

# David E Machugh

## List of Publications by Citations

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126  
papers

5,439  
citations

39  
h-index

70  
g-index

139  
ext. papers

6,879  
ext. citations

4.8  
avg, IF

5.28  
L-index

| #   | Paper  | IF   | Citations |
|-----|--|------|-----------|
| 126 | Genetic evidence for Near-Eastern origins of European cattle. <i>Nature</i> , <b>2001</b> , 410, 1088-91   | 50.4 | 436       |
| 125 | Mitochondrial diversity and the origins of African and European cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1996</b> , 93, 5131-5  | 11.5 | 387       |
| 124 | Microsatellite DNA variation and the evolution, domestication and phylogeography of taurine and zebu cattle ( <i>Bos taurus</i> and <i>Bos indicus</i> ). <i>Genetics</i> , <b>1997</b> , 146, 1071-86   | 4    | 308       |
| 123 | Transcriptional profiling of immune genes in bovine monocyte-derived macrophages exposed to bacterial antigens. <i>Veterinary Immunology and Immunopathology</i> , <b>2011</b> , 140, 130-9  | 2    | 239       |
| 122 | Prehistoric genomes reveal the genetic foundation and cost of horse domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E5661-9   | 11.5 | 197       |
| 121 | Livestock genetic origins: goats buck the trend. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2001</b> , 98, 5382-4   | 11.5 | 136       |
| 120 | Genetic structure of seven European cattle breeds assessed using 20 microsatellite markers. <i>Animal Genetics</i> , <b>1998</b> , 29, 333-40  | 2.5  | 134       |
| 119 | Circulating microRNAs as Potential Biomarkers of Infectious Disease. <i>Frontiers in Immunology</i> , <b>2017</b> , 8, 118   | 8.4  | 131       |
| 118 | Genome sequencing of the extinct Eurasian wild aurochs, <i>Bos primigenius</i> , illuminates the phylogeography and evolution of cattle. <i>Genome Biology</i> , <b>2015</b> , 16, 234   | 18.3 | 127       |
| 117 | A microsatellite survey of cattle from a centre of origin: the Near East. <i>Molecular Ecology</i> , <b>1999</b> , 8, 2015-27  | 3.7  | 125       |
| 116 | A sequence polymorphism in MSTN predicts sprinting ability and racing stamina in thoroughbred horses. <i>PLoS ONE</i> , <b>2010</b> , 5, e8645   | 3.7  | 122       |
| 115 | A genome-wide SNP-association study confirms a sequence variant (g.66493737C>T) in the equine myostatin (MSTN) gene as the most powerful predictor of optimum racing distance for Thoroughbred racehorses. <i>BMC Genomics</i> , <b>2010</b> , 11, 552 | 4.5  | 105       |
| 114 | A genome scan for positive selection in thoroughbred horses. <i>PLoS ONE</i> , <b>2009</b> , 4, e5767  | 3.7  | 102       |
| 113 | Selection signatures in worldwide sheep populations. <i>PLoS ONE</i> , <b>2014</b> , 9, e103813  | 3.7  | 101       |
| 112 | Phylogenetic analysis of the tribe Bovini using microsatellites. <i>Animal Genetics</i> , <b>2000</b> , 31, 178-85   | 2.5  | 94        |
| 111 | Genetics and domestic cattle origins. <i>Evolutionary Anthropology</i> , <b>1998</b> , 6, 79-86  | 4.7  | 83        |
| 110 | Taming the Past: Ancient DNA and the Study of Animal Domestication. <i>Annual Review of Animal Biosciences</i> , <b>2017</b> , 5, 329-351  | 13.7 | 78        |

