

Robert D Schnabel

List of Publications by Year in descending order

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122
papers

12,157
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38742

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9478
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#	ARTICLE	IF	CITATIONS
1	Exploring genetic variation and population structure in a threatened species, <i>Noturus placidus</i> , with whole-genome sequence data. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	1
2	A Non-Synonymous Point Mutation in a WD-40 Domain Repeat of EML5 Leads to Decreased Bovine Sperm Quality and Fertility. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 872740.	3.7	3
3	Evidence of rare misassemblies in the bovine reference genome revealed by population genetic metrics. <i>Animal Genetics</i> , 2022, 53, 498-505.	1.7	2
4	Genome-wide association and genotype by environment interactions for growth traits in U.S. Red Angus cattle. <i>BMC Genomics</i> , 2022, 23, .	2.8	11
5	Introgression, admixture, and selection facilitate genetic adaptation to high-altitude environments in cattle. <i>Genomics</i> , 2021, 113, 1491-1503.	2.9	10
6	Genome-wide association analyses identify genotype-by-environment interactions of growth traits in Simmental cattle. <i>Scientific Reports</i> , 2021, 11, 13335.	3.3	22
7	Powerful detection of polygenic selection and evidence of environmental adaptation in US beef cattle. <i>PLoS Genetics</i> , 2021, 17, e1009652.	3.5	23
8	Taurine and Indicine Haplotype Representation in Advanced Generation Individuals From Three American Breeds. <i>Frontiers in Genetics</i> , 2021, 12, 758394.	2.3	1
9	Spliced genes in muscle from Nelore Cattle and their association with carcass and meat quality. <i>Scientific Reports</i> , 2020, 10, 14701.	3.3	21
10	Using online tools at the Bovine Genome Database to manually annotate genes in the new reference genome. <i>Animal Genetics</i> , 2020, 51, 675-682.	1.7	2
11	Symposium review: Advances in sequencing technology herald a new frontier in cattle genomics and genome-enabled selection. <i>Journal of Dairy Science</i> , 2020, 103, 5278-5290.	3.4	15
12	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	6.4	380
13	QTL-mapping and genomic prediction for bovine respiratory disease in U.S. Holsteins using sequence imputation and feature selection. <i>BMC Genomics</i> , 2019, 20, 555.	2.8	6
14	Neuronal ceroid lipofuscinosis in a German Shorthaired Pointer associated with a previously reported CLN8 nonsense variant. <i>Molecular Genetics and Metabolism Reports</i> , 2019, 21, 100521.	1.1	4
15	CRUMBLER: A tool for the prediction of ancestry in cattle. <i>PLoS ONE</i> , 2019, 14, e0221471.	2.5	7
16	Identification of bovine CpG SNPs as potential targets for epigenetic regulation via DNA methylation. <i>PLoS ONE</i> , 2019, 14, e0222329.	2.5	8
17	Genome-Wide SNP Discovery in Indigenous Cattle Breeds of South Africa. <i>Frontiers in Genetics</i> , 2019, 10, 273.	2.3	35
18	Genome-wide association and genotype by environment interactions for growth traits in U.S. Gelbvieh cattle. <i>BMC Genomics</i> , 2019, 20, 926.	2.8	37

