James M Reecy

List of Publications by Year
in descending order

93 papers	8,596 citations	76031 42 h-index	54771 88 g-index
95 all docs	95 docs citations	95 times ranked	13691 citing authors

#	Article	IF	Citations
1	Analyses of pig genomes provide insight into porcine demography and evolution. Nature, 2012, 491, 393-398.	13.7	1,190
2	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	6.0	1,038
3	The BioMart community portal: an innovative alternative to large, centralized data repositories. Nucleic Acids Research, 2015, 43, W589-W598.	6.5	682
4	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	9.4	506
5	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. PLoS Genetics, 2014, 10, e1004254.	1.5	391
6	Animal QTLdb: an improved database tool for livestock animal QTL/association data dissemination in the post-genome era. Nucleic Acids Research, 2013, 41, D871-D879.	6.5	331
7	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. Genome Biology, 2015, 16, 57.	3.8	331
8	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. Nature Genetics, 2018, 50, 362-367.	9.4	286
9	Developmental progress and current status of the Animal QTLdb. Nucleic Acids Research, 2016, 44, D827-D833.	6.5	272
10	Building a livestock genetic and genomic information knowledgebase through integrative developments of Animal QTLdb and CorrDB. Nucleic Acids Research, 2019, 47, D701-D710.	6.5	268
11	AnimalQTLdb: a livestock QTL database tool set for positional QTL information mining and beyond. Nucleic Acids Research, 2007, 35, D604-D609.	6.5	181
12	A QTL resource and comparison tool for pigs: PigQTLDB. Mammalian Genome, 2005, 16, 792-800.	1.0	125
13	Bringing the Animal QTLdb and CorrDB into the future: meeting new challenges and providing updated services. Nucleic Acids Research, 2022, 50, D956-D961.	6.5	125
14	Genome-wide association study for intramuscular fat deposition and composition in Nellore cattle. BMC Genetics, 2014, 15, 39.	2.7	121
15	Genome to Phenome: Improving Animal Health, Production, and Well-Being – A New USDA Blueprint for Animal Genome Research 2018–2027. Frontiers in Genetics, 2019, 10, 327.	1.1	118
16	Putative Regulatory Factors Associated with Intramuscular Fat Content. PLoS ONE, 2015, 10, e0128350.	1.1	116
17	Transcriptional profiling of myostatin–knockout mice implicates Wnt signaling in postnatal skeletal muscle growth and hypertrophy. FASEB Journal, 2006, 20, 580-582.	0.2	115
18	Integration of machine learning and meta-analysis identifies the transcriptomic bio-signature of mastitis disease in cattle. PLoS ONE, 2018, 13, e0191227.	1.1	115

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19	Identification of upstream regulatory regions in the heart-expressed homeobox gene *Nkx2-5*. Development (Cambridge), 1999, 126, 839-849.	1.2	100
20	Differential gene expression in the rat soleus muscle during early work overload-induced hypertrophy. FASEB Journal, 2002, 16, 1-21.	0.2	91
21	Lipid metabolism, adipocyte depot physiology and utilization of meat animals as experimental models for metabolic research. International Journal of Biological Sciences, 2010, 6, 691-699.	2.6	89
22	TACE release of TNF-α mediates mechanotransduction-induced activation of p38 MAPK and myogenesis. Journal of Cell Science, 2007, 120, 692-701.	1.2	85
23	Design and validation of a 90K SNP genotyping assay for the water buffalo (Bubalus bubalis). PLoS ONE, 2017, 12, e0185220.	1.1	76
24	Animal QTLdb: beyond a repository. Mammalian Genome, 2007, 18, 1-4.	1.0	75
25	Interleukin-8, Interleukin-1β, and Interferon-γ Levels Are Linked to PRRS Virus Clearance. Viral Immunology, 2010, 23, 127-134.	0.6	72
26	Genome-wide association and prediction of direct genomic breeding values for composition of fatty acids in Angus beef cattlea. BMC Genomics, 2013, 14, 730.	1.2	67
27	Murine Tbx2 contains domains that activate and repress gene transcription. Gene, 2002, 283, 117-124.	1.0	66
28	Functional and phylogenetic analyses of a melanocortin-4 receptor mutation in domestic pigs. Domestic Animal Endocrinology, 2004, 26, 75-86.	0.8	66
29	GO–FAANG meeting: a Gathering On Functional Annotation of Animal Genomes. Animal Genetics, 2016, 47, 528-533.	0.6	65
30	A Vision for Development and Utilization of High-Throughput Phenotyping and Big Data Analytics in Livestock. Frontiers in Genetics, 2019, 10, 1197.	1.1	64
31	Network Analysis Reveals Putative Genes Affecting Meat Quality in Angus Cattle. Frontiers in Genetics, 2017, 8, 171.	1.1	63
32	Identification of differentially expressed gene categories in microarray studies using nonparametric multivariate analysis. Bioinformatics, 2008, 24, 192-201.	1.8	60
33	Chicken Nkx-2.8: A Novel Homeobox Gene Expressed in Early Heart Progenitor Cells and Pharyngeal Pouch-2 and -3 Endoderm. Developmental Biology, 1997, 188, 295-311.	0.9	59
34	Allied Industry Approaches to Alter Intramuscular Fat Content and Composition in Beef Animals. Journal of Food Science, 2010, 75, R1-8.	1.5	59
35	Differences in the skeletal muscle transcriptome profile associated with extreme values of fatty acids content. BMC Genomics, 2016, 17, 961.	1.2	54
36	Gene Co-expression Analysis Indicates Potential Pathways and Regulators of Beef Tenderness in Nellore Cattle. Frontiers in Genetics, 2018, 9, 441.	1.1	54

