

Michel Georges

List of Publications by Year in descending order

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138
papers

29,606
citations

22146

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10445

139
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154
all docs

154
docs citations

154
times ranked

33190
citing authors

#	ARTICLE	IF	CITATIONS
1	Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. Nature, 2012, 491, 119-124.	27.8	4,038
2	Resistance to HIV-1 infection in Caucasian individuals bearing mutant alleles of the CCR-5 chemokine receptor gene. Nature, 1996, 382, 722-725.	27.8	2,782
3	Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. Nature Genetics, 2008, 40, 955-962.	21.4	2,422
4	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. Nature Genetics, 2010, 42, 1118-1125.	21.4	2,284
5	A deletion in the bovine myostatin gene causes the double-musled phenotype in cattle. Nature Genetics, 1997, 17, 71-74.	21.4	1,323
6	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nature Genetics, 2011, 43, 246-252.	21.4	1,201
7	A mutation creating a potential illegitimate microRNA target site in the myostatin gene affects muscularity in sheep. Nature Genetics, 2006, 38, 813-818.	21.4	1,125
8	Positional Candidate Cloning of a QTL in Dairy Cattle: Identification of a Missense Mutation in the Bovine <i>DGAT1</i> Gene with Major Effect on Milk Yield and Composition. Genome Research, 2002, 12, 222-231.	5.5	803
9	A regulatory mutation in IGF2 causes a major QTL effect on muscle growth in the pig. Nature, 2003, 425, 832-836.	27.8	791
10	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	21.4	590
11	Domestic-animal genomics: deciphering the genetics of complex traits. Nature Reviews Genetics, 2004, 5, 202-212.	16.3	516
12	Novel Crohn Disease Locus Identified by Genome-Wide Association Maps to a Gene Desert on 5p13.1 and Modulates Expression of PTGER4. PLoS Genetics, 2007, 3, e58.	3.5	506
13	Fine-mapping inflammatory bowel disease loci to single-variant resolution. Nature, 2017, 547, 173-178.	27.8	473
14	Common variants at five new loci associated with early-onset inflammatory bowel disease. Nature Genetics, 2009, 41, 1335-1340.	21.4	459
15	Molecular definition of an allelic series of mutations disrupting the myostatin function and causing double-muscling in cattle. Mammalian Genome, 1998, 9, 210-213.	2.2	422
16	Molecular Dissection of a Quantitative Trait Locus: A Phenylalanine-to-Tyrosine Substitution in the Transmembrane Domain of the Bovine Growth Hormone Receptor Is Associated With a Major Effect on Milk Yield and Composition. Genetics, 2003, 163, 253-266.	2.9	390
17	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
18	An imprinted QTL with major effect on muscle mass and fat deposition maps to the IGF2 locus in pigs. Nature Genetics, 1999, 21, 155-156.	21.4	376