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19	A multi-breed reference panel and additional rare variants maximize imputation accuracy in cattle. <i>Genetics Selection Evolution</i> , 2019, 51, 77.	3.0	42
20	Review: Genomics of bull fertility. <i>Animal</i> , 2018, 12, s172-s183.	3.3	63
21	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. <i>Nature Genetics</i> , 2018, 50, 362-367.	21.4	286
22	Identification of genomic variants causing sperm abnormalities and reduced male fertility. <i>Animal Reproduction Science</i> , 2018, 194, 57-62.	1.5	32
23	Scans for signatures of selection in Russian cattle breed genomes reveal new candidate genes for environmental adaptation and acclimation. <i>Scientific Reports</i> , 2018, 8, 12984.	3.3	85
24	Association of single nucleotide polymorphisms in candidate genes previously related to genetic variation in fertility with phenotypic measurements of reproductive function in Holstein cows. <i>Journal of Dairy Science</i> , 2017, 100, 3725-3734.	3.4	32
25	A homozygous PIGN missense mutation in Soft-Coated Wheaten Terriers with a canine paroxysmal dyskinesia. <i>Neurogenetics</i> , 2017, 18, 39-47.	1.4	23
26	Homozygous <i>PPT1</i> Splice Donor Mutation in a Cane Corso Dog With Neuronal Ceroid Lipofuscinosis. <i>Journal of Veterinary Internal Medicine</i> , 2017, 31, 149-157.	1.6	24
27	<i>GM2</i> Gangliosidosis in Shiba Inu Dogs with an InFrame Deletion in <i>HEXB</i> . <i>Journal of Veterinary Internal Medicine</i> , 2017, 31, 1520-1526.	1.6	16
28	Genome-wide association study for feed efficiency and growth traits in U.S. beef cattle. <i>BMC Genomics</i> , 2017, 18, 386.	2.8	159
29	Tissue Tropism in Host Transcriptional Response to Members of the Bovine Respiratory Disease Complex. <i>Scientific Reports</i> , 2017, 7, 17938.	3.3	28
30	Candidate lethal haplotypes and causal mutations in Angus cattle. <i>BMC Genomics</i> , 2017, 18, 799.	2.8	42
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	Gene expression differences in Longissimus muscle of Nelore steers genetically divergent for residual feed intake. <i>Scientific Reports</i> , 2016, 6, 39493.	3.3	57
33	Lessons for livestock genomics from genome and transcriptome sequencing in cattle and other mammals. <i>Genetics Selection Evolution</i> , 2016, 48, 59.	3.0	25
34	Australian Cattle Dogs with Neuronal Ceroid Lipofuscinosis are Homozygous for a <i>CLN5</i> Nonsense Mutation Previously Identified in Border Collies. <i>Journal of Veterinary Internal Medicine</i> , 2016, 30, 1149-1158.	1.6	34
35	Early cave art and ancient DNA record the origin of European bison. <i>Nature Communications</i> , 2016, 7, 13158.	12.8	81
36	Origins of cattle on Chirikof Island, Alaska, elucidated from genome-wide SNP genotypes. <i>Heredity</i> , 2016, 116, 502-505.	2.6	16

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37	A mutation in the Warburg syndrome gene, RAB3GAP1, causes a similar syndrome with polyneuropathy and neuronal vacuolation in Black Russian Terrier dogs. <i>Neurobiology of Disease</i> , 2016, 86, 75-85.	4.4	22
38	Bottlenecks and selective sweeps during domestication have increased deleterious genetic variation in dogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 152-157.	7.1	265
39	The players may change but the game remains: network analyses of ruminal microbiomes suggest taxonomic differences mask functional similarity. <i>Nucleic Acids Research</i> , 2015, 43, gkv973.	14.5	98
40	Whatâ€™s in your next-generation sequence data? An exploration of unmapped DNA and RNA sequence reads from the bovine reference individual. <i>BMC Genomics</i> , 2015, 16, 1114.	2.8	32
41	Immunological Response to Single Pathogen Challenge with Agents of the Bovine Respiratory Disease Complex: An RNA-Sequence Analysis of the Bronchial Lymph Node Transcriptome. <i>PLoS ONE</i> , 2015, 10, e0131459.	2.5	51
42	Genome-Wide Scan for Visceral Leishmaniasis in Mixed-Breed Dogs Identifies Candidate Genes Involved in T Helper Cells and Macrophage Signaling. <i>PLoS ONE</i> , 2015, 10, e0136749.	2.5	19
43	RAPTR-SV: a hybrid method for the detection of structural variants. <i>Bioinformatics</i> , 2015, 31, 2084-2090.	4.1	18
44	Golden Retriever dogs with neuronal ceroid lipofuscinosis have a two-base-pair deletion and frameshift in CLN5. <i>Molecular Genetics and Metabolism</i> , 2015, 115, 101-109.	1.1	36
45	Detection of quantitative trait loci for mineral content of Nelore longissimus dorsi muscle. <i>Genetics Selection Evolution</i> , 2015, 47, 15.	3.0	40
46	Comparison of Bayesian models to estimate direct genomic values in multi-breed commercial beef cattle. <i>Genetics Selection Evolution</i> , 2015, 47, 23.	3.0	38
47	Global liver gene expression differences in Nelore steers with divergent residual feed intake phenotypes. <i>BMC Genomics</i> , 2015, 16, 242.	2.8	109
48	A simple procedure for directly obtaining haplotype sequences of diploid genomes. <i>BMC Genomics</i> , 2015, 16, 642.	2.8	2
49	QTLs associated with dry matter intake, metabolic mid-test weight, growth and feed efficiency have little overlap across 4 beef cattle studies. <i>BMC Genomics</i> , 2014, 15, 1004.	2.8	97
50	Genome-wide DNA methylation analysis in precursor B-cells. <i>Epigenetics</i> , 2014, 9, 1588-1595.	2.7	22
51	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004254.	3.5	391
52	A Homozygous <i>KCNJ10</i> Mutation in Jack Russell Terriers and Related Breeds with Spinocerebellar Ataxia with Myokymia, Seizures, or Both. <i>Journal of Veterinary Internal Medicine</i> , 2014, 28, 871-877.	1.6	60
53	Results of the BRD CAP project: progress toward identifying genetic markers associated with BRD susceptibility. <i>Animal Health Research Reviews</i> , 2014, 15, 157-160.	3.1	8
54	Recombination locations and rates in beef cattle assessed from parent-offspring pairs. <i>Genetics Selection Evolution</i> , 2014, 46, 34.	3.0	52

