

# 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	Genome assembly of the Australian black tiger shrimp ( <i>Penaeus monodon</i> ) reveals a novel fragmented IHNV EVE sequence. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	9
2	A low-density SNP genotyping panel for the accurate prediction of cattle breeds. <i>Journal of Animal Science</i> , 2020, 98, .	0.5	10
3	Gene expression identifies metabolic and functional differences between intramuscular and subcutaneous adipocytes in cattle. <i>BMC Genomics</i> , 2020, 21, 77.	2.8	16
4	Changed Patterns of Genomic Variation Following Recent Domestication: Selection Sweeps in Farmed Atlantic Salmon. <i>Frontiers in Genetics</i> , 2020, 11, 264.	2.3	15
5	Polygenic and sex specific architecture for two maturation traits in farmed Atlantic salmon. <i>BMC Genomics</i> , 2019, 20, 139.	2.8	25
6	Greenlip Abalone ( <i>Haliotis laevis</i> ) Genome and Protein Analysis Provides Insights into Maturation and Spawning. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3067-3078.	1.8	14
7	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
8	Evolution of Sex Determination Loci in Atlantic Salmon. <i>Scientific Reports</i> , 2018, 8, 5664.	3.3	51
9	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
10	Genome Sequencing of Blacklip and Greenlip Abalone for Development and Validation of a SNP Based Genotyping Tool. <i>Frontiers in Genetics</i> , 2018, 9, 687.	2.3	14
11	Genomic correlation: harnessing the benefit of combining two unrelated populations for genomic selection. <i>Genetics Selection Evolution</i> , 2015, 47, 84.	3.0	35
12	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
13	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
14	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
15	SNP discovery in nonmodel organisms: strand bias and base substitution errors reduce conversion rates. <i>Molecular Ecology Resources</i> , 2015, 15, 723-736.	4.8	9
16	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
17	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
18	Evidence for positive selection of taurine genes within a QTL region on chromosome X associated with testicular size in Australian Brahman cattle. <i>BMC Genetics</i> , 2014, 15, 6.	2.7	21

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19	Exploiting genomic data to identify proteins involved in abalone reproduction. <i>Journal of Proteomics</i> , 2014, 108, 337-353.	2.4	15
20	Post-partum anoestrus in tropical beef cattle: A systems approach combining gene expression and genome-wide association results. <i>Livestock Science</i> , 2014, 166, 158-166.	1.6	11
21	Information compression exploits patterns of genome composition to discriminate populations and highlight regions of evolutionary interest. <i>BMC Bioinformatics</i> , 2014, 15, 66.	2.6	15
22	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	12.6	436
23	Next-generation sequencing: a challenge to meet the increasing demand for training workshops in Australia. <i>Briefings in Bioinformatics</i> , 2013, 14, 563-574.	6.5	17
24	Next generation sequencing of African and Indicine cattle to identify single nucleotide polymorphisms. <i>Animal Production Science</i> , 2012, 52, 133.	1.3	11
25	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
26	Analysis of copy number variants in the cattle genome. <i>Gene</i> , 2011, 482, 73-77.	2.2	34
27	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
28	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
29	Skeletal muscle specific genes networks in cattle. <i>Functional and Integrative Genomics</i> , 2010, 10, 609-618.	3.5	25
30	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
31	Bovine proteins containing poly-glutamine repeats are often polymorphic and enriched for components of transcriptional regulatory complexes. <i>BMC Genomics</i> , 2010, 11, 654.	2.8	15
32	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
33	Analysis of the complement and molecular evolution of tRNA genes in cow. <i>BMC Genomics</i> , 2009, 10, 188.	2.8	21
34	A multiway analysis for identifying high integrity bovine BACs. <i>BMC Genomics</i> , 2009, 10, 46.	2.8	4
35	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
36	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038

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37	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	12.6	746
38	Gene expression patterns during intramuscular fat development in cattle1. <i>Journal of Animal Science</i> , 2009, 87, 119-130.	0.5	161
39	A Genome Wide Survey of SNP Variation Reveals the Genetic Structure of Sheep Breeds. <i>PLoS ONE</i> , 2009, 4, e4668.	2.5	269
40	A high-resolution comparative radiation hybrid map of ovine chromosomal regions that are homologous to human chromosome 6 (HSA6). <i>Animal Genetics</i> , 2008, 39, 459-467.	1.7	13
41	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
42	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
43	Identification of a gene network contributing to hypertrophy in callipyge skeletal muscle. <i>Physiological Genomics</i> , 2007, 28, 253-272.	2.3	66
44	Using comparative genomics to reorder the human genome sequence into a virtual sheep genome. <i>Genome Biology</i> , 2007, 8, R152.	9.6	77
45	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
46	A gene coexpression network for bovine skeletal muscle inferred from microarray data. <i>Physiological Genomics</i> , 2006, 28, 76-83.	2.3	38
47	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
48	Gene expression profiling of muscle tissue in Brahman steers during nutritional restriction1. <i>Journal of Animal Science</i> , 2005, 83, 1-12.	0.5	109
49	Construction and validation of a Bovine Innate Immune Microarray. <i>BMC Genomics</i> , 2005, 6, 135.	2.8	75
50	Transcriptional profiling of skeletal muscle tissue from two breeds of cattle. <i>Mammalian Genome</i> , 2005, 16, 201-210.	2.2	135
51	Characterisation and application of a bovine U6 promoter for expression of short hairpin RNAs. <i>BMC Biotechnology</i> , 2005, 5, 13.	3.3	26
52	A rapid method for computationally inferring transcriptome coverage and microarray sensitivity. <i>Bioinformatics</i> , 2005, 21, 80-89.	4.1	28
53	Validation of alternative methods of data normalization in gene co-expression studies. <i>Bioinformatics</i> , 2005, 21, 1112-1120.	4.1	80
54	Construction of gene interaction and regulatory networks in bovine skeletal muscle from expression data. <i>Australian Journal of Experimental Agriculture</i> , 2005, 45, 821.	1.0	12

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55	An interactive bovine in silico SNP database (IBISS). <i>Mammalian Genome</i> , 2004, 15, 819-827.	2.2	60
56	Mapping of 12 bovine ribosomal protein genes using a bovine radiation hybrid panel. <i>Animal Genetics</i> , 2001, 32, 269-273.	1.7	16
57	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
58	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
59	Complex Genome Organization in the GNS-L Intergenic Region of Adelaide River Rhabdovirus. <i>Virology</i> , 1994, 203, 63-72.	2.4	36
60	The genome of bovine ephemeral fever rhabdovirus contains two related glycoprotein genes. <i>Virology</i> , 1992, 191, 49-61.	2.4	80