

# Michel Georges

## List of Publications by Year in descending order

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138  
papers

29,606  
citations

25423

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11946

139  
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154  
docs citations

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times ranked

36543  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping and analysis of a spatiotemporal H3K27ac and gene expression spectrum in pigs. <i>Science China Life Sciences</i> , 2022, 65, 1517-1534.	2.3	21
2	Benchmarking phasing software with a whole-genome sequenced cattle pedigree. <i>BMC Genomics</i> , 2022, 23, 130.	1.2	3
3	ABO genotype alters the gut microbiota by regulating GalNAc levels in pigs. <i>Nature</i> , 2022, 606, 358-367.	13.7	67
4	Association Between Human Gut Microbiome and N-Glycan Composition of Total Plasma Proteome. <i>Frontiers in Microbiology</i> , 2022, 13, 811922.	1.5	1
5	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.	3.3	24
6	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, .	0.6	6
7	PCIP-seq: simultaneous sequencing of integrated viral genomes and their insertion sites with long reads. <i>Genome Biology</i> , 2021, 22, 97.	3.8	24
8	Wobble tRNA modification and hydrophilic amino acid patterns dictate protein fate. <i>Nature Communications</i> , 2021, 12, 2170.	5.8	16
9	New approach to determine the healthy immune variations by combining clustering methods. <i>Scientific Reports</i> , 2021, 11, 8917.	1.6	2
10	Non-additive association analysis using proxy phenotypes identifies novel cattle syndromes. <i>Nature Genetics</i> , 2021, 53, 949-954.	9.4	34
11	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.	1.5	25
12	Identification of tissue-specific and common methylation quantitative trait loci in healthy individuals using MAGAR. <i>Epigenetics and Chromatin</i> , 2021, 14, 44.	1.8	3
13	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021, 53, 1300-1310.	9.4	590
14	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	13.5	388
15	Genetic architecture of individual variation in recombination rate on the X chromosome in cattle. <i>Heredity</i> , 2020, 125, 304-316.	1.2	10
16	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.	1.5	5
17	CRELD1 modulates homeostasis of the immune system in mice and humans. <i>Nature Immunology</i> , 2020, 21, 1517-1527.	7.0	13
18	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.	2.4	1

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19	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. <i>Science Advances</i> , 2020, 6, eaax0301.	4.7	90
20	Genome wide association study of 40 clinical measurements in eight dog breeds. <i>Scientific Reports</i> , 2020, 10, 6520.	1.6	8
21	Defining the genetic control of human blood plasma N-glycome using genome-wide association study. <i>Human Molecular Genetics</i> , 2019, 28, 2062-2077.	1.4	40
22	Harnessing genomic information for livestock improvement. <i>Nature Reviews Genetics</i> , 2019, 20, 135-156.	7.7	262
23	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.	0.6	26
24	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.	9.4	106
25	IBD risk loci are enriched in multigenic regulatory modules encompassing putative causative genes. <i>Nature Communications</i> , 2018, 9, 2427.	5.8	159
26	Codon-specific translation reprogramming promotes resistance to targeted therapy. <i>Nature</i> , 2018, 558, 605-609.	13.7	177
27	Cis-perturbation of cancer drivers by the HTLV-1/BLV proviruses is an early determinant of leukemogenesis. <i>Nature Communications</i> , 2017, 8, 15264.	5.8	77
28	CCDC88B is required for pathogenesis of inflammatory bowel disease. <i>Nature Communications</i> , 2017, 8, 932.	5.8	21
29	Fine-mapping inflammatory bowel disease loci to single-variant resolution. <i>Nature</i> , 2017, 547, 173-178.	13.7	473
30	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.	0.9	12
31	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.	2.6	21
32	Characterization of novel Bovine Leukemia Virus (BLV) antisense transcripts by deep sequencing reveals constitutive expression in tumors and transcriptional interaction with viral microRNAs. <i>Retrovirology</i> , 2016, 13, 33.	0.9	59
33	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. <i>Genome Research</i> , 2016, 26, 1323-1332.	2.4	77
34	NGS-based reverse genetic screen for common embryonic lethal mutations compromising fertility in livestock. <i>Genome Research</i> , 2016, 26, 1333-1341.	2.4	71
35	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.	0.6	21
36	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.	0.6	11

