

# Robert D Schnabel

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9022/publications.pdf>

Version: 2024-02-01

122  
papers

12,157  
citations

38742

50  
h-index

27406

106  
g-index

134  
all docs

134  
docs citations

134  
times ranked

9478  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
2	Invited Review: Reliability of genomic predictions for North American Holstein bulls. <i>Journal of Dairy Science</i> , 2009, 92, 16-24.	3.4	1,008
3	Development and Characterization of a High Density SNP Genotyping Assay for Cattle. <i>PLoS ONE</i> , 2009, 4, e5350.	2.5	813
4	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	12.6	746
5	Design of a High Density SNP Genotyping Assay in the Pig Using SNPs Identified and Characterized by Next Generation Sequencing Technology. <i>PLoS ONE</i> , 2009, 4, e6524.	2.5	568
6	SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. <i>Nature Methods</i> , 2008, 5, 247-252.	19.0	534
7	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004254.	3.5	391
8	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	6.4	380
9	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
10	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
11	Copy number variation of individual cattle genomes using next-generation sequencing. <i>Genome Research</i> , 2012, 22, 778-790.	5.5	259
12	Distribution and location of genetic effects for dairy traits. <i>Journal of Dairy Science</i> , 2009, 92, 2931-2946.	3.4	210
13	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
14	Extent of genome-wide linkage disequilibrium in Australian Holstein-Friesian cattle based on a high-density SNP panel. <i>BMC Genomics</i> , 2008, 9, 187.	2.8	203
15	Whole genome linkage disequilibrium maps in cattle. <i>BMC Genetics</i> , 2007, 8, 74.	2.7	201
16	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18644-18649.	7.1	196
17	Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds. <i>BMC Genomics</i> , 2014, 15, 442.	2.8	191
18	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

#	ARTICLE	IF	CITATIONS
19	Selection of single-nucleotide polymorphisms and quality of genotypes used in genomic evaluation of dairy cattle in the United States and Canada. <i>Journal of Dairy Science</i> , 2009, 92, 3431-3436.	3.4	163
20	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
21	New World cattle show ancestry from multiple independent domestication events. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1398-406.	7.1	126
22	Genome scan for meat quality traits in Nelore beef cattle. <i>Physiological Genomics</i> , 2013, 45, 1012-1020.	2.3	123
23	Genome-wide association analysis for feed efficiency in Angus cattle. <i>Animal Genetics</i> , 2012, 43, 367-374.	1.7	110
24	A truncating mutation in ATP13A2 is responsible for adult-onset neuronal ceroid lipofuscinosis in Tibetan terriers. <i>Neurobiology of Disease</i> , 2011, 42, 468-474.	4.4	109
25	Global liver gene expression differences in Nelore steers with divergent residual feed intake phenotypes. <i>BMC Genomics</i> , 2015, 16, 242.	2.8	109
26	Detection of selective sweeps in cattle using genome-wide SNP data. <i>BMC Genomics</i> , 2013, 14, 382.	2.8	102
27	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
28	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
29	Fine-mapping milk production quantitative trait loci on BTA6: Analysis of the bovine osteopontin gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 6896-6901.	7.1	95
30	An assessment of population structure in eight breeds of cattle using a whole genome SNP panel. <i>BMC Genetics</i> , 2008, 9, 37.	2.7	95
31	A whole genome association analysis identifies loci associated with <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> infection status in US holstein cattle. <i>Animal Genetics</i> , 2009, 40, 655-662.	1.7	92
32	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
33	Evaluation of approaches for identifying population informative markers from high density SNP Chips. <i>BMC Genetics</i> , 2011, 12, 45.	2.7	83
34	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
35	Early cave art and ancient DNA record the origin of European bison. <i>Nature Communications</i> , 2016, 7, 13158.	12.8	81
36	Genome-wide association analysis for quantitative trait loci influencing <i>Warriner</i> <i>B</i> ratzler shear force in five taurine cattle breeds. <i>Animal Genetics</i> , 2012, 43, 662-673.	1.7	76

