

James M Reecy

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

88

papers

6,084

citations

35

h-index

77

g-index

95

ext. papers

7,748

ext. citations

6.3

avg, IF

5.28

L-index

#	Paper	IF	Citations
88	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012 , 491, 393-8	50.4	928
87	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863
86	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , 2015 , 43, W589-98	20.1	468
85	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008 , 26, 889-96	44.5	417
84	Worldwide patterns of ancestry, divergence, and admixture in domesticated cattle. <i>PLoS Genetics</i> , 2014 , 10, e1004254	6	271
83	Animal QTLdb: an improved database tool for livestock animal QTL/association data dissemination in the post-genome era. <i>Nucleic Acids Research</i> , 2013 , 41, D871-9	20.1	266
82	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015 , 16, 57	18.3	196
81	Developmental progress and current status of the Animal QTLdb. <i>Nucleic Acids Research</i> , 2016 , 44, D827-831	23.1	185
80	Building a livestock genetic and genomic information knowledgebase through integrative developments of Animal QTLdb and CorrDB. <i>Nucleic Acids Research</i> , 2019 , 47, D701-D710	20.1	157
79	AnimalQTLdb: a livestock QTL database tool set for positional QTL information mining and beyond. <i>Nucleic Acids Research</i> , 2007 , 35, D604-9	20.1	148
78	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	36.3	139
77	A QTL resource and comparison tool for pigs: PigQTLDB. <i>Mammalian Genome</i> , 2005 , 16, 792-800	3.2	106
76	Transcriptional profiling of myostatin-knockout mice implicates Wnt signaling in postnatal skeletal muscle growth and hypertrophy. <i>FASEB Journal</i> , 2006 , 20, 580-2	0.9	103
75	Identification of upstream regulatory regions in the heart-expressed homeobox gene Nkx2-5. <i>Development (Cambridge)</i> , 1999 , 126, 839-849	6.6	90
74	Differential gene expression in the rat soleus muscle during early work overload-induced hypertrophy. <i>FASEB Journal</i> , 2002 , 16, 207-9	0.9	80
73	Genome-wide association study for intramuscular fat deposition and composition in Nellore cattle. <i>BMC Genetics</i> , 2014 , 15, 39	2.6	73
72	Lipid metabolism, adipocyte depot physiology and utilization of meat animals as experimental models for metabolic research. <i>International Journal of Biological Sciences</i> , 2010 , 6, 691-9	11.2	73

71	TACE release of TNF-alpha mediates mechanotransduction-induced activation of p38 MAPK and myogenesis. <i>Journal of Cell Science</i> , 2007 , 120, 692-701	5.3	72
70	Animal QTLdb: beyond a repository. A public platform for QTL comparisons and integration with diverse types of structural genomic information. <i>Mammalian Genome</i> , 2007 , 18, 1-4	3.2	68
69	Murine Tbx2 contains domains that activate and repress gene transcription. <i>Gene</i> , 2002 , 283, 117-24	3.8	64
68	Interleukin-8, interleukin-1beta, and interferon-gamma levels are linked to PRRS virus clearance. <i>Viral Immunology</i> , 2010 , 23, 127-34	1.7	60
67	Functional and phylogenetic analyses of a melanocortin-4 receptor mutation in domestic pigs. <i>Domestic Animal Endocrinology</i> , 2004 , 26, 75-86	2.3	57
66	Chicken Nkx-2.8: a novel homeobox gene expressed in early heart progenitor cells and pharyngeal pouch-2 and -3 endoderm. <i>Developmental Biology</i> , 1997 , 188, 295-311	3.1	56
65	Allied industry approaches to alter intramuscular fat content and composition in beef animals. <i>Journal of Food Science</i> , 2010 , 75, R1-8	3.4	53
64	Genome-wide association and prediction of direct genomic breeding values for composition of fatty acids in Angus beef cattle. <i>BMC Genomics</i> , 2013 , 14, 730	4.5	51
63	Putative regulatory factors associated with intramuscular fat content. <i>PLoS ONE</i> , 2015 , 10, e0128350	3.7	50
62	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	4.5	47
61	Identification of differentially expressed gene categories in microarray studies using nonparametric multivariate analysis. <i>Bioinformatics</i> , 2008 , 24, 192-201	7.2	47
60	Design and validation of a 90K SNP genotyping assay for the water buffalo (<i>Bubalus bubalis</i>). <i>PLoS ONE</i> , 2017 , 12, e0185220	3.7	44
59	Skeletal muscle stem cells from animals I. Basic cell biology. <i>International Journal of Biological Sciences</i> , 2010 , 6, 465-74	11.2	42
58	Integration of machine learning and meta-analysis identifies the transcriptomic bio-signature of mastitis disease in cattle. <i>PLoS ONE</i> , 2018 , 13, e0191227	3.7	42
57	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. <i>Journal of Dairy Science</i> , 2013 , 96, 6007-21	4	38
56	GO-FAANG meeting: a Gathering On Functional Annotation of Animal Genomes. <i>Animal Genetics</i> , 2016 , 47, 528-33	2.5	37
55	A nonsense mutation in cGMP-dependent type II protein kinase (PRKG2) causes dwarfism in American Angus cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 19250-5	11.5	36
54	A Vision for Development and Utilization of High-Throughput Phenotyping and Big Data Analytics in Livestock. <i>Frontiers in Genetics</i> , 2019 , 10, 1197	4.5	35