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19	Genetic and functional confirmation of the causality of the DGAT1 K232A quantitative trait nucleotide in affecting milk yield and composition. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 2398-2403.	7.1	370
20	Extensive Genome-wide Linkage Disequilibrium in Cattle. Genome Research, 2000, 10, 220-227.	5.5	304
21	CCDC39 is required for assembly of inner dynein arms and the dynein regulatory complex and for normal ciliary motility in humans and dogs. Nature Genetics, 2011, 43, 72-78.	21.4	302
22	RNAi-Mediated Allelic trans-Interaction at the Imprinted Rtl1/Peg11 Locus. Current Biology, 2005, 15, 743-749.	3.9	301
23	Variants modulating the expression of a chromosome domain encompassing PLAG1 influence bovine stature. Nature Genetics, 2011, 43, 405-413.	21.4	300
24	Gigantism and Acromegaly Due to Xq26 Microduplications and <i>GPR101</i> Mutation. New England Journal of Medicine, 2014, 371, 2363-2374.	27.0	292
25	Highly effective SNP-based association mapping and management of recessive defects in livestock. Nature Genetics, 2008, 40, 449-454.	21.4	263
26	Harnessing genomic information for livestock improvement. Nature Reviews Genetics, 2019, 20, 135-156.	16.3	262
27	A Hidden Markov Model Combining Linkage and Linkage Disequilibrium Information for Haplotype Reconstruction and Quantitative Trait Locus Fine Mapping. Genetics, 2010, 184, 789-798.	2.9	178
28	Codon-specific translation reprogramming promotes resistance to targeted therapy. Nature, 2018, 558, 605-609.	27.8	177
29	Resequencing of positional candidates identifies low frequency IL23R coding variants protecting against inflammatory bowel disease. Nature Genetics, 2011, 43, 43-47.	21.4	175
30	The callipyge mutation enhances the expression of coregulated imprinted genes in cis without affecting their imprinting status. Nature Genetics, 2001, 27, 367-369.	21.4	160
31	IBD risk loci are enriched in multigenic regulatory modules encompassing putative causative genes. Nature Communications, 2018, 9, 2427.	12.8	159
32	The Role of the Bovine Growth Hormone Receptor and Prolactin Receptor Genes in Milk, Fat and Protein Production in Finnish Ayrshire Dairy Cattle. Genetics, 2006, 173, 2151-2164.	2.9	154
33	Modulating skeletal muscle mass by postnatal, muscle-specific inactivation of the myostatin gene. Genesis, 2003, 35, 227-238.	1.6	152
34	Genetical metabolomics of flavonoid biosynthesis in <i>Populus</i> : a case study. Plant Journal, 2006, 47, 224-237.	5.7	140
35	Serial translocation by means of circular intermediates underlies colour sidedness in cattle. Nature, 2012, 482, 81-84.	27.8	137
36	The callipyge locus: evidence for the trans interaction of reciprocally imprinted genes. Trends in Genetics, 2003, 19, 248-252.	6.7	136

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37	Polymorphic miRNA-mediated gene regulation: contribution to phenotypic variation and disease. <i>Current Opinion in Genetics and Development</i> , 2007, 17, 166-176.	3.3	131
38	Genetic Variants in REC8, RNF212, and PRDM9 Influence Male Recombination in Cattle. <i>PLoS Genetics</i> , 2012, 8, e1002854.	3.5	128
39	Patrocles: a database of polymorphic miRNA-mediated gene regulation in vertebrates. <i>Nucleic Acids Research</i> , 2010, 38, D640-D651.	14.5	126
40	A 660-Kb Deletion with Antagonistic Effects on Fertility and Milk Production Segregates at High Frequency in Nordic Red Cattle: Additional Evidence for the Common Occurrence of Balancing Selection in Livestock. <i>PLoS Genetics</i> , 2014, 10, e1004049.	3.5	126
41	Microsatellite mapping of a gene affecting horn development in <i>Bos taurus</i> . <i>Nature Genetics</i> , 1993, 4, 206-210.	21.4	122
42	Comparative Sequence Analysis of the Imprinted <i>Dlk1</i> Locus in Three Mammalian Species Reveals Highly Conserved Genomic Elements and Refines Comparison with the <i>Igf2</i> Region. <i>Genome Research</i> , 2001, 11, 2085-2094.	5.5	116
43	Ectopic Expression of DLK1 Protein in Skeletal Muscle of Padumnal Heterozygotes Causes the Callipyge Phenotype. <i>Current Biology</i> , 2004, 14, 1858-1862.	3.9	114
44	A QTL with major effect on milk yield and composition maps to bovine Chromosome 14. <i>Mammalian Genome</i> , 1998, 9, 540-544.	2.2	110
45	Mapping, Fine Mapping, and Molecular Dissection of Quantitative Trait Loci in Domestic Animals. <i>Annual Review of Genomics and Human Genetics</i> , 2007, 8, 131-162.	6.2	108
46	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. <i>Nature Genetics</i> , 2018, 50, 1072-1080.	21.4	106
47	Haplotype diversity of the myostatin gene among beef cattlebreeds. <i>Genetics Selection Evolution</i> , 2003, 35, 103-18.	3.0	104
48	Deep sequencing reveals abundant noncanonical retroviral microRNAs in B-cell leukemia/lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2306-2311.	7.1	101
49	Simultaneous Mining of Linkage and Linkage Disequilibrium to Fine Map Quantitative Trait Loci in Outbred Half-Sib Pedigrees: Revisiting the Location of a Quantitative Trait Locus With Major Effect on Milk Production on Bovine Chromosome 14. <i>Genetics</i> , 2002, 161, 275-287.	2.9	101
50	LUPA: A European initiative taking advantage of the canine genome architecture for unravelling complex disorders in both human and dogs. <i>Veterinary Journal</i> , 2011, 189, 155-159.	1.7	95
51	Mosaicism of Solid Gold Supports the Causality of a Noncoding A-to-G Transition in the Determinism of the Callipyge Phenotype. <i>Genetics</i> , 2003, 163, 453-456.	2.9	94
52	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. <i>Science Advances</i> , 2020, 6, eaax0301.	10.3	90
53	Effects of Character Weighting and Species Sampling on Phylogeny Reconstruction: A Case Study Based on DNA Sequence Data in Cetaceans. <i>Genetics</i> , 1996, 144, 1817-1833.	2.9	85
54	On the use of DNA fingerprints for linkage studies in cattle. <i>Genomics</i> , 1990, 6, 461-474.	2.9	83

