

# Michael P Heaton

## List of Publications by Year in descending order

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77  
papers

3,989  
citations

159525

30  
h-index

128225

60  
g-index

81  
all docs

81  
docs citations

81  
times ranked

4268  
citing authors

#	ARTICLE	IF	CITATIONS
1	Development and Characterization of a High Density SNP Genotyping Assay for Cattle. PLoS ONE, 2009, 4, e5350.	1.1	813
2	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. PLoS Genetics, 2014, 10, e1004254.	1.5	391
3	A Genome Wide Survey of SNP Variation Reveals the Genetic Structure of Sheep Breeds. PLoS ONE, 2009, 4, e4668.	1.1	269
4	Selection and use of SNP markers for animal identification and paternity analysis in U.S. beef cattle. Mammalian Genome, 2002, 13, 272-281.	1.0	199
5	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.	3.3	196
6	Prion gene sequence variation within diverse groups of U.S. sheep, beef cattle, and deer. Mammalian Genome, 2003, 14, 765-777.	1.0	104
7	Sequence Evaluation of Four Pooled-Tissue Normalized Bovine cDNA Libraries and Construction of a Gene Index for Cattle. Genome Research, 2001, 11, 626-630.	2.4	98
8	Mobilization of vancomycin resistance by transposon-mediated fusion of a VanA plasmid with an Enterococcus faecium sex pheromone-response plasmid. Gene, 1996, 171, 9-17.	1.0	95
9	Biosynthesis of D-alanyl-lipoteichoic acid: cloning, nucleotide sequence, and expression of the Lactobacillus casei gene for the D-alanine-activating enzyme. Journal of Bacteriology, 1992, 174, 4707-4717.	1.0	92
10	SNPs for Parentage Testing and Traceability in Globally Diverse Breeds of Sheep. PLoS ONE, 2014, 9, e94851.	1.1	88
11	Role of the D-alanyl carrier protein in the biosynthesis of D-alanyl-lipoteichoic acid. Journal of Bacteriology, 1994, 176, 681-690.	1.0	84
12	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. Nature Communications, 2020, 11, 2071.	5.8	84
13	Characterization of Ovine Nectin-4, a Novel Peste des Petits Ruminants Virus Receptor. Journal of Virology, 2013, 87, 4756-4761.	1.5	82
14	Reduced Lentivirus Susceptibility in Sheep with TMEM154 Mutations. PLoS Genetics, 2012, 8, e1002467.	1.5	78
15	Association of Escherichia coli O157:H7 tir polymorphisms with human infection. BMC Infectious Diseases, 2007, 7, 98.	1.3	64
16	Single nucleotide polymorphism (SNP) discovery and linkage mapping of bovine cytokine genes. Mammalian Genome, 1999, 10, 1062-1069.	1.0	61
17	The D-Alanyl carrier protein in Lactobacillus casei: cloning, sequencing, and expression of dltC. Journal of Bacteriology, 1996, 178, 3869-3876.	1.0	59
18	Consistent divergence times and allele sharing measured from cross-species application of SNP chips developed for three domestic species. Molecular Ecology Resources, 2012, 12, 1145-1150.	2.2	56

