

# George E Liu

## List of Publications by Year in descending order

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135  
papers

7,696  
citations

76196  
40  
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58464  
82  
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141  
all docs

141  
docs citations

141  
times ranked

7055  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	6.0	1,038
2	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	6.0	746
3	Single-molecule sequencing and chromatin conformation capture enable de novo reference assembly of the domestic goat genome. <i>Nature Genetics</i> , 2017, 49, 643-650.	9.4	600
4	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	3.3	380
5	Analysis of copy number variations among diverse cattle breeds. <i>Genome Research</i> , 2010, 20, 693-703.	2.4	280
6	Copy number variation of individual cattle genomes using next-generation sequencing. <i>Genome Research</i> , 2012, 22, 778-790.	2.4	259
7	Genomic characteristics of cattle copy number variations. <i>BMC Genomics</i> , 2011, 12, 127.	1.2	201
8	Genomic Signatures Reveal New Evidences for Selection of Important Traits in Domestic Cattle. <i>Molecular Biology and Evolution</i> , 2015, 32, 711-725.	3.5	173
9	Cattle Sex-Specific Recombination and Genetic Control from a Large Pedigree Analysis. <i>PLoS Genetics</i> , 2015, 11, e1005387.	1.5	168
10	Effect of Artificial Selection on Runs of Homozygosity in U.S. Holstein Cattle. <i>PLoS ONE</i> , 2013, 8, e80813.	1.1	165
11	Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. <i>BMC Genomics</i> , 2013, 14, 876.	1.2	142
12	Transcriptional profiling of mammary gland in Holstein cows with extremely different milk protein and fat percentage using RNA sequencing. <i>BMC Genomics</i> , 2014, 15, 226.	1.2	138
13	The challenges and importance of structural variation detection in livestock. <i>Frontiers in Genetics</i> , 2014, 5, 37.	1.1	104
14	Genetic Architecture and Selection of Chinese Cattle Revealed by Whole Genome Resequencing. <i>Molecular Biology and Evolution</i> , 2018, 35, 688-699.	3.5	97
15	Comprehensive analyses of 723 transcriptomes enhance genetic and biological interpretations for complex traits in cattle. <i>Genome Research</i> , 2020, 30, 790-801.	2.4	97
16	Population-genetic properties of differentiated copy number variations in cattle. <i>Scientific Reports</i> , 2016, 6, 23161.	1.6	91
17	Fine mapping of copy number variations on two cattle genome assemblies using high density SNP array. <i>BMC Genomics</i> , 2012, 13, 376.	1.2	90
18	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. <i>BMC Genomics</i> , 2014, 15, 683.	1.2	89

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19	Genomic regions showing copy number variations associate with resistance or susceptibility to gastrointestinal nematodes in Angus cattle. <i>Functional and Integrative Genomics</i> , 2012, 12, 81-92.	1.4	87
20	CNV discovery for milk composition traits in dairy cattle using whole genome resequencing. <i>BMC Genomics</i> , 2017, 18, 265.	1.2	87
21	Analysis of recent segmental duplications in the bovine genome. <i>BMC Genomics</i> , 2009, 10, 571.	1.2	86
22	Assessing signatures of selection through variation in linkage disequilibrium between taurine and indicine cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 19.	1.2	79
23	Comparative analysis of <i>Alu</i> repeats in primate genomes. <i>Genome Research</i> , 2009, 19, 876-885.	2.4	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 4 $\alpha$ . <i>Journal of Biological Chemistry</i> , 2009, 284, 27042-27053.	1.6	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. <i>PLoS ONE</i> , 2014, 9, e92769.	1.1	69
26	Genome-wide CNV analysis reveals variants associated with growth traits in <i>Bos indicus</i> . <i>BMC Genomics</i> , 2016, 17, 419.	1.2	69
27	GWAS and fine-mapping of livability and six disease traits in Holstein cattle. <i>BMC Genomics</i> , 2020, 21, 41.	1.2	66
28	Copy number variation in the cattle genome. <i>Functional and Integrative Genomics</i> , 2012, 12, 609-624.	1.4	60
29	Comparative whole genome DNA methylation profiling of cattle sperm and somatic tissues reveals striking hypomethylated patterns in sperm. <i>GigaScience</i> , 2018, 7, .	3.3	60
30	Diversity and population-genetic properties of copy number variations and multicopy genes in cattle. <i>DNA Research</i> , 2016, 23, 253-262.	1.5	59
31	Evidence of evolutionary history and selective sweeps in the genome of Meishan pig reveals its genetic and phenotypic characterization. <i>GigaScience</i> , 2018, 7, .	3.3	56
32	Diversity of copy number variation in a worldwide population of sheep. <i>Genomics</i> , 2018, 110, 143-148.	1.3	53
33	Genome-wide copy number variant analysis reveals variants associated with 10 diverse production traits in Holstein cattle. <i>BMC Genomics</i> , 2018, 19, 314.	1.2	52
34	Analysis of copy number variations in Holstein cows identify potential mechanisms contributing to differences in residual feed intake. <i>Functional and Integrative Genomics</i> , 2012, 12, 717-723.	1.4	51
35	Functional annotation of the cattle genome through systematic discovery and characterization of chromatin states and butyrate-induced variations. <i>BMC Biology</i> , 2019, 17, 68.	1.7	48
36	A genome-wide association study for mastitis resistance in phenotypically well-characterized Holstein dairy cattle using a selective genotyping approach. <i>Immunogenetics</i> , 2019, 71, 35-47.	1.2	47

