

George E Liu

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

132
papers

5,034
citations

33
h-index

69
g-index

141
ext. papers

6,750
ext. citations

5
avg, IF

5.04
L-index

#	Paper	IF	Citations
132	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	4.3	0
131	Genome-wide recombination map construction from single sperm sequencing in cattle.. <i>BMC Genomics</i> , 2022 , 23, 181	4.5	1
130	Transcriptional atlas analysis from multiple tissues reveals the expression specificity patterns in beef cattle.. <i>BMC Biology</i> , 2022 , 20, 79	7.3	2
129	Towards the detection of copy number variation from single sperm sequencing in cattle.. <i>BMC Genomics</i> , 2022 , 23, 215	4.5	
128	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	4.5	0
127	Initial Analysis of Structural Variation Detections in Cattle Using Long-Read Sequencing Methods. <i>Genes</i> , 2022 , 13, 828	4.2	0
126	The Dynamics of Chromatin Accessibility Prompted by Butyrate-Induced Chromatin Modification in Bovine Cells. <i>Ruminants</i> , 2022 , 2, 226-243		0
125	Insights from Initial Variant Detection by Sequencing Single Sperm in Cattle. <i>Dairy</i> , 2021 , 2, 649-657	2.6	1
124	Distribution of copy number variation in Chinese goats and its associations with milk production traits. <i>Animal Biotechnology</i> , 2021 , 1-6	1.4	1
123	Genome-wide association study reveals 14 new SNPs and confirms two structural variants highly associated with the horned/polled phenotype in goats. <i>BMC Genomics</i> , 2021 , 22, 769	4.5	3
122	Detection of copy number variants in African goats using whole genome sequence data. <i>BMC Genomics</i> , 2021 , 22, 398	4.5	0
121	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	4.9	1
120	Effect of Temperature and Maternal Age on Recombination Rate in Cattle. <i>Frontiers in Genetics</i> , 2021 , 12, 682718	4.5	
119	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	8.3	6
118	Genomic sequencing analysis reveals copy number variations and their associations with economically important traits in beef cattle. <i>Genomics</i> , 2021 , 113, 812-820	4.3	2
117	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	1.4	2
116	Single-cell transcriptomic analyses of dairy cattle ruminal epithelial cells during weaning. <i>Genomics</i> , 2021 , 113, 2045-2055	4.3	3

115	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	7.3	2
114	Comprehensive analyses of 723 transcriptomes enhance genetic and biological interpretations for complex traits in cattle. <i>Genome Research</i> , 2020 , 30, 790-801	9.7	40
113	Comparative whole genome DNA methylation profiling across cattle tissues reveals global and tissue-specific methylation patterns. <i>BMC Biology</i> , 2020 , 18, 85	7.3	11
112	Epigenomics and genotype-phenotype association analyses reveal conserved genetic architecture of complex traits in cattle and human. <i>BMC Biology</i> , 2020 , 18, 80	7.3	12
111	GWAS and fine-mapping of livability and six disease traits in Holstein cattle. <i>BMC Genomics</i> , 2020 , 21, 41	4.5	26
110	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	1.2	1
109	Comparative analyses of copy number variations between <i>Bos taurus</i> and <i>Bos indicus</i> . <i>BMC Genomics</i> , 2020 , 21, 682	4.5	8
108	Copy number variation analysis reveals variants associated with milk production traits in dairy goats. <i>Genomics</i> , 2020 , 112, 4934-4937	4.3	4
107	PRE-1 Revealed Previous Unknown Introgression Events in Eurasian Boars during the Middle Pleistocene. <i>Genome Biology and Evolution</i> , 2020 , 12, 1751-1764	3.9	1
106	Integrating RNA-Seq with GWAS reveals novel insights into the molecular mechanism underpinning ketosis in cattle. <i>BMC Genomics</i> , 2020 , 21, 489	4.5	10
105	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	3.6	4
104	Genome-Wide Assessment of Runs of Homozygosity in Chinese Wagyu Beef Cattle. <i>Animals</i> , 2020 , 10,	3.1	7
103	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	4.5	0
102	Genome-wide CNV analysis revealed variants associated with growth traits in African indigenous goats. <i>Genomics</i> , 2020 , 112, 1477-1480	4.3	4
101	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020 , 9,	7.6	140
100	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	7.3	22
99	<i>Bos taurus-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	2.6	2
98	Genomic Analysis Reveals Specific Patterns of Homozygosity and Heterozygosity in Inbred Pigs. <i>Animals</i> , 2019 , 9,	3.1	7

