

Toni Reverter-Gomez

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183
papers

5,644
citations

47
h-index

66
g-index

201
ext. papers

7,317
ext. citations

3.3
avg, IF

5.62
L-index

#	Paper	IF	Citations
183	Combining partial correlation and an information theory approach to the reversed engineering of gene co-expression networks. <i>Bioinformatics</i> , 2008 , 24, 2491-7	7.2	212
182	A differential wiring analysis of expression data correctly identifies the gene containing the causal mutation. <i>PLoS Computational Biology</i> , 2009 , 5, e1000382	5	150
181	A multi-trait, meta-analysis for detecting pleiotropic polymorphisms for stature, fatness and reproduction in beef cattle. <i>PLoS Genetics</i> , 2014 , 10, e1004198	6	139
180	A validated whole-genome association study of efficient food conversion in cattle. <i>Genetics</i> , 2007 , 176, 1893-905	4	138
179	Gene expression patterns during intramuscular fat development in cattle. <i>Journal of Animal Science</i> , 2009 , 87, 119-30	0.7	137
178	Transcriptional profiling of skeletal muscle tissue from two breeds of cattle. <i>Mammalian Genome</i> , 2005 , 16, 201-10	3.2	124
177	Regulatory impact factors: unraveling the transcriptional regulation of complex traits from expression data. <i>Bioinformatics</i> , 2010 , 26, 896-904	7.2	116
176	Accuracy of prediction of genomic breeding values for residual feed intake and carcass and meat quality traits in <i>Bos taurus</i> , <i>Bos indicus</i> , and composite beef cattle. <i>Journal of Animal Science</i> , 2013 , 91, 3088-104	0.7	111
175	Genome-wide association studies of female reproduction in tropically adapted beef cattle. <i>Journal of Animal Science</i> , 2012 , 90, 1398-410	0.7	106
174	Gene regulatory network inference: evaluation and application to ovarian cancer allows the prioritization of drug targets. <i>Genome Medicine</i> , 2012 , 4, 41	14.4	104
173	Association weight matrix for the genetic dissection of puberty in beef cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 13642-7	11.5	104
172	Gene expression studies of developing bovine longissimus muscle from two different beef cattle breeds. <i>BMC Developmental Biology</i> , 2007 , 7, 95	3.1	102
171	Gene expression profiling of muscle tissue in Brahman steers during nutritional restriction. <i>Journal of Animal Science</i> , 2005 , 83, 1-12	0.7	96
170	Identification of immune genes and proteins involved in the response of bovine mammary tissue to <i>Staphylococcus aureus</i> infection. <i>BMC Veterinary Research</i> , 2008 , 4, 18	2.7	85
169	Genetic and phenotypic characterisation of animal, carcass, and meat quality traits from temperate and tropically adapted beef breeds. 4. Correlations among animal, carcass, and meat quality traits. <i>Australian Journal of Agricultural Research</i> , 2003 , 54, 149		82
168	A single nucleotide polymorphism-derived regulatory gene network underlying puberty in 2 tropical breeds of beef cattle. <i>Journal of Animal Science</i> , 2011 , 89, 1669-83	0.7	79
167	Gastrointestinal nematode challenge induces some conserved gene expression changes in the gut mucosa of genetically resistant sheep. <i>International Journal for Parasitology</i> , 2008 , 38, 431-42	4.3	78