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37	Initial analysis of copy number variations in cattle selected for resistance or susceptibility to intestinal nematodes. <i>Mammalian Genome</i> , 2011, 22, 111-121.	1.0	46
38	Comparative analyses across cattle genders and breeds reveal the pitfalls caused by false positive and lineage-differential copy number variations. <i>Scientific Reports</i> , 2016, 6, 29219.	1.6	44
39	A PLAG1 mutation contributed to stature recovery in modern cattle. <i>Scientific Reports</i> , 2017, 7, 17140.	1.6	42
40	Diversity of copy number variation in the worldwide goat population. <i>Heredity</i> , 2019, 122, 636-646.	1.2	42
41	Genetic and epigenetic architecture of paternal origin contribute to gestation length in cattle. <i>Communications Biology</i> , 2019, 2, 100.	2.0	41
42	Muscle transcriptomic analyses in Angus cattle with divergent tenderness. <i>Molecular Biology Reports</i> , 2012, 39, 4185-4193.	1.0	40
43	Genomic Patterns of Homozygosity in Chinese Local Cattle. <i>Scientific Reports</i> , 2019, 9, 16977.	1.6	40
44	Genome changes due to artificial selection in U.S. Holstein cattle. <i>BMC Genomics</i> , 2019, 20, 128.	1.2	39
45	Functional Genomic Analysis of Variation on Beef Tenderness Induced by Acute Stress in Angus Cattle. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-11.	2.0	38
46	Protein Accumulation in the Germinating <i>Uromyces appendiculatus</i> Uredospore. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 857-866.	1.4	37
47	Comparative Analysis of CNV Calling Algorithms: Literature Survey and a Case Study Using Bovine High-Density SNP Data. <i>Microarrays (Basel, Switzerland)</i> , 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. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 217-223.	0.8	36
49	Functional proteomic and interactome analysis of proteins associated with beef tenderness in Angus cattle. <i>Livestock Science</i> , 2014, 161, 201-209.	0.6	35
50	Genome-wide scan reveals genetic divergence and diverse adaptive selection in Chinese local cattle. <i>BMC Genomics</i> , 2019, 20, 494.	1.2	34
51	Array CGH-based detection of CNV regions and their potential association with reproduction and other economic traits in Holsteins. <i>BMC Genomics</i> , 2019, 20, 181.	1.2	34
52	Comparative whole genome DNA methylation profiling across cattle tissues reveals global and tissue-specific methylation patterns. <i>BMC Biology</i> , 2020, 18, 85.	1.7	34
53	Genomic divergences among cattle, dog and human estimated from large-scale alignments of genomic sequences. <i>BMC Genomics</i> , 2006, 7, 140.	1.2	33
54	The essence of appetite: does olfactory receptor variation play a role?. <i>Journal of Animal Science</i> , 2018, 96, 1551-1558.	0.2	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> ). <i>Molecular Biology and Evolution</i> , 2021, 38, 1122-1136.	3.5	32
56	Comprehensive transcriptome and methylome analysis delineates the biological basis of hair follicle development and wool-related traits in Merino sheep. <i>BMC Biology</i> , 2021, 19, 197.	1.7	31
57	Reduced representation bisulphite sequencing of ten bovine somatic tissues reveals DNA methylation patterns and their impacts on gene expression. <i>BMC Genomics</i> , 2016, 17, 779.	1.2	30
58	Genome-wide analysis reveals differential selection involved with copy number variation in diverse Chinese Cattle. <i>Scientific Reports</i> , 2017, 7, 14299.	1.6	30
59	Epigenomics and genotype-phenotype association analyses reveal conserved genetic architecture of complex traits in cattle and human. <i>BMC Biology</i> , 2020, 18, 80.	1.7	28
60	MicroRNA-guided prioritization of genome-wide association signals reveals the importance of microRNA-target gene networks for complex traits in cattle. <i>Scientific Reports</i> , 2018, 8, 9345.	1.6	27
61	Copy number variation-based genome wide association study reveals additional variants contributing to meat quality in Swine. <i>Scientific Reports</i> , 2015, 5, 12535.	1.6	26
62	Mucin biosynthesis in the bovine goblet cell induced by <i>Cooperia oncophora</i> infection. <i>Veterinary Parasitology</i> , 2009, 165, 281-289.	0.7	25
63	Comparative analyses of sperm DNA methylomes among human, mouse and cattle provide insights into epigenomic evolution and complex traits. <i>Epigenetics</i> , 2019, 14, 260-276.	1.3	25
64	A genome-wide survey reveals a deletion polymorphism associated with resistance to gastrointestinal nematodes in Angus cattle. <i>Functional and Integrative Genomics</i> , 2014, 14, 333-339.	1.4	24
65	Integrating RNA-Seq with GWAS reveals novel insights into the molecular mechanism underpinning ketosis in cattle. <i>BMC Genomics</i> , 2020, 21, 489.	1.2	24
66	Probe-based association analysis identifies several deletions associated with average daily gain in beef cattle. <i>BMC Genomics</i> , 2019, 20, 31.	1.2	22
67	Genome-Wide Assessment of Runs of Homozygosity in Chinese Wagyu Beef Cattle. <i>Animals</i> , 2020, 10, 1425.	1.0	22
68	Comparative analyses of copy number variations between <i>Bos taurus</i> and <i>Bos indicus</i> . <i>BMC Genomics</i> , 2020, 21, 682.	1.2	21
69	Systematic profiling of short tandem repeats in the cattle genome. <i>Genome Biology and Evolution</i> , 2016, 9, evw256.	1.1	20
70	miRNA-dysregulation associated with tenderness variation induced by acute stress in Angus cattle. <i>Journal of Animal Science and Biotechnology</i> , 2012, 3, 12.	2.1	19
71	Analyses of inter-individual variations of sperm DNA methylation and their potential implications in cattle. <i>BMC Genomics</i> , 2019, 20, 888.	1.2	19
72	Fine Mapping for Weaver Syndrome in Brown Swiss Cattle and the Identification of 41 Concordant Mutations across NRCAM, PNPLA8 and CTTNBP2. <i>PLoS ONE</i> , 2013, 8, e59251.	1.1	18

