

# Sean M McWilliam

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

4,756  
citations

159585

30  
h-index

133252

59  
g-index

63  
all docs

63  
docs citations

63  
times ranked

5757  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
2	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	12.6	746
3	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	12.6	436
4	A Genome Wide Survey of SNP Variation Reveals the Genetic Structure of Sheep Breeds. <i>PLoS ONE</i> , 2009, 4, e4668.	2.5	269
5	Gene expression patterns during intramuscular fat development in cattle <sup>1</sup> . <i>Journal of Animal Science</i> , 2009, 87, 119-130.	0.5	161
6	Transcriptional profiling of skeletal muscle tissue from two breeds of cattle. <i>Mammalian Genome</i> , 2005, 16, 201-210.	2.2	135
7	Origin, Evolution, and Biological Role of miRNA Cluster in DLK-DIO3 Genomic Region in Placental Mammals. <i>Molecular Biology and Evolution</i> , 2008, 25, 939-948.	8.9	127
8	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. <i>Nature Communications</i> , 2018, 9, 859.	12.8	126
9	Gene expression profiling of muscle tissue in Brahman steers during nutritional restriction <sup>1</sup> . <i>Journal of Animal Science</i> , 2005, 83, 1-12.	0.5	109
10	Transcriptomics of a Giant Freshwater Prawn ( <i>Macrobrachium rosenbergii</i> ): De Novo Assembly, Annotation and Marker Discovery. <i>PLoS ONE</i> , 2011, 6, e27938.	2.5	94
11	The genome of bovine ephemeral fever rhabdovirus contains two related glycoprotein genes. <i>Virology</i> , 1992, 191, 49-61.	2.4	80
12	Validation of alternative methods of data normalization in gene co-expression studies. <i>Bioinformatics</i> , 2005, 21, 1112-1120.	4.1	80
13	Using comparative genomics to reorder the human genome sequence into a virtual sheep genome. <i>Genome Biology</i> , 2007, 8, R152.	9.6	77
14	Construction and validation of a Bovine Innate Immune Microarray. <i>BMC Genomics</i> , 2005, 6, 135.	2.8	75
15	Whole-genome resequencing uncovers molecular signatures of natural and sexual selection in wild bighorn sheep. <i>Molecular Ecology</i> , 2015, 24, 5616-5632.	3.9	73
16	Identification of a gene network contributing to hypertrophy in callipyge skeletal muscle. <i>Physiological Genomics</i> , 2007, 28, 253-272.	2.3	66
17	An interactive bovine in silico SNP database (IBISS). <i>Mammalian Genome</i> , 2004, 15, 819-827.	2.2	60
18	Genome organization and transcription strategy in the complex GNS-L intergenic region of bovine ephemeral fever rhabdovirus.. <i>Journal of General Virology</i> , 1997, 78, 1309-1317.	2.9	56

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19	Gene expression profiling of bovine in vitro adipogenesis using a cDNA microarray. <i>Functional and Integrative Genomics</i> , 2006, 6, 235-249.	3.5	53
20	Using Regulatory and Epistatic Networks to Extend the Findings of a Genome Scan: Identifying the Gene Drivers of Pigmentation in Merino Sheep. <i>PLoS ONE</i> , 2011, 6, e21158.	2.5	52
21	Evolution of Sex Determination Loci in Atlantic Salmon. <i>Scientific Reports</i> , 2018, 8, 5664.	3.3	51
22	De novo assembly, characterization, functional annotation and expression patterns of the black tiger shrimp ( <i>Penaeus monodon</i> ) transcriptome. <i>Scientific Reports</i> , 2018, 8, 13553.	3.3	48
23	Gene expression profiling of Hereford Shorthorn cattle following challenge with <i>Boophilus microplus</i> tick larvae. <i>Australian Journal of Experimental Agriculture</i> , 2007, 47, 1397.	1.0	48
24	Comparison of microsatellite and SNP DNA markers for pedigree assignment in Black Tiger shrimp, <i>Penaeus monodon</i> . <i>Aquaculture Research</i> , 2014, 45, 417-426.	1.8	47
25	Structural and antigenic analysis of the nucleoprotein of bovine ephemeral fever rhabdovirus. <i>Journal of General Virology</i> , 1994, 75, 1889-1899.	2.9	45
26	A gene coexpression network for bovine skeletal muscle inferred from microarray data. <i>Physiological Genomics</i> , 2006, 28, 76-83.	2.3	38
27	Complex Genome Organization in the GNS-L Intergenic Region of Adelaide River Rhabdovirus. <i>Virology</i> , 1994, 203, 63-72.	2.4	36
28	Genomic correlation: harnessing the benefit of combining two unrelated populations for genomic selection. <i>Genetics Selection Evolution</i> , 2015, 47, 84.	3.0	35
29	Analysis of copy number variants in the cattle genome. <i>Gene</i> , 2011, 482, 73-77.	2.2	34
30	Non-synonymous mutations mapped to chromosome X associated with andrological and growth traits in beef cattle. <i>BMC Genomics</i> , 2015, 16, 384.	2.8	34
31	A rapid method for computationally inferring transcriptome coverage and microarray sensitivity. <i>Bioinformatics</i> , 2005, 21, 80-89.	4.1	28
32	Characterisation and application of a bovine U6 promoter for expression of short hairpin RNAs. <i>BMC Biotechnology</i> , 2005, 5, 13.	3.3	26
33	Skeletal muscle specific genes networks in cattle. <i>Functional and Integrative Genomics</i> , 2010, 10, 609-618.	3.5	25
34	A genomics-informed, SNP association study reveals FBLN1 and FABP4 as contributing to resistance to fleece rot in Australian Merino sheep. <i>BMC Veterinary Research</i> , 2010, 6, 27.	1.9	25
35	Transcriptome Profiles of <i>Penaeus (Marsupenaeus) japonicus</i> Animal and Vegetal Half-Embryos: Identification of Sex Determination, Germ Line, Mesoderm, and Other Developmental Genes. <i>Marine Biotechnology</i> , 2015, 17, 252-265.	2.4	25
36	Polygenic and sex specific architecture for two maturation traits in farmed Atlantic salmon. <i>BMC Genomics</i> , 2019, 20, 139.	2.8	25