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37	Skeletal Muscle Stem Cells from Animals I. Basic Cell Biology. International Journal of Biological Sciences, 2010, 6, 465-474.	2.6	53
38	Integrative analysis of microRNAs and mRNAs revealed regulation of composition and metabolism in Nelore cattle. BMC Genomics, 2018, 19, 126.	1.2	53
39	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	52
40	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. BMC Genomics, 2018, 19, 499.	1.2	51
41	A nonsense mutation in cGMP-dependent type II protein kinase (*PRKG2*) causes dwarfism in American Angus cattle. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19250-19255.	3.3	48
42	Association of polymorphisms in solute carrier family 27, isoform A6 (SLC27A6) and fatty acid-binding protein-3 and fatty acid-binding protein-4 (FABP3 and FABP4) with fatty acid composition of bovine milk. Journal of Dairy Science, 2013, 96, 6007-6021.	1.4	48
43	The Vertebrate Trait Ontology: a controlled vocabulary for the annotation of trait data across species. Journal of Biomedical Semantics, 2013, 4, 13.	0.9	42
44	In vitro neutralization of HoBi-like viruses by antibodies in serum of cattle immunized with inactivated or modified live vaccines of bovine viral diarrhea viruses 1 and 2. Veterinary Microbiology, 2013, 166, 242-245.	0.8	33
45	Haplotype-based genome-wide association studies for carcass and growth traits in chicken. Poultry Science, 2020, 99, 2349-2361.	1.5	32
46	Pig immune response to general stimulus and to porcine reproductive and respiratory syndrome virus infection: a meta-analysis approach. BMC Genomics, 2013, 14, 220.	1.2	31
47	Myostatin genotype regulates muscle-specific miRNA expression in mouse pectoralis muscle. BMC Research Notes, 2010, 3, 297.	0.6	30
48	Integration of genome wide association studies and whole genome sequencing provides novel insights into fat deposition in chicken. Scientific Reports, 2018, 8, 16222.	1.6	29
49	ANEXdb: an integrated animal ANnotation and microarray EXpression database. Mammalian Genome, 2009, 20, 768-777.	1.0	28
50	Use of SNP genotyping to determine pedigree and breed composition of dairy cattle in Kenya. Journal of Animal Breeding and Genetics, 2010, 127, 348-351.	0.8	28
51	Prediction of key regulators and downstream targets of E. coli induced mastitis. Journal of Applied Genetics, 2019, 60, 367-373.	1.0	28
52	Sterol regulatory element binding transcription factor 1 (SREBF1) polymorphism and milk fatty acid composition. Journal of Dairy Science, 2013, 96, 2605-2616.	1.4	23
53	Whole genome analysis of infectious bovine keratoconjunctivitis in Angus cattle using Bayesian threshold models. BMC Proceedings, 2011, 5, S22.	1.8	22
54	Co-Expression Networks Reveal Potential Regulatory Roles of miRNAs in Fatty Acid Composition of Nelore Cattle. Frontiers in Genetics, 2019, 10, 651.	1.1	22