166	Finding genes for economically important traits: Brahman cattle puberty. <i>Animal Production Science</i> , 2012 , 52, 143	1.4	75
165	The extent of linkage disequilibrium in beef cattle breeds using high-density SNP genotypes. <i>Genetics Selection Evolution</i> , 2014 , 46, 22	4.9	73
164	Beyond differential expression: the quest for causal mutations and effector molecules. <i>BMC Genomics</i> , 2012 , 13, 356	4.5	73
163	Evidence for pleiotropism and recent selection in the PLAG1 region in Australian Beef cattle. <i>Animal Genetics</i> , 2013 , 44, 636-47	2.5	72
162	Multi-tissue omics analyses reveal molecular regulatory networks for puberty in composite beef cattle. <i>PLoS ONE</i> , 2014 , 9, e102551	3.7	71
161	Genetic analyses of live-animal ultrasound and abattoir carcass traits in Australian Angus and Hereford cattle. <i>Journal of Animal Science</i> , 2000 , 78, 1786-95	0.7	71
160	The genetic architecture of climatic adaptation of tropical cattle. <i>PLoS ONE</i> , 2014 , 9, e113284	3.7	68
159	Linkage disequilibrium over short physical distances measured in sheep using a high-density SNP chip. <i>Animal Genetics</i> , 2014 , 45, 754-7	2.5	65
158	PCIT: an R package for weighted gene co-expression networks based on partial correlation and information theory approaches. <i>Bioinformatics</i> , 2010 , 26, 411-3	7.2	63
157	Genome-wide association study for inhibin, luteinizing hormone, insulin-like growth factor 1, testicular size and semen traits in bovine species. <i>Andrology</i> , 2013 , 1, 644-50	4.2	62
156	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. <i>Nature Communications</i> , 2018 , 9, 859	17.4	61
155	Identification of a gene network contributing to hypertrophy in callipyge skeletal muscle. <i>Physiological Genomics</i> , 2007 , 28, 253-72	3.6	60
154	Genetic and phenotypic characterisation of animal, carcass, and meat quality traits from temperate and tropically adapted beef breeds. 3. Meat quality traits. <i>Australian Journal of Agricultural Research</i> , 2003 , 54, 135		60
153	Candidate genes associated with testicular development, sperm quality, and hormone levels of inhibin, luteinizing hormone, and insulin-like growth factor 1 in Brahman bulls. <i>Biology of Reproduction</i> , 2012 , 87, 58	3.9	59
152	Method R variance components procedure: application on the simple breeding value model. <i>Journal of Animal Science</i> , 1994 , 72, 2247-53	0.7	57
151	Prospecting major genes in dairy buffaloes. <i>BMC Genomics</i> , 2015 , 16, 872	4.5	56
150	Simultaneous identification of differential gene expression and connectivity in inflammation, adipogenesis and cancer. <i>Bioinformatics</i> , 2006 , 22, 2396-404	7.2	56
149	Stress-induced gene expression profiling in the black tiger shrimp <i>Penaeus monodon</i> . <i>Physiological Genomics</i> , 2007 , 31, 126-38	3.6	55

148	Genomic Prediction of Breeding Values Using a Subset of SNPs Identified by Three Machine Learning Methods. <i>Frontiers in Genetics</i> , 2018 , 9, 237	4.5	54
147	Gene expression profiling of bovine skeletal muscle in response to and during recovery from chronic and severe undernutrition. <i>Journal of Animal Science</i> , 2006 , 84, 3239-50	0.7	54
146	The evolution of tropical adaptation: comparing taurine and zebu cattle. <i>Animal Genetics</i> , 2010 , 41, 467-775		53
145	Construction and validation of a Bovine Innate Immune Microarray. <i>BMC Genomics</i> , 2005 , 6, 135	4.5	53
144	Semi-parametric estimates of population accuracy and bias of predictions of breeding values and future phenotypes using the LR method. <i>Genetics Selection Evolution</i> , 2018 , 50, 53	4.9	52
143	Inferring the transcriptional landscape of bovine skeletal muscle by integrating co-expression networks. <i>PLoS ONE</i> , 2009 , 4, e7249	3.7	51
142	Gene network analyses of first service conception in Brangus heifers: use of genome and trait associations, hypothalamic-transcriptome information, and transcription factors. <i>Journal of Animal Science</i> , 2012 , 90, 2894-906	0.7	50
141	A Boolean-based systems biology approach to predict novel genes associated with cancer: Application to colorectal cancer. <i>BMC Systems Biology</i> , 2011 , 5, 35	3.5	50
140	Transcriptional response of sugarcane roots to methyl jasmonate. <i>Plant Science</i> , 2005 , 168, 761-772	5.3	50
139	Gene expression profiling of bovine in vitro adipogenesis using a cDNA microarray. <i>Functional and Integrative Genomics</i> , 2006 , 6, 235-49	3.8	50
138	Identification of Gene Networks for Residual Feed Intake in Angus Cattle Using Genomic Prediction and RNA-seq. <i>PLoS ONE</i> , 2016 , 11, e0152274	3.7	50
137	Genetic and phenotypic characterisation of animal, carcass, and meat quality traits from temperate and tropically adapted beef breeds. 2. Abattoir carcass traits. <i>Australian Journal of Agricultural Research</i> , 2003 , 54, 119		47
136	Breeding and Genetics Symposium: networks and pathways to guide genomic selection. <i>Journal of Animal Science</i> , 2013 , 91, 537-52	0.7	46
135	Validation of alternative methods of data normalization in gene co-expression studies. <i>Bioinformatics</i> , 2005 , 21, 1112-20	7.2	46
134	A marker-derived gene network reveals the regulatory role of PPARGC1A, HNF4G, and FOXP3 in intramuscular fat deposition of beef cattle. <i>Journal of Animal Science</i> , 2014 , 92, 2832-45	0.7	45
133	A systems biology approach using metabolomic data reveals genes and pathways interacting to modulate divergent growth in cattle. <i>BMC Genomics</i> , 2013 , 14, 798	4.5	42
132	Differential gene expression of wheat progeny with contrasting levels of transpiration efficiency. <i>Plant Molecular Biology</i> , 2006 , 61, 863-81	4.6	42
131	Non-additive genetic variation in growth, carcass and fertility traits of beef cattle. <i>Genetics Selection Evolution</i> , 2015 , 47, 26	4.9	40