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55	A Deletion in the Bovine FANCI Gene Compromises Fertility by Causing Fetal Death and Brachyspina. PLoS ONE, 2012, 7, e43085.	2.5	82
56	Comparative sequence analysis of the INS-IGF2-H19 gene cluster in pigs. Mammalian Genome, 2002, 13, 388-398.	2.2	80
57	Coding and noncoding variants in <i>HFM1</i> , <i>MLH3</i> , <i>MSH4</i> , <i>MSH5</i> , <i>RNF212</i> , and <i>RNF212B</i> affect recombination rate in cattle. Genome Research, 2016, 26, 1323-1332.	5.5	77
58	Cis-perturbation of cancer drivers by the HTLV-1/BLV proviruses is an early determinant of leukemogenesis. Nature Communications, 2017, 8, 15264.	12.8	77
59	Balancing Selection of a Frame-Shift Mutation in the MRC2 Gene Accounts for the Outbreak of the Crooked Tail Syndrome in Belgian Blue Cattle. PLoS Genetics, 2009, 5, e1000666.	3.5	74
60	NGS-based reverse genetic screen for common embryonic lethal mutations compromising fertility in livestock. Genome Research, 2016, 26, 1333-1341.	5.5	71
61	ABO genotype alters the gut microbiota by regulating GalNAc levels in pigs. Nature, 2022, 606, 358-367.	27.8	67
62	Characterization of a set of variable number of tandem repeat markers conserved in Bovidae. Genomics, 1991, 11, 24-32.	2.9	64
63	Characterization of the bovine pseudoautosomal boundary: Documenting the evolutionary history of mammalian sex chromosomes. Genome Research, 2008, 18, 1884-1895.	5.5	60
64	Characterization of novel Bovine Leukemia Virus (BLV) antisense transcripts by deep sequencing reveals constitutive expression in tumors and transcriptional interaction with viral microRNAs. Retrovirology, 2016, 13, 33.	2.0	59
65	Results of a whole genome scan targeting QTL for growth and carcass traits in a PiÅ©train Å— Large White intercross. Genetics Selection Evolution, 2002, 34, 371-87.	3.0	57
66	Haplotype Sharing Refines the Location of an Imprinted Quantitative Trait Locus With Major Effect on Muscle Mass to a 250-kb Chromosome Segment Containing the Porcine <i>IGF2</i> Gene. Genetics, 2003, 165, 277-285.	2.9	53
67	Evidence for Significant Overlap between Common Risk Variants for Crohn's Disease and Ankylosing Spondylitis. PLoS ONE, 2010, 5, e13795.	2.5	51
68	A polymorphic satellite sequence maps to the pericentric region of the bovine Y chromosome. Genomics, 1990, 6, 482-490.	2.9	50
69	A nonsense mutation in cGMP-dependent type II protein kinase (<i>PRKG2</i>) causes dwarfism in American Angus cattle. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19250-19255.	7.1	48
70	Selection in action: dissecting the molecular underpinnings of the increasing muscle mass of Belgian Blue Cattle. BMC Genomics, 2014, 15, 796.	2.8	47
71	The callipyge mutation enhances bidirectional long-range DLK1-GTL2 intergenic transcription in cis. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8119-8124.	7.1	46
72	Fine-mapping and construction of a bovine contig spanning the ovine callipyge locus. Mammalian Genome, 2001, 12, 141-149.	2.2	45

