

David E Machugh

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6277514/publications.pdf>

Version: 2024-02-01

124
papers

7,679
citations

50170

46
h-index

56606

83
g-index

139
all docs

139
docs citations

139
times ranked

7280
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome Profiling of Developing Ovine Fat Tail Tissue Reveals an Important Role for MTFP1 in Regulation of Adipogenesis. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 839731.	1.8	7
2	Inbreeding depression and the probability of racing in the Thoroughbred horse. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	10
3	Genome-wide local ancestry and evidence for mitonuclear coadaptation in African hybrid cattle populations. <i>IScience</i> , 2022, 25, 104672.	1.9	8
4	Integrative genomics of the mammalian alveolar macrophage response to intracellular mycobacteria. <i>BMC Genomics</i> , 2021, 22, 343.	1.2	11
5	RNA-Seq Transcriptome Analysis of Peripheral Blood From Cattle Infected With <i>Mycobacterium bovis</i> Across an Experimental Time Course. <i>Frontiers in Veterinary Science</i> , 2021, 8, 662002.	0.9	8
6	Transcriptomic Analysis of Ovine Hepatic Lymph Node Following <i>Fasciola hepatica</i> Infection – Inhibition of NK Cell and IgE-Mediated Signaling. <i>Frontiers in Immunology</i> , 2021, 12, 687579.	2.2	9
7	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. <i>Frontiers in Immunology</i> , 2021, 12, 729217.	2.2	4
8	Identification of novel molecular markers of mastitis caused by <i>Staphylococcus aureus</i> using gene expression profiling in two consecutive generations of Chinese Holstein dairy cattle. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 98.	2.1	26
9	Selection in Australian Thoroughbred horses acts on a locus associated with early two-year old speed. <i>PLoS ONE</i> , 2020, 15, e0227212.	1.1	11
10	Genomic inbreeding trends, influential sire lines and selection in the global Thoroughbred horse population. <i>Scientific Reports</i> , 2020, 10, 466.	1.6	33
11	Domestication of cattle: Two or three events?. <i>Evolutionary Applications</i> , 2019, 12, 123-136.	1.5	80
12	A genomic prediction model for racecourse starts in the Thoroughbred horse. <i>Animal Genetics</i> , 2019, 50, 347-357.	0.6	12
13	Refinement of Global Domestic Horse Biogeography Using Historic Landrace Chinese Mongolian Populations. <i>Journal of Heredity</i> , 2019, 110, 769-781.	1.0	8
14	Analysis of genetic variation contributing to measured speed in Thoroughbreds identifies genomic regions involved in the transcriptional response to exercise. <i>Animal Genetics</i> , 2019, 50, 670-685.	0.6	15
15	A Population Genomics Analysis of the Native Irish Galway Sheep Breed. <i>Frontiers in Genetics</i> , 2019, 10, 927.	1.1	8
16	<i>Fasciola hepatica</i> Infection in Cattle: Analyzing Responses of Peripheral Blood Mononuclear Cells (PBMC) Using a Transcriptomics Approach. <i>Frontiers in Immunology</i> , 2019, 10, 2081.	2.2	25
17	Chinese Mongolian horses may retain early domestic male genetic lineages yet to be discovered. <i>Animal Genetics</i> , 2019, 50, 399-402.	0.6	17
18	The bovine alveolar macrophage DNA methylome is resilient to infection with <i>Mycobacterium bovis</i> . <i>Scientific Reports</i> , 2019, 9, 1510.	1.6	8