130	Chronic exposure to anabolic steroids induces the muscle expression of oxytocin and a more than fiftyfold increase in circulating oxytocin in cattle. <i>Physiological Genomics</i> , 2011 , 43, 467-78	3.6	38
129	Gene expression profiling of Hereford Shorthorn cattle following challenge with <i>Boophilus microplus</i> tick larvae. <i>Australian Journal of Experimental Agriculture</i> , 2007 , 47, 1397		38
128	Physiology and Endocrinology Symposium: How single nucleotide polymorphism chips will advance our knowledge of factors controlling puberty and aid in selecting replacement beef females. <i>Journal of Animal Science</i> , 2012 , 90, 1152-65	0.7	36
127	Genomic regions associated with fertility traits in male and female cattle: advances from microsatellites to high-density chips and beyond. <i>Animal Reproduction Science</i> , 2013 , 141, 1-19	2.1	35
126	Gene expression phenotypes for lipid metabolism and intramuscular fat in skeletal muscle of cattle. <i>Journal of Animal Science</i> , 2013 , 91, 1112-28	0.7	35
125	A mixed-model approach for the analysis of cDNA microarray gene expression data from extreme-performing pigs after infection with <i>Actinobacillus pleuropneumoniae</i> . <i>Journal of Animal Science</i> , 2004 , 82, 1261-71	0.7	34
124	Genetic and phenotypic characterisation of animal, carcass, and meat quality traits from temperate and tropically adapted beef breeds.. <i>Australian Journal of Agricultural Research</i> , 2003 , 54, 107		34
123	Detection of quantitative trait loci in <i>Bos indicus</i> and <i>Bos taurus</i> cattle using genome-wide association studies. <i>Genetics Selection Evolution</i> , 2013 , 45, 43	4.9	33
122	Convergent Evolution of Slick Coat in Cattle through Truncation Mutations in the Prolactin Receptor. <i>Frontiers in Genetics</i> , 2018 , 9, 57	4.5	32
121	Longitudinal muscle gene expression patterns associated with differential intramuscular fat in cattle. <i>Animal</i> , 2015 , 9, 650-9	3.1	32
120	Effects of growth curve parameters on cow efficiency. <i>Journal of Animal Science</i> , 1992 , 70, 2668-72	0.7	32
119	From SNP co-association to RNA co-expression: novel insights into gene networks for intramuscular fatty acid composition in porcine. <i>BMC Genomics</i> , 2014 , 15, 232	4.5	31
118	Transcriptional profiling of muscle tissue in growing Japanese Black cattle to identify genes involved with the development of intramuscular fat. <i>Australian Journal of Experimental Agriculture</i> , 2005 , 45, 809		31
117	Purebred-crossbred performance and genetic evaluation of postweaning growth and carcass traits in <i>Bos indicus</i> x <i>Bos taurus</i> crosses in Australia. <i>Journal of Animal Science</i> , 2002 , 80, 1801-8	0.7	30
116	Nematode challenge induces differential expression of oxidant, antioxidant and mucous genes down the longitudinal axis of the sheep gut. <i>Parasite Immunology</i> , 2010 , 32, 36-46	2.2	29
115	Transcription profiling provides insights into gene pathways involved in horn and scurs development in cattle. <i>BMC Genomics</i> , 2010 , 11, 370	4.5	29
114	Mining tissue specificity, gene connectivity and disease association to reveal a set of genes that modify the action of disease causing genes. <i>BioData Mining</i> , 2008 , 1, 8	4.3	28
113	Proteomics of Breast Muscle Tissue Associated with the Phenotypic Expression of Feed Efficiency within a Pedigree Male Broiler Line: I. Highlight on Mitochondria. <i>PLoS ONE</i> , 2016 , 11, e0155679	3.7	28