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37	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.	0.6	4
38	Ectopic Expression of Retrotransposon-Derived PEG11/RTL1 Contributes to the Callipyge Muscular Hypertrophy. <i>PLoS ONE</i> , 2015, 10, e0140594.	1.1	14
39	LINKPHASE3: an improved pedigree-based phasing algorithm robust to genotyping and map errors. <i>Bioinformatics</i> , 2015, 31, 1677-1679.	1.8	40
40	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 arthrogyposis in Belgian Blue cattle. <i>BMC Genomics</i> , 2015, 16, 316.	1.2	13
41	Selection in action: dissecting the molecular underpinnings of the increasing muscle mass of Belgian Blue Cattle. <i>BMC Genomics</i> , 2014, 15, 796.	1.2	47
42	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.	1.5	126
43	Gigantism and Acromegaly Due to Xq26 Microduplications and <i>GPR101</i> Mutation. <i>New England Journal of Medicine</i> , 2014, 371, 2363-2374.	13.9	292
44	Experimental evaluation does not reveal a direct effect of microRNA from the callipyge locus on DLK1 expression. <i>BMC Genomics</i> , 2014, 15, 944.	1.2	3
45	Towards sequence-based genomic selection of cattle. <i>Nature Genetics</i> , 2014, 46, 807-809.	9.4	17
46	Cis- and Trans-Effects Underlying Polar Overdominance at the Callipyge Locus. , 2013, , 89-106.		1
47	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.	3.3	101
48	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.	1.1	9
49	A Genome Scan Conducted in a Multigenerational Pedigree with Convergent Strabismus Supports a Complex Genetic Determinism. <i>PLoS ONE</i> , 2013, 8, e83574.	1.1	2
50	A Splice Site Variant in the Bovine RNF11 Gene Compromises Growth and Regulation of the Inflammatory Response. <i>PLoS Genetics</i> , 2012, 8, e1002581.	1.5	40
51	Genetic Variants in REC8, RNF212, and PRDM9 Influence Male Recombination in Cattle. <i>PLoS Genetics</i> , 2012, 8, e1002854.	1.5	128
52	Serial translocation by means of circular intermediates underlies colour sidedness in cattle. <i>Nature</i> , 2012, 482, 81-84.	13.7	137
53	Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. <i>Nature</i> , 2012, 491, 119-124.	13.7	4,038
54	A Deletion in the Bovine FANCI Gene Compromises Fertility by Causing Fetal Death and Brachyspina. <i>PLoS ONE</i> , 2012, 7, e43085.	1.1	82

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55	CCDC39 is required for assembly of inner dynein arms and the dynein regulatory complex and for normal ciliary motility in humans and dogs. <i>Nature Genetics</i> , 2011, 43, 72-78.	9.4	302
56	Resequencing of positional candidates identifies low frequency IL23R coding variants protecting against inflammatory bowel disease. <i>Nature Genetics</i> , 2011, 43, 43-47.	9.4	175
57	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. <i>Nature Genetics</i> , 2011, 43, 246-252.	9.4	1,201
58	Variants modulating the expression of a chromosome domain encompassing PLAG1 influence bovine stature. <i>Nature Genetics</i> , 2011, 43, 405-413.	9.4	300
59	The long and winding road from correlation to causation. <i>Nature Genetics</i> , 2011, 43, 180-181.	9.4	16
60	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.	0.6	95
61	Results of a haplotype-based GWAS for recurrent laryngeal neuropathy in the horse. <i>Mammalian Genome</i> , 2011, 22, 613-620.	1.0	45
62	Improved risk prediction for Crohn's disease with a multi-locus approach. <i>Human Molecular Genetics</i> , 2011, 20, 2435-2442.	1.4	42
63	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
64	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. <i>Nature Genetics</i> , 2010, 42, 1118-1125.	9.4	2,284
65	Evidence for Significant Overlap between Common Risk Variants for Crohn's Disease and Ankylosing Spondylitis. <i>PLoS ONE</i> , 2010, 5, e13795.	1.1	51
66	A Hidden Markov Model Combining Linkage and Linkage Disequilibrium Information for Haplotype Reconstruction and Quantitative Trait Locus Fine Mapping. <i>Genetics</i> , 2010, 184, 789-798.	1.2	178
67	Demonstrating polymorphic miRNA-mediated gene regulation in vivo: Application to the <i>g+6223Gâ†’A</i> mutation of Texel sheep. <i>Rna</i> , 2010, 16, 1854-1863.	1.6	10
68	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.	2.4	38
69	Patrocles: a database of polymorphic miRNA-mediated gene regulation in vertebrates. <i>Nucleic Acids Research</i> , 2010, 38, D640-D651.	6.5	126
70	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.	1.3	5
71	Balancing Selection of a Frame-Shift Mutation in the MRC2 Gene Accounts for the Outbreak of the Crooked Tail Syndrome in Belgian Blue Cattle. <i>PLoS Genetics</i> , 2009, 5, e1000666.	1.5	74
72	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.	1.5	25