#	ARTICLE	IF	CITATIONS
19	Unlocking the origins and biology of domestic animals using ancient DNA and paleogenomics. BMC Biology, 2019, 17, 98.	1.7	48
20	Expression Quantitative Trait Loci in Equine Skeletal Muscle Reveals Heritable Variation in Metabolism and the Training Responsive Transcriptome. Frontiers in Genetics, 2019, 10, 1215.	1.1	11
21	The contribution of myostatin (<i>MSTN</i>) and additional modifying genetic loci to race distance aptitude in Thoroughbred horses racing in different geographic regions. Equine Veterinary Journal, 2019, 51, 625-633.	0.9	14
22	Alveolar Macrophage Chromatin Is Modified to Orchestrate Host Response to Mycobacterium bovis Infection. Frontiers in Genetics, 2019, 10, 1386.	1.1	19
23	CHAPTER 4. MicroRNAs and Mycobacterial Infections in Humans and Domestic Animals. RSC Drug Discovery Series, 2019, , 105-132.	0.2	1
24	Ancient cattle genomics, origins, and rapid turnover in the Fertile Crescent. Science, 2019, 365, 173-176.	6.0	138
25	Genetic contributions to precocity traits in racing Thoroughbreds. Animal Genetics, 2018, 49, 193-204.	0.6	11
26	Genomic Characterisation of the Indigenous Irish Kerry Cattle Breed. Frontiers in Genetics, 2018, 9, 51.	1.1	33
27	RNA Sequencing (RNA-Seq) Reveals Extremely Low Levels of Reticulocyte-Derived Globin Gene Transcripts in Peripheral Blood From Horses (<i>Equus caballus</i>) and Cattle (<i>Bos taurus</i>). Frontiers in Genetics, 2018, 9, 278.	1.1	13
28	Comparative 'omics analyses differentiate Mycobacterium tuberculosis and Mycobacterium bovis and reveal distinct macrophage responses to infection with the human and bovine tubercle bacilli. Microbial Genomics, 2018, 4, .	1.0	57
29	Differential gene expression in the endometrium reveals cytoskeletal and immunological genes in lactating dairy cows genetically divergent for fertility traits. Reproduction, Fertility and Development, 2017, 29, 274.	0.1	55
30	Taming the Past: Ancient DNA and the Study of Animal Domestication. Annual Review of Animal Biosciences, 2017, 5, 329-351.	3.6	120
31	Genetic origin, admixture and population history of aurochs (<i>Bos primigenius</i>) and primitive European cattle. Heredity, 2017, 118, 169-176.	1.2	80
32	Equine skeletal muscle adaptations to exercise and training: evidence of differential regulation of autophagosomal and mitochondrial components. BMC Genomics, 2017, 18, 595.	1.2	33
33	Genome-Wide microRNA Binding Site Variation between Extinct Wild Aurochs and Modern Cattle Identifies Candidate microRNA-Regulated Domestication Genes. Frontiers in Genetics, 2017, 8, 3.	1.1	24
34	Circulating microRNAs as Potential Biomarkers of Infectious Disease. Frontiers in Immunology, 2017, 8, 118.	2.2	189
35	How Modern and Ancient Genomic Analyses can Reveal Complex Domestic Histories Using Cattle as a Case Study. , 2017, , 30-44.		0
36	Iodine supplementation of the pregnant dam alters intestinal gene expression and immunoglobulin uptake in the newborn lamb. Animal, 2016, 10, 598-606.	1.3	8

#	ARTICLE	IF	CITATIONS
37	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> , 2016, 17, 126.	1.2	40
38	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> , 2016, 97, 154-162.	0.8	33
39	RNA sequencing provides exquisite insight into the manipulation of the alveolar macrophage by tubercle bacilli. <i>Scientific Reports</i> , 2015, 5, 13629.	1.6	50
40	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> , 2015, 16, 1046.	1.2	13
41	Analysis of the Bovine Monocyte-Derived Macrophage Response to <i>Mycobacterium avium</i> Subspecies Paratuberculosis Infection Using RNA-seq. <i>Frontiers in Immunology</i> , 2015, 6, 23.	2.2	61
42	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> , 2015, 95, 60-67.	0.8	64
43	Genomic imprinting effects on complex traits in domesticated animal species. <i>Frontiers in Genetics</i> , 2015, 6, 156.	1.1	25
44	Genome sequencing of the extinct Eurasian wild aurochs, <i>Bos primigenius</i> , illuminates the phylogeography and evolution of cattle. <i>Genome Biology</i> , 2015, 16, 234.	3.8	178
45	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> , 2015, 10, e0134310.	1.1	57
46	Definition of the Cattle Killer Cell Ig-like Receptor Gene Family: Comparison with Aurochs and Human Counterparts. <i>Journal of Immunology</i> , 2014, 193, 6016-6030.	0.4	29
47	RNA-seq Transcriptional Profiling of Peripheral Blood Leukocytes from Cattle Infected with <i>Mycobacterium bovis</i> . <i>Frontiers in Immunology</i> , 2014, 5, 396.	2.2	65
48	Key Hub and Bottleneck Genes Differentiate the Macrophage Response to Virulent and Attenuated <i>Mycobacterium bovis</i> . <i>Frontiers in Immunology</i> , 2014, 5, 422.	2.2	29
49	Comparative Functional Genomics and the Bovine Macrophage Response to Strains of the <i>Mycobacterium</i> Genus. <i>Frontiers in Immunology</i> , 2014, 5, 536.	2.2	38
50	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> , 2014, 111, E5661-9.	3.3	260
51	Selection Signatures in Worldwide Sheep Populations. <i>PLoS ONE</i> , 2014, 9, e103813.	1.1	197
52	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> , 2014, 94, 441-450.	0.8	38
53	Imprinted loci in domestic livestock species as epigenomic targets for artificial selection of complex traits. <i>Animal Genetics</i> , 2014, 45, 25-39.	0.6	21
54	Interrogation of modern and ancient genomes reveals the complex domestic history of cattle. <i>Animal Frontiers</i> , 2014, 4, 7-22.	0.8	57