97	Probe-based association analysis identifies several deletions associated with average daily gain in beef cattle. <i>BMC Genomics</i> , 2019 , 20, 31	4.5	11
96	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,	2.3	9
95	Genome-wide scan reveals genetic divergence and diverse adaptive selection in Chinese local cattle. <i>BMC Genomics</i> , 2019 , 20, 494	4.5	9
94	Epigenetics and heritable phenotypic variations in livestock 2019 , 283-313		
93	Timing and Extent of Inbreeding in African Goats. <i>Frontiers in Genetics</i> , 2019 , 10, 537	4.5	8
92	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	2.5	4
91	Genetic and epigenetic architecture of paternal origin contribute to gestation length in cattle. <i>Communications Biology</i> , 2019 , 2, 100	6.7	21
90	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	5.7	14
89	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	4.5	11
88	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	3.8	3
87	Genome changes due to artificial selection in U.S. Holstein cattle. <i>BMC Genomics</i> , 2019 , 20, 128	4.5	18
86	Divergence Analyses of Sperm DNA Methylomes between Monozygotic Twin AI Bulls.. <i>Epigenomes</i> , 2019 , 3,	2.3	5
85	Genomic Patterns of Homozygosity in Chinese Local Cattle. <i>Scientific Reports</i> , 2019 , 9, 16977	4.9	17
84	Analyses of inter-individual variations of sperm DNA methylation and their potential implications in cattle. <i>BMC Genomics</i> , 2019 , 20, 888	4.5	13
83	Diversity of copy number variation in the worldwide goat population. <i>Heredity</i> , 2019 , 122, 636-646	3.6	29
82	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	3.2	20
81	Comparative sequence alignment reveals River Buffalo genomic structural differences compared with cattle. <i>Genomics</i> , 2019 , 111, 418-425	4.3	5
80	The essence of appetite: does olfactory receptor variation play a role?. <i>Journal of Animal Science</i> , 2018 , 96, 1551-1558	0.7	10

79	Comparative whole genome DNA methylation profiling of cattle sperm and somatic tissues reveals striking hypomethylated patterns in sperm. <i>GigaScience</i> , 2018 , 7,	7.6	34
78	Genetic Architecture and Selection of Chinese Cattle Revealed by Whole Genome Resequencing. <i>Molecular Biology and Evolution</i> , 2018 , 35, 688-699	8.3	47
77	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	4.5	7
76	Characterization of recombination features and the genetic basis in multiple cattle breeds. <i>BMC Genomics</i> , 2018 , 19, 304	4.5	10
75	Diversity of copy number variation in a worldwide population of sheep. <i>Genomics</i> , 2018 , 110, 143-148	4.3	32
74	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	4.9	17
73	Genomic predictions combining SNP markers and copy number variations in Nellore cattle. <i>BMC Genomics</i> , 2018 , 19, 441	4.5	8
72	Genome-wide copy number variant analysis reveals variants associated with 10 diverse production traits in Holstein cattle. <i>BMC Genomics</i> , 2018 , 19, 314	4.5	25
71	Statistical Detection of Genome Differences Based on CNV Segments. <i>Methods in Molecular Biology</i> , 2018 , 1833, 49-59	1.4	1
70	Analysis of Population-Genetic Properties of Copy Number Variations. <i>Methods in Molecular Biology</i> , 2018 , 1833, 179-186	1.4	1
69	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	6	5
68	Evidence of evolutionary history and selective sweeps in the genome of Meishan pig reveals its genetic and phenotypic characterization. <i>GigaScience</i> , 2018 , 7,	7.6	19
67	Genomic structural differences between cattle and River Buffalo identified through comparative genomic and transcriptomic analysis. <i>Data in Brief</i> , 2018 , 19, 236-239	1.2	7
66	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	36.3	323
65	Genome-wide analysis reveals differential selection involved with copy number variation in diverse Chinese Cattle. <i>Scientific Reports</i> , 2017 , 7, 14299	4.9	17
64	CNV Analysis of Host Responses to Porcine Reproductive and Respiratory Syndrome Virus Infection. <i>Journal of Genomics</i> , 2017 , 5, 58-63	0.9	5
63	Systematic Profiling of Short Tandem Repeats in the Cattle Genome. <i>Genome Biology and Evolution</i> , 2017 , 9, 20-31	3.9	8
62	A PLAG1 mutation contributed to stature recovery in modern cattle. <i>Scientific Reports</i> , 2017 , 7, 17140	4.9	32

