List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	12.6	1,038
2	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. Science, 2009, 324, 528-532.	12.6	746
3	Single-molecule sequencing and chromatin conformation capture enable de novo reference assembly of the domestic goat genome. Nature Genetics, 2017, 49, 643-650.	21.4	600
4	De novo assembly of the cattle reference genome with single-molecule sequencing. GigaScience, 2020, 9, .	6.4	380
5	Analysis of copy number variations among diverse cattle breeds. Genome Research, 2010, 20, 693-703.	5.5	280
6	Copy number variation of individual cattle genomes using next-generation sequencing. Genome Research, 2012, 22, 778-790.	5.5	259
7	Genomic characteristics of cattle copy number variations. BMC Genomics, 2011, 12, 127.	2.8	201
8	Genomic Signatures Reveal New Evidences for Selection of Important Traits in Domestic Cattle. Molecular Biology and Evolution, 2015, 32, 711-725.	8.9	173
9	Cattle Sex-Specific Recombination and Genetic Control from a Large Pedigree Analysis. PLoS Genetics, 2015, 11, e1005387.	3.5	168
10	Effect of Artificial Selection on Runs of Homozygosity in U.S. Holstein Cattle. PLoS ONE, 2013, 8, e80813.	2.5	165
11	Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. BMC Genomics, 2013, 14, 876.	2.8	142
12	Transcriptional profiling of mammary gland in Holstein cows with extremely different milk protein and fat percentage using RNA sequencing. BMC Genomics, 2014, 15, 226.	2.8	138
13	The challenges and importance of structural variation detection in livestock. Frontiers in Genetics, 2014, 5, 37.	2.3	104
14	Genetic Architecture and Selection of Chinese Cattle Revealed by Whole Genome Resequencing. Molecular Biology and Evolution, 2018, 35, 688-699.	8.9	97
15	Comprehensive analyses of 723 transcriptomes enhance genetic and biological interpretations for complex traits in cattle. Genome Research, 2020, 30, 790-801.	5.5	97
16	Population-genetic properties of differentiated copy number variations in cattle. Scientific Reports, 2016, 6, 23161.	3.3	91
17	Fine mapping of copy number variations on two cattle genome assemblies using high density SNP array. BMC Genomics, 2012, 13, 376.	2.8	90
18	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. BMC Genomics, 2014, 15, 683.	2.8	89

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19	Genomic regions showing copy number variations associate with resistance or susceptibility to gastrointestinal nematodes in Angus cattle. Functional and Integrative Genomics, 2012, 12, 81-92.	3.5	87
20	CNV discovery for milk composition traits in dairy cattle using whole genome resequencing. BMC Genomics, 2017, 18, 265.	2.8	87
21	Analysis of recent segmental duplications in the bovine genome. BMC Genomics, 2009, 10, 571.	2.8	86
22	Assessing signatures of selection through variation in linkage disequilibrium between taurine and indicine cattle. Genetics Selection Evolution, 2014, 46, 19.	3.0	79
23	Comparative analysis of <i>Alu</i> repeats in primate genomes. Genome Research, 2009, 19, 876-885.	5.5	71
24	Activation of SIRT1 by Resveratrol Represses Transcription of the Gene for the Cytosolic Form of Phosphoenolpyruvate Carboxykinase (GTP) by Deacetylating Hepatic Nuclear Factor 4α. Journal of Biological Chemistry, 2009, 284, 27042-27053.	3.4	70
25	Bovine Exome Sequence Analysis and Targeted SNP Genotyping of Recessive Fertility Defects BH1, HH2, and HH3 Reveal a Putative Causative Mutation in SMC2 for HH3. PLoS ONE, 2014, 9, e92769.	2.5	69
26	Genome-wide CNV analysis reveals variants associated with growth traits in Bos indicus. BMC Genomics, 2016, 17, 419.	2.8	69
27	GWAS and fine-mapping of livability and six disease traits in Holstein cattle. BMC Genomics, 2020, 21, 41.	2.8	66
28	Copy number variation in the cattle genome. Functional and Integrative Genomics, 2012, 12, 609-624.	3.5	60
29	Comparative whole genome DNA methylation profiling of cattle sperm and somatic tissues reveals striking hypomethylated patterns in sperm. GigaScience, 2018, 7, .	6.4	60
30	Diversity and population-genetic properties of copy number variations and multicopy genes in cattle. DNA Research, 2016, 23, 253-262.	3.4	59