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73	RAPTR-SV: a hybrid method for the detection of structural variants. <i>Bioinformatics</i> , 2015, 31, 2084-2090.	1.8	18
74	Genomic predictions combining SNP markers and copy number variations in Nellore cattle. <i>BMC Genomics</i> , 2018, 19, 441.	1.2	18
75	Alternative splicing variants and DNA methylation status of BDNF in inbred chicken lines. <i>Brain Research</i> , 2009, 1269, 1-10.	1.1	17
76	Characterization of recombination features and the genetic basis in multiple cattle breeds. <i>BMC Genomics</i> , 2018, 19, 304.	1.2	17
77	CNV Analysis of Host Responses to Porcine Reproductive and Respiratory Syndrome Virus Infection. <i>Journal of Genomics</i> , 2017, 5, 58-63.	0.6	16
78	Single-cell transcriptomic analyses of dairy cattle ruminal epithelial cells during weaning. <i>Genomics</i> , 2021, 113, 2045-2055.	1.3	16
79	Construction of PRDM9 allele-specific recombination maps in cattle using large-scale pedigree analysis and genome-wide single sperm genomics. <i>DNA Research</i> , 2018, 25, 183-194.	1.5	15
80	Timing and Extent of Inbreeding in African Goats. <i>Frontiers in Genetics</i> , 2019, 10, 537.	1.1	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. <i>Genetics Selection Evolution</i> , 2021, 53, 56.	1.2	15
82	Genome-wide CNV analysis revealed variants associated with growth traits in African indigenous goats. <i>Genomics</i> , 2020, 112, 1477-1480.	1.3	14
83	Co-Expression Analysis of Fetal Weight-Related Genes in Ovine Skeletal Muscle during Mid and Late Fetal Development Stages. <i>International Journal of Biological Sciences</i> , 2014, 10, 1039-1050.	2.6	13
84	Integrating Signals from Sperm Methylome Analysis and Genome-Wide Association Study for a Better Understanding of Male Fertility in Cattle. <i>Epigenomes</i> , 2019, 3, 10.	0.8	12
85	Recent Applications of DNA Sequencing Technologies in Food, Nutrition and Agriculture. <i>Recent Patents on Food, Nutrition &amp; Agriculture</i> , 2011, 3, 187-195.	0.5	12
86	Transcriptional atlas analysis from multiple tissues reveals the expression specificity patterns in beef cattle. <i>BMC Biology</i> , 2022, 20, 79.	1.7	12
87	Refinement of <i>Bos taurus</i> sequence assembly based on BAC-FISH experiments. <i>BMC Genomics</i> , 2011, 12, 639.	1.2	11
88	Identification of Candidate Transcription Factor Binding Sites in the Cattle Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 195-198.	3.0	11
89	Transcriptome profiling of CTLs regulated by rapamycin using RNA-Seq. <i>Immunogenetics</i> , 2014, 66, 625-633.	1.2	11
90	Copy number variation analysis reveals variants associated with milk production traits in dairy goats. <i>Genomics</i> , 2020, 112, 4934-4937.	1.3	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. <i>PLoS ONE</i> , 2009, 4, e7978.	1.1	10