61	Ruminant-specific multiple duplication events of PRDM9 before speciation. <i>BMC Evolutionary Biology</i> , 2017 , 17, 79	3	3
60	CNV discovery for milk composition traits in dairy cattle using whole genome resequencing. <i>BMC Genomics</i> , 2017 , 18, 265	4.5	40
59	Characterization of Copy Number Variation & Potential Role in Marek's Disease. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	6
58	Population-genetic properties of differentiated copy number variations in cattle. <i>Scientific Reports</i> , 2016 , 6, 23161	4.9	52
57	Diversity and population-genetic properties of copy number variations and multicopy genes in cattle. <i>DNA Research</i> , 2016 , 23, 253-62	4.5	46
56	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	4.5	20
55	Genome-wide CNV analysis reveals variants associated with growth traits in <i>Bos indicus</i> . <i>BMC Genomics</i> , 2016 , 17, 419	4.5	44
54	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	4.9	16
53	Genomic signatures reveal new evidences for selection of important traits in domestic cattle. <i>Molecular Biology and Evolution</i> , 2015 , 32, 711-25	8.3	93
52	Copy number variation-based genome wide association study reveals additional variants contributing to meat quality in Swine. <i>Scientific Reports</i> , 2015 , 5, 12535	4.9	19
51	Transcriptomic Profiling of Spleen in Grass-Fed and Grain-Fed Angus Cattle. <i>PLoS ONE</i> , 2015 , 10, e0135637	3.9	6
50	RAPTR-SV: a hybrid method for the detection of structural variants. <i>Bioinformatics</i> , 2015 , 31, 2084-90	7.2	14
49	Cattle Sex-Specific Recombination and Genetic Control from a Large Pedigree Analysis. <i>PLoS Genetics</i> , 2015 , 11, e1005387	6	112
48	A high-resolution whole-genome map of the distinctive epigenomic landscape induced by butyrate in bovine cells. <i>Animal Genetics</i> , 2014 , 45 Suppl 1, 40-50	2.5	5
47	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. <i>BMC Genomics</i> , 2014 , 15, 683	4.5	63
46	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, 333-9	3.8	22
45	Assessing signatures of selection through variation in linkage disequilibrium between taurine and indicine cattle. <i>Genetics Selection Evolution</i> , 2014 , 46, 19	4.9	50
44	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	4.5	93

43	Functional proteomic and interactome analysis of proteins associated with beef tenderness in Angus cattle. <i>Livestock Science</i> , 2014 , 161, 201-209	1.7	23
42	The challenges and importance of structural variation detection in livestock. <i>Frontiers in Genetics</i> , 2014 , 5, 37	4.5	61
41	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	3.7	55
40	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, 1039-50	11.2	8
39	Transcriptome profiling of CTLs regulated by rapamycin using RNA-Seq. <i>Immunogenetics</i> , 2014 , 66, 625-332	3.3	6
38	Identification of candidate transcription factor binding sites in the cattle genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2013 , 11, 195-8	6.5	10
37	Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. <i>BMC Genomics</i> , 2013 , 14, 876	4.5	93
36	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, 171-85		32
35	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, 217-23	3.2	28
34	Butyrate Induced IGF2 Activation Correlated with Distinct Chromatin Signatures Due to Histone Modification. <i>Gene Regulation and Systems Biology</i> , 2013 , 7, 57-70	2	5
33	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	3.7	12
32	Effect of artificial selection on runs of homozygosity in u.s. Holstein cattle. <i>PLoS ONE</i> , 2013 , 8, e80813	3.7	114
31	Muscle transcriptomic analyses in Angus cattle with divergent tenderness. <i>Molecular Biology Reports</i> , 2012 , 39, 4185-93	2.8	33
30	Copy number variation in the cattle genome. <i>Functional and Integrative Genomics</i> , 2012 , 12, 609-24	3.8	38
29	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, 717-23	3.8	45
28	miRNA-dysregulation associated with tenderness variation induced by acute stress in Angus cattle. <i>Journal of Animal Science and Biotechnology</i> , 2012 , 3, 12	6	13
27	Copy number variation of individual cattle genomes using next-generation sequencing. <i>Genome Research</i> , 2012 , 22, 778-90	9.7	204
26	Fine mapping of copy number variations on two cattle genome assemblies using high density SNP array. <i>BMC Genomics</i> , 2012 , 13, 376	4.5	71