31	Evidence of evolutionary history and selective sweeps in the genome of Meishan pig reveals its genetic and phenotypic characterization. GigaScience, 2018, 7, .	6.4	56
32	Diversity of copy number variation in a worldwide population of sheep. Genomics, 2018, 110, 143-148.	2.9	53
33	Genome-wide copy number variant analysis reveals variants associated with 10 diverse production traits in Holstein cattle. BMC Genomics, 2018, 19, 314.	2.8	52
34	Analysis of copy number variations in Holstein cows identify potential mechanisms contributing to differences in residual feed intake. Functional and Integrative Genomics, 2012, 12, 717-723.	3.5	51
35	Functional annotation of the cattle genome through systematic discovery and characterization of chromatin states and butyrate-induced variations. BMC Biology, 2019, 17, 68.	3.8	48
36	A genome-wide association study for mastitis resistance in phenotypically well-characterized Holstein dairy cattle using a selective genotyping approach. Immunogenetics, 2019, 71, 35-47.	2.4	47

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37	Initial analysis of copy number variations in cattle selected for resistance or susceptibility to intestinal nematodes. Mammalian Genome, 2011, 22, 111-121.	2.2	46
38	Comparative analyses across cattle genders and breeds reveal the pitfalls caused by false positive and lineage-differential copy number variations. Scientific Reports, 2016, 6, 29219.	3.3	44
39	A PLAG1 mutation contributed to stature recovery in modern cattle. Scientific Reports, 2017, 7, 17140.	3.3	42
40	Diversity of copy number variation in the worldwide goat population. Heredity, 2019, 122, 636-646.	2.6	42
41	Genetic and epigenetic architecture of paternal origin contribute to gestation length in cattle. Communications Biology, 2019, 2, 100.	4.4	41
42	Muscle transcriptomic analyses in Angus cattle with divergent tenderness. Molecular Biology Reports, 2012, 39, 4185-4193.	2.3	40
43	Genomic Patterns of Homozygosity in Chinese Local Cattle. Scientific Reports, 2019, 9, 16977.	3.3	40
44	Genome changes due to artificial selection in U.S. Holstein cattle. BMC Genomics, 2019, 20, 128.	2.8	39
45	Functional Genomic Analysis of Variation on Beef Tenderness Induced by Acute Stress in Angus Cattle. Comparative and Functional Genomics, 2012, 2012, 1-11.	2.0	38
46	Protein Accumulation in the Germinating Uromyces appendiculatus Uredospore. Molecular Plant-Microbe Interactions, 2007, 20, 857-866.	2.6	37
47	Comparative Analysis of CNV Calling Algorithms: Literature Survey and a Case Study Using Bovine High-Density SNP Data. Microarrays (Basel, Switzerland), 2013, 2, 171-185.	1.4	37
48	Genome-Wide Copy Number Variant Analysis in Inbred Chickens Lines With Different Susceptibility to Marek's Disease. G3: Genes, Genomes, Genetics, 2013, 3, 217-223.	1.8	36
49	Functional proteomic and interactome analysis of proteins associated with beef tenderness in Angus cattle. Livestock Science, 2014, 161, 201-209.	1.6	35
50	Genome-wide scan reveals genetic divergence and diverse adaptive selection in ChineseÂlocal cattle. BMC Genomics, 2019, 20, 494.	2.8	34
51	Array CGH-based detection of CNV regions and their potential association with reproduction and other economic traits in Holsteins. BMC Genomics, 2019, 20, 181.	2.8	34
52	Comparative whole genome DNA methylation profiling across cattle tissues reveals global and tissue-specific methylation patterns. BMC Biology, 2020, 18, 85.	3.8	34
53	Genomic divergences among cattle, dog and human estimated from large-scale alignments of genomic sequences. BMC Genomics, 2006, 7, 140.	2.8	33
54	The essence of appetite: does olfactory receptor variation play a role?. Journal of Animal Science, 2018, 96, 1551-1558.	0.5	32

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55	Genomic Analysis Revealed a Convergent Evolution of LINE-1 in Coat Color: A Case Study in Water Buffaloes (<i>Bubalus bubalis</i>). Molecular Biology and Evolution, 2021, 38, 1122-1136.	8.9	32
56	Comprehensive transcriptome and methylome analysis delineates the biological basis of hair follicle development and wool-related traits in Merino sheep. BMC Biology, 2021, 19, 197.	3.8	31