112	Breeding and Genetics Symposium: building single nucleotide polymorphism-derived gene regulatory networks: Towards functional genomewide association studies. <i>Journal of Animal Science</i> , 2013 , 91, 530-6	0.7	27
111	Detection of chromosome segments of zebu and taurine origin and their effect on beef production and growth. <i>Journal of Animal Science</i> , 2011 , 89, 2050-60	0.7	27
110	A rapid method for computationally inferring transcriptome coverage and microarray sensitivity. <i>Bioinformatics</i> , 2005 , 21, 80-9	7.2	27
109	Using regulatory and epistatic networks to extend the findings of a genome scan: identifying the gene drivers of pigmentation in merino sheep. <i>PLoS ONE</i> , 2011 , 6, e21158	3.7	27
108	A gene coexpression network for bovine skeletal muscle inferred from microarray data. <i>Physiological Genomics</i> , 2006 , 28, 76-83	3.6	26
107	Systems biology analysis merging phenotype, metabolomic and genomic data identifies Non-SMC Condensin I Complex, Subunit G (NCAPG) and cellular maintenance processes as major contributors to genetic variability in bovine feed efficiency. <i>PLoS ONE</i> , 2015 , 10, e0124574	3.7	26
106	Sources of variation in mechanical shear force measures of tenderness in beef from tropically adapted genotypes, effects of data editing and their implications for genetic parameter estimation. <i>Australian Journal of Experimental Agriculture</i> , 2001 , 41, 991		25
105	Genomic correlation: harnessing the benefit of combining two unrelated populations for genomic selection. <i>Genetics Selection Evolution</i> , 2015 , 47, 84	4.9	24
104	Microarray-based detection of viruses causing vesicular or vesicular-like lesions in livestock animals. <i>Veterinary Microbiology</i> , 2009 , 133, 145-53	3.3	23
103	Combining multi-OMICs information to identify key-regulator genes for pleiotropic effect on fertility and production traits in beef cattle. <i>PLoS ONE</i> , 2018 , 13, e0205295	3.7	22
102	Progesterone signalling in broiler skeletal muscle is associated with divergent feed efficiency. <i>BMC Systems Biology</i> , 2017 , 11, 29	3.5	21
101	Proteomic analysis of the abomasal mucosal response following infection by the nematode, <i>Haemonchus contortus</i> , in genetically resistant and susceptible sheep. <i>Journal of Proteomics</i> , 2012 , 75, 2141-52	3.9	21
100	Skeletal muscle specific genes networks in cattle. <i>Functional and Integrative Genomics</i> , 2010 , 10, 609-18	3.8	21
99	Genomic structure and marker-derived gene networks for growth and meat quality traits of Brazilian Nelore beef cattle. <i>BMC Genomics</i> , 2016 , 17, 235	4.5	21
98	Characterization of the porcine nutrient and taste receptor gene repertoire in domestic and wild populations across the globe. <i>BMC Genomics</i> , 2014 , 15, 1057	4.5	20
97	The integrity of sperm chromatin in young tropical composite bulls. <i>Theriogenology</i> , 2012 , 78, 326-33, 333.e1-4	2.8	20
96	Mammalian genomic regulatory regions predicted by utilizing human genomics, transcriptomics, and epigenetics data. <i>GigaScience</i> , 2018 , 7, 1-17	7.6	19
95	The combined effect of SNP-marker and phenotype attributes in genome-wide association studies. <i>Animal Genetics</i> , 2009 , 40, 149-56	2.5	19

