

Michael P Heaton

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7844352/publications.pdf>

Version: 2024-02-01

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	An improved ovine reference genome assembly to facilitate in-depth functional annotation of the sheep genome. <i>GigaScience</i> , 2022, 11, .	3.3	24
2	Gaur genome reveals expansion of sperm odorant receptors in domesticated cattle. <i>BMC Genomics</i> , 2022, 23, 344.	1.2	3
3	Structural variant-based pangenome construction has low sensitivity to variability of haplotype-resolved bovine assemblies. <i>Nature Communications</i> , 2022, 13, .	5.8	19
4	A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i>. <i>Journal of Heredity</i> , 2021, 112, 184-191.	1.0	25
5	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i>. <i>Journal of Heredity</i> , 2021, 112, 174-183.	1.0	14
6	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
7	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
8	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
9	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. <i>Nature Communications</i> , 2020, 11, 2071.	5.8	84
10	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	3.3	46
11	Using triallelic SNPs for determining parentage in North American yak (<i>Bos grunniens</i>) and estimating cattle (<i>B. taurus</i>) introgression. <i>F1000Research</i> , 2020, 9, 1096.	0.8	1
12	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
13	Using triallelic SNPs for determining parentage in North American yak (<i>Bos grunniens</i>) and estimating cattle (<i>B. taurus</i>) introgression. <i>F1000Research</i> , 2020, 9, 1096.	0.8	1
14	Cardiopulmonary remodeling in fattened beef cattle: a naturally occurring large animal model of obesityâ€™associated pulmonary hypertension with left heart disease. <i>Pulmonary Circulation</i> , 2019, 9, 1-13.	0.8	14
15	Association of TMEM154 variants with visna/maedi virus infection in Turkish sheep. <i>Small Ruminant Research</i> , 2019, 177, 61-67.	0.6	16
16	Evaluation of EPAS1 variants for association with bovine congestive heart failure. <i>F1000Research</i> , 2019, 8, 1189.	0.8	8
17	First Complete Genome Sequence of a Genotype A2, Subgroup 4 Small Ruminant Lentivirus. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	4
18	Structure-Guided Identification of a Nonhuman Morbillivirus with Zoonotic Potential. <i>Journal of Virology</i> , 2018, 92, .	1.5	23

#	ARTICLE	IF	CITATIONS
19	A SNP resource for studying North American moose. <i>F1000Research</i> , 2018, 7, 40.	0.8	7
20	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
21	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
22	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
23	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
24	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
25	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
26	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
27	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
28	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
29	Design of a DNA panel for genomic studies in Russian cattle breeds. <i>Russian Journal of Genetics: Applied Research</i> , 2015, 5, 21-25.	0.4	1
30	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
31	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004254.	1.5	391
32	SNPs for Parentage Testing and Traceability in Globally Diverse Breeds of Sheep. <i>PLoS ONE</i> , 2014, 9, e94851.	1.1	88
33	Characterization of Ovine Nectin-4, a Novel Peste des Petits Ruminants Virus Receptor. <i>Journal of Virology</i> , 2013, 87, 4756-4761.	1.5	82
34	Small ruminant lentivirus genetic subgroups associate with sheep TMEM154 genotypes. <i>Veterinary Research</i> , 2013, 44, 64.	1.1	19
35	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
36	Effects of TMEM154 haplotypes 1 and 3 on susceptibility to ovine progressive pneumonia virus following natural exposure in sheep ^{1,2,3} . <i>Journal of Animal Science</i> , 2013, 91, 5114-5121.	0.2	27