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73	Genetics of ulcerative colitis: the come-back of interleukin 10. <i>Gut</i> , 2009, 58, 1173-1176.	6.1	21
74	Mapping QTL influencing gastrointestinal nematode burden in Dutch Holstein-Friesian dairy cattle. <i>BMC Genomics</i> , 2009, 10, 96.	1.2	39
75	Common variants at five new loci associated with early-onset inflammatory bowel disease. <i>Nature Genetics</i> , 2009, 41, 1335-1340.	9.4	459
76	A nonsense mutation in cGMP-dependent type II protein kinase ( <i>PRKG2</i> ) causes dwarfism in American Angus cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19250-19255.	3.3	48
77	Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. <i>Nature Genetics</i> , 2008, 40, 955-962.	9.4	2,422
78	Highly effective SNP-based association mapping and management of recessive defects in livestock. <i>Nature Genetics</i> , 2008, 40, 449-454.	9.4	263
79	Characterization of the bovine pseudoautosomal boundary: Documenting the evolutionary history of mammalian sex chromosomes. <i>Genome Research</i> , 2008, 18, 1884-1895.	2.4	60
80	On the Detection of Imprinted Quantitative Trait Loci in Line Crosses: Effect of Linkage Disequilibrium. <i>Genetics</i> , 2008, 180, 1167-1175.	1.2	18
81	Polymorphic miRNA-mediated gene regulation: contribution to phenotypic variation and disease. <i>Current Opinion in Genetics and Development</i> , 2007, 17, 166-176.	1.5	131
82	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.	2.5	108
83	Novel Crohn Disease Locus Identified by Genome-Wide Association Maps to a Gene Desert on 5p13.1 and Modulates Expression of PTGER4. <i>PLoS Genetics</i> , 2007, 3, e58.	1.5	506
84	Differential expression of sarcoplasmic proteins in four heterogeneous ovine skeletal muscles. <i>Proteomics</i> , 2007, 7, 271-280.	1.3	41
85	The Role of the Bovine Growth Hormone Receptor and Prolactin Receptor Genes in Milk, Fat and Protein Production in Finnish Ayrshire Dairy Cattle. <i>Genetics</i> , 2006, 173, 2151-2164.	1.2	154
86	Genetical metabolomics of flavonoid biosynthesis in <i>Populus</i> : a case study. <i>Plant Journal</i> , 2006, 47, 224-237.	2.8	140
87	A mutation creating a potential illegitimate microRNA target site in the myostatin gene affects muscularity in sheep. <i>Nature Genetics</i> , 2006, 38, 813-818.	9.4	1,125
88	Genetic identification of distinct loci controlling mammary tumor multiplicity, latency, and aggressiveness in the rat. <i>Mammalian Genome</i> , 2006, 17, 310-321.	1.0	28
89	The callipyge mutation enhances bidirectional long-range DLK1-GTL2 intergenic transcription in cis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8119-8124.	3.3	46
90	Linkage Disequilibrium on the Bovine X Chromosome: Characterization and Use in Quantitative Trait Locus Mapping. <i>Genetics</i> , 2006, 173, 1777-1786.	1.2	24

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91	RNAi-Mediated Allelic trans-Interaction at the Imprinted Rtl1/Peg11 Locus. <i>Current Biology</i> , 2005, 15, 743-749.	1.8	301
92	The callipyge mutation and other genes that affect muscle hypertrophy in sheep. <i>Genetics Selection Evolution</i> , 2005, 37, S65-81.	1.2	41
93	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.	1.0	19
94	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.	3.3	38
95	Genetic and functional confirmation of the causality of the DGAT1 K232A quantitative trait nucleotide in affecting milk yield and composition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2398-2403.	3.3	370
96	Domestic-animal genomics: deciphering the genetics of complex traits. <i>Nature Reviews Genetics</i> , 2004, 5, 202-212.	7.7	516
97	Ectopic Expression of DLK1 Protein in Skeletal Muscle of Padumnal Heterozygotes Causes the Callipyge Phenotype. <i>Current Biology</i> , 2004, 14, 1858-1862.	1.8	114
98	Haplotype diversity of the myostatin gene among beef cattlebreeds. <i>Genetics Selection Evolution</i> , 2003, 35, 103-18.	1.2	104
99	The callipyge locus: evidence for the trans interaction of reciprocally imprinted genes. <i>Trends in Genetics</i> , 2003, 19, 248-252.	2.9	136
100	Modulating skeletal muscle mass by postnatal, muscle-specific inactivation of the myostatin gene. <i>Genesis</i> , 2003, 35, 227-238.	0.8	152
101	A regulatory mutation in IGF2 causes a major QTL effect on muscle growth in the pig. <i>Nature</i> , 2003, 425, 832-836.	13.7	791
102	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. <i>Genetics</i> , 2003, 163, 253-266.	1.2	390
103	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.	1.2	94
104	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. <i>Genetics</i> , 2003, 165, 277-285.	1.2	53
105	Positional Candidate Cloning of a QTL in Dairy Cattle: Identification of a Missense Mutation in the Bovine DGAT1 Gene with Major Effect on Milk Yield and Composition. <i>Genome Research</i> , 2002, 12, 222-231.	2.4	803
106	Results of a whole genome scan targeting QTL for growth and carcass traits in a PiÃ©train Ã— Large White intercross. <i>Genetics Selection Evolution</i> , 2002, 34, 371-87.	1.2	57
107	Comparative sequence analysis of the INS-IGF2-H19 gene cluster in pigs. <i>Mammalian Genome</i> , 2002, 13, 388-398.	1.0	80
108	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.	1.2	101