94	Dominance and epistatic genetic variances for litter size in pigs using genomic models. <i>Genetics Selection Evolution</i> , 2018 , 50, 71	4.9	19
93	Genomic analyses of tropical beef cattle fertility based on genotyping pools of Brahman cows with unknown pedigree. <i>Journal of Animal Science</i> , 2016 , 94, 4096-4108	0.7	18
92	A genomics-informed, SNP association study reveals FBLN1 and FABP4 as contributing to resistance to fleece rot in Australian Merino sheep. <i>BMC Veterinary Research</i> , 2010 , 6, 27	2.7	18
91	Genomic inbreeding depression for climatic adaptation of tropical beef cattle. <i>Journal of Animal Science</i> , 2017 , 95, 3809-3821	0.7	18
90	Biological Network Approach for the Identification of Regulatory Long Non-Coding RNAs Associated With Metabolic Efficiency in Cattle. <i>Frontiers in Genetics</i> , 2019 , 10, 1130	4.5	18
89	Proteogenomics Reveals Enriched Ribosome Assembly and Protein Translation in of High Feed Efficiency Pedigree Broiler Males. <i>Frontiers in Physiology</i> , 2017 , 8, 306	4.6	17
88	Potential for recombinant <i>Babesia bovis</i> antigens to protect against a highly virulent isolate. <i>Parasite Immunology</i> , 2005 , 27, 439-45	2.2	17
87	,, and Emerge as Predicted Regulators of 452 Differentially Expressed Genes Associated With Puberty in Brahman Heifers. <i>Frontiers in Genetics</i> , 2018 , 9, 87	4.5	16
86	Transcriptome analyses identify five transcription factors differentially expressed in the hypothalamus of post- versus prepubertal Brahman heifers. <i>Journal of Animal Science</i> , 2016 , 94, 3693-3707	4.7	16
85	Systems Biology Reveals and as Key Regulators of Feed Efficiency in Beef Cattle. <i>Frontiers in Genetics</i> , 2019 , 10, 230	4.5	15
84	Gene expression-based approaches to beef quality research. <i>Australian Journal of Experimental Agriculture</i> , 2006 , 46, 165		15
83	Gene expression profiling of ovine skin and wool follicle development using a combined ovine - bovine skin cDNA microarray. <i>Australian Journal of Experimental Agriculture</i> , 2005 , 45, 867		15
82	The rate of L-lactate production: a feasible parameter for the fresh diluted boar semen quality analysis. <i>Animal Reproduction Science</i> , 1996 , 43, 161-172	2.1	15
81	Association weight matrix: a network-based approach towards functional genome-wide association studies. <i>Methods in Molecular Biology</i> , 2013 , 1019, 437-47	1.4	14
80	Porcine tissue-specific regulatory networks derived from meta-analysis of the transcriptome. <i>PLoS ONE</i> , 2012 , 7, e46159	3.7	13
79	Chicken muscle mitochondrial content appears co-ordinately regulated and is associated with performance phenotypes. <i>Biology Open</i> , 2017 , 6, 50-58	2.2	12
78	Information compression exploits patterns of genome composition to discriminate populations and highlight regions of evolutionary interest. <i>BMC Bioinformatics</i> , 2014 , 15, 66	3.6	12
77	Genome-wide patterns of promoter sharing and co-expression in bovine skeletal muscle. <i>BMC Genomics</i> , 2011 , 12, 23	4.5	12

