome-wide association study for birth weight in Nelore cattle points to previously described orthologous genes affecting human and bovine height. <i>BMC Genetics</i> , 2013 , 14, 52	2.6	83
76	Heritability estimates of methane emissions from sheep. <i>Animal</i> , 2013 , 7 Suppl 2, 316-21	3.1	133
75	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
74	Imputation of microsatellite alleles from dense SNP genotypes for parentage verification across multiple Bos taurus and Bos indicus breeds. <i>Frontiers in Genetics</i> , 2013 , 4, 176	4.5	12
73	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
72	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
71	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
70	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
69	Repeatability of methane emissions from sheep. <i>Animal Feed Science and Technology</i> , 2011 , 166-167, 210-218	3	49
68	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

67	The sheep genome reference sequence: a work in progress. <i>Animal Genetics</i> , 2010 , 41, 449-53	2.5	128
66	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
65	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
64	Phylogenetic reconstruction and the identification of ancient polymorphism in the Bovini tribe (Bovidae, Bovinae). <i>BMC Genomics</i> , 2009 , 10, 177	4.5	45
63	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
62	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
61	A multiway analysis for identifying high integrity bovine BACs. <i>BMC Genomics</i> , 2009 , 10, 46	4.5	2
60	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863
59	Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. <i>Science</i> , 2009 , 324, 528-32	33.3	612
58	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
57	A genome wide survey of SNP variation reveals the genetic structure of sheep breeds. <i>PLoS ONE</i> , 2009 , 4, e4668	3.7	208
56	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
55	Future perspectives for the implementation of genetic markers for parasite resistance in sheep. <i>Tropical Biomedicine</i> , 2008 , 25, 18-33	0.5	9
54	A QTL study of growth and body shape in the inter-species hybrid of Pê David deer (<i>Elaphurus davidianus</i>) and red deer (<i>Cervus elaphus</i>). <i>Animal Genetics</i> , 2007 , 38, 270-6	2.5	5
53	Inference of transcriptional regulation using gene expression data from the bovine and human genomes. <i>BMC Genomics</i> , 2007 , 8, 265	4.5	6
52	Expansion of the Bactericidal/Permeability Increasing-like (BPI-like) protein locus in cattle. <i>BMC Genomics</i> , 2007 , 8, 75	4.5	21
51	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
50	Fatty acid synthase effects on bovine adipose fat and milk fat. <i>Mammalian Genome</i> , 2007 , 18, 64-74	3.2	102

49	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
48	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
47	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
46	Comparative mapping of sheep chromosome 2q. <i>Cytogenetic and Genome Research</i> , 2007 , 116, 85-92	1.9	1
45	A physical map of the bovine genome. <i>Genome Biology</i> , 2007 , 8, R165	18.3	67
44	Using comparative genomics to reorder the human genome sequence into a virtual sheep genome. <i>Genome Biology</i> , 2007 , 8, R152	18.3	65
43	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	
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	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
40	Establishment of a pipeline to analyse non-synonymous SNPs in Bos taurus. <i>BMC Genomics</i> , 2006 , 7, 298	4.5	18
39	Gene expression profiling of naïve sheep genetically resistant and susceptible to gastrointestinal nematodes. <i>BMC Genomics</i> , 2006 , 7, 42	4.5	71
38	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
37	Carcass composition and meat quality differences between pasture-reared ewe and ram lambs. <i>Meat Science</i> , 2005 , 71, 383-91	6.4	38
36	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
35	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
34	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
33	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
32	Physical mapping of the stearoyl-CoA desaturase (SCD) locus in sheep. <i>Animal Genetics</i> , 2004 , 35, 163	2.5	3

31	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
30	Economic benefits in selection for weight and composition of lamb cuts predicted by computer tomography. <i>Livestock Science</i> , 2004 , 90, 123-133		15
29	Bone density in sheep: genetic variation and quantitative trait loci localisation. <i>Bone</i> , 2003 , 33, 540-8	4.7	31
28	Linkage disequilibrium in domestic sheep. <i>Genetics</i> , 2002 , 160, 1113-22	4	124
27	Selection for high or low backfat depth in Coopworth sheep: breeding-ewe traits. <i>Animal Science</i> , 2001 , 73, 241-252		12
26	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
25	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
24	Catalase gene is associated with facial eczema disease resistance in sheep. <i>Animal Genetics</i> , 1999 , 30, 286-95	2.5	12
23	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
22	Economic values for ewe prolificacy and lamb survival in New Zealand sheep. <i>Livestock Science</i> , 1999 , 58, 75-90		77
21	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
20	Finding disease resistance QTL in sheep. <i>Animal Biotechnology</i> , 1997 , 8, 13-22	1.4	9
19	Selection for high or low backfat depth in Coopworth sheep: juvenile traits. <i>Animal Science</i> , 1997 , 65, 93-103		28
18	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
17	Phenotypic markers for selection of nematode-resistant sheep. <i>International Journal for Parasitology</i> , 1996 , 26, 899-911	4.3	51
16	Exclusion probabilities for pedigree testing farm animals. <i>Theoretical and Applied Genetics</i> , 1996 , 92, 966-75	6	53
15	Exclusion probabilities for pedigree testing farm animals 1996 , 92, 966		4
14	Liveweight, fleece weight and prolificacy of Romney ewes carrying the Inverdale prolificacy gene (FecXI) located on the X-chromosome. <i>Livestock Science</i> , 1993 , 34, 83-91		12

13	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
12	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
11	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
10	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
9	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
8	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
7	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
6	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
5	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
4	Cytological monitoring of nickel sinter plant workers. <i>Annals of the New York Academy of Sciences</i> , 1976 , 271, 365-9	6.5	8
3	Construction of relatedness matrices using genotyping-by-sequencing data		2
2	Utilization of high throughput genome sequencing technology for large scale single nucleotide polymorphism discovery in red deer and Canadian elk		14
1	Linkage Disequilibrium Estimation in Low Coverage High-Throughput Sequencing Data		1