#	ARTICLE	IF	CITATIONS
55	Profiling microRNA expression in bovine alveolar macrophages using RNA-seq. <i>Veterinary Immunology and Immunopathology</i> , 2013, 155, 238-244.	0.5	44
56	Whole-transcriptome, high-throughput RNA sequence analysis of the bovine macrophage response to <i>Mycobacterium bovis</i> infection in vitro. <i>BMC Genomics</i> , 2013, 14, 230.	1.2	49
57	Receptor-mediated recognition of mycobacterial pathogens. <i>Cellular Microbiology</i> , 2013, 15, 1484-1495.	1.1	104
58	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> , 2013, 44, 408-412.	0.6	13
59	<i>MSTN</i> genotype (g.66493737C/T) association with speed indices in Thoroughbred racehorses. <i>Journal of Applied Physiology</i> , 2012, 112, 86-90.	1.2	32
60	Impact of delayed processing of bovine peripheral blood on differential gene expression. <i>Veterinary Immunology and Immunopathology</i> , 2012, 145, 199-205.	0.5	6
61	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> , 2012, 43, 25.	1.1	64
62	The genetic origin and history of speed in the Thoroughbred racehorse. <i>Nature Communications</i> , 2012, 3, 643.	5.8	77
63	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> , 2012, 7, e32034.	1.1	45
64	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> , 2012, 44, 878-888.	1.0	30
65	Single nucleotide polymorphisms in the imprinted bovine <i>insulin-like growth factor 2 receptor</i> gene (<i>IGF2R</i>) are associated with body size traits in Irish Holstein-Friesian cattle. <i>Animal Genetics</i> , 2012, 43, 81-87.	0.6	19
66	Functional characterisation of bovine interleukin 8 promoter haplotypes in vitro. <i>Molecular Immunology</i> , 2012, 50, 108-116.	1.0	15
67	PGC encoded by the <i>PPARGC1A</i> gene regulates oxidative energy metabolism in equine skeletal muscle during exercise. <i>Animal Genetics</i> , 2012, 43, 153-162.	0.6	36
68	<i>PHLDA2</i> is an imprinted gene in cattle. <i>Animal Genetics</i> , 2012, 43, 587-590.	0.6	10
69	<i>MSTN</i> genotypes in Thoroughbred horses influence skeletal muscle gene expression and racetrack performance. <i>Animal Genetics</i> , 2012, 43, 810-812.	0.6	42
70	Polymorphism discovery and allele frequency estimation using high-throughput DNA sequencing of target-enriched pooled DNA samples. <i>BMC Genomics</i> , 2012, 13, 16.	1.2	18
71	Horses for Courses: a DNA-based Test for Race Distance Aptitude in Thoroughbred Racehorses. <i>Recent Patents on DNA & Gene Sequences</i> , 2012, 6, 203-208.	0.7	14
72	DNA sequence polymorphisms within the bovine guanine nucleotide-binding protein Gs subunit alpha (<i>Gs</i>)-encoding (<i>GNAS</i>) genomic imprinting domain are associated with performance traits. <i>BMC Genetics</i> , 2011, 12, 4.	2.7	32