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73	Results of a haplotype-based GWAS for recurrent laryngeal neuropathy in the horse. <i>Mammalian Genome</i> , 2011, 22, 613-620.	2.2	45
74	A Rank-Based Nonparametric Method for Mapping Quantitative Trait Loci in Outbred Half-Sib Pedigrees: Application to Milk Production in a Granddaughter Design. <i>Genetics</i> , 1998, 149, 1547-1555.	2.9	43
75	Improved risk prediction for Crohn's disease with a multi-locus approach. <i>Human Molecular Genetics</i> , 2011, 20, 2435-2442.	2.9	42
76	The callipyge mutation and other genes that affect muscle hypertrophy in sheep. <i>Genetics Selection Evolution</i> , 2005, 37, S65-81.	3.0	41
77	Differential expression of sarcoplasmic proteins in four heterogeneous ovine skeletal muscles. <i>Proteomics</i> , 2007, 7, 271-280.	2.2	41
78	DNA fingerprinting in man using a mouse probe related to part of the <i>Drosophila</i> α -Per TM gene. <i>Nucleic Acids Research</i> , 1987, 15, 7193-7193.	14.5	40
79	Somatic cell mapping, polymorphism, and linkage analysis of bovine prolactin-related proteins and placental lactogen. <i>Genomics</i> , 1992, 14, 137-143.	2.9	40
80	A Splice Site Variant in the Bovine RNF11 Gene Compromises Growth and Regulation of the Inflammatory Response. <i>PLoS Genetics</i> , 2012, 8, e1002581.	3.5	40
81	LINKPHASE3: an improved pedigree-based phasing algorithm robust to genotyping and map errors. <i>Bioinformatics</i> , 2015, 31, 1677-1679.	4.1	40
82	Defining the genetic control of human blood plasma N-glycome using genome-wide association study. <i>Human Molecular Genetics</i> , 2019, 28, 2062-2077.	2.9	40
83	A genetic map of DNA loci on bovine chromosome 1. <i>Genomics</i> , 1993, 18, 602-608.	2.9	39
84	Mapping QTL influencing gastrointestinal nematode burden in Dutch Holstein-Friesian dairy cattle. <i>BMC Genomics</i> , 2009, 10, 96.	2.8	39
85	Transgenic engineering of male-specific muscular hypertrophy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 6413-6418.	7.1	38
86	Assessing the effect of the CLPG mutation on the microRNA catalog of skeletal muscle using high-throughput sequencing. <i>Genome Research</i> , 2010, 20, 1651-1662.	5.5	38
87	Generation of bovine multisite haplotypes using random cosmid clones. <i>Genomics</i> , 1991, 10, 889-904.	2.9	35
88	Non-additive association analysis using proxy phenotypes identifies novel cattle syndromes. <i>Nature Genetics</i> , 2021, 53, 949-954.	21.4	34
89	Genetic identification of distinct loci controlling mammary tumor multiplicity, latency, and aggressiveness in the rat. <i>Mammalian Genome</i> , 2006, 17, 310-321.	2.2	28
90	Analysis of Genes Associated With Monogenic Primary Immunodeficiency Identifies Rare Variants in XIAP in Patients With Crohn's Disease. <i>Gastroenterology</i> , 2018, 154, 2165-2177.	1.3	26