#	ARTICLE	IF	CITATIONS
37	A physical map of the bovine genome. <i>Genome Biology</i> , 2007, 8, R165.	9.6	73
38	Whole-genome scan to detect QTL for milk production, conformation, fertility and functional traits in two US Holstein families. <i>Animal Genetics</i> , 2005, 36, 408-416.	1.7	70
39	Identification of loci associated with tolerance to Johne's disease in Holstein cattle. <i>Animal Genetics</i> , 2011, 42, 28-38.	1.7	63
40	Accuracy of direct genomic breeding values for nationally evaluated traits in US Limousin and Simmental beef cattle. <i>Genetics Selection Evolution</i> , 2012, 44, 38.	3.0	63
41	Review: Genomics of bull fertility. <i>Animal</i> , 2018, 12, s172-s183.	3.3	63
42	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
43	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
44	Validation of 15 microsatellites for parentage testing in North American bison, Bison bison and domestic cattle. <i>Animal Genetics</i> , 2000, 31, 360-366.	1.7	57
45	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
46	BOARD-INVITED REVIEW: Applications of genomic information in livestock1. <i>Journal of Animal Science</i> , 2007, 85, 3148-3158.	0.5	56
47	Comparison of molecular breeding values based on within- and across-breed training in beef cattle. <i>Genetics Selection Evolution</i> , 2013, 45, 30.	3.0	56
48	An ADAMTS17 Splice Donor Site Mutation in Dogs with Primary Lens Luxation. , 2010, 51, 4716.		55
49	A Novel Mutation in the Maternally Imprinted PEG3 Domain Results in a Loss of MIMT1 Expression and Causes Abortions and Stillbirths in Cattle ( <i>Bos taurus</i> ). <i>PLoS ONE</i> , 2010, 5, e15116.	2.5	55
50	Recombination locations and rates in beef cattle assessed from parent-offspring pairs. <i>Genetics Selection Evolution</i> , 2014, 46, 34.	3.0	52
51	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
52	Conservation genomics: disequilibrium mapping of domestic cattle chromosomal segments in North American bison populations. <i>Molecular Ecology</i> , 2005, 14, 2343-2362.	3.9	50
53	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
54	Predicting expected progeny difference for marbling score in Angus cattle using artificial neural networks and Bayesian regression models. <i>Genetics Selection Evolution</i> , 2013, 45, 34.	3.0	50

#	ARTICLE	IF	CITATIONS
55	Association analysis of adiponectin and somatostatin polymorphisms on BTA1 with growth and carcass traits in Angus cattle. <i>Animal Genetics</i> , 2006, 37, 554-562.	1.7	49
56	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
57	SNPchiMp: a database to disentangle the SNPchip jungle in bovine livestock. <i>BMC Genomics</i> , 2014, 15, 123.	2.8	47
58	Linkage disequilibrium and signatures of selection on chromosomes 19 and 29 in beef and dairy cattle. <i>Animal Genetics</i> , 2008, 39, 597-605.	1.7	42
59	Candidate lethal haplotypes and causal mutations in Angus cattle. <i>BMC Genomics</i> , 2017, 18, 799.	2.8	42
60	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
61	An ensemble-based approach to imputation of moderate-density genotypes for genomic selection with application to Angus cattle. <i>Genetical Research</i> , 2012, 94, 133-150.	0.9	40
62	Detection of quantitative trait loci for mineral content of Nelore longissimus dorsi muscle. <i>Genetics Selection Evolution</i> , 2015, 47, 15.	3.0	40
63	A CLN8 nonsense mutation in the whole genome sequence of a mixed breed dog with neuronal ceroid lipofuscinosis and Australian Shepherd ancestry. <i>Molecular Genetics and Metabolism</i> , 2014, 112, 302-309.	1.1	38
64	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
65	Genetic Mapping of Canine Multiple System Degeneration and Ectodermal Dysplasia Loci. <i>Journal of Heredity</i> , 2005, 96, 727-734.	2.4	37
66	A novel analytical method, Birth Date Selection Mapping, detects response of the Angus ( <i>Bos taurus</i> ) genome to selection on complex traits. <i>BMC Genomics</i> , 2012, 13, 606.	2.8	37
67	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
68	Construction of bovine whole-genome radiation hybrid and linkage maps using high-throughput genotyping. <i>Animal Genetics</i> , 2007, 38, 120-125.	1.7	36
69	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
70	A rare homozygous MFSD8 single-base-pair deletion and frameshift in the whole genome sequence of a Chinese Crested dog with neuronal ceroid lipofuscinosis. <i>BMC Veterinary Research</i> , 2014, 10, 960.	1.9	35
71	Genome-Wide SNP Discovery in Indigenous Cattle Breeds of South Africa. <i>Frontiers in Genetics</i> , 2019, 10, 273.	2.3	35
72	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

#	ARTICLE	IF	CITATIONS
73	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
74	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
75	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
76	Identification of genomic variants causing sperm abnormalities and reduced male fertility. <i>Animal Reproduction Science</i> , 2018, 194, 57-62.	1.5	32
77	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
78	Depot-specific gene expression profiles during differentiation and transdifferentiation of bovine muscle satellite cells, and differentiation of preadipocytes. <i>Genomics</i> , 2012, 100, 195-202.	2.9	30
79	Imputation of microsatellite alleles from dense SNP genotypes for parentage verification across multiple <i>Bos taurus</i> and <i>Bos indicus</i> breeds. <i>Frontiers in Genetics</i> , 2013, 4, 176.	2.3	29
80	Differential introgression of uniparentally inherited markers in bison populations with hybrid ancestries. <i>Animal Genetics</i> , 2001, 32, 89-91.	1.7	28
81	Mapping of fertility traits in Finnish Ayrshire by genome-wide association analysis. <i>Animal Genetics</i> , 2011, 42, 263-269.	1.7	28
82	Tissue Tropism in Host Transcriptional Response to Members of the Bovine Respiratory Disease Complex. <i>Scientific Reports</i> , 2017, 7, 17938.	3.3	28
83	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
84	Assessment of DNA extracted from FTAâ€™ cards for use on the Illumina iSelect BeadChip. <i>BMC Research Notes</i> , 2009, 2, 107.	1.4	24
85	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
86	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
87	Powerful detection of polygenic selection and evidence of environmental adaptation in US beef cattle. <i>PLoS Genetics</i> , 2021, 17, e1009652.	3.5	23
88	A neonatal encephalopathy with seizures in standard poodle dogs with a missense mutation in the canine ortholog of ATF2. <i>Neurogenetics</i> , 2008, 9, 41-49.	1.4	22
89	Genome-wide DNA methylation analysis in precursor B-cells. <i>Epigenetics</i> , 2014, 9, 1588-1595.	2.7	22
90	A mutation in the Warburg syndrome gene, <i>RAB3GAP1</i> , 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