53	The Vertebrate Trait Ontology: a controlled vocabulary for the annotation of trait data across species. <i>Journal of Biomedical Semantics</i> , 2013 , 4, 13	2.2	32
52	Network Analysis Reveals Putative Genes Affecting Meat Quality in Angus Cattle. <i>Frontiers in Genetics</i> , 2017 , 8, 171	4.5	29
51	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	28
50	Pig immune response to general stimulus and to porcine reproductive and respiratory syndrome virus infection: a meta-analysis approach. <i>BMC Genomics</i> , 2013 , 14, 220	4.5	27
49	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. <i>Veterinary Microbiology</i> , 2013 , 166, 242-5	3.3	27
48	Integrative analysis of microRNAs and mRNAs revealed regulation of composition and metabolism in Nelore cattle. <i>BMC Genomics</i> , 2018 , 19, 126	4.5	26
47	Myostatin genotype regulates muscle-specific miRNA expression in mouse pectoralis muscle. <i>BMC Research Notes</i> , 2010 , 3, 297	2.3	26
46	Differences in the skeletal muscle transcriptome profile associated with extreme values of fatty acids content. <i>BMC Genomics</i> , 2016 , 17, 961	4.5	25
45	ANEXdb: an integrated animal ANnotation and microarray EXpression database. <i>Mammalian Genome</i> , 2009 , 20, 768-77	3.2	23
44	Use of SNP genotyping to determine pedigree and breed composition of dairy cattle in Kenya. <i>Journal of Animal Breeding and Genetics</i> , 2010 , 127, 348-51	2.9	22
43	Lactate dehydrogenase expression at the onset of altered loading in rat soleus muscle. <i>Journal of Applied Physiology</i> , 2004 , 97, 1424-30	3.7	19
42	Gene Co-expression Analysis Indicates Potential Pathways and Regulators of Beef Tenderness in Nellore Cattle. <i>Frontiers in Genetics</i> , 2018 , 9, 441	4.5	19
41	Whole genome analysis of infectious bovine keratoconjunctivitis in Angus cattle using Bayesian threshold models. <i>BMC Proceedings</i> , 2011 , 5 Suppl 4, S22	2.3	18
40	Transient cardiac expression of the tinman-family homeobox gene, XNkx2-10. <i>Mechanisms of Development</i> , 2000 , 91, 369-73	1.7	18
39	Serum Response Factor-NK Homeodomain Factor Interactions, Role in Cardiac Development 1999 , 273-290		18
38	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. <i>BMC Genomics</i> , 2018 , 19, 499	4.5	17
37	Association of toll-like receptor four single nucleotide polymorphisms with incidence of infectious bovine keratoconjunctivitis (IBK) in cattle. <i>Immunogenetics</i> , 2011 , 63, 115-9	3.2	16
36	Integration of genome wide association studies and whole genome sequencing provides novel insights into fat deposition in chicken. <i>Scientific Reports</i> , 2018 , 8, 16222	4.9	16

