

# David E Machugh

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	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
125	Integrative genomics of the mammalian alveolar macrophage response to intracellular mycobacteria. <i>BMC Genomics</i> , <b>2021</b> , 22, 343	4.5	1
124	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
123	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
122	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
121	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
120	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
119	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
118	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
117	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
116	Alveolar Macrophage Chromatin Is Modified to Orchestrate Host Response to Infection. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 1386	4.5	8
115	Domestication of cattle: Two or three events?. <i>Evolutionary Applications</i> , <b>2019</b> , 12, 123-136	4.8	42
114	A genomic prediction model for racecourse starts in the Thoroughbred horse. <i>Animal Genetics</i> , <b>2019</b> , 50, 347-357	2.5	4
113	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
112	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
111	A Population Genomics Analysis of the Native Irish Galway Sheep Breed. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 927	4.5	2
110	Ancient cattle genomics, origins, and rapid turnover in the Fertile Crescent. <i>Science</i> , <b>2019</b> , 365, 173-176	33.3	77

109	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
108	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
107	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
106	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
105	Genetic contributions to precocity traits in racing Thoroughbreds. <i>Animal Genetics</i> , <b>2018</b> , 49, 193-204	2.5	5
104	Genomic Characterisation of the Indigenous Irish Kerry Cattle Breed. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 51	4.5	16
103	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
102	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
101	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
100	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
99	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
98	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
97	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
96	Circulating microRNAs as Potential Biomarkers of Infectious Disease. <i>Frontiers in Immunology</i> , <b>2017</b> , 8, 118	8.4	131
95	How Modern and Ancient Genomic Analyses can Reveal Complex Domestic Histories Using Cattle as a Case Study <b>2017</b> , 30-44		
94	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
93	The MarR family transcription factor Rv1404 coordinates adaptation of <i>Mycobacterium tuberculosis</i> to acid stress via controlled expression of Rv1405c, a virulence-associated methyltransferase. <i>Tuberculosis</i> , <b>2016</b> , 97, 154-62	2.6	18
92	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

91	Genomic imprinting effects on complex traits in domesticated animal species. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 156	4.5	16
90	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
89	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
88	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
87	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
86	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
85	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
84	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
83	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
82	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
81	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
80	Key Hub and Bottleneck Genes Differentiate the Macrophage Response to Virulent and Attenuated <i>Mycobacterium bovis</i> . <i>Frontiers in Immunology</i> , <b>2014</b> , 5, 422	8.4	12
79	Comparative functional genomics and the bovine macrophage response to strains of the <i>Mycobacterium</i> genus. <i>Frontiers in Immunology</i> , <b>2014</b> , 5, 536	8.4	22
78	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
77	Selection signatures in worldwide sheep populations. <i>PLoS ONE</i> , <b>2014</b> , 9, e103813	3.7	101
76	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
75	Profiling microRNA expression in bovine alveolar macrophages using RNA-seq. <i>Veterinary Immunology and Immunopathology</i> , <b>2013</b> , 155, 238-44	2	24
74	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

73	Receptor-mediated recognition of mycobacterial pathogens. <i>Cellular Microbiology</i> , <b>2013</b> , 15, 1484-95	3.9	73
72	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
71	Genomics of Performance <b>2013</b> , 265-283		1
70	Functional characterisation of bovine interleukin 8 promoter haplotypes in vitro. <i>Molecular Immunology</i> , <b>2012</b> , 50, 108-16	4.3	13
69	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
68	PHLDA2 is an imprinted gene in cattle. <i>Animal Genetics</i> , <b>2012</b> , 43, 587-90	2.5	9
67	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
66	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
65	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
64	Pan-genomic analysis of bovine monocyte-derived macrophage gene expression in response to in vitro infection with <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> . <i>Veterinary Research</i> , <b>2012</b> , 43, 25	3.8	42
63	The genetic origin and history of speed in the Thoroughbred racehorse. <i>Nature Communications</i> , <b>2012</b> , 3, 643	17.4	55
62	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
61	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
60	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
59	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
58	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
57	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
56	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

