

Derek M Bickhart

List of Publications by Year in descending order

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Version: 2024-02-01

78
papers

6,303
citations

101543

36
h-index

82547

72
g-index

95
all docs

95
docs citations

95
times ranked

6664
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	21.4	600
2	metaFlye: scalable long-read metagenome assembly using repeat graphs. <i>Nature Methods</i> , 2020, 17, 1103-1110.	19.0	430
3	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	6.4	380
4	Genome characteristics of facultatively symbiotic <i>Frankia</i> sp. strains reflect host range and host plant biogeography. <i>Genome Research</i> , 2006, 17, 7-15.	5.5	352
5	De novo assembly of haplotype-resolved genomes with trio binning. <i>Nature Biotechnology</i> , 2018, 36, 1174-1182.	17.5	352
6	Copy number variation of individual cattle genomes using next-generation sequencing. <i>Genome Research</i> , 2012, 22, 778-790.	5.5	259
7	On the chimeric nature, thermophilic origin, and phylogenetic placement of the Thermotogales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5865-5870.	7.1	221
8	Genomic characteristics of cattle copy number variations. <i>BMC Genomics</i> , 2011, 12, 127.	2.8	201
9	Scaffolding of long read assemblies using long range contact information. <i>BMC Genomics</i> , 2017, 18, 527.	2.8	194
10	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020, 9, .	6.4	187
11	Genomic Signatures Reveal New Evidences for Selection of Important Traits in Domestic Cattle. <i>Molecular Biology and Evolution</i> , 2015, 32, 711-725.	8.9	173
12	Cattle Sex-Specific Recombination and Genetic Control from a Large Pedigree Analysis. <i>PLoS Genetics</i> , 2015, 11, e1005387.	3.5	168
13	Chromosome-level assembly of the water buffalo genome surpasses human and goat genomes in sequence contiguity. <i>Nature Communications</i> , 2019, 10, 260.	12.8	161
14	Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. <i>BMC Genomics</i> , 2013, 14, 876.	2.8	142
15	Genome to Phenome: Improving Animal Health, Production, and Well-Being – A New USDA Blueprint for Animal Genome Research 2018–2027. <i>Frontiers in Genetics</i> , 2019, 10, 327.	2.3	118
16	Selecting sequence variants to improve genomic predictions for dairy cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 32.	3.0	113
17	The challenges and importance of structural variation detection in livestock. <i>Frontiers in Genetics</i> , 2014, 5, 37.	2.3	104
18	Generating lineage-resolved, complete metagenome-assembled genomes from complex microbial communities. <i>Nature Biotechnology</i> , 2022, 40, 711-719.	17.5	99

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19	Population-genetic properties of differentiated copy number variations in cattle. <i>Scientific Reports</i> , 2016, 6, 23161.	3.3	91
20	Fine mapping of copy number variations on two cattle genome assemblies using high density SNP array. <i>BMC Genomics</i> , 2012, 13, 376.	2.8	90
21	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. <i>BMC Genomics</i> , 2014, 15, 683.	2.8	89
22	Identification of a Nonsense Mutation in CWC15 Associated with Decreased Reproductive Efficiency in Jersey Cattle. <i>PLoS ONE</i> , 2013, 8, e54872.	2.5	88
23	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.	3.5	87
24	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. <i>Nature Communications</i> , 2020, 11, 2071.	12.8	84
25	Assessing signatures of selection through variation in linkage disequilibrium between taurine and indicine cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 19.	3.0	79
26	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.	2.5	69
27	Genome-wide CNV analysis reveals variants associated with growth traits in <i>Bos indicus</i> . <i>BMC Genomics</i> , 2016, 17, 419.	2.8	69
28	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation. <i>Genome Biology</i> , 2019, 20, 153.	8.8	66
29	Copy number variation in the cattle genome. <i>Functional and Integrative Genomics</i> , 2012, 12, 609-624.	3.5	60
30	Comparative whole genome DNA methylation profiling of cattle sperm and somatic tissues reveals striking hypomethylated patterns in sperm. <i>GigaScience</i> , 2018, 7, .	6.4	60
31	Diversity and population-genetic properties of copy number variations and multicopy genes in cattle. <i>DNA Research</i> , 2016, 23, 253-262.	3.4	59
32	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.	3.5	51
33	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	6.4	46
34	Convergent Evolution of Slick Coat in Cattle through Truncation Mutations in the Prolactin Receptor. <i>Frontiers in Genetics</i> , 2018, 9, 57.	2.3	45
35	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.	3.3	44
36	A PLAG1 mutation contributed to stature recovery in modern cattle. <i>Scientific Reports</i> , 2017, 7, 17140.	3.3	42