#	ARTICLE	IF	CITATIONS
91	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
92	Characterization of the rat developmental liver transcriptome. <i>Physiological Genomics</i> , 2013, 45, 301-311.	2.3	21
93	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
94	High density linkage disequilibrium maps of chromosome 14 in Holstein and Angus cattle. <i>BMC Genetics</i> , 2008, 9, 45.	2.7	20
95	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
96	RAPTR-SV: a hybrid method for the detection of structural variants. <i>Bioinformatics</i> , 2015, 31, 2084-2090.	4.1	18
97	Characterization of DGAT1 Allelic Effects in a Sample of North American Holstein Cattle. <i>Animal Biotechnology</i> , 2010, 21, 88-99.	1.5	17
98	Origins of cattle on Chirikof Island, Alaska, elucidated from genome-wide SNP genotypes. <i>Heredity</i> , 2016, 116, 502-505.	2.6	16
99	<sc>GM</sc>2 Gangliosidosis in Shiba Inu Dogs with an Inâ€Frame Deletion in <i><sc>HEXB</sc></i>. <i>Journal of Veterinary Internal Medicine</i> , 2017, 31, 1520-1526.	1.6	16
100	The color of a Dalmatian's spots: linkage evidence to support the TYRP1 gene. <i>BMC Veterinary Research</i> , 2005, 1, 1.	1.9	15
101	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
102	Genetic Variation at a Metallothionein2APromoter 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
103	Gene expression profiles during differentiation and transdifferentiation of bovine myogenic satellite cells. <i>Genes and Genomics</i> , 2012, 34, 133-148.	1.4	13
104	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
105	Development of a linkage map and QTL scan for growth traits in North American bison. <i>Cytogenetic and Genome Research</i> , 2003, 102, 59-64.	1.1	10
106	Introgression, admixture, and selection facilitate genetic adaptation to high-altitude environments in cattle. <i>Genomics</i> , 2021, 113, 1491-1503.	2.9	10
107	The accuracies of DNA-based estimates of genetic merit derived from Angus or multibreed beef cattle training populations1,2,3. <i>Journal of Animal Science</i> , 2012, 90, 4191-4202.	0.5	8
108	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

#	ARTICLE	IF	CITATIONS
109	Identification of bovine CpG SNPs as potential targets for epigenetic regulation via DNA methylation. PLoS ONE, 2019, 14, e0222329.	2.5	8
110	Development and Application of Bovine and Porcine Oligonucleotide Arrays with Protein-Based Annotation. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-11.	3.0	7
111	CRUMBLER: A tool for the prediction of ancestry in cattle. PLoS ONE, 2019, 14, e0221471.	2.5	7
112	QTL-mapping and genomic prediction for bovine respiratory disease in U.S. Holsteins using sequence imputation and feature selection. BMC Genomics, 2019, 20, 555.	2.8	6
113	Assignment of Canine MSS1 Microsatellite Markers to Chromosomes by Linkage Data. DNA Sequence, 2004, 15, 209-212.	0.7	4
114	Neuronal ceroid lipofuscinosis in a German Shorthaired Pointer associated with a previously reported CLN8 nonsense variant. Molecular Genetics and Metabolism Reports, 2019, 21, 100521.	1.1	4
115	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
116	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
117	A Non-Synonymous Point Mutation in a WD-40 Domain Repeat of EML5 Leads to Decreased Bovine Sperm Quality and Fertility. Frontiers in Cell and Developmental Biology, 2022, 10, 872740.	3.7	3
118	A simple procedure for directly obtaining haplotype sequences of diploid genomes. BMC Genomics, 2015, 16, 642.	2.8	2
119	Using online tools at the Bovine Genome Database to manually annotate genes in the new reference genome. Animal Genetics, 2020, 51, 675-682.	1.7	2
120	Evidence of rare misassemblies in the bovine reference genome revealed by population genetic metrics. Animal Genetics, 2022, 53, 498-505.	1.7	2
121	Taurine and Indicine Haplotype Representation in Advanced Generation Individuals From Three American Breeds. Frontiers in Genetics, 2021, 12, 758394.	2.3	1
122	Exploring genetic variation and population structure in a threatened species, <i>Noturus placidus</i> , with whole-genome sequence data. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	1