76	Gene expression profiling of porcine peripheral blood leukocytes after infection with <i>Actinobacillus pleuropneumoniae</i> . <i>Veterinary Immunology and Immunopathology</i> , 2008 , 121, 260-74	2	12
75	Inferring the in vivo cellular program of developing bovine skeletal muscle from expression data. <i>Gene Expression Patterns</i> , 2013 , 13, 109-25	1.5	11
74	Construction of gene interaction and regulatory networks in bovine skeletal muscle from expression data. <i>Australian Journal of Experimental Agriculture</i> , 2005 , 45, 821		11
73	Eukaryotic evolutionary transitions are associated with extreme codon bias in functionally-related proteins. <i>PLoS ONE</i> , 2011 , 6, e25457	3.7	11
72	Selection signatures in tropical cattle are enriched for promoter and coding regions and reveal missense mutations in the damage response gene HELB. <i>Genetics Selection Evolution</i> , 2020 , 52, 27	4.9	10
71	Approximate confidence intervals for heritability from method R estimates. <i>Journal of Animal Science</i> , 1997 , 75, 2041-6	0.7	10
70	Global differential gene expression in the pituitary gland and the ovaries of pre- and postpubertal Brahman heifers. <i>Journal of Animal Science</i> , 2017 , 95, 599	0.7	10
69	Gene expression identifies metabolic and functional differences between intramuscular and subcutaneous adipocytes in cattle. <i>BMC Genomics</i> , 2020 , 21, 77	4.5	9
68	Parasitic castration by the digenian trematode <i>Allopodocotyle</i> sp. alters gene expression in the brain of the host mollusc <i>Haliotis asinina</i> . <i>FEBS Letters</i> , 2006 , 580, 3769-74	3.8	9
67	The <i>Bos taurus</i> - <i>Bos indicus</i> balance in fertility and milk related genes. <i>PLoS ONE</i> , 2017 , 12, e0181930	3.7	9
66	Neuropeptidome of the Hypothalamus and Pituitary Gland of Indicine Taurine Heifers: Evidence of Differential Neuropeptide Processing in the Pituitary Gland before and after Puberty. <i>Journal of Proteome Research</i> , 2018 , 17, 1852-1865	5.6	8
65	Polymorphisms and genes associated with puberty in heifers. <i>Theriogenology</i> , 2016 , 86, 333-9	2.8	8
64	Evaluation of nonadditive effects in yearling weight of tropical beef cattle. <i>Journal of Animal Science</i> , 2018 , 96, 4028-4034	0.7	8
63	Pooled genotyping strategies for the rapid construction of genomic reference populations1. <i>Journal of Animal Science</i> , 2019 , 97, 4761-4769	0.7	8
62	Molecular regulation of high muscle mass in developing Blonde d'Aquitaine cattle fetuses. <i>Biology Open</i> , 2017 , 6, 1483-1492	2.2	8
61	Genome-wide association for the outcome of fixed-time artificial insemination of Brahman heifers in northern Australia. <i>Journal of Animal Science</i> , 2015 , 93, 5119-27	0.7	8
60	Divergent ghrelin expression patterns in sheep genetically resistant or susceptible to gastrointestinal nematodes. <i>Veterinary Parasitology</i> , 2011 , 181, 194-202	2.8	8
59	Pre- and post-puberty expression of genes and proteins in the uterus of <i>Bos indicus</i> heifers: the luteal phase effect post-puberty. <i>Animal Genetics</i> , 2018 , 49, 539-549	2.5	8