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91	Coinfection with Two Closely Related Alphaherpesviruses Results in a Highly Diversified Recombination Mosaic Displaying Negative Genetic Interference. <i>Journal of Virology</i> , 2009, 83, 3127-3137.	3.4	25
92	A 12 kb multi-allelic copy number variation encompassing a GC gene enhancer is associated with mastitis resistance in dairy cattle. <i>PLoS Genetics</i> , 2021, 17, e1009331.	3.5	25
93	Linkage Disequilibrium on the Bovine X Chromosome: Characterization and Use in Quantitative Trait Locus Mapping. <i>Genetics</i> , 2006, 173, 1777-1786.	2.9	24
94	Targeted deep sequencing reveals clonal and subclonal mutational signatures in Adult T-cell leukemia/lymphoma and defines an unfavorable indolent subtype. <i>Leukemia</i> , 2021, 35, 764-776.	7.2	24
95	PCIP-seq: simultaneous sequencing of integrated viral genomes and their insertion sites with long reads. <i>Genome Biology</i> , 2021, 22, 97.	8.8	24
96	Physical mapping of inhibin β -A in domestic cattle. <i>Mammalian Genome</i> , 1993, 4, 328-332.	2.2	23
97	Genetics of ulcerative colitis: the come-back of interleukin 10. <i>Gut</i> , 2009, 58, 1173-1176.	12.1	21
98	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. <i>American Journal of Human Genetics</i> , 2016, 98, 857-868.	6.2	21
99	Reverse genetic screen for loss-of-function mutations uncovers a frameshifting deletion in the <i>melanophilin</i> gene accountable for a distinctive coat color in Belgian Blue cattle. <i>Animal Genetics</i> , 2016, 47, 110-113.	1.7	21
100	CCDC88B is required for pathogenesis of inflammatory bowel disease. <i>Nature Communications</i> , 2017, 8, 932.	12.8	21
101	Mapping and analysis of a spatiotemporal H3K27ac and gene expression spectrum in pigs. <i>Science China Life Sciences</i> , 2022, 65, 1517-1534.	4.9	21
102	Towards marker assisted selection in livestock. <i>Reproduction, Nutrition, Development</i> , 1999, 39, 555-561.	1.9	20
103	Breakpoint mapping positions the callipyge gene within a 450-kilobase chromosome segment containing the DLK1 and GTL2 genes. <i>Mammalian Genome</i> , 2001, 12, 183-185.	2.2	20
104	BEGAIN: A novel imprinted gene that generates paternally expressed transcripts in a tissue- and promoter-specific manner in sheep. <i>Mammalian Genome</i> , 2005, 16, 801-814.	2.2	19
105	On the Detection of Imprinted Quantitative Trait Loci in Line Crosses: Effect of Linkage Disequilibrium. <i>Genetics</i> , 2008, 180, 1167-1175.	2.9	18
106	Towards sequence-based genomic selection of cattle. <i>Nature Genetics</i> , 2014, 46, 807-809.	21.4	17
107	The long and winding road from correlation to causation. <i>Nature Genetics</i> , 2011, 43, 180-181.	21.4	16
108	Wobble tRNA modification and hydrophilic amino acid patterns dictate protein fate. <i>Nature Communications</i> , 2021, 12, 2170.	12.8	16