35	Sterol regulatory element binding transcription factor 1 (SREBF1) polymorphism and milk fatty acid composition. <i>Journal of Dairy Science</i> , 2013 , 96, 2605-2616	4	15
34	Associations between infectious bovine keratoconjunctivitis at weaning and ultrasonographically measured body composition traits in yearling cattle. <i>Journal of the American Veterinary Medical Association</i> , 2014 , 244, 100-6	1	14
33	Prediction of altered 3'UTR miRNA-binding sites from RNA-Seq data: the swine leukocyte antigen complex (SLA) as a model region. <i>PLoS ONE</i> , 2012 , 7, e48607	3.7	14
32	Polymorphisms in lipogenic genes and milk fatty acid composition in Holstein dairy cattle. <i>Genomics</i> , 2014 , 104, 572-81	4.3	12
31	Genomic Analysis Suggests KITLG is Responsible for a Roan Pattern in two Pakistani Goat Breeds. <i>Journal of Heredity</i> , 2018 , 109, 315-319	2.4	11
30	Perspectives on the formation of an interdisciplinary research team. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 391, 1155-7	3.4	11
29	Bringing the Animal QTLdb and CorrDB into the future: meeting new challenges and providing updated services. <i>Nucleic Acids Research</i> , 2021 ,	20.1	11
28	Haplotype-based genome-wide association studies for carcass and growth traits in chicken. <i>Poultry Science</i> , 2020 , 99, 2349-2361	3.9	10
27	Co-Expression Networks Reveal Potential Regulatory Roles of miRNAs in Fatty Acid Composition of Nelore Cattle. <i>Frontiers in Genetics</i> , 2019 , 10, 651	4.5	10
26	Sire breed effect on beef longissimus mineral concentrations and their relationships with carcass and palatability traits. <i>Meat Science</i> , 2015 , 106, 25-30	6.4	9
25	Gene co-expression network analysis provides novel insights into myostatin regulation at three different mouse developmental timepoints. <i>PLoS ONE</i> , 2015 , 10, e0117607	3.7	9
24	Structure and regulation of the porcine skeletal alpha-actin-encoding gene. <i>Gene</i> , 1996 , 180, 23-8	3.8	8
23	Discovery of biological networks using an optimized partial correlation coefficient with information theory algorithm on StampedeX Xeon and Xeon Phi processors. <i>Concurrency Computation Practice and Experience</i> , 2014 , 26, 2178-2190	1.4	7
22	Genome-wide association scan for QTL and their positional candidate genes associated with internal organ traits in chickens. <i>BMC Genomics</i> , 2019 , 20, 669	4.5	6
21	Prediction of key regulators and downstream targets of E. coli induced mastitis. <i>Journal of Applied Genetics</i> , 2019 , 60, 367-373	2.5	6
20	Unraveling genomic associations with feed efficiency and body weight traits in chickens through an integrative approach. <i>BMC Genetics</i> , 2019 , 20, 83	2.6	6
19	The effect of postruminal amino acid flow on muscle cell proliferation and protein turnover. <i>Journal of Animal Science</i> , 1996 , 74, 2158-69	0.7	6
18	Body composition and gene expression QTL mapping in mice reveals imprinting and interaction effects. <i>BMC Genetics</i> , 2013 , 14, 103	2.6	5

17	Abomasal casein infusion enhances the mitogenic activity of serum from protein-restricted steers. <i>Journal of Nutrition</i> , 1994 , 124, 67-77	4.1	5
16	Whole Genome Sequence Data Provides Novel Insights Into the Genetic Architecture of Meat Quality Traits in Beef. <i>Frontiers in Genetics</i> , 2020 , 11, 538640	4.5	5
15	Design database for quantitative trait loci (QTL) data warehouse, data mining, and meta-analysis. <i>Methods in Molecular Biology</i> , 2012 , 871, 121-44	1.4	4
14	BEAP: The BLAST Extension and Alignment Program- a tool for contig construction and analysis of preliminary genome sequence. <i>BMC Research Notes</i> , 2009 , 2, 11	2.3	4
13	Comparative analysis of GDF 8 (myostatin) in <i>Bos indicus</i> and <i>Bos taurus</i> . <i>DNA Sequence</i> , 2006 , 17, 311-3		4
12	Cloning and expression of the porcine myogenin gene. <i>Animal Biotechnology</i> , 1995 , 6, 79-92	1.4	4
11	Deriving Gene Networks from SNP Associated with Triacylglycerol and Phospholipid Fatty Acid Fractions from Ribeyes of Angus Cattle. <i>Frontiers in Genetics</i> , 2016 , 7, 116	4.5	4
10	Transcriptional profiling of PRKG2-null growth plate identifies putative down-stream targets of PRKG2. <i>BMC Research Notes</i> , 2015 , 8, 177	2.3	3
9	Use of Genome Sequence Information for Meat Quality Trait QTL Mining for Causal Genes and Mutations on Pig Chromosome 17. <i>Frontiers in Genetics</i> , 2011 , 2, 43	4.5	3
8	Multiple regions of the porcine alpha-skeletal actin gene modulate muscle-specific expression in cell culture and directly injected skeletal muscle. <i>Animal Biotechnology</i> , 1998 , 9, 101-20	1.4	3
7	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. <i>Livestock Science</i> , 2021 , 248, 104515	1.7	3
6	Gene expression in tonsils in swine following infection with porcine reproductive and respiratory syndrome virus. <i>BMC Veterinary Research</i> , 2021 , 17, 88	2.7	2
5	Phenotypic variation of mineral contents in beef. <i>FASEB Journal</i> , 2009 , 23, LB412	0.9	1
4	Whole-genome SNP markers reveal runs of homozygosity in indigenous cattle breeds of Pakistan.. <i>Animal Biotechnology</i> , 2022 , 1-13	1.4	0
3	Ten simple rules to ruin a collaborative environment.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009957	5	0
2	Genetic regulation of milk fatty acid composition-developing tools for use in selection.. <i>FASEB Journal</i> , 2008 , 22, 695-695	0.9	
1	Differential effects of two different beta-adrenergic agonists, clenbuterol and ractopamine, on muscle growth in rats. <i>FASEB Journal</i> , 2010 , 24, lb680	0.9	