57	Reduced representation bisulphite sequencing of ten bovine somatic tissues reveals DNA methylation patterns and their impacts on gene expression. BMC Genomics, 2016, 17, 779.	2.8	30
58	Genome-wide analysis reveals differential selection involved with copy number variation in diverse Chinese Cattle. Scientific Reports, 2017, 7, 14299.	3.3	30
59	Epigenomics and genotype-phenotype association analyses reveal conserved genetic architecture of complex traits in cattle and human. BMC Biology, 2020, 18, 80.	3.8	28
60	MicroRNA-guided prioritization of genome-wide association signals reveals the importance of microRNA-target gene networks for complex traits in cattle. Scientific Reports, 2018, 8, 9345.	3.3	27
61	Copy number variation-based genome wide association study reveals additional variants contributing to meat quality in Swine. Scientific Reports, 2015, 5, 12535.	3.3	26
62	Mucin biosynthesis in the bovine goblet cell induced by Cooperia oncophora infection. Veterinary Parasitology, 2009, 165, 281-289.	1.8	25
63	Comparative analyses of sperm DNA methylomes among human, mouse and cattle provide insights into epigenomic evolution and complex traits. Epigenetics, 2019, 14, 260-276.	2.7	25
64	A genome-wide survey reveals a deletion polymorphism associated with resistance to gastrointestinal nematodes in Angus cattle. Functional and Integrative Genomics, 2014, 14, 333-339.	3.5	24
65	Integrating RNA-Seq with GWAS reveals novel insights into the molecular mechanism underpinning ketosis in cattle. BMC Genomics, 2020, 21, 489.	2.8	24
66	Probe-based association analysis identifies several deletions associated with average daily gain in beef cattle. BMC Genomics, 2019, 20, 31.	2.8	22
67	Genome-Wide Assessment of Runs of Homozygosity in Chinese Wagyu Beef Cattle. Animals, 2020, 10, 1425.	2.3	22
68	Comparative analyses of copy number variations between Bos taurus and Bos indicus. BMC Genomics, 2020, 21, 682.	2.8	21
69	Systematic profiling of short tandem repeats in the cattle genome. Genome Biology and Evolution, 2016, 9, evw256.	2.5	20
70	miRNA-dysregulation associated with tenderness variation induced by acute stress in Angus cattle. Journal of Animal Science and Biotechnology, 2012, 3, 12.	5.3	19
71	Analyses of inter-individual variations of sperm DNA methylation and their potential implications in cattle. BMC Genomics, 2019, 20, 888.	2.8	19
72	Fine Mapping for Weaver Syndrome in Brown Swiss Cattle and the Identification of 41 Concordant Mutations across NRCAM, PNPLA8 and CTTNBP2. PLoS ONE, 2013, 8, e59251.	2.5	18

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73	RAPTR-SV: a hybrid method for the detection of structural variants. Bioinformatics, 2015, 31, 2084-2090.	4.1	18
74	Genomic predictions combining SNP markers and copy number variations in Nellore cattle. BMC Genomics, 2018, 19, 441.	2.8	18
75	Alternative splicing variants and DNA methylation status of BDNF in inbred chicken lines. Brain Research, 2009, 1269, 1-10.	2.2	17
76	Characterization of recombination features and the genetic basis in multiple cattle breeds. BMC Genomics, 2018, 19, 304.	2.8	17
77	CNV Analysis of Host Responses to Porcine Reproductive and Respiratory Syndrome Virus Infection. Journal of Genomics, 2017, 5, 58-63.	0.9	16
78	Single-cell transcriptomic analyses of dairy cattle ruminal epithelial cells during weaning. Genomics, 2021, 113, 2045-2055.	2.9	16
79	Construction of PRDM9 allele-specific recombination maps in cattle using large-scale pedigree analysis and genome-wide single sperm genomics. DNA Research, 2018, 25, 183-194.	3.4	15
80	Timing and Extent of Inbreeding in African Goats. Frontiers in Genetics, 2019, 10, 537.	2.3	15
81	Integration of a single-step genome-wide association study with a multi-tissue transcriptome analysis provides novel insights into the genetic basis of wool and weight traits in sheep. Genetics Selection Evolution, 2021, 53, 56.	3.0	15
82	Genome-wide CNV analysis revealed variants associated with growth traits in African indigenous goats. Genomics, 2020, 112, 1477-1480.	2.9	14
83	Co-Expression Analysis of Fetal Weight-Related Genes in Ovine Skeletal Muscle during Mid and Late Fetal Development Stages. International Journal of Biological Sciences, 2014, 10, 1039-1050.	6.4	13