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55	SNPchiMp: a database to disentangle the SNPchip jungle in bovine livestock. BMC Genomics, 2014, 15, 123.	2.8	47
56	Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds. BMC Genomics, 2014, 15, 442.	2.8	191
57	A CLN8 nonsense mutation in the whole genome sequence of a mixed breed dog with neuronal ceroid lipofuscinosis and Australian Shepherd ancestry. Molecular Genetics and Metabolism, 2014, 112, 302-309.	1.1	38
58	A rare homozygous MFSD8 single-base-pair deletion and frameshift in the whole genome sequence of a Chinese Crested dog with neuronal ceroid lipofuscinosis. BMC Veterinary Research, 2014, 10, 960.	1.9	35
59	Detection of selective sweeps in cattle using genome-wide SNP data. BMC Genomics, 2013, 14, 382.	2.8	102
60	Predicting expected progeny difference for marbling score in Angus cattle using artificial neural networks and Bayesian regression models. Genetics Selection Evolution, 2013, 45, 34.	3.0	50
61	Comparison of molecular breeding values based on within- and across-breed training in beef cattle. Genetics Selection Evolution, 2013, 45, 30.	3.0	56
62	Characterization of the rat developmental liver transcriptome. Physiological Genomics, 2013, 45, 301-311.	2.3	21
63	New World cattle show ancestry from multiple independent domestication events. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E1398-406.	7.1	126
64	Genome scan for meat quality traits in Nelore beef cattle. Physiological Genomics, 2013, 45, 1012-1020.	2.3	123
65	Imputation of microsatellite alleles from dense SNP genotypes for parentage verification across multiple Bos taurus and Bos indicus breeds. Frontiers in Genetics, 2013, 4, 176.	2.3	29
66	An ensemble-based approach to imputation of moderate-density genotypes for genomic selection with application to Angus cattle. Genetical Research, 2012, 94, 133-150.	0.9	40
67	Depot-specific gene expression profiles during differentiation and transdifferentiation of bovine muscle satellite cells, and differentiation of preadipocytes. Genomics, 2012, 100, 195-202.	2.9	30
68	Accuracy of direct genomic breeding values for nationally evaluated traits in US Limousin and Simmental beef cattle. Genetics Selection Evolution, 2012, 44, 38.	3.0	63
69	Copy number variation of individual cattle genomes using next-generation sequencing. Genome Research, 2012, 22, 778-790.	5.5	259
70	A novel analytical method, Birth Date Selection Mapping, detects response of the Angus (Bos taurus) genome to selection on complex traits. BMC Genomics, 2012, 13, 606.	2.8	37
71	The accuracies of DNA-based estimates of genetic merit derived from Angus or multibreed beef cattle training populations ^{1,2,3} . Journal of Animal Science, 2012, 90, 4191-4202.	0.5	8
72	Gene expression profiles during differentiation and transdifferentiation of bovine myogenic satellite cells. Genes and Genomics, 2012, 34, 133-148.	1.4	13