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19	Estimation of DNA sequence diversity in bovine cytokine genes. <i>Mammalian Genome</i> , 2001, 12, 32-37.	1.0	51
20	Use of bovine single nucleotide polymorphism markers to verify sample tracking in beef processing. <i>Journal of the American Veterinary Medical Association</i> , 2005, 226, 1311-1314.	0.2	46
21	Prevalence of the prion protein gene E211K variant in U.S. cattle. <i>BMC Veterinary Research</i> , 2008, 4, 25.	0.7	46
22	Genomic signatures of <i>Mannheimia haemolytica</i> that associate with the lungs of cattle with respiratory disease, an integrative conjugative element, and antibiotic resistance genes. <i>BMC Genomics</i> , 2016, 17, 982.	1.2	46
23	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	3.3	46
24	Association of bovine neonatal Fc receptor a-chain gene (FCGRT) haplotypes with serum IgG concentration in newborn calves. <i>Mammalian Genome</i> , 2002, 13, 704-710.	1.0	42
25	Interleukin-8 haplotype structure from nucleotide sequence variation in commercial populations of U.S. beef cattle. <i>Mammalian Genome</i> , 2001, 12, 219-226.	1.0	38
26	Prion gene haplotypes of U.S. cattle. <i>BMC Genetics</i> , 2006, 7, 51.	2.7	36
27	Scrapie Resistance in ARQ Sheep. <i>Journal of Virology</i> , 2008, 82, 10318-10320.	1.5	36
28	Conjugative Mobilization of a Vancomycin Resistance Plasmid by a Putative <i>Enterococcus faecium</i> Sex Pheromone Response Plasmid. <i>Microbial Drug Resistance</i> , 1995, 1, 177-183.	0.9	35
29	Association of a Bovine Prion Gene Haplotype with Atypical BSE. <i>PLoS ONE</i> , 2008, 3, e1830.	1.1	34
30	Beta-2-microglobulin haplotypes in U.S. beef cattle and association with failure of passive transfer in newborn calves. <i>Mammalian Genome</i> , 2004, 15, 227-236.	1.0	33
31	Resolving <i>Bovine viral diarrhea virus</i> subtypes from persistently infected U.S. beef calves with complete genome sequence. <i>Journal of Veterinary Diagnostic Investigation</i> , 2016, 28, 519-528.	0.5	31
32	Genetic Testing for TMEM154 Mutations Associated with Lentivirus Susceptibility in Sheep. <i>PLoS ONE</i> , 2013, 8, e55490.	1.1	28
33	Effects of TMEM154 haplotypes 1 and 3 on susceptibility to ovine progressive pneumonia virus following natural exposure in sheep <sup>1,2,3</sup> . <i>Journal of Animal Science</i> , 2013, 91, 5114-5121.	0.2	27
34	Using diverse U.S. beef cattle genomes to identify missense mutations in EPAS1, a gene associated with high-altitude pulmonary hypertension. <i>F1000Research</i> , 2016, 5, 2003.	0.8	27
35	Characterization of 954 bovine full-CDS cDNA sequences. <i>BMC Genomics</i> , 2005, 6, 166.	1.2	26
36	Evaluation of a Real-Time PCR Kit for Detecting <i>Escherichia coli</i> O157 in Bovine Fecal Samples. <i>Applied and Environmental Microbiology</i> , 2004, 70, 1855-1857.	1.4	25

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37	Gene expression profiling of bovine macrophages in response to O157:H7 lipopolysaccharide. <i>Developmental and Comparative Immunology</i> , 2004, 28, 635-645.	1.0	25
38	A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i> . <i>Journal of Heredity</i> , 2021, 112, 184-191.	1.0	25
39	An improved ovine reference genome assembly to facilitate in-depth functional annotation of the sheep genome. <i>GigaScience</i> , 2022, 11, .	3.3	24
40	Structure-Guided Identification of a Nonhuman Morbillivirus with Zoonotic Potential. <i>Journal of Virology</i> , 2018, 92, .	1.5	23
41	Using diverse U.S. beef cattle genomes to identify missense mutations in EPAS1, a gene associated with pulmonary hypertension. <i>F1000Research</i> , 2016, 5, 2003.	0.8	21
42	Small ruminant lentivirus genetic subgroups associate with sheep TMEM154 genotypes. <i>Veterinary Research</i> , 2013, 44, 64.	1.1	19
43	Complete Closed Genome Sequences of <i>Mannheimia haemolytica</i> Serotypes A1 and A6, Isolated from Cattle. <i>Genome Announcements</i> , 2013, 1, .	0.8	19
44	Structural variant-based pangenome construction has low sensitivity to variability of haplotype-resolved bovine assemblies. <i>Nature Communications</i> , 2022, 13, .	5.8	19
45	Using sheep genomes from diverse U.S. breeds to identify missense variants in genes affecting fecundity. <i>F1000Research</i> , 2017, 6, 1303.	0.8	18
46	Association of TMEM154 variants with visna/maedi virus infection in Turkish sheep. <i>Small Ruminant Research</i> , 2019, 177, 61-67.	0.6	16
47	Directed cosmid isolation of bovine markers for physical assignment by fish. <i>Animal Biotechnology</i> , 1997, 8, 167-177.	0.7	15
48	Cardiopulmonary remodeling in fattened beef cattle: a naturally occurring large animal model of obesity-associated pulmonary hypertension with left heart disease. <i>Pulmonary Circulation</i> , 2019, 9, 1-13.	0.8	14
49	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . <i>Journal of Heredity</i> , 2021, 112, 174-183.	1.0	14
50	Identification and genetic mapping of bovine chemokine genes expressed in epithelial cells. <i>Mammalian Genome</i> , 1999, 10, 128-133.	1.0	13
51	Genetic subgroup of small ruminant lentiviruses that infects sheep homozygous for TMEM154 frameshift deletion mutation A41>53. <i>Veterinary Research</i> , 2015, 46, 22.	1.1	13
52	Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. <i>F1000Research</i> , 2013, 2, 244.	0.8	13
53	Frequent Missense and Insertion/Deletion Polymorphisms in the Ovine Shadoo Gene Parallel Species-Specific Variation in PrP. <i>PLoS ONE</i> , 2009, 4, e5338.	1.1	13
54	Ovine reference materials and assays for prion genetic testing. <i>BMC Veterinary Research</i> , 2010, 6, 23.	0.7	12