55	Erratum to Associations between novel single nucleotide polymorphisms in the Bos taurus 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	
54	Associations between newly discovered polymorphisms in the Bos taurus 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
53	Genome-wide transcriptional profiling of peripheral blood leukocytes from cattle infected with Mycobacterium bovis reveals suppression of host immune genes. <i>BMC Genomics</i> , <b>2011</b> , 12, 611	4.5	26
52	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
51	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
50	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
49	Technical note: High fidelity of whole-genome amplified sheep (Ovis aries) 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
48	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
47	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
46	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
45	Associations between novel single nucleotide polymorphisms in the Bos taurus 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
44	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
43	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
42	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
41	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
40	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
39	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
38	A complete mitochondrial genome sequence from a mesolithic wild aurochs (Bos primigenius). <i>PLoS ONE</i> , <b>2010</b> , 5, e9255	3.7	64

37	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
36	Gene expression profiling of the host response to Mycobacterium bovis infection in cattle. <i>Transboundary and Emerging Diseases</i> , <b>2009</b> , 56, 204-14	4.2	24
35	Divergent antimicrobial peptide (AMP) and acute phase protein (APP) responses to Trypanosoma congolense infection in trypanotolerant and trypanosusceptible cattle. <i>Molecular Immunology</i> , <b>2009</b> , 47, 196-204	4.3	7
34	Transcriptional profiling of cattle infected with Trypanosoma congolense highlights gene expression signatures underlying trypanotolerance and trypanosusceptibility. <i>BMC Genomics</i> , <b>2009</b> , 10, 207	4.5	34
33	A genome scan for positive selection in thoroughbred horses. <i>PLoS ONE</i> , <b>2009</b> , 4, e5767	3.7	102
32	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
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	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
29	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
28	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
27	Innate gene repression associated with Mycobacterium bovis infection in cattle: toward a gene signature of disease. <i>BMC Genomics</i> , <b>2007</b> , 8, 400	4.5	54
26	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
25	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
24	Gene expression profiling of peripheral blood mononuclear cells (PBMC) from Mycobacterium bovis 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
23	Cytokine mRNA profiling of peripheral blood mononuclear cells from trypanotolerant and trypanosusceptible cattle infected with Trypanosoma congolense. <i>Physiological Genomics</i> , <b>2006</b> , 28, 53-61	3.6	39
22	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
21	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
20	Understanding bovine trypanosomiasis and trypanotolerance: the promise of functional genomics. <i>Veterinary Immunology and Immunopathology</i> , <b>2005</b> , 105, 247-58	2	46

19	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	
18	Admixture and diversity in West African cattle populations. <i>Molecular Ecology</i> , <b>2004</b> , 13, 3477-87	5.7	73
17	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
16	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
15	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
14	Genetic evidence for Near-Eastern origins of European cattle. <i>Nature</i> , <b>2001</b> , 410, 1088-91	50.4	436
13	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
12	Y-specific microsatellite polymorphisms in a range of bovid species. <i>Animal Genetics</i> , <b>2000</b> , 31, 127-30	2.5	37
11	Phylogenetic analysis of the tribe Bovini using microsatellites. <i>Animal Genetics</i> , <b>2000</b> , 31, 178-85	2.5	94
10	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
9	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
8	Genetics and domestic cattle origins. <i>Evolutionary Anthropology</i> , <b>1998</b> , 6, 79-86	4.7	83
7	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
6	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
5	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
4	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		1
3	Alveolar macrophage chromatin is modified to orchestrate host response to <i>Mycobacterium bovis</i> infection		1
2	Timing of transcriptomic peripheral blood mononuclear cell responses of sheep to <i>Fasciola hepatica</i> infection differs from those of cattle, reflecting different disease phenotypes		1



- 1 Genome-wide local ancestry and direct evidence for mitonuclear co-adaptation in African hybrid cattle populations (*Bos taurus/indicus*)

1