25	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	3.8	71
24	Functional genomic analysis of variation on beef tenderness induced by acute stress in angus cattle. <i>Comparative and Functional Genomics</i> , 2012 , 2012, 756284		34
23	Initial analysis of copy number variations in cattle selected for resistance or susceptibility to intestinal nematodes. <i>Mammalian Genome</i> , 2011 , 22, 111-21	3.2	36
22	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	0.8	5
21	Genomic characteristics of cattle copy number variations. <i>BMC Genomics</i> , 2011 , 12, 127	4.5	156
20	Refinement of Bos taurus sequence assembly based on BAC-FISH experiments. <i>BMC Genomics</i> , 2011 , 12, 639	4.5	10
19	Recent applications of DNA sequencing technologies in food, nutrition and agriculture. <i>Recent Patents on Food, Nutrition & Agriculture</i> , 2011 , 3, 187-95	1.9	8
18	Analysis of copy number variations among diverse cattle breeds. <i>Genome Research</i> , 2010 , 20, 693-703	9.7	214
17	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	3.7	10
16	Applications and case studies of the next-generation sequencing technologies in food, nutrition and agriculture. <i>Recent Patents on Food, Nutrition & Agriculture</i> , 2009 , 1, 75-9	1.9	8
15	Activation of SIRT1 by resveratrol represses transcription of the gene for the cytosolic form of phosphoenolpyruvate carboxykinase (GTP) by deacetylating hepatic nuclear factor 4alpha. <i>Journal of Biological Chemistry</i> , 2009 , 284, 27042-53	5.4	64
14	Calibration of mutation rates reveals diverse subfamily structure of galliform CR1 repeats. <i>Genome Biology and Evolution</i> , 2009 , 1, 119-30	3.9	4
13	Comparative analysis of Alu repeats in primate genomes. <i>Genome Research</i> , 2009 , 19, 876-85	9.7	55
12	Analysis of recent segmental duplications in the bovine genome. <i>BMC Genomics</i> , 2009 , 10, 571	4.5	67
11	Alternative splicing variants and DNA methylation status of BDNF in inbred chicken lines. <i>Brain Research</i> , 2009 , 1269, 1-10	3.7	15
10	Genomic expression analysis by single-cell mRNA differential display of quiescent CD8 T cells from tumour-infiltrating lymphocytes obtained from in vivo liver tumours. <i>Immunology</i> , 2009 , 127, 83-90	7.8	5
9	Mucin biosynthesis in the bovine goblet cell induced by Cooperia oncophora infection. <i>Veterinary Parasitology</i> , 2009 , 165, 281-9	2.8	22
8	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863

7	Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. <i>Science</i> , 2009 , 324, 528-32	33.3	612
6	Characterization of a novel microdeletion polymorphism on BTA5 in cattle. <i>Animal Genetics</i> , 2008 , 39, 655-8	2.5	3
5	Identification of conserved regulatory elements in mammalian promoter regions: a case study using the PCK1 promoter. <i>Genomics, Proteomics and Bioinformatics</i> , 2008 , 6, 129-43	6.5	8
4	Protein accumulation in the germinating <i>Uromyces appendiculatus</i> uredospore. <i>Molecular Plant-Microbe Interactions</i> , 2007 , 20, 857-66	3.6	34
3	Genomic divergences among cattle, dog and human estimated from large-scale alignments of genomic sequences. <i>BMC Genomics</i> , 2006 , 7, 140	4.5	28
2	Single-molecule sequencing and conformational capture enable de novo mammalian reference genomes		12
1	A comprehensive catalogue of regulatory variants in the cattle transcriptome		6