92	Genomic structural differences between cattle and River Buffalo identified through comparative genomic and transcriptomic analysis. <i>Data in Brief</i> , 2018, 19, 236-239.	0.5	10
93	Divergence Analyses of Sperm DNA Methylomes between Monozygotic Twin AI Bulls. <i>Epigenomes</i> , 2019, 3, 21.	0.8	10
94	Genomic sequencing analysis reveals copy number variations and their associations with economically important traits in beef cattle. <i>Genomics</i> , 2021, 113, 812-820.	1.3	10
95	Genome-wide association study reveals 14 new SNPs and confirms two structural variants highly associated with the horned/poled phenotype in goats. <i>BMC Genomics</i> , 2021, 22, 769.	1.2	10
96	Applications and Case Studies of the Next-Generation Sequencing Technologies in Food, Nutrition and Agriculture. <i>Recent Patents on Food, Nutrition &amp; Agriculture</i> , 2009, 1, 75-79.	0.5	9
97	Genomic expression analysis by single-cell mRNA differential display of quiescent CD8 T cells from tumour-infiltrating lymphocytes obtained from <i>in vivo</i> liver tumours. <i>Immunology</i> , 2009, 127, 83-90.	2.0	9
98	Transcriptomic Profiling of Spleen in Grass-Fed and Grain-Fed Angus Cattle. <i>PLoS ONE</i> , 2015, 10, e0135670.	1.1	9
99	Characterization of Copy Number Variation's Potential Role in Marek's Disease. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1020.	1.8	9
100	Genetic assessment of inbred chicken lines indicates genomic signatures of resistance to Marek's disease. <i>Journal of Animal Science and Biotechnology</i> , 2018, 9, 65.	2.1	9
101	Copy number variation of bovine SHH gene is associated with body conformation traits in Chinese beef cattle. <i>Journal of Applied Genetics</i> , 2019, 60, 199-207.	1.0	9
102	PRE-1 Revealed Previous Unknown Introgression Events in Eurasian Boars during the Middle Pleistocene. <i>Genome Biology and Evolution</i> , 2020, 12, 1751-1764.	1.1	9
103	Identification of Conserved Regulatory Elements in Mammalian Promoter Regions: A Case Study Using the PCK1 Promoter. <i>Genomics, Proteomics and Bioinformatics</i> , 2008, 6, 129-143.	3.0	8
104	Calibration of Mutation Rates Reveals Diverse Subfamily Structure of Galliform CR1 Repeats. <i>Genome Biology and Evolution</i> , 2009, 1, 119-130.	1.1	8
105	Genomic Analysis Reveals Specific Patterns of Homozygosity and Heterozygosity in Inbred Pigs. <i>Animals</i> , 2019, 9, 314.	1.0	8
106	Comparative sequence alignment reveals River Buffalo genomic structural differences compared with cattle. <i>Genomics</i> , 2019, 111, 418-425.	1.3	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. <i>Heliyon</i> , 2020, 6, e04112.	1.4	8
108	Butyrate Induced IGF2 Activation Correlated with Distinct Chromatin Signatures Due to Histone Modification. <i>Gene Regulation and Systems Biology</i> , 2013, 7, GRSB.S11243.	2.3	7

