

# 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	Generating lineage-resolved, complete metagenome-assembled genomes from complex microbial communities. <i>Nature Biotechnology</i> , 2022, 40, 711-719.	9.4	99
2	An improved ovine reference genome assembly to facilitate in-depth functional annotation of the sheep genome. <i>GigaScience</i> , 2022, 11, .	3.3	24
3	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
4	Gaur genome reveals expansion of sperm odorant receptors in domesticated cattle. <i>BMC Genomics</i> , 2022, 23, 344.	1.2	3
5	Structural variant-based pangenome construction has low sensitivity to variability of haplotype-resolved bovine assemblies. <i>Nature Communications</i> , 2022, 13, .	5.8	19
6	A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i> . <i>Journal of Heredity</i> , 2021, 112, 184-191.	1.0	25
7	Characterization of the domestic goat $\beta$ T cell receptor gene loci and gene usage. <i>Immunogenetics</i> , 2021, 73, 187-201.	1.2	10
8	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
9	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . <i>Journal of Heredity</i> , 2021, 112, 174-183.	1.0	14
10	Variants at the ASIP locus contribute to coat color darkening in Nellore cattle. <i>Genetics Selection Evolution</i> , 2021, 53, 40.	1.2	25
11	Development of polymorphic markers in the immune gene complex loci of cattle. <i>Journal of Dairy Science</i> , 2021, 104, 6897-6908.	1.4	2
12	metaFlye: scalable long-read metagenome assembly using repeat graphs. <i>Nature Methods</i> , 2020, 17, 1103-1110.	9.0	430
13	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020, 9, .	3.3	187
14	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
15	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
16	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	3.3	46
17	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	3.3	380
18	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

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19	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
20	The Structure, Evolution, and Gene Expression Within the Caprine Leukocyte Receptor Complex. <i>Frontiers in Immunology</i> , 2019, 10, 2302.	2.2	17
21	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
22	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
23	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
24	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
25	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
26	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
27	Comparative sequence alignment reveals River Buffalo genomic structural differences compared with cattle. <i>Genomics</i> , 2019, 111, 418-425.	1.3	8
28	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
29	The antibody loci of the domestic goat ( <i>Capra hircus</i> ). <i>Immunogenetics</i> , 2018, 70, 317-326.	1.2	35
30	De novo assembly of haplotype-resolved genomes with trio binning. <i>Nature Biotechnology</i> , 2018, 36, 1174-1182.	9.4	352
31	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
32	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
33	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
34	Genomic predictions combining SNP markers and copy number variations in Nellore cattle. <i>BMC Genomics</i> , 2018, 19, 441.	1.2	18
35	Statistical Detection of Genome Differences Based on CNV Segments. <i>Methods in Molecular Biology</i> , 2018, 1833, 49-59.	0.4	1
36	Analysis of Population-Genetic Properties of Copy Number Variations. <i>Methods in Molecular Biology</i> , 2018, 1833, 179-186.	0.4	1

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37	Use of RAPTR-SV to Identify SVs from Read Pairing and Split Read Signatures. <i>Methods in Molecular Biology</i> , 2018, 1833, 143-153.	0.4	1
38	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
39	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
40	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
41	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
42	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
43	A PLAG1 mutation contributed to stature recovery in modern cattle. <i>Scientific Reports</i> , 2017, 7, 17140.	1.6	42
44	Selecting sequence variants to improve genomic predictions for dairy cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 32.	1.2	113
45	Scaffolding of long read assemblies using long range contact information. <i>BMC Genomics</i> , 2017, 18, 527.	1.2	194
46	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
47	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
48	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
49	Revealing misassembled segments in the bovine reference genome by high resolution linkage disequilibrium scan. <i>BMC Genomics</i> , 2016, 17, 705.	1.2	41
50	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
51	Systematic profiling of short tandem repeats in the cattle genome. <i>Genome Biology and Evolution</i> , 2016, 9, evw256.	1.1	20
52	Population-genetic properties of differentiated copy number variations in cattle. <i>Scientific Reports</i> , 2016, 6, 23161.	1.6	91
53	RAPTR-SV: a hybrid method for the detection of structural variants. <i>Bioinformatics</i> , 2015, 31, 2084-2090.	1.8	18
54	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

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55	Cattle Sex-Specific Recombination and Genetic Control from a Large Pedigree Analysis. <i>PLoS Genetics</i> , 2015, 11, e1005387.	1.5	168
56	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
57	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. <i>BMC Genomics</i> , 2014, 15, 683.	1.2	89
58	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
59	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
60	The challenges and importance of structural variation detection in livestock. <i>Frontiers in Genetics</i> , 2014, 5, 37.	1.1	104
61	Identification of Candidate Transcription Factor Binding Sites in the Cattle Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 195-198.	3.0	11
62	Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. <i>BMC Genomics</i> , 2013, 14, 876.	1.2	142
63	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
64	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
65	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
66	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
67	Copy number variation in the cattle genome. <i>Functional and Integrative Genomics</i> , 2012, 12, 609-624.	1.4	60
68	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
69	Copy number variation of individual cattle genomes using next-generation sequencing. <i>Genome Research</i> , 2012, 22, 778-790.	2.4	259
70	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
71	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
72	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

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73	Genomic characteristics of cattle copy number variations. BMC Genomics, 2011, 12, 127.	1.2	201
74	Transcriptomes of Frankia sp. strain Ccl3 in growth transitions. BMC Microbiology, 2011, 11, 192.	1.3	26
75	Insertion sequence content reflects genome plasticity in strains of the root nodule actinobacterium Frankia. BMC Genomics, 2009, 10, 468.	1.2	34
76	On the chimeric nature, thermophilic origin, and phylogenetic placement of the Thermotogales. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5865-5870.	3.3	221
77	Genome characteristics of facultatively symbiotic Frankia sp. strains reflect host range and host plant biogeography. Genome Research, 2006, 17, 7-15.	2.4	352
78	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