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|-----|--|------|----|
| 109 | Ancient cattle genomics, origins, and rapid turnover in the Fertile Crescent. <i>Science</i> , <b>2019</b> , 365, 173-176  | 33.3 | 77 |
| 108 | Receptor-mediated recognition of mycobacterial pathogens. <i>Cellular Microbiology</i> , <b>2013</b> , 15, 1484-95   | 3.9  | 73 |
| 107 | Admixture and diversity in West African cattle populations. <i>Molecular Ecology</i> , <b>2004</b> , 13, 3477-87   | 5.7  | 73 |
| 106 | Ancient DNA analysis of 101 cattle remains: limits and prospects. <i>Journal of Archaeological Science</i> , <b>2004</b> , 31, 695-710   | 2.9  | 67 |
| 105 | A complete mitochondrial genome sequence from a mesolithic wild aurochs ( <i>Bos primigenius</i> ). <i>PLoS ONE</i> , <b>2010</b> , 5, e9255   | 3.7  | 64 |
| 104 | Tumour necrosis factor-alpha (TNF-alpha) increases nuclear factor kappaB (NFkappaB) activity in and interleukin-8 (IL-8) release from bovine mammary epithelial cells. <i>Veterinary Immunology and Immunopathology</i> , <b>2007</b> , 116, 59-68 | 2    | 63 |
| 103 | Characterization of the equine skeletal muscle transcriptome identifies novel functional responses to exercise training. <i>BMC Genomics</i> , <b>2010</b> , 11, 398   | 4.5  | 61 |
| 102 | The genetic origin and history of speed in the Thoroughbred racehorse. <i>Nature Communications</i> , <b>2012</b> , 3, 643   | 17.4 | 55 |
| 101 | Genetic origin, admixture and population history of aurochs ( <i>Bos primigenius</i> ) and primitive European cattle. <i>Heredity</i> , <b>2017</b> , 118, 169-176   | 3.6  | 54 |
| 100 | Innate gene repression associated with <i>Mycobacterium bovis</i> infection in cattle: toward a gene signature of disease. <i>BMC Genomics</i> , <b>2007</b> , 8, 400  | 4.5  | 54 |
| 99  | Targets of selection in the Thoroughbred genome contain exercise-relevant gene SNPs associated with elite racecourse performance. <i>Animal Genetics</i> , <b>2010</b> , 41 Suppl 2, 56-63   | 2.5  | 51 |
| 98  | Sequence variation in the mitochondrial DNA control region of wild African cheetahs ( <i>Acinonyx jubatus</i> ). <i>Heredity</i> , <b>2001</b> , 86, 355-62  | 3.6  | 51 |
| 97  | Evidence for biogeographic patterning of mitochondrial DNA sequences in Eastern horse populations. <i>Animal Genetics</i> , <b>2006</b> , 37, 494-7  | 2.5  | 50 |
| 96  | Understanding bovine trypanosomiasis and trypanotolerance: the promise of functional genomics. <i>Veterinary Immunology and Immunopathology</i> , <b>2005</b> , 105, 247-58  | 2    | 46 |
| 95  | Alterations in oxidative gene expression in equine skeletal muscle following exercise and training. <i>Physiological Genomics</i> , <b>2010</b> , 40, 83-93  | 3.6  | 44 |
| 94  | Association of sequence variants in CKM (creatine kinase, muscle) and COX4I2 (cytochrome c oxidase, subunit 4, isoform 2) genes with racing performance in Thoroughbred horses. <i>Equine Veterinary Journal</i> , <b>2010</b> , 42, 569-75        | 2.4  | 44 |
| 93  | Domestication of cattle: Two or three events?. <i>Evolutionary Applications</i> , <b>2019</b> , 12, 123-136  | 4.8  | 42 |
| 92  | RNA-seq Transcriptional Profiling of Peripheral Blood Leukocytes from Cattle Infected with <i>Mycobacterium bovis</i> . <i>Frontiers in Immunology</i> , <b>2014</b> , 5, 396  | 8.4  | 42 |