#	ARTICLE	IF	CITATIONS
73	Transcriptional profiling of immune genes in bovine monocyte-derived macrophages exposed to bacterial antigens. <i>Veterinary Immunology and Immunopathology</i> , 2011, 140, 130-139.	0.5	309
74	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" (<i>J. Dairy Sci.</i> 93:5959-5969). <i>Journal of Dairy Science</i> , 2011, 94, 1069.	1.4	0
75	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> , 2011, 42, 39-49.	0.6	49
76	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> , 2011, 12, 611.	1.2	40
77	Single nucleotide polymorphisms at the imprinted bovine insulin-like growth factor 2 (<i>IGF2</i>) locus are associated with dairy performance in Irish Holstein-Friesian cattle. <i>Journal of Dairy Research</i> , 2011, 78, 1-8.	0.7	41
78	Single Nucleotide Polymorphisms within the Bovine DLK1-DIO3 Imprinted Domain Are Associated with Economically Important Production Traits in Cattle. <i>Journal of Heredity</i> , 2011, 102, 94-101.	1.0	29
79	A catalogue of validated single nucleotide polymorphisms in bovine orthologs of mammalian imprinted genes and associations with beef production traits. <i>Animal</i> , 2010, 4, 1958-1970.	1.3	15
80	Genome-wide SNP association-based localization of a dwarfism gene in Friesian dwarf horses. <i>Animal Genetics</i> , 2010, 41, 2-7.	0.6	31
81	Targets of selection in the Thoroughbred genome contain exercise-relevant gene SNPs associated with elite racecourse performance. <i>Animal Genetics</i> , 2010, 41, 56-63.	0.6	65
82	Characterization of the equine skeletal muscle transcriptome identifies novel functional responses to exercise training. <i>BMC Genomics</i> , 2010, 11, 398.	1.2	81
83	A genome-wide SNP-association study confirms a sequence variant (g.66493737C>T) in the equine myostatin (<i>MSTN</i>) gene as the most powerful predictor of optimum racing distance for Thoroughbred racehorses. <i>BMC Genomics</i> , 2010, 11, 552.	1.2	125
84	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> , 2010, 11, 93.	2.7	49
85	A Sequence Polymorphism in <i>MSTN</i> Predicts Sprinting Ability and Racing Stamina in Thoroughbred Horses. <i>PLoS ONE</i> , 2010, 5, e8645.	1.1	154
86	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 platform1. <i>Journal of Animal Science</i> , 2010, 88, 3183-3186.	0.2	11
87	High Concordance of Bovine Single Nucleotide Polymorphism Genotypes Generated Using Two Independent Genotyping Strategies. <i>Animal Biotechnology</i> , 2010, 21, 257-262.	0.7	1
88	Alterations in oxidative gene expression in equine skeletal muscle following exercise and training. <i>Physiological Genomics</i> , 2010, 40, 83-93.	1.0	64
89	Association of sequence variants in <i>CKM</i> (creatine kinase, muscle) and <i>COX4I2</i> (cytochrome c oxidase subunit 4) in Thoroughbred horses. <i>Veterinary Journal</i> , 2010, 42, 569-575.	0.9	57
90	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> , 2010, 93, 5959-5969.	1.4	31