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73	Genome-wide association analysis for feed efficiency in Angus cattle. <i>Animal Genetics</i> , 2012, 43, 367-374.	1.7	110
74	Genome-wide association analysis for quantitative trait loci influencing <i>W</i> and <i>B</i> ratzler shear force in five taurine cattle breeds. <i>Animal Genetics</i> , 2012, 43, 662-673.	1.7	76
75	Evaluation of approaches for identifying population informative markers from high density SNP Chips. <i>BMC Genetics</i> , 2011, 12, 45.	2.7	83
76	A Truncated Retrotransposon Disrupts the <i>GRM1</i> Coding Sequence in Coton de Tulear Dogs with Bandera's Neonatal Ataxia. <i>Journal of Veterinary Internal Medicine</i> , 2011, 25, 267-272.	1.6	34
77	Identification of loci associated with tolerance to Johne's disease in Holstein cattle. <i>Animal Genetics</i> , 2011, 42, 28-38.	1.7	63
78	Mapping of fertility traits in Finnish Ayrshire by genome-wide association analysis. <i>Animal Genetics</i> , 2011, 42, 263-269.	1.7	28
79	A truncating mutation in <i>ATP13A2</i> is responsible for adult-onset neuronal ceroid lipofuscinosis in Tibetan terriers. <i>Neurobiology of Disease</i> , 2011, 42, 468-474.	4.4	109
80	Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. <i>Genetics Selection Evolution</i> , 2011, 43, 40.	3.0	174
81	Evolution of the Bovine TLR Gene Family and Member Associations with <i>Mycobacterium avium</i> Subspecies Paratuberculosis Infection. <i>PLoS ONE</i> , 2011, 6, e27744.	2.5	48
82	Impact of reduced marker set estimation of genomic relationship matrices on genomic selection for feed efficiency in Angus cattle. <i>BMC Genetics</i> , 2010, 11, 24.	2.7	50
83	A genome scan for quantitative trait loci influencing carcass, postnatal growth and reproductive traits in commercial Angus cattle. <i>Animal Genetics</i> , 2010, 41, 597-607.	1.7	209
84	An <i>ADAMTS17</i> Splice Donor Site Mutation in Dogs with Primary Lens Luxation. , 2010, 51, 4716.		55
85	Diversity and evolution of 11 innate immune genes in <i>Bos taurus taurus</i> and <i>Bos taurus indicus</i> cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 151-156.	7.1	81
86	Development and Application of Bovine and Porcine Oligonucleotide Arrays with Protein-Based Annotation. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-11.	3.0	7
87	Characterization and Mode of Inheritance of a Paroxysmal Dyskinesia in Chinook Dogs. <i>Journal of Veterinary Internal Medicine</i> , 2010, 24, 1305-1313.	1.6	30
88	Characterization of <i>DGAT1</i> Allelic Effects in a Sample of North American Holstein Cattle. <i>Animal Biotechnology</i> , 2010, 21, 88-99.	1.5	17
89	Genetic Variation at a Metallothionein2A Promoter Single-Nucleotide Polymorphism in White and Black Females in Midwestern United States. <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2010, 73, 1283-1287.	2.3	14
90	A Novel Mutation in the Maternally Imprinted <i>PEG3</i> Domain Results in a Loss of <i>MIMT1</i> Expression and Causes Abortions and Stillbirths in Cattle (<i>Bos taurus</i>). <i>PLoS ONE</i> , 2010, 5, e15116.	2.5	55