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109	A high-resolution whole-genome map of the distinctive epigenomic landscape induced by butyrate in bovine cells. <i>Animal Genetics</i> , 2014, 45, 40-50.	0.6	7
110	Computational detection and experimental validation of segmental duplications and associated copy number variations in water buffalo ( <i>Bubalus bubalis</i> ). <i>Functional and Integrative Genomics</i> , 2019, 19, 409-419.	1.4	7
111	Identification and population genetic analyses of copy number variations in six domestic goat breeds and Bezoar ibexes using next-generation sequencing. <i>BMC Genomics</i> , 2020, 21, 840.	1.2	7
112	Assessment of genome integrity with array CGH in cattle transgenic cell lines produced by homologous recombination and somatic cell cloning. <i>Genome Integrity</i> , 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. <i>BMC Genomics</i> , 2022, 23, 338.	1.2	6
114	Detection of copy number variants in African goats using whole genome sequence data. <i>BMC Genomics</i> , 2021, 22, 398.	1.2	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. <i>Genomics</i> , 2022, 114, 110296.	1.3	4
116	Genome-wide recombination map construction from single sperm sequencing in cattle. <i>BMC Genomics</i> , 2022, 23, 181.	1.2	4
117	Characterization of Accessible Chromatin Regions in Cattle Rumen Epithelial Tissue during Weaning. <i>Genes</i> , 2022, 13, 535.	1.0	4
118	Initial Analysis of Structural Variation Detections in Cattle Using Long-Read Sequencing Methods. <i>Genes</i> , 2022, 13, 828.	1.0	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. <i>BMC Genomics</i> , 2022, 23, .	1.2	4
120	Characterization of a novel microdeletion polymorphism on BTA5 in cattle. <i>Animal Genetics</i> , 2008, 39, 655-658.	0.6	3
121	Ruminant-specific multiple duplication events of PRDM9 before speciation. <i>BMC Evolutionary Biology</i> , 2017, 17, 79.	3.2	3
122	<i>Bos taurus</i> – <i>B. indicus</i> hybridization correlates with intralocus sexual-conflict effects of PRDM9 on male and female fertility in Holstein cattle. <i>BMC Genetics</i> , 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. <i>Data in Brief</i> , 2020, 28, 104983.	0.5	3
124	Distribution of DGAT1 copy number variation in Chinese goats and its associations with milk production traits. <i>Animal Biotechnology</i> , 2021, , 1-6.	0.7	3
125	Genome-wide association study between copy number variation regions and carcass- and meat-quality traits in Nellore cattle. <i>Animal Production Science</i> , 2021, 61, 731.	0.6	2
126	Mining Unknown Porcine Protein Isoforms by Tissue-based Map of Proteome Enhances Pig Genome Annotation. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 772-786.	3.0	2



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127	Towards the detection of copy number variation from single sperm sequencing in cattle. BMC Genomics, 2022, 23, 215.	1.2	2
128	The Dynamics of Chromatin Accessibility Prompted by Butyrate-Induced Chromatin Modification in Bovine Cells. Ruminants, 2022, 2, 226-243.	0.4	2
129	Statistical Detection of Genome Differences Based on CNV Segments. Methods in Molecular Biology, 2018, 1833, 49-59.	0.4	1
130	Analysis of Population-Genetic Properties of Copy Number Variations. Methods in Molecular Biology, 2018, 1833, 179-186.	0.4	1
131	Effect of Temperature and Maternal Age on Recombination Rate in Cattle. Frontiers in Genetics, 2021, 12, 682718.	1.1	1
132	Transcriptional Reprogramming in Rumen Epithelium during the Developmental Transition of Pre-Ruminant to the Ruminant in Cattle. Animals, 2021, 11, 2870.	1.0	1
133	Insights from Initial Variant Detection by Sequencing Single Sperm in Cattle. Dairy, 2021, 2, 649-657.	0.7	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