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55	Full-Length Coding Sequences for 12 Bovine Viral Diarrhea Virus Isolates from Persistently Infected Cattle in a Feedyard in Kansas. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
56	Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. <i>F1000Research</i> , 2013, 2, 244.	0.8	9
57	Evaluation of EPAS1 variants for association with bovine congestive heart failure. <i>F1000Research</i> , 2019, 8, 1189.	0.8	8
58	A SNP resource for studying North American moose. <i>F1000Research</i> , 2018, 7, 40.	0.8	7
59	Linkage disequilibrium across six prion gene regions spanning 20 kbp in U.S. sheep. <i>Mammalian Genome</i> , 2006, 17, 1121-1129.	1.0	6
60	Association of ARRDC3 and NFIA variants with bovine congestive heart failure in feedlot cattle. <i>F1000Research</i> , 0, 11, 385.	0.8	6
61	Controlled cell lysis and protoplast formation by enhancement of inhibitors of alanine racemase by glycine. <i>Biochemical and Biophysical Research Communications</i> , 1987, 149, 576-579.	1.0	5
62	Complete Closed Genome Sequences of a <i>Mannheimia haemolytica</i> Serotype A1 Leukotoxin Deletion Mutant and Its Wild-Type Parent Strain. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
63	Complete Genome Sequences of Two Genotype A2 Small Ruminant Lentiviruses Isolated from Infected U.S. Sheep. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
64	Structure of the genes for porcine endometrial secreted and membrane folate binding proteins. <i>Domestic Animal Endocrinology</i> , 2001, 21, 55-72.	0.8	4
65	First Complete Genome Sequence of a Genotype A2, Subgroup 4 Small Ruminant Lentivirus. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	4
66	Detection of bovine viral diarrhea virus in stable flies following consumption of blood from persistently infected cattle. <i>Journal of Veterinary Diagnostic Investigation</i> , 2020, 32, 108-111.	0.5	4
67	A bovine CD18 signal peptide variant with increased binding activity to <i>Mannheimia hemolytica</i> leukotoxin. <i>F1000Research</i> , 2018, 7, 1985.	0.8	4
68	Evaluating Large Spontaneous Deletions in a Bovine Cell Line Selected for Bovine Viral Diarrhea Virus Resistance. <i>Viruses</i> , 2021, 13, 2147.	1.5	4
69	Gaur genome reveals expansion of sperm odorant receptors in domesticated cattle. <i>BMC Genomics</i> , 2022, 23, 344.	1.2	3
70	A sequencing strategy for identifying variation throughout the prion gene of BSE-affected cattle. <i>BMC Research Notes</i> , 2008, 1, 32.	0.6	2
71	Association of TLR2 haplotypes encoding Q650 with reduced susceptibility to ovine Johneâ€™s disease in Turkish sheep. <i>Scientific Reports</i> , 2021, 11, 7088.	1.6	2
72	Classification of small ruminant lentivirus subtype A2, subgroups 1 and 2 based on whole genome comparisons and complex recombination patterns. <i>F1000Research</i> , 2020, 9, 1449.	0.8	2

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73	Design of a DNA panel for genomic studies in Russian cattle breeds. Russian Journal of Genetics: Applied Research, 2015, 5, 21-25.	0.4	1
74	Classification of small ruminant lentivirus subtype A2, subgroups 1 and 2 based on whole genome comparisons and complex recombination patterns. F1000Research, 0, 9, 1449.	0.8	1
75	Using triallelic SNPs for determining parentage in North American yak ( <i>Bos grunniens</i> ) and estimating cattle ( <i>B. taurus</i> ) introgression. F1000Research, 2020, 9, 1096.	0.8	1
76	Using triallelic SNPs for determining parentage in North American yak ( <i>Bos grunniens</i> ) and estimating cattle ( <i>B. taurus</i> ) introgression. F1000Research, 2020, 9, 1096.	0.8	1
77	Discovery, validation and characterization of 1039 cattle single nucleotide polymorphisms. Animal Genetics, 2010, 41, 421-423.	0.6	0