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55	Lactate dehydrogenase expression at the onset of altered loading in rat soleus muscle. Journal of Applied Physiology, 2004, 97, 1424-1430.	1.2	21
56	Association of toll-like receptor four single nucleotide polymorphisms with incidence of infectious bovine keratoconjunctivitis (IBK) in cattle. Immunogenetics, 2011, 63, 115-119.	1.2	21
57	Serum Response Factor-NK Homeodomain Factor Interactions, Role in Cardiac Development. , 1999, , 273-290.		19
58	Transient cardiac expression of the tinman-family homeobox gene, XNkx2-10. Mechanisms of Development, 2000, 91, 369-373.	1.7	18
59	Effects of increasing dietary oil inclusion from different sources on growth performance, carcass and meat quality traits, and fatty acid profile in genetically lean immunocastrated male pigs. Livestock Science, 2021, 248, 104515.	0.6	18
60	Genomic Analysis Suggests KITLG is Responsible for a Roan Pattern in two Pakistani Goat Breeds. Journal of Heredity, 2018, 109, 315-319.	1.0	17
61	Genome-wide association scan for QTL and their positional candidate genes associated with internal organ traits in chickens. BMC Genomics, 2019, 20, 669.	1.2	17
62	Polymorphisms in lipogenic genes and milk fatty acid composition in Holstein dairy cattle. Genomics, 2014, 104, 572-581.	1.3	16
63	Associations between infectious bovine keratoconjunctivitis at weaning and ultrasongraphically measured body composition traits in yearling cattle. Journal of the American Veterinary Medical Association, 2014, 244, 100-106.	0.2	15
64	Prediction of Altered 3â€²- UTR miRNA-Binding Sites from RNA-Seq Data: The Swine Leukocyte Antigen Complex (SLA) as a Model Region. PLoS ONE, 2012, 7, e48607.	1.1	15
65	Sire breed effect on beef longissimus mineral concentrations and their relationships with carcass and palatability traits. Meat Science, 2015, 106, 25-30.	2.7	14
66	Perspectives on the formation of an interdisciplinary research team. Biochemical and Biophysical Research Communications, 2010, 391, 1155-1157.	1.0	13
67	The effect of postruminal amino acid flow on muscle cell proliferation and protein turnover.. Journal of Animal Science, 1996, 74, 2158.	0.2	12
68	Whole Genome Sequence Data Provides Novel Insights Into the Genetic Architecture of Meat Quality Traits in Beef. Frontiers in Genetics, 2020, 11, 538640.	1.1	12
69	Gene expression in tonsils in swine following infection with porcine reproductive and respiratory syndrome virus. BMC Veterinary Research, 2021, 17, 88.	0.7	12
70	Gene Co-Expression Network Analysis Provides Novel Insights into Myostatin Regulation at Three Different Mouse Developmental Timepoints. PLoS ONE, 2015, 10, e0117607.	1.1	12
71	Structure and regulation of the porcine skeletal Î±-actin-encoding gene. Gene, 1996, 180, 23-28.	1.0	11
72	Deriving Gene Networks from SNP Associated with Triacylglycerol and Phospholipid Fatty Acid Fractions from Ribeyes of Angus Cattle. Frontiers in Genetics, 2016, 7, 116.	1.1	10

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73	Unraveling genomic associations with feed efficiency and body weight traits in chickens through an integrative approach. BMC Genetics, 2019, 20, 83.	2.7	10
74	Abomasal Casein Infusion Enhances the Mitogenic Activity of Serum from Protein-Restricted Steers. Journal of Nutrition, 1994, 124, 67-77.	1.3	9
75	Transcriptional profiling of PRKG2-null growth plate identifies putative down-stream targets of PRKG2. BMC Research Notes, 2015, 8, 177.	0.6	9
76	Discovery of biological networks using an optimized partial correlation coefficient with information theory algorithm on Stampede's Xeon and Xeon Phi processors. Concurrency Computation Practice and Experience, 2014, 26, 2178-2190.	1.4	8
77	Effect of dietary soybean oil inclusion on liver-related transcription factors in a pig model for metabolic diseases. Scientific Reports, 2022, 12, .	1.6	8
78	Comparative analysis of GDF 8 (myostatin) inBos indicusandBos taurus. DNA Sequence, 2006, 17, 311-313.	0.7	7
79	Body composition and gene expression QTL mapping in mice reveals imprinting and interaction effects. BMC Genetics, 2013, 14, 103.	2.7	6
80	Cloning and expression of the porcine myogenin gene. Animal Biotechnology, 1995, 6, 79-92.	0.7	5
81	Multiple regions of the porcine α€skeletal actin gene modulate muscle€specific expression in cell culture and directly injected skeletal muscle. Animal Biotechnology, 1998, 9, 101-120.	0.7	5
82	BEAP: The BLAST Extension and Alignment Program- a tool for contig construction and analysis of preliminary genome sequence. BMC Research Notes, 2009, 2, 11.	0.6	5
83	Differential Gene Expression Associated with Soybean Oil Level in the Diet of Pigs. Animals, 2022, 12, 1632.	1.0	5
84	Use of Genome Sequence Information for Meat Quality Trait QTL Mining for Casual Genes and Mutations on Pig Chromosome 17. Frontiers in Genetics, 2011, 2, 43.	1.1	4
85	Design Database for Quantitative Trait Loci (QTL) Data Warehouse, Data Mining, and Meta-Analysis. Methods in Molecular Biology, 2012, 871, 121-144.	0.4	4
86	Whole-genome SNP markers reveal runs of homozygosity in indigenous cattle breeds of Pakistan. Animal Biotechnology, 2023, 34, 1384-1396.	0.7	3
87	Systems Biology€"Derived Genetic Signatures of Mastitis in Dairy Cattle: A New Avenue for Drug Repurposing. Animals, 2022, 12, 29.	1.0	3
88	Phenotypic variation of mineral contents in beef. FASEB Journal, 2009, 23, LB412.	0.2	1
89	Ten simple rules to ruin a collaborative environment. PLoS Computational Biology, 2022, 18, e1009957.	1.5	1
90	Extension of Animal QTLdb. , 2011, , .		0

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91	Genetic regulation of milk fatty acid composition—developing tools for use in selection.. FASEB Journal, 2008, 22, 695-695.	0.2	0
92	Differential effects of two different beta—adrenergic agonists, clenbuterol and ractopamine, on muscle growth in rats. FASEB Journal, 2010, 24, lb680.	0.2	0
93	Genetic Improvement of Production and Adaptive Traits in Livestock. Indian Journal of Plant Genetic Resources, 2016, 29, 382.	0.1	0