84	Integrating Signals from Sperm Methylome Analysis and Genome-Wide Association Study for a Better Understanding of Male Fertility in Cattle. Epigenomes, 2019, 3, 10.	1.8	12
85	Recent Applications of DNA Sequencing Technologies in Food, Nutrition and Agriculture. Recent Patents on Food, Nutrition & Agriculture, 2011, 3, 187-195.	0.9	12
86	Transcriptional atlas analysis from multiple tissues reveals the expression specificity patterns in beef cattle. BMC Biology, 2022, 20, 79.	3.8	12
87	Refinement of Bos taurus sequence assembly based on BAC-FISH experiments. BMC Genomics, 2011, 12, 639.	2.8	11
88	Identification of Candidate Transcription Factor Binding Sites in the Cattle Genome. Genomics, Proteomics and Bioinformatics, 2013, 11, 195-198.	6.9	11
89	Transcriptome profiling of CTLs regulated by rapamycin using RNA-Seq. Immunogenetics, 2014, 66, 625-633.	2.4	11
90	Copy number variation analysis reveals variants associated with milk production traits in dairy goats. Genomics, 2020, 112, 4934-4937.	2.9	11

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91	A Genome-Wide Analysis of Array-Based Comparative Genomic Hybridization (CGH) Data to Detect Intra-Species Variations and Evolutionary Relationships. PLoS ONE, 2009, 4, e7978.	2.5	10
92	Genomic structural differences between cattle and River Buffalo identified through comparative genomic and transcriptomic analysis. Data in Brief, 2018, 19, 236-239.	1.0	10
93	Divergence Analyses of Sperm DNA Methylomes between Monozygotic Twin Al Bulls. Epigenomes, 2019, 3, 21.	1.8	10
94	Genomic sequencing analysis reveals copy number variations and their associations with economically important traits in beef cattle. Genomics, 2021, 113, 812-820.	2.9	10
95	Genome-wide association study reveals 14 new SNPs and confirms two structural variants highly associated with the horned/polled phenotype in goats. BMC Genomics, 2021, 22, 769.	2.8	10
96	Applications and Case Studies of the Next-Generation Sequencing Technologies in Food, Nutrition and Agriculture. Recent Patents on Food, Nutrition & Agriculture, 2009, 1, 75-79.	0.9	9
97	Genomic expression analysis by singleâ€cell mRNA differential display of quiescent CD8 T cells from tumourâ€infiltrating lymphocytes obtained from <i>in vivo</i> liver tumours. Immunology, 2009, 127, 83-90.	4.4	9
98	Transcriptomic Profiling of Spleen in Grass-Fed and Grain-Fed Angus Cattle. PLoS ONE, 2015, 10, e0135670.	2.5	9
99	Characterization of Copy Number Variation's Potential Role in Marek's Disease. International Journal of Molecular Sciences, 2017, 18, 1020.	4.1	9
100	Genetic assessment of inbred chicken lines indicates genomic signatures of resistance to Marek's disease. Journal of Animal Science and Biotechnology, 2018, 9, 65.	5.3	9
101	Copy number variation of bovine SHH gene is associated with body conformation traits in Chinese beef cattle. Journal of Applied Genetics, 2019, 60, 199-207.	1.9	9
102	PRE-1 Revealed Previous Unknown Introgression Events in Eurasian Boars during the Middle Pleistocene. Genome Biology and Evolution, 2020, 12, 1751-1764.	2.5	9
103	Identification of Conserved Regulatory Elements in Mammalian Promoter Regions: A Case Study Using the PCK1 Promoter. Genomics, Proteomics and Bioinformatics, 2008, 6, 129-143.	6.9	8
104	Calibration of Mutation Rates Reveals Diverse Subfamily Structure of Galliform CR1 Repeats. Genome Biology and Evolution, 2009, 1, 119-130.	2.5	8
105	Genomic Analysis Reveals Specific Patterns of Homozygosity and Heterozygosity in Inbred Pigs. Animals, 2019, 9, 314.	2.3	8
106	Comparative sequence alignment reveals River Buffalo genomic structural differences compared with cattle. Genomics, 2019, 111, 418-425.	2.9	8
107	Establishment and transcriptomic analyses of a cattle rumen epithelial primary cells (REPC) culture by bulk and single-cell RNA sequencing to elucidate interactions of butyrate and rumen development. Heliyon, 2020, 6, e04112.	3.2	8
108	Butyrate Induced IGF2 Activation Correlated with Distinct Chromatin Signatures Due to Histone Modification. Gene Regulation and Systems Biology, 2013, 7, GRSB.S11243.	2.3	7