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109	QTL Mapping to QTL Cloning: Mice to the Rescue. <i>Genome Research</i> , 1997, 7, 663-665.	5.5	14
110	Ectopic Expression of Retrotransposon-Derived PEG11/RTL1 Contributes to the Callipyge Muscular Hypertrophy. <i>PLoS ONE</i> , 2015, 10, e0140594.	2.5	14
111	Genome-wide next-generation DNA and RNA sequencing reveals a mutation that perturbs splicing of the phosphatidylinositol glycan anchor biosynthesis class H gene (PIGH) and causes arthrogyriposis in Belgian Blue cattle. <i>BMC Genomics</i> , 2015, 16, 316.	2.8	13
112	CRELD1 modulates homeostasis of the immune system in mice and humans. <i>Nature Immunology</i> , 2020, 21, 1517-1527.	14.5	13
113	Evaluation of a New Fine-mapping Method Exploiting Linkage Disequilibrium: a Case Study Analysing a QTL with Major Effect on Milk Composition on Bovine Chromosome 14. <i>Asian-Australasian Journal of Animal Sciences</i> , 2002, 15, 1250-1256.	2.4	13
114	Genome-Wide Copy Number Variation Scan Identifies Complement Component C4 as Novel Susceptibility Gene for Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 505-515.	1.9	12
115	When Less Means More: Impact of Myostatin in Animal Breeding. <i>Immunology, Endocrine and Metabolic Agents in Medicinal Chemistry</i> , 2010, 10, 240-248.	0.5	11
116	A stop-gain in the <i>laminin, alpha 3</i> gene causes recessive junctional epidermolysis bullosa in Belgian Blue cattle. <i>Animal Genetics</i> , 2015, 46, 566-570.	1.7	11
117	Demonstrating polymorphic miRNA-mediated gene regulation in vivo: Application to the <i>g+6223G>A</i> mutation of Texel sheep. <i>Rna</i> , 2010, 16, 1854-1863.	3.5	10
118	Genetic architecture of individual variation in recombination rate on the X chromosome in cattle. <i>Heredity</i> , 2020, 125, 304-316.	2.6	10
119	Denmark's approach to marker-assisted selection. <i>Animal Biotechnology</i> , 1992, 3, 95-109.	1.5	9
120	A Triad of Highly Divergent Polymeric Immunoglobulin Receptor (PIGR) Haplotypes with Major Effect on IgA Concentration in Bovine Milk. <i>PLoS ONE</i> , 2013, 8, e57219.	2.5	9
121	A genetic map of index DNA loci on bovine chromosome 21. <i>Genomics</i> , 1993, 18, 598-601.	2.9	8
122	The great-grand-daughter design: a simple strategy to increase the power of a grand-daughter design for QTL mapping. <i>Genetical Research</i> , 1999, 74, 189-199.	0.9	8
123	Genome wide association study of 40 clinical measurements in eight dog breeds. <i>Scientific Reports</i> , 2020, 10, 6520.	3.3	8
124	Quantitative estimation of chimerism in mice using microsatellite markers. <i>Molecular Reproduction and Development</i> , 1993, 34, 127-132.	2.0	7
125	Alzheimer's disease genetic risk and sleep phenotypes in healthy young men: association with more slow waves and daytime sleepiness. <i>Sleep</i> , 2021, 44, .	1.1	6
126	Methylation analysis of the imprinted DLK1-GTL2 domain supports the random parental origin of the IGH-involving del(14q) in B-cell malignancies. <i>Epigenetics</i> , 2009, 4, 469-475.	2.7	5

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127	An Improved Sequencing-Based Bioinformatics Pipeline to Track the Distribution and Clonal Architecture of Proviral Integration Sites. <i>Frontiers in Microbiology</i> , 2020, 11, 587306.	3.5	5
128	On the use of the transmission disequilibrium test to detect pseudo-autosomal variants affecting traits with sex-limited expression. <i>Animal Genetics</i> , 2015, 46, 395-402.	1.7	4
129	High-resolution, human–bovine comparative mapping based on a closed YAC contig spanning the bovine mh locus. <i>Mammalian Genome</i> , 1999, 10, 289-293.	2.2	3
130	Experimental evaluation does not reveal a direct effect of microRNA from the callipyge locus on DLK1 expression. <i>BMC Genomics</i> , 2014, 15, 944.	2.8	3
131	Identification of tissue-specific and common methylation quantitative trait loci in healthy individuals using MAGAR. <i>Epigenetics and Chromatin</i> , 2021, 14, 44.	3.9	3
132	From phenotype to genotype : towards positional cloning of QTL in livestock?. <i>The Journal of Animal Genetics</i> , 1999, 27, 33-43.	0.1	3
133	Benchmarking phasing software with a whole-genome sequenced cattle pedigree. <i>BMC Genomics</i> , 2022, 23, 130.	2.8	3
134	A Genome Scan Conducted in a Multigenerational Pedigree with Convergent Strabismus Supports a Complex Genetic Determinism. <i>PLoS ONE</i> , 2013, 8, e83574.	2.5	2
135	New approach to determine the healthy immune variations by combining clustering methods. <i>Scientific Reports</i> , 2021, 11, 8917.	3.3	2
136	Cis- and Trans-Effects Underlying Polar Overdominance at the Callipyge Locus. , 2013, , 89-106.		1
137	SNP-based quantitative deconvolution of biological mixtures: application to the detection of cows with subclinical mastitis by whole-genome sequencing of tank milk. <i>Genome Research</i> , 2020, 30, 1201-1207.	5.5	1
138	Association Between Human Gut Microbiome and N-Glycan Composition of Total Plasma Proteome. <i>Frontiers in Microbiology</i> , 2022, 13, 811922.	3.5	1