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91	Development and Characterization of a High Density SNP Genotyping Assay for Cattle. PLoS ONE, 2009, 4, e5350.	2.5	813
92	Design of a High Density SNP Genotyping Assay in the Pig Using SNPs Identified and Characterized by Next Generation Sequencing Technology. PLoS ONE, 2009, 4, e6524.	2.5	568
93	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18644-18649.	7.1	196
94	Assessment of DNA extracted from FTA [®] cards for use on the Illumina iSelect BeadChip. BMC Research Notes, 2009, 2, 107.	1.4	24
95	A whole genome association analysis identifies loci associated with <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> infection status in US holstein cattle. Animal Genetics, 2009, 40, 655-662.	1.7	92
96	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	12.6	1,038
97	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. Science, 2009, 324, 528-532.	12.6	746
98	Invited Review: Reliability of genomic predictions for North American Holstein bulls. Journal of Dairy Science, 2009, 92, 16-24.	3.4	1,008
99	Selection of single-nucleotide polymorphisms and quality of genotypes used in genomic evaluation of dairy cattle in the United States and Canada. Journal of Dairy Science, 2009, 92, 3431-3436.	3.4	163
100	Distribution and location of genetic effects for dairy traits. Journal of Dairy Science, 2009, 92, 2931-2946.	3.4	210
101	A neonatal encephalopathy with seizures in standard poodle dogs with a missense mutation in the canine ortholog of ATF2. Neurogenetics, 2008, 9, 41-49.	1.4	22
102	An assessment of population structure in eight breeds of cattle using a whole genome SNP panel. BMC Genetics, 2008, 9, 37.	2.7	95
103	High density linkage disequilibrium maps of chromosome 14 in Holstein and Angus cattle. BMC Genetics, 2008, 9, 45.	2.7	20
104	SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. Nature Methods, 2008, 5, 247-252.	19.0	534
105	Linkage disequilibrium and signatures of selection on chromosomes 19 and 29 in beef and dairy cattle. Animal Genetics, 2008, 39, 597-605.	1.7	42
106	Extent of genome-wide linkage disequilibrium in Australian Holstein-Friesian cattle based on a high-density SNP panel. BMC Genomics, 2008, 9, 187.	2.8	203
107	A physical map of the bovine genome. Genome Biology, 2007, 8, R165.	9.6	73
108	BOARD-INVITED REVIEW: Applications of genomic information in livestock1. Journal of Animal Science, 2007, 85, 3148-3158.	0.5	56

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109	Whole genome linkage disequilibrium maps in cattle. BMC Genetics, 2007, 8, 74.	2.7	201
110	Construction of bovine whole-genome radiation hybrid and linkage maps using high-throughput genotyping. Animal Genetics, 2007, 38, 120-125.	1.7	36
111	Association analysis of adiponectin and somatostatin polymorphisms on BTA1 with growth and carcass traits in Angus cattle. Animal Genetics, 2006, 37, 554-562.	1.7	49
112	Comparative mapping of bovine chromosome 27 with human chromosome 8 near a dairy form QTL in cattle. Cytogenetic and Genome Research, 2006, 112, 98-102.	1.1	3
113	Impaired collagen chaperone results in preterm PROM. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13267-13268.	7.1	3
114	Conservation genomics: disequilibrium mapping of domestic cattle chromosomal segments in North American bison populations. Molecular Ecology, 2005, 14, 2343-2362.	3.9	50
115	Whole-genome scan to detect QTL for milk production, conformation, fertility and functional traits in two US Holstein families. Animal Genetics, 2005, 36, 408-416.	1.7	70
116	The color of a Dalmatian's spots: linkage evidence to support the TYRP1 gene. BMC Veterinary Research, 2005, 1, 1.	1.9	15
117	Fine-mapping milk production quantitative trait loci on BTA6: Analysis of the bovine osteopontin gene. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 6896-6901.	7.1	95
118	Genetic Mapping of Canine Multiple System Degeneration and Ectodermal Dysplasia Loci. Journal of Heredity, 2005, 96, 727-734.	2.4	37
119	Assignment of Canine MSS1 Microsatellite Markers to Chromosomes by Linkage Data. DNA Sequence, 2004, 15, 209-212.	0.7	4
120	Development of a linkage map and QTL scan for growth traits in North American bison. Cytogenetic and Genome Research, 2003, 102, 59-64.	1.1	10
121	Differential introgression of uniparentally inherited markers in bison populations with hybrid ancestries. Animal Genetics, 2001, 32, 89-91.	1.7	28
122	Validation of 15 microsatellites for parentage testing in North American bison, Bison bison and domestic cattle. Animal Genetics, 2000, 31, 360-366.	1.7	57