#	ARTICLE	IF	CITATIONS
91	A Complete Mitochondrial Genome Sequence from a Mesolithic Wild Aurochs (<i>Bos primigenius</i>). PLoS ONE, 2010, 5, e9255.	1.1	73
92	Transcriptional adaptations following exercise in Thoroughbred horse skeletal muscle highlights molecular mechanisms that lead to muscle hypertrophy. BMC Genomics, 2009, 10, 638.	1.2	57
93	Gene Expression Profiling of the Host Response to <i>Mycobacterium bovis</i> Infection in Cattle. Transboundary and Emerging Diseases, 2009, 56, 204-214.	1.3	26
94	Divergent antimicrobial peptide (AMP) and acute phase protein (APP) responses to <i>Trypanosoma congolense</i> infection in trypanotolerant and trypanosusceptible cattle. Molecular Immunology, 2009, 47, 196-204.	1.0	11
95	Transcriptional profiling of cattle infected with <i>Trypanosoma congolense</i> highlights gene expression signatures underlying trypanotolerance and trypanosusceptibility. BMC Genomics, 2009, 10, 207.	1.2	41
96	A Genome Scan for Positive Selection in Thoroughbred Horses. PLoS ONE, 2009, 4, e5767.	1.1	123
97	Transmission ratio distortion at the growth hormone gene (<i>GH1</i>) in bovine preimplantation embryos: An in vitro culture-induced phenomenon?. Molecular Reproduction and Development, 2008, 75, 715-722.	1.0	7
98	Antigen stimulation of peripheral blood mononuclear cells from <i>Mycobacterium bovis</i> infected cattle yields evidence for a novel gene expression program. BMC Genomics, 2008, 9, 447.	1.2	20
99	Inbreeding effects on postweaning production traits, conformation, and calving performance in Irish beef cattle. Journal of Animal Science, 2008, 86, 3338-3347.	0.2	11
100	Tumour necrosis factor- α (TNF- α) increases nuclear factor κ B (NF κ B) activity in and interleukin-8 (IL-8) release from bovine mammary epithelial cells. Veterinary Immunology and Immunopathology, 2007, 116, 59-68.	0.5	77
101	Long-term stability of RNA in post-mortem bovine skeletal muscle, liver and subcutaneous adipose tissues. BMC Molecular Biology, 2007, 8, 108.	3.0	45
102	Taurine and zebu admixture in Near Eastern cattle: a comparison of mitochondrial, autosomal and Y-chromosomal data. Animal Genetics, 2007, 38, 520-524.	0.6	63
103	Innate gene repression associated with <i>Mycobacterium bovis</i> infection in cattle: toward a gene signature of disease. BMC Genomics, 2007, 8, 400.	1.2	65
104	Linkage mapping of the locus for inherited ovine arthrogryposis (IOA) to sheep Chromosome 5. Mammalian Genome, 2007, 18, 43-52.	1.0	10
105	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). Veterinary Immunology and Immunopathology, 2006, 113, 73-89.	0.5	30
106	Cytokine mRNA profiling of peripheral blood mononuclear cells from trypanotolerant and trypanosusceptible cattle infected with <i>Trypanosoma congolense</i> . Physiological Genomics, 2006, 28, 53-61.	1.0	49
107	Evidence for biogeographic patterning of mitochondrial DNA sequences in Eastern horse populations. Animal Genetics, 2006, 37, 494-497.	0.6	60
108	Mitochondrial DNA sequence diversity in extant Irish horse populations and in ancient horses. Animal Genetics, 2006, 37, 498-502.	0.6	49

#	ARTICLE	IF	CITATIONS
109	Convenient detection of single nucleotide polymorphism haplotypes in the bovine growth hormone gene using amplification-created restriction sites. <i>Animal Genetics</i> , 2005, 36, 175-177.	0.6	0
110	Understanding bovine trypanosomiasis and trypanotolerance: the promise of functional genomics. <i>Veterinary Immunology and Immunopathology</i> , 2005, 105, 247-258.	0.5	74
111	Admixture and diversity in West African cattle populations. <i>Molecular Ecology</i> , 2004, 13, 3477-3487.	2.0	89
112	Ancient DNA analysis of 101 cattle remains: limits and prospects. <i>Journal of Archaeological Science</i> , 2004, 31, 695-710.	1.2	76
113	Feasibility and utility of microsatellite markers in archaeological cattle remains from a Viking Age settlement in Dublin. <i>Animal Genetics</i> , 2003, 34, 410-416.	0.6	18
114	Sequence variation in the mitochondrial DNA control region of wild African cheetahs (<i>Acinonyx</i>). <i>Journal of Molecular Evolution</i> , 2001, 53, 101-107.	1.2	67
115	Genetic evidence for Near-Eastern origins of European cattle. <i>Nature</i> , 2001, 410, 1088-1091.	13.7	547
116	Livestock genetic origins: Goats buck the trend. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 5382-5384.	3.3	194
117	Yâ€specific microsatellite polymorphisms in a range of bovid species. <i>Animal Genetics</i> , 2000, 31, 127-130.	0.6	50
118	Phylogenetic analysis of the tribe Bovini using microsatellites. <i>Animal Genetics</i> , 2000, 31, 178-185.	0.6	111
119	A microsatellite survey of cattle from a centre of origin: the Near East. <i>Molecular Ecology</i> , 1999, 8, 2015-2022.	2.0	160
120	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> , 1999, 354, 99-109.	1.8	45
121	Genetics and domestic cattle origins. <i>Evolutionary Anthropology</i> , 1998, 6, 79-86.	1.7	127
122	Genetic structure of seven European cattle breeds assessed using 20 microsatellite markers. <i>Animal Genetics</i> , 1998, 29, 333-340.	0.6	177
123	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> , 1997, 146, 1071-1086.	1.2	430
124	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> , 1996, 93, 5131-5135.	3.3	476