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|----|---|-----|----|
| 91 | Pan-genomic analysis of bovine monocyte-derived macrophage gene expression in response to in vitro infection with <i>Mycobacterium avium</i> subspecies paratuberculosis. <i>Veterinary Research</i> , <b>2012</b> , 43, 25                               | 3.8 | 42 |
| 90 | Associations between newly discovered polymorphisms in the <i>Bos taurus</i> growth hormone receptor gene and performance traits in Holstein-Friesian dairy cattle. <i>Animal Genetics</i> , <b>2011</b> , 42, 39-49                                      | 2.5 | 41 |
| 89 | MicroRNA profiling of the bovine alveolar macrophage response to <i>Mycobacterium bovis</i> infection suggests pathogen survival is enhanced by microRNA regulation of endocytosis and lysosome trafficking. <i>Tuberculosis</i> , <b>2015</b> , 95, 60-7 | 2.6 | 40 |
| 88 | DNA sequence polymorphisms in a panel of eight candidate bovine imprinted genes and their association with performance traits in Irish Holstein-Friesian cattle. <i>BMC Genetics</i> , <b>2010</b> , 11, 93   | 2.6 | 40 |
| 87 | Global gene expression and systems biology analysis of bovine monocyte-derived macrophages in response to in vitro challenge with <i>Mycobacterium bovis</i> . <i>PLoS ONE</i> , <b>2012</b> , 7, e32034  | 3.7 | 39 |
| 86 | Long-term stability of RNA in post-mortem bovine skeletal muscle, liver and subcutaneous adipose tissues. <i>BMC Molecular Biology</i> , <b>2007</b> , 8, 108   | 4.5 | 39 |
| 85 | Cytokine mRNA profiling of peripheral blood mononuclear cells from trypanotolerant and trypanosusceptible cattle infected with <i>Trypanosoma congolense</i> . <i>Physiological Genomics</i> , <b>2006</b> , 28, 53-61                                    | 3.6 | 39 |
| 84 | Transcriptional adaptations following exercise in thoroughbred horse skeletal muscle highlights molecular mechanisms that lead to muscle hypertrophy. <i>BMC Genomics</i> , <b>2009</b> , 10, 638   | 4.5 | 38 |
| 83 | Y-specific microsatellite polymorphisms in a range of bovid species. <i>Animal Genetics</i> , <b>2000</b> , 31, 127-30  | 2.5 | 37 |
| 82 | Single nucleotide polymorphisms at the imprinted bovine insulin-like growth factor 2 (IGF2) locus are associated with dairy performance in Irish Holstein-Friesian cattle. <i>Journal of Dairy Research</i> , <b>2011</b> , 78, 1-8                       | 1.6 | 36 |
| 81 | The Identification of Circulating MiRNA in Bovine Serum and Their Potential as Novel Biomarkers of Early <i>Mycobacterium avium</i> subsp paratuberculosis Infection. <i>PLoS ONE</i> , <b>2015</b> , 10, e0134310  | 3.7 | 35 |
| 80 | MSTN genotypes in Thoroughbred horses influence skeletal muscle gene expression and racetrack performance. <i>Animal Genetics</i> , <b>2012</b> , 43, 810-2   | 2.5 | 34 |
| 79 | Whole-transcriptome, high-throughput RNA sequence analysis of the bovine macrophage response to <i>Mycobacterium bovis</i> infection in vitro. <i>BMC Genomics</i> , <b>2013</b> , 14, 230  | 4.5 | 34 |
| 78 | Transcriptional profiling of cattle infected with <i>Trypanosoma congolense</i> highlights gene expression signatures underlying trypanotolerance and trypanosusceptibility. <i>BMC Genomics</i> , <b>2009</b> , 10, 207                                  | 4.5 | 34 |
| 77 | Mitochondrial DNA sequence diversity in extant Irish horse populations and in ancient horses. <i>Animal Genetics</i> , <b>2006</b> , 37, 498-502  | 2.5 | 34 |
| 76 | Taurine and zebu admixture in Near Eastern cattle: a comparison of mitochondrial, autosomal and Y-chromosomal data. <i>Animal Genetics</i> , <b>2007</b> , 38, 520-4  | 2.5 | 32 |
| 75 | Genome-wide SNP association-based localization of a dwarfism gene in Friesian dwarf horses. <i>Animal Genetics</i> , <b>2010</b> , 41 Suppl 2, 2-7  | 2.5 | 29 |
| 74 | Early medieval cattle remains from a Scandinavian settlement in Dublin: genetic analysis and comparison with extant breeds. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>1999</b> , 354, 99-108; discussion 108-9   | 5.8 | 29 |