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109	A highâ€resolution wholeâ€genome map of the distinctive epigenomic landscape induced by butyrate in bovine cells. Animal Genetics, 2014, 45, 40-50.	1.7	7
110	Computational detection and experimental validation of segmental duplications and associated copy number variations in water buffalo (Bubalus bubalis). Functional and Integrative Genomics, 2019, 19, 409-419.	3.5	7
111	Identification and population genetic analyses of copy number variations in six domestic goat breeds and Bezoar ibexes using next-generation sequencing. BMC Genomics, 2020, 21, 840.	2.8	7
112	Assessment of genome integrity with array CGH in cattle transgenic cell lines produced by homologous recombination and somatic cell cloning. Genome Integrity, 2011, 2, 6.	1.0	6
113	Single-cell transcriptomic and chromatin accessibility analyses of dairy cattle peripheral blood mononuclear cells and their responses to lipopolysaccharide. BMC Genomics, 2022, 23, 338.	2.8	6
114	Detection of copy number variants in African goats using whole genome sequence data. BMC Genomics, 2021, 22, 398.	2.8	4
115	Functional annotation of regulatory elements in cattle genome reveals the roles of extracellular interaction and dynamic change of chromatin states in rumen development during weaning. Genomics, 2022, 114, 110296.	2.9	4
116	Genome-wide recombination map construction from single sperm sequencing in cattle. BMC Genomics, 2022, 23, 181.	2.8	4
117	Characterization of Accessible Chromatin Regions in Cattle Rumen Epithelial Tissue during Weaning. Genes, 2022, 13, 535.	2.4	4
118	Initial Analysis of Structural Variation Detections in Cattle Using Long-Read Sequencing Methods. Genes, 2022, 13, 828.	2.4	4
119	A 13.42-kb tandem duplication at the ASIP locus is strongly associated with the depigmentation phenotype of non-classic Swiss markings in goats. BMC Genomics, 2022, 23, .	2.8	4
120	Characterization of a novel microdeletion polymorphism on BTA5 in cattle. Animal Genetics, 2008, 39, 655-658.	1.7	3
121	Ruminant-specific multiple duplication events of PRDM9 before speciation. BMC Evolutionary Biology, 2017, 17, 79.	3.2	3
122	Bos taurus–indicus hybridization correlates with intralocus sexual-conflict effects of PRDM9 on male and female fertility in Holstein cattle. BMC Genetics, 2019, 20, 71.	2.7	3
123	Data of epigenomic profiling of histone marks and CTCF binding sites in bovine rumen epithelial primary cells before and after butyrate treatment. Data in Brief, 2020, 28, 104983.	1.0	3
124	Distribution of DGAT1 copy number variation in Chinese goats and its associations with milk production traits. Animal Biotechnology, 2021, , 1-6.	1.5	3
125	Genome-wide association study between copy number variation regions and carcass- and meat-quality traits in Nellore cattle. Animal Production Science, 2021, 61, 731.	1.3	2
126	Mining Unknown Porcine Protein Isoforms by Tissue-based Map of Proteome Enhances Pig Genome Annotation. Genomics, Proteomics and Bioinformatics, 2021, 19, 772-786.	6.9	2

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127	Towards the detection of copy number variation from single sperm sequencing in cattle. BMC Genomics, 2022, 23, 215.	2.8	2
128	The Dynamics of Chromatin Accessibility Prompted by Butyrate-Induced Chromatin Modification in Bovine Cells. Ruminants, 2022, 2, 226-243.	1.1	2
129	Statistical Detection of Genome Differences Based on CNV Segments. Methods in Molecular Biology, 2018, 1833, 49-59.	0.9	1
130	Analysis of Population-Genetic Properties of Copy Number Variations. Methods in Molecular Biology, 2018, 1833, 179-186.	0.9	1
131	Effect of Temperature and Maternal Age on Recombination Rate in Cattle. Frontiers in Genetics, 2021, 12, 682718.	2.3	1
132	Transcriptional Reprogramming in Rumen Epithelium during the Developmental Transition of Pre-Ruminant to the Ruminant in Cattle. Animals, 2021, 11, 2870.	2.3	1
133	Insights from Initial Variant Detection by Sequencing Single Sperm in Cattle. Dairy, 2021, 2, 649-657.	2.0	1
134	Distinct Turn-Over Patterns of Common Repeats Correlate with Genome Size Differences Among Cattle, Dog and Human. , 2009, , .		0
135	Epigenetics and heritable phenotypic variations in livestock. , 2019, , 283-313.		0