

# Derek M Bickhart

## List of Publications by Year in descending order

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78  
papers

6,303  
citations

101384

36  
h-index

82410

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.	9.4	600
2	metaFlye: scalable long-read metagenome assembly using repeat graphs. <i>Nature Methods</i> , 2020, 17, 1103-1110.	9.0	430
3	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	3.3	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.	2.4	352
5	De novo assembly of haplotype-resolved genomes with trio binning. <i>Nature Biotechnology</i> , 2018, 36, 1174-1182.	9.4	352
6	Copy number variation of individual cattle genomes using next-generation sequencing. <i>Genome Research</i> , 2012, 22, 778-790.	2.4	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.	3.3	221
8	Genomic characteristics of cattle copy number variations. <i>BMC Genomics</i> , 2011, 12, 127.	1.2	201
9	Scaffolding of long read assemblies using long range contact information. <i>BMC Genomics</i> , 2017, 18, 527.	1.2	194
10	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020, 9, .	3.3	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.	3.5	173
12	Cattle Sex-Specific Recombination and Genetic Control from a Large Pedigree Analysis. <i>PLoS Genetics</i> , 2015, 11, e1005387.	1.5	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.	5.8	161
14	Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. <i>BMC Genomics</i> , 2013, 14, 876.	1.2	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.	1.1	118
16	Selecting sequence variants to improve genomic predictions for dairy cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 32.	1.2	113
17	The challenges and importance of structural variation detection in livestock. <i>Frontiers in Genetics</i> , 2014, 5, 37.	1.1	104
18	Generating lineage-resolved, complete metagenome-assembled genomes from complex microbial communities. <i>Nature Biotechnology</i> , 2022, 40, 711-719.	9.4	99

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19	Population-genetic properties of differentiated copy number variations in cattle. <i>Scientific Reports</i> , 2016, 6, 23161.	1.6	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.	1.2	90
21	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. <i>BMC Genomics</i> , 2014, 15, 683.	1.2	89
22	Identification of a Nonsense Mutation in CWC15 Associated with Decreased Reproductive Efficiency in Jersey Cattle. <i>PLoS ONE</i> , 2013, 8, e54872.	1.1	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.	1.4	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.	5.8	84
25	Assessing signatures of selection through variation in linkage disequilibrium between taurine and indicine cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 19.	1.2	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.	1.1	69
27	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
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.	3.8	66
29	Copy number variation in the cattle genome. <i>Functional and Integrative Genomics</i> , 2012, 12, 609-624.	1.4	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, .	3.3	60
31	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
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.	1.4	51
33	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	3.3	46
34	Convergent Evolution of Slick Coat in Cattle through Truncation Mutations in the Prolactin Receptor. <i>Frontiers in Genetics</i> , 2018, 9, 57.	1.1	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.	1.6	44
36	A PLAG1 mutation contributed to stature recovery in modern cattle. <i>Scientific Reports</i> , 2017, 7, 17140.	1.6	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.	1.2	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.	1.2	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.	1.4	36
41	The antibody loci of the domestic goat ( <i>Capra hircus</i> ). <i>Immunogenetics</i> , 2018, 70, 317-326.	1.2	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.	1.2	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.	1.2	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.	1.2	30
45	Transcriptomes of <i>Frankia</i> sp. strain Ccl3 in growth transitions. <i>BMC Microbiology</i> , 2011, 11, 192.	1.3	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.	1.3	25
47	A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i> . <i>Journal of Heredity</i> , 2021, 112, 184-191.	1.0	25
48	Variants at the ASIP locus contribute to coat color darkening in Nellore cattle. <i>Genetics Selection Evolution</i> , 2021, 53, 40.	1.2	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.	1.4	24
50	An improved ovine reference genome assembly to facilitate in-depth functional annotation of the sheep genome. <i>GigaScience</i> , 2022, 11, .	3.3	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.	1.2	21
52	Systematic profiling of short tandem repeats in the cattle genome. <i>Genome Biology and Evolution</i> , 2016, 9, evw256.	1.1	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.	0.8	20
54	Structural variant-based pangenome construction has low sensitivity to variability of haplotype-resolved bovine assemblies. <i>Nature Communications</i> , 2022, 13, .	5.8	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. <i>PLoS ONE</i> , 2013, 8, e59251.	1.1	18
56	RAPTR-SV: a hybrid method for the detection of structural variants. <i>Bioinformatics</i> , 2015, 31, 2084-2090.	1.8	18
57	Genomic predictions combining SNP markers and copy number variations in Nellore cattle. <i>BMC Genomics</i> , 2018, 19, 441.	1.2	18
58	The Structure, Evolution, and Gene Expression Within the Caprine Leukocyte Receptor Complex. <i>Frontiers in Immunology</i> , 2019, 10, 2302.	2.2	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. <i>Scientific Reports</i> , 2019, 9, 790.	1.6	16
60	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . <i>Journal of Heredity</i> , 2021, 112, 174-183.	1.0	14
61	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
62	Identification of Candidate Transcription Factor Binding Sites in the Cattle Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 195-198.	3.0	11
63	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
64	Characterization of the domestic goat $\beta$ T cell receptor gene loci and gene usage. <i>Immunogenetics</i> , 2021, 73, 187-201.	1.2	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. <i>Journal of Dairy Science</i> , 2018, 101, 10478-10494.	1.4	8
66	Comparative sequence alignment reveals River Buffalo genomic structural differences compared with cattle. <i>Genomics</i> , 2019, 111, 418-425.	1.3	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. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	8
68	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
69	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
70	Chromosome-scale assembly of the highly heterozygous genome of red clover ( <i>Trifolium pratense</i> L.), an allogamous forage crop species. <i>GigaByte</i> , 0, 2022, 1-13.	0.0	6
71	Defining the caprine $\beta$ T cell WC1 multigenic array and evaluation of its expressed sequences and gene structure conservation among goat breeds and relative to cattle. <i>Immunogenetics</i> , 2022, 74, 347-365.	1.2	4
72	Examination of the xanthosine response on gene expression of mammary epithelial cells using RNA-seq technology. <i>Journal of Animal Science and Technology</i> , 2018, 60, 18.	0.8	3

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73	Gaur genome reveals expansion of sperm odorant receptors in domesticated cattle. BMC Genomics, 2022, 23, 344.	1.2	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.	0.6	2
75	Development of polymorphic markers in the immune gene complex loci of cattle. Journal of Dairy Science, 2021, 104, 6897-6908.	1.4	2
76	Statistical Detection of Genome Differences Based on CNV Segments. Methods in Molecular Biology, 2018, 1833, 49-59.	0.4	1
77	Analysis of Population-Genetic Properties of Copy Number Variations. Methods in Molecular Biology, 2018, 1833, 179-186.	0.4	1
78	Use of RAPTR-SV to Identify SVs from Read Pairing and Split Read Signatures. Methods in Molecular Biology, 2018, 1833, 143-153.	0.4	1