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|----|---|-----|----|
| 73 | DNA sequence polymorphisms within the bovine guanine nucleotide-binding protein Gs subunit alpha (Gs $\alpha$ )-encoding (GNAS) genomic imprinting domain are associated with performance traits. <i>BMC Genetics</i> , <b>2011</b> , 12, 4   | 2.6 | 27 |
| 72 | RNA sequencing provides exquisite insight into the manipulation of the alveolar macrophage by tubercle bacilli. <i>Scientific Reports</i> , <b>2015</b> , 5, 13629  | 4.9 | 26 |
| 71 | Genome-wide transcriptional profiling of peripheral blood leukocytes from cattle infected with <i>Mycobacterium bovis</i> reveals suppression of host immune genes. <i>BMC Genomics</i> , <b>2011</b> , 12, 611   | 4.5 | 26 |
| 70 | Gene expression profiling of peripheral blood mononuclear cells (PBMC) from <i>Mycobacterium bovis</i> infected cattle after in vitro antigenic stimulation with purified protein derivative of tuberculin (PPD). <i>Veterinary Immunology and Immunopathology</i> , <b>2006</b> , 113, 73-89 | 2   | 26 |
| 69 | Interrogation of modern and ancient genomes reveals the complex domestic history of cattle. <i>Animal Frontiers</i> , <b>2014</b> , 4, 7-22   | 5.5 | 25 |
| 68 | Associations between novel single nucleotide polymorphisms in the <i>Bos taurus</i> growth hormone gene and performance traits in Holstein-Friesian dairy cattle. <i>Journal of Dairy Science</i> , <b>2010</b> , 93, 5959-69   | 4   | 25 |
| 67 | Comparative 'omics analyses differentiate <i>Mycobacterium tuberculosis</i> and <i>Mycobacterium bovis</i> and reveal distinct macrophage responses to infection with the human and bovine tubercle bacilli. <i>Microbial Genomics</i> , <b>2018</b> , 4,                                     | 4.4 | 25 |
| 66 | Profiling microRNA expression in bovine alveolar macrophages using RNA-seq. <i>Veterinary Immunology and Immunopathology</i> , <b>2013</b> , 155, 238-44  | 2   | 24 |
| 65 | Analysis of the Bovine Monocyte-Derived Macrophage Response to <i>Mycobacterium avium</i> Subspecies Paratuberculosis Infection Using RNA-seq. <i>Frontiers in Immunology</i> , <b>2015</b> , 6, 23   | 8.4 | 24 |
| 64 | Innate cytokine profiling of bovine alveolar macrophages reveals commonalities and divergence in the response to <i>Mycobacterium bovis</i> and <i>Mycobacterium tuberculosis</i> infection. <i>Tuberculosis</i> , <b>2014</b> , 94, 441-50   | 2.6 | 24 |
| 63 | Dietary n-3 polyunsaturated fatty acid supplementation alters the expression of genes involved in the control of fertility in the bovine uterine endometrium. <i>Physiological Genomics</i> , <b>2012</b> , 44, 878-88  | 3.6 | 24 |
| 62 | Gene expression profiling of the host response to <i>Mycobacterium bovis</i> infection in cattle. <i>Transboundary and Emerging Diseases</i> , <b>2009</b> , 56, 204-14   | 4.2 | 24 |
| 61 | Single nucleotide polymorphisms within the bovine DLK1-DIO3 imprinted domain are associated with economically important production traits in cattle. <i>Journal of Heredity</i> , <b>2011</b> , 102, 94-101   | 2.4 | 23 |
| 60 | MSTN genotype (g.66493737C/T) association with speed indices in Thoroughbred racehorses. <i>Journal of Applied Physiology</i> , <b>2012</b> , 112, 86-90  | 3.7 | 23 |
| 59 | Unlocking the origins and biology of domestic animals using ancient DNA and paleogenomics. <i>BMC Biology</i> , <b>2019</b> , 17, 98  | 7.3 | 23 |
| 58 | PGC-1 $\beta$ -encoded by the PPARGC1A gene regulates oxidative energy metabolism in equine skeletal muscle during exercise. <i>Animal Genetics</i> , <b>2012</b> , 43, 153-62  | 2.5 | 22 |
| 57 | Comparative functional genomics and the bovine macrophage response to strains of the mycobacterium genus. <i>Frontiers in Immunology</i> , <b>2014</b> , 5, 536   | 8.4 | 22 |
| 56 | Differential gene expression in the endometrium reveals cytoskeletal and immunological genes in lactating dairy cows genetically divergent for fertility traits. <i>Reproduction, Fertility and Development</i> , <b>2017</b> , 29, 274-282   | 1.8 | 20 |