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109	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
110	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.	1.0	20
111	Fine-mapping and construction of a bovine contig spanning the ovine callipyge locus. <i>Mammalian Genome</i> , 2001, 12, 141-149.	1.0	45
112	The callipyge mutation enhances the expression of coregulated imprinted genes in cis without affecting their imprinting status. <i>Nature Genetics</i> , 2001, 27, 367-369.	9.4	160
113	Comparative Sequence Analysis of the Imprinted Dlk1-Gtl2 Locus in Three Mammalian Species Reveals Highly Conserved Genomic Elements and Refines Comparison with the Igf2-H19 Region. <i>Genome Research</i> , 2001, 11, 2085-2094.	2.4	116
114	Extensive Genome-wide Linkage Disequilibrium in Cattle. <i>Genome Research</i> , 2000, 10, 220-227.	2.4	304
115	Towards marker assisted selection in livestock. <i>Reproduction, Nutrition, Development</i> , 1999, 39, 555-561.	1.9	20
116	An imprinted QTL with major effect on muscle mass and fat deposition maps to the IGF2 locus in pigs. <i>Nature Genetics</i> , 1999, 21, 155-156.	9.4	376
117	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.	1.0	3
118	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.	0.3	8
119	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
120	Molecular definition of an allelic series of mutations disrupting the myostatin function and causing double-muscling in cattle. <i>Mammalian Genome</i> , 1998, 9, 210-213.	1.0	422
121	A QTL with major effect on milk yield and composition maps to bovine Chromosome 14. <i>Mammalian Genome</i> , 1998, 9, 540-544.	1.0	110
122	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.	1.2	43
123	QTL Mapping to QTL Cloning: Mice to the Rescue. <i>Genome Research</i> , 1997, 7, 663-665.	2.4	14
124	A deletion in the bovine myostatin gene causes the double-muscling phenotype in cattle. <i>Nature Genetics</i> , 1997, 17, 71-74.	9.4	1,323
125	Resistance to HIV-1 infection in Caucasian individuals bearing mutant alleles of the CCR-5 chemokine receptor gene. <i>Nature</i> , 1996, 382, 722-725.	13.7	2,782
126	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.	1.2	85



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127	Physical mapping of inhibin $\beta$ -A in domestic cattle. <i>Mammalian Genome</i> , 1993, 4, 328-332.	1.0	23
128	Microsatellite mapping of a gene affecting horn development in <i>Bos taurus</i> . <i>Nature Genetics</i> , 1993, 4, 206-210.	9.4	122
129	Quantitative estimation of chimerism in mice using microsatellite markers. <i>Molecular Reproduction and Development</i> , 1993, 34, 127-132.	1.0	7
130	A genetic map of index DNA loci on bovine chromosome 21. <i>Genomics</i> , 1993, 18, 598-601.	1.3	8
131	A genetic map of DNA loci on bovine chromosome 1. <i>Genomics</i> , 1993, 18, 602-608.	1.3	39
132	Genmark's approach to marker-assisted selection. <i>Animal Biotechnology</i> , 1992, 3, 95-109.	0.7	9
133	Somatic cell mapping, polymorphism, and linkage analysis of bovine prolactin-related proteins and placental lactogen. <i>Genomics</i> , 1992, 14, 137-143.	1.3	40
134	Generation of bovine multisite haplotypes using random cosmid clones. <i>Genomics</i> , 1991, 10, 889-904.	1.3	35
135	Characterization of a set of variable number of tandem repeat markers conserved in Bovidae. <i>Genomics</i> , 1991, 11, 24-32.	1.3	64
136	On the use of DNA fingerprints for linkage studies in cattle. <i>Genomics</i> , 1990, 6, 461-474.	1.3	83
137	A polymorphic satellite sequence maps to the pericentric region of the bovine Y chromosome. <i>Genomics</i> , 1990, 6, 482-490.	1.3	50
138	DNA fingerprinting in man using a mouse probe related to part of the <i>Drosophila</i> $\omega$ gene. <i>Nucleic Acids Research</i> , 1987, 15, 7193-7193.	6.5	40