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37	Analysis of the complement and molecular evolution of tRNA genes in cow. BMC Genomics, 2009, 10, 188.	2.8	21
38	Evidence for positive selection of taurine genes within a QTL region on chromosome X associated with testicular size in Australian Brahman cattle. BMC Genetics, 2014, 15, 6.	2.7	21
39	Next-generation sequencing: a challenge to meet the increasing demand for training workshops in Australia. Briefings in Bioinformatics, 2013, 14, 563-574.	6.5	17
40	Mapping of 12 bovine ribosomal protein genes using a bovine radiation hybrid panel. Animal Genetics, 2001, 32, 269-273.	1.7	16
41	Gene expression identifies metabolic and functional differences between intramuscular and subcutaneous adipocytes in cattle. BMC Genomics, 2020, 21, 77.	2.8	16
42	Bovine proteins containing poly-glutamine repeats are often polymorphic and enriched for components of transcriptional regulatory complexes. BMC Genomics, 2010, 11, 654.	2.8	15
43	Exploiting genomic data to identify proteins involved in abalone reproduction. Journal of Proteomics, 2014, 108, 337-353.	2.4	15
44	Information compression exploits patterns of genome composition to discriminate populations and highlight regions of evolutionary interest. BMC Bioinformatics, 2014, 15, 66.	2.6	15
45	Changed Patterns of Genomic Variation Following Recent Domestication: Selection Sweeps in Farmed Atlantic Salmon. Frontiers in Genetics, 2020, 11, 264.	2.3	15
46	Greenlip Abalone ( <i>Haliotis laevis</i> ) Genome and Protein Analysis Provides Insights into Maturation and Spawning. G3: Genes, Genomes, Genetics, 2019, 9, 3067-3078.	1.8	14
47	Genome Sequencing of Blacklip and Greenlip Abalone for Development and Validation of a SNP Based Genotyping Tool. Frontiers in Genetics, 2018, 9, 687.	2.3	14
48	A high-resolution comparative radiation hybrid map of ovine chromosomal regions that are homologous to human chromosome 6 (HSA6). Animal Genetics, 2008, 39, 459-467.	1.7	13
49	Construction of gene interaction and regulatory networks in bovine skeletal muscle from expression data. Australian Journal of Experimental Agriculture, 2005, 45, 821.	1.0	12
50	Next generation sequencing of African and Indicine cattle to identify single nucleotide polymorphisms. Animal Production Science, 2012, 52, 133.	1.3	11
51	Post-partum anoestrus in tropical beef cattle: A systems approach combining gene expression and genome-wide association results. Livestock Science, 2014, 166, 158-166.	1.6	11
52	A low-density SNP genotyping panel for the accurate prediction of cattle breeds. Journal of Animal Science, 2020, 98, .	0.5	10
53	SNP discovery in nonmodel organisms: strand bias and base substitution errors reduce conversion rates. Molecular Ecology Resources, 2015, 15, 723-736.	4.8	9
54	Genome assembly of the Australian black tiger shrimp ( <i>Penaeus monodon</i> ) reveals a novel fragmented IHHNV EVE sequence. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	9

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55	A radiation hybrid comparative map of ovine chromosome 1 aligned to the virtual sheep genome. <i>Animal Genetics</i> , 2009, 40, 435-455.	1.7	6
56	A multiway analysis for identifying high integrity bovine BACs. <i>BMC Genomics</i> , 2009, 10, 46.	2.8	4
57	Using paired-end sequences to optimise parameters for alignment of sequence reads against related genomes. <i>BMC Genomics</i> , 2010, 11, 458.	2.8	3
58	Dissection of beef quality phenotypes using a myogenin network-anchored systems biology approach. <i>Australian Journal of Experimental Agriculture</i> , 2008, 48, 1053.	1.0	1
59	Variation in genes involved in epigenetic processes offers insights into tropically adapted cattle diversity. <i>Frontiers in Genetics</i> , 2014, 5, 89.	2.3	1
60	Insight Into Differential Gene Expression of <i>Enterococcus Faecium</i> , an IBD Associated Bacterium, Using RNA-Seq. <i>Gastroenterology</i> , 2011, 140, S-30.	1.3	0