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|----|--|-----|----|
| 55 | Definition of the cattle killer cell Ig-like receptor gene family: comparison with aurochs and human counterparts. <i>Journal of Immunology</i> , <b>2014</b> , 193, 6016-30   | 5.3 | 20 |
| 54 | The MarR family transcription factor Rv1404 coordinates adaptation of Mycobacterium tuberculosis to acid stress via controlled expression of Rv1405c, a virulence-associated methyltransferase. <i>Tuberculosis</i> , <b>2016</b> , 97, 154-62 | 2.6 | 18 |
| 53 | Infection in Cattle: Analyzing Responses of Peripheral Blood Mononuclear Cells (PBMC) Using a Transcriptomics Approach. <i>Frontiers in Immunology</i> , <b>2019</b> , 10, 2081  | 8.4 | 17 |
| 52 | Genome-Wide microRNA Binding Site Variation between Extinct Wild Aurochs and Modern Cattle Identifies Candidate microRNA-Regulated Domestication Genes. <i>Frontiers in Genetics</i> , <b>2017</b> , 8, 3                                      | 4.5 | 17 |
| 51 | Antigen stimulation of peripheral blood mononuclear cells from Mycobacterium bovis infected cattle yields evidence for a novel gene expression program. <i>BMC Genomics</i> , <b>2008</b> , 9, 447   | 4.5 | 17 |
| 50 | Feasibility and utility of microsatellite markers in archaeological cattle remains from a Viking Age settlement in Dublin. <i>Animal Genetics</i> , <b>2003</b> , 34, 410-6  | 2.5 | 17 |
| 49 | Genomic imprinting effects on complex traits in domesticated animal species. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 156   | 4.5 | 16 |
| 48 | GOexpress: an R/Bioconductor package for the identification and visualisation of robust gene ontology signatures through supervised learning of gene expression data. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 126                        | 3.6 | 16 |
| 47 | Genomic Characterisation of the Indigenous Irish Kerry Cattle Breed. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 51  | 4.5 | 16 |
| 46 | Equine skeletal muscle adaptations to exercise and training: evidence of differential regulation of autophagosomal and mitochondrial components. <i>BMC Genomics</i> , <b>2017</b> , 18, 595   | 4.5 | 16 |
| 45 | Genomic inbreeding trends, influential sire lines and selection in the global Thoroughbred horse population. <i>Scientific Reports</i> , <b>2020</b> , 10, 466   | 4.9 | 15 |
| 44 | Imprinted loci in domestic livestock species as epigenomic targets for artificial selection of complex traits. <i>Animal Genetics</i> , <b>2014</b> , 45 Suppl 1, 25-39  | 2.5 | 14 |
| 43 | Single nucleotide polymorphisms in the imprinted bovine insulin-like growth factor 2 receptor gene (IGF2R) are associated with body size traits in Irish Holstein-Friesian cattle. <i>Animal Genetics</i> , <b>2012</b> , 43, 81-7             | 2.5 | 14 |
| 42 | Functional characterisation of bovine interleukin 8 promoter haplotypes in vitro. <i>Molecular Immunology</i> , <b>2012</b> , 50, 108-16   | 4.3 | 13 |
| 41 | Polymorphism discovery and allele frequency estimation using high-throughput DNA sequencing of target-enriched pooled DNA samples. <i>BMC Genomics</i> , <b>2012</b> , 13, 16  | 4.5 | 13 |
| 40 | Genome-wide association study of osteochondrosis in the tarsocrural joint of Dutch Warmblood horses identifies susceptibility loci on chromosomes 3 and 10. <i>Animal Genetics</i> , <b>2013</b> , 44, 408-12                                  | 2.5 | 13 |
| 39 | A catalogue of validated single nucleotide polymorphisms in bovine orthologs of mammalian imprinted genes and associations with beef production traits. <i>Animal</i> , <b>2010</b> , 4, 1958-70   | 3.1 | 13 |
| 38 | Key Hub and Bottleneck Genes Differentiate the Macrophage Response to Virulent and Attenuated Mycobacterium bovis. <i>Frontiers in Immunology</i> , <b>2014</b> , 5, 422   | 8.4 | 12 |