#	ARTICLE	IF	CITATIONS
37	Genetic Testing for TMEM154 Mutations Associated with Lentivirus Susceptibility in Sheep. PLoS ONE, 2013, 8, e55490.	1.1	28
38	Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. F1000Research, 2013, 2, 244.	0.8	13
39	Mapping whole genome shotgun sequence and variant calling in mammalian species without their reference genomes. F1000Research, 2013, 2, 244.	0.8	9
40	Reduced Lentivirus Susceptibility in Sheep with TMEM154 Mutations. PLoS Genetics, 2012, 8, e1002467.	1.5	78
41	Consistent divergence times and allele sharing measured from cross-species application of <sc>SNP</sc> chips developed for three domestic species. Molecular Ecology Resources, 2012, 12, 1145-1150.	2.2	56
42	Discovery, validation and characterization of 1039 cattle single nucleotide polymorphisms. Animal Genetics, 2010, 41, 421-423.	0.6	0
43	Ovine reference materials and assays for prion genetic testing. BMC Veterinary Research, 2010, 6, 23.	0.7	12
44	Development and Characterization of a High Density SNP Genotyping Assay for Cattle. PLoS ONE, 2009, 4, e5350.	1.1	813
45	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
46	A Genome Wide Survey of SNP Variation Reveals the Genetic Structure of Sheep Breeds. PLoS ONE, 2009, 4, e4668.	1.1	269
47	Frequent Missense and Insertion/Deletion Polymorphisms in the Ovine Shadoo Gene Parallel Species-Specific Variation in PrP. PLoS ONE, 2009, 4, e6538.	1.1	13
48	Prevalence of the prion protein gene E211K variant in U.S. cattle. BMC Veterinary Research, 2008, 4, 25.	0.7	46
49	A sequencing strategy for identifying variation throughout the prion gene of BSE-affected cattle. BMC Research Notes, 2008, 1, 32.	0.6	2
50	Scrapie Resistance in ARQ Sheep. Journal of Virology, 2008, 82, 10318-10320.	1.5	36
51	Association of a Bovine Prion Gene Haplotype with Atypical BSE. PLoS ONE, 2008, 3, e1830.	1.1	34
52	Association of Escherichia coli O157:H7 tirpolymorphisms with human infection. BMC Infectious Diseases, 2007, 7, 98.	1.3	64
53	Prion gene haplotypes of U.S. cattle. BMC Genetics, 2006, 7, 51.	2.7	36
54	Linkage disequilibrium across six prion gene regions spanning 20 kbp in U.S. sheep. Mammalian Genome, 2006, 17, 1121-1129.	1.0	6

#	ARTICLE	IF	CITATIONS
55	Characterization of 954 bovine full-CDS cDNA sequences. BMC Genomics, 2005, 6, 166.	1.2	26
56	Use of bovine single nucleotide polymorphism markers to verify sample tracking in beef processing. Journal of the American Veterinary Medical Association, 2005, 226, 1311-1314.	0.2	46
57	Evaluation of a Real-Time PCR Kit for Detecting Escherichia coli O157 in Bovine Fecal Samples. Applied and Environmental Microbiology, 2004, 70, 1855-1857.	1.4	25
58	Beta-2-microglobulin haplotypes in U.S. beef cattle and association with failure of passive transfer in newborn calves. Mammalian Genome, 2004, 15, 227-236.	1.0	33
59	Gene expression profiling of bovine macrophages in response to O157:H7 lipopolysaccharide. Developmental and Comparative Immunology, 2004, 28, 635-645.	1.0	25
60	Prion gene sequence variation within diverse groups of U.S. sheep, beef cattle, and deer. Mammalian Genome, 2003, 14, 765-777.	1.0	104
61	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
62	Association of bovine neonatal Fc receptor a-chain gene (FCGRT) haplotypes with serum IgG concentration in newborn calves. Mammalian Genome, 2002, 13, 704-710.	1.0	42
63	Structure of the genes for porcine endometrial secreted and membrane folate binding proteins. Domestic Animal Endocrinology, 2001, 21, 55-72.	0.8	4
64	Estimation of DNA sequence diversity in bovine cytokine genes. Mammalian Genome, 2001, 12, 32-37.	1.0	51
65	Interleukin-8 haplotype structure from nucleotide sequence variation in commercial populations of U.S. beef cattle. Mammalian Genome, 2001, 12, 219-226.	1.0	38
66	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
67	Identification and genetic mapping of bovine chemokine genes expressed in epithelial cells. Mammalian Genome, 1999, 10, 128-133.	1.0	13
68	Single nucleotide polymorphism (SNP) discovery and linkage mapping of bovine cytokine genes. Mammalian Genome, 1999, 10, 1062-1069.	1.0	61
69	Directed cosmid isolation of bovine markers for physical assignment by fish. Animal Biotechnology, 1997, 8, 167-177.	0.7	15
70	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
71	The D-Alanyl carrier protein in Lactobacillus casei: cloning, sequencing, and expression of dltC. Journal of Bacteriology, 1996, 178, 3869-3876.	1.0	59
72	Conjugative Mobilization of a Vancomycin Resistance Plasmid by a Putative Enterococcus faecium Sex Pheromone Response Plasmid. Microbial Drug Resistance, 1995, 1, 177-183.	0.9	35

#	ARTICLE	IF	CITATIONS
73	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
74	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
75	Controlled cell lysis and protoplast formation by enhancement of inhibitors of alanine racemase by glycine. Biochemical and Biophysical Research Communications, 1987, 149, 576-579.	1.0	5
76	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
77	Association of ARRDC3 and NFIA variants with bovine congestive heart failure in feedlot cattle. F1000Research, 0, 11, 385.	0.8	6