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37	Revealing misassembled segments in the bovine reference genome by high resolution linkage disequilibrium scan. <i>BMC Genomics</i> , 2016, 17, 705.	2.8	41
38	The evolution of the natural killer complex; a comparison between mammals using new high-quality genome assemblies and targeted annotation. <i>Immunogenetics</i> , 2017, 69, 255-269.	2.4	40
39	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
40	The Biology of <i>Frankia</i> sp. Strains in the Post-Genome Era. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 1310-1316.	2.6	36
41	The antibody loci of the domestic goat (<i>Capra hircus</i>). <i>Immunogenetics</i> , 2018, 70, 317-326.	2.4	35
42	Insertion sequence content reflects genome plasticity in strains of the root nodule actinobacterium <i>Frankia</i> . <i>BMC Genomics</i> , 2009, 10, 468.	2.8	34
43	Misidentification of runs of homozygosity islands in cattle caused by interference with copy number variation or large intermarker distances. <i>Genetics Selection Evolution</i> , 2018, 50, 43.	3.0	32
44	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.	2.8	30
45	Transcriptomes of <i>Frankia</i> sp. strain Ccl3 in growth transitions. <i>BMC Microbiology</i> , 2011, 11, 192.	3.3	26
46	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.	2.7	25
47	A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i> . <i>Journal of Heredity</i> , 2021, 112, 184-191.	2.4	25
48	Variants at the ASIP locus contribute to coat color darkening in Nellore cattle. <i>Genetics Selection Evolution</i> , 2021, 53, 40.	3.0	25
49	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.	3.5	24
50	An improved ovine reference genome assembly to facilitate in-depth functional annotation of the sheep genome. <i>GigaScience</i> , 2022, 11, .	6.4	24
51	New insights into mammalian sex chromosome structure and evolution using high-quality sequences from bovine X and Y chromosomes. <i>BMC Genomics</i> , 2019, 20, 1000.	2.8	21
52	Systematic profiling of short tandem repeats in the cattle genome. <i>Genome Biology and Evolution</i> , 2016, 9, evw256.	2.5	20
53	Annotated Draft Genome Assemblies for the Northern Bobwhite (<i>Colinus virginianus</i>) and the Scaled Quail (<i>Callipepla squamata</i>) Reveal Disparate Estimates of Modern Genome Diversity and Historic Effective Population Size. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3047-3058.	1.8	20
54	Structural variant-based pangenome construction has low sensitivity to variability of haplotype-resolved bovine assemblies. <i>Nature Communications</i> , 2022, 13, .	12.8	19

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55	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
56	RAPTR-SV: a hybrid method for the detection of structural variants. Bioinformatics, 2015, 31, 2084-2090.	4.1	18
57	Genomic predictions combining SNP markers and copy number variations in Nellore cattle. BMC Genomics, 2018, 19, 441.	2.8	18
58	The Structure, Evolution, and Gene Expression Within the Caprine Leukocyte Receptor Complex. Frontiers in Immunology, 2019, 10, 2302.	4.8	17
59	Transcriptomics analysis of host liver and meta-transcriptome analysis of rumen epimural microbial community in young calves treated with artificial dosing of rumen content from adult donor cow. Scientific Reports, 2019, 9, 790.	3.3	16
60	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . Journal of Heredity, 2021, 112, 174-183.	2.4	14
61	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
62	Identification of Candidate Transcription Factor Binding Sites in the Cattle Genome. Genomics, Proteomics and Bioinformatics, 2013, 11, 195-198.	6.9	11
63	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
64	Characterization of the domestic goat β T cell receptor gene loci and gene usage. Immunogenetics, 2021, 73, 187-201.	2.4	10
65	Effect of consuming endophyte-infected fescue seed on transcript abundance in the mammary gland of lactating and dry cows, as assessed by RNA sequencing. Journal of Dairy Science, 2018, 101, 10478-10494.	3.4	8
66	Comparative sequence alignment reveals River Buffalo genomic structural differences compared with cattle. Genomics, 2019, 111, 418-425.	2.9	8
67	Validating the Use of Bovine Buccal Sampling as a Proxy for the Rumen Microbiota by Using a Time Course and Random Forest Classification Approach. Applied and Environmental Microbiology, 2020, 86, .	3.1	8
68	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
69	Computational detection and experimental validation of segmental duplications and associated copy number variations in water buffalo (<i>Bubalus bubalis</i>). Functional and Integrative Genomics, 2019, 19, 409-419.	3.5	7
70	Chromosome-scale assembly of the highly heterozygous genome of red clover (<i>Trifolium pratense</i> L.), an allogamous forage crop species. GigaByte, 0, 2022, 1-13.	0.0	6
71	Defining the caprine β T cell WC1 multigenic array and evaluation of its expressed sequences and gene structure conservation among goat breeds and relative to cattle. Immunogenetics, 2022, 74, 347-365.	2.4	4
72	Examination of the xanthosine response on gene expression of mammary epithelial cells using RNA-seq technology. Journal of Animal Science and Technology, 2018, 60, 18.	2.5	3

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73	Gaur genome reveals expansion of sperm odorant receptors in domesticated cattle. BMC Genomics, 2022, 23, 344.	2.8	3
74	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
75	Development of polymorphic markers in the immune gene complex loci of cattle. Journal of Dairy Science, 2021, 104, 6897-6908.	3.4	2
76	Statistical Detection of Genome Differences Based on CNV Segments. Methods in Molecular Biology, 2018, 1833, 49-59.	0.9	1
77	Analysis of Population-Genetic Properties of Copy Number Variations. Methods in Molecular Biology, 2018, 1833, 179-186.	0.9	1
78	Use of RAPTR-SV to Identify SVs from Read Pairing and Split Read Signatures. Methods in Molecular Biology, 2018, 1833, 143-153.	0.9	1