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|----|--|-----|----|
| 37 | Horses for courses: a DNA-based test for race distance aptitude in thoroughbred racehorses. <i>Recent Patents on DNA &amp; Gene Sequences</i> , <b>2012</b> , 6, 203-8   |     | 10 |
| 36 | PHLDA2 is an imprinted gene in cattle. <i>Animal Genetics</i> , <b>2012</b> , 43, 587-90   | 2.5 | 9  |
| 35 | Linkage mapping of the locus for inherited ovine arthrogyrosis (IOA) to sheep chromosome 5. <i>Mammalian Genome</i> , <b>2007</b> , 18, 43-52  | 3.2 | 9  |
| 34 | Alveolar Macrophage Chromatin Is Modified to Orchestrate Host Response to Infection. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 1386   | 4.5 | 8  |
| 33 | RNA Sequencing (RNA-Seq) Reveals Extremely Low Levels of Reticulocyte-Derived Globin Gene Transcripts in Peripheral Blood From Horses () and Cattle (). <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 278  | 4.5 | 8  |
| 32 | Technical note: High fidelity of whole-genome amplified sheep ( <i>Ovis aries</i> ) deoxyribonucleic acid using a high-density single nucleotide polymorphism array-based genotyping platform. <i>Journal of Animal Science</i> , <b>2010</b> , 88, 3183-6 | 0.7 | 8  |
| 31 | Inbreeding effects on postweaning production traits, conformation, and calving performance in Irish beef cattle. <i>Journal of Animal Science</i> , <b>2008</b> , 86, 3338-47  | 0.7 | 8  |
| 30 | High-throughput transcriptomics reveals common and strain-specific responses of human macrophages to infection with <i>Mycobacterium abscessus</i> Smooth and Rough variants. <i>BMC Genomics</i> , <b>2015</b> , 16, 1046                                 | 4.5 | 7  |
| 29 | Divergent antimicrobial peptide (AMP) and acute phase protein (APP) responses to <i>Trypanosoma congolense</i> infection in trypanotolerant and trypanosusceptible cattle. <i>Molecular Immunology</i> , <b>2009</b> , 47, 196-204                         | 4.3 | 7  |
| 28 | Identification of novel molecular markers of mastitis caused by using gene expression profiling in two consecutive generations of Chinese Holstein dairy cattle. <i>Journal of Animal Science and Biotechnology</i> , <b>2020</b> , 11, 98                 | 6   | 7  |
| 27 | The bovine alveolar macrophage DNA methylome is resilient to infection with <i>Mycobacterium bovis</i> . <i>Scientific Reports</i> , <b>2019</b> , 9, 1510   | 4.9 | 7  |
| 26 | Selection in Australian Thoroughbred horses acts on a locus associated with early two-year old speed. <i>PLoS ONE</i> , <b>2020</b> , 15, e0227212   | 3.7 | 6  |
| 25 | Analysis of genetic variation contributing to measured speed in Thoroughbreds identifies genomic regions involved in the transcriptional response to exercise. <i>Animal Genetics</i> , <b>2019</b> , 50, 670-685  | 2.5 | 6  |
| 24 | Impact of delayed processing of bovine peripheral blood on differential gene expression. <i>Veterinary Immunology and Immunopathology</i> , <b>2012</b> , 145, 199-205   | 2   | 6  |
| 23 | Transmission ratio distortion at the growth hormone gene (GH1) in bovine preimplantation embryos: An in vitro culture-induced phenomenon?. <i>Molecular Reproduction and Development</i> , <b>2008</b> , 75, 715-22  | 2.6 | 6  |
| 22 | Iodine supplementation of the pregnant dam alters intestinal gene expression and immunoglobulin uptake in the newborn lamb. <i>Animal</i> , <b>2016</b> , 10, 598-606  | 3.1 | 6  |
| 21 | The contribution of myostatin (MSTN) and additional modifying genetic loci to race distance aptitude in Thoroughbred horses racing in different geographic regions. <i>Equine Veterinary Journal</i> , <b>2019</b> , 51, 625-633                           | 2.4 | 6  |
| 20 | Genetic contributions to precocity traits in racing Thoroughbreds. <i>Animal Genetics</i> , <b>2018</b> , 49, 193-204  | 2.5 | 5  |

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|----|--|-----|---|
| 19 | A genomic prediction model for racecourse starts in the Thoroughbred horse. <i>Animal Genetics</i> , <b>2019</b> , 50, 347-357   | 2.5 | 4 |
| 18 | Transcriptomic Analysis of Ovine Hepatic Lymph Node Following Infection - Inhibition of NK Cell and IgE-Mediated Signaling. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 687579  | 8.4 | 4 |
| 17 | Chinese Mongolian horses may retain early domestic male genetic lineages yet to be discovered. <i>Animal Genetics</i> , <b>2019</b> , 50, 399-402  | 2.5 | 3 |
| 16 | Expression Quantitative Trait Loci in Equine Skeletal Muscle Reveals Heritable Variation in Metabolism and the Training Responsive Transcriptome. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 1215  | 4.5 | 3 |
| 15 | A Population Genomics Analysis of the Native Irish Galway Sheep Breed. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 927  | 4.5 | 2 |
| 14 | RNA-Seq Transcriptome Analysis of Peripheral Blood From Cattle Infected With Across an Experimental Time Course. <i>Frontiers in Veterinary Science</i> , <b>2021</b> , 8, 662002  | 3.1 | 2 |
| 13 | Refinement of Global Domestic Horse Biogeography Using Historic Landrace Chinese Mongolian Populations. <i>Journal of Heredity</i> , <b>2019</b> , 110, 769-781  | 2.4 | 1 |
| 12 | Genomics of Performance <b>2013</b> , 265-283  |     | 1 |
| 11 | High concordance of bovine single nucleotide polymorphism genotypes generated using two independent genotyping strategies. <i>Animal Biotechnology</i> , <b>2010</b> , 21, 257-62  | 1.4 | 1 |
| 10 | Comparative Omics analyses differentiate Mycobacterium tuberculosis and Mycobacterium bovis and reveal distinct macrophage responses to infection with the human and bovine tubercle bacilli   |     | 1 |
| 9  | Alveolar macrophage chromatin is modified to orchestrate host response to Mycobacterium bovis infection  |     | 1 |
| 8  | Integrative genomics of the mammalian alveolar macrophage response to intracellular mycobacteria. <i>BMC Genomics</i> , <b>2021</b> , 22, 343  | 4.5 | 1 |
| 7  | Timing of transcriptomic peripheral blood mononuclear cell responses of sheep to Fasciola hepatica infection differs from those of cattle, reflecting different disease phenotypes   |     | 1 |
| 6  | Genome-wide local ancestry and direct evidence for mitonuclear co-adaptation in African hybrid cattle populations ( <i>Bos taurus/indicus</i> )  |     | 1 |
| 5  | Timing of Transcriptomic Peripheral Blood Mononuclear Cell Responses of Sheep to Infection Differs From Those of Cattle, Reflecting Different Disease Phenotypes. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 729217  | 8.4 | 1 |
| 4  | Transcriptome Profiling of Developing Ovine Fat Tail Tissue Reveals an Important Role for in Regulation of Adipogenesis.. <i>Frontiers in Cell and Developmental Biology</i> , <b>2022</b> , 10, 839731  | 5.7 | 1 |
| 3  | Erratum to Associations between novel single nucleotide polymorphisms in the <i>Bos taurus</i> growth hormone gene and performance traits in Holstein-Friesian dairy cattle (J. Dairy Sci. 93:5959-5969). <i>Journal of Dairy Science</i> , <b>2011</b> , 94, 1069 | 4   |   |
| 2  | Convenient detection of single nucleotide polymorphism haplotypes in the bovine growth hormone gene using amplification-created restriction sites. <i>Animal Genetics</i> , <b>2005</b> , 36, 175-7  | 2.5 |   |



- 1 How Modern and Ancient Genomic Analyses can Reveal Complex Domestic Histories Using Cattle as a Case Study **2017**, 30-44