58	Mitochondrial metabolism: a driver of energy utilisation and product quality?. <i>Animal Production Science</i> , 2017 , 57, 2204	1.4	7
57	Post-partum anoestrus in tropical beef cattle: A systems approach combining gene expression and genome-wide association results. <i>Livestock Science</i> , 2014 , 166, 158-166	1.7	7
56	Numerical analysis of intensity signals resulting from genotyping pooled DNA samples in beef cattle and broiler chicken. <i>Journal of Animal Science</i> , 2014 , 92, 1874-85	0.7	7
55	INSPeCT: INtegrative Platform for Cancer Transcriptomics. <i>Cancer Informatics</i> , 2014 , 13, 59-66	2.4	7
54	Assessing the efficiency of multiplicative mixed model equations to account for heterogeneous variance across herds in carcass scan traits from beef cattle. <i>Journal of Animal Science</i> , 1997 , 75, 1477-85 ^{0.7}	0.7	7
53	Estimation of genetic covariances with method R. <i>Journal of Animal Science</i> , 2001 , 79, 605-15	0.7	7
52	Exploring the Regulatory Potential of Long Non-Coding RNA in Feed Efficiency of Indicine Cattle. <i>Genes</i> , 2020 , 11,	4.2	7
51	A Pathway-Centered Analysis of Pig Domestication and Breeding in Eurasia. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 2171-2184	3.2	6
50	Gene Networks Driving Genetic Variation in Milk and Cheese-Making Traits of Spanish Assaf Sheep. <i>Genes</i> , 2020 , 11,	4.2	6
49	Compression distance can discriminate animals by genetic profile, build relationship matrices and estimate breeding values. <i>Genetics Selection Evolution</i> , 2015 , 47, 78	4.9	6
48	A gene co-association network regulating gut microbial communities in a Duroc pig population. <i>Microbiome</i> , 2021 , 9, 52	16.6	6
47	Multi-Tissue Transcriptome Profiling of North American Derived Atlantic Salmon. <i>Frontiers in Genetics</i> , 2018 , 9, 369	4.5	6
46	The 'heritability' of domestication and its functional partitioning in the pig. <i>Heredity</i> , 2017 , 118, 160-168 ^{3.6}	3.6	5
45	Sensory rewiring in an echolocator: genome-wide modification of retinogenic and auditory genes in the bat <i>Myotis davidii</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1825-35	3.2	5
44	Sire and growth-path effects on sheep meat production. 3. Fascicular structure of lamb loin muscle (m. longissimus lumborum) and the impact on eating quality. <i>Animal Production Science</i> , 2009 , 49, 239	1.4	5
43	The interplay between evolution, regulation and tissue specificity in the Human Hereditary Diseaseome. <i>BMC Genomics</i> , 2010 , 11 Suppl 4, S23	4.5	5
42	A regulatory gene network related to the porcine umami taste receptor (TAS1R1/TAS1R3). <i>Animal Genetics</i> , 2016 , 47, 114-9	2.5	5
41	Greenlip Abalone () Genome and Protein Analysis Provides Insights into Maturation and Spawning. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 3067-3078	3.2	5

40	Identification of Predictor Genes for Feed Efficiency in Beef Cattle by Applying Machine Learning Methods to Multi-Tissue Transcriptome Data. <i>Frontiers in Genetics</i> , 2021 , 12, 619857	4.5	5
39	A systems biology framework integrating GWAS and RNA-seq to shed light on the molecular basis of sperm quality in swine. <i>Genetics Selection Evolution</i> , 2020 , 52, 72	4.9	4
38	Identification and Annotation of Potential Function of Regulatory Antisense Long Non-Coding RNAs Related to Feed Efficiency in Bulls. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	4
37	Weighting genomic and genealogical information for genetic parameter estimation and breeding value prediction in tropical beef cattle. <i>Journal of Animal Science</i> , 2018 , 96, 612-617	0.7	4
36	Data compression can discriminate broilers by selection line, detect haplotypes, and estimate genetic potential for complex phenotypes. <i>Poultry Science</i> , 2017 , 96, 3031-3038	3.9	4
35	Evaluation of non-additive genetic variation in feed-related traits of broiler chickens. <i>Poultry Science</i> , 2017 , 96, 754-763	3.9	4
34	An Always Correlated gene expression landscape for ovine skeletal muscle, lessons learnt from comparison with an "equivalent" bovine landscape. <i>BMC Research Notes</i> , 2012 , 5, 632	2.3	4
33	Model selection in a global analysis of a microarray experiment. <i>Journal of Animal Science</i> , 2009 , 87, 88-98.7		4
32	Using a 3D virtual muscle model to link gene expression changes during myogenesis to protein spatial location in muscle. <i>BMC Systems Biology</i> , 2008 , 2, 88	3.5	4
31	Genetic regulators of mineral amount in Nelore cattle muscle predicted by a new co-expression and regulatory impact factor approach. <i>Scientific Reports</i> , 2020 , 10, 8436	4.9	4
30	Chromatin accessibility and regulatory vocabulary across indicine cattle tissues. <i>Genome Biology</i> , 2021 , 22, 273	18.3	4
29	Identification of differentially expressed reproductive and metabolic proteins in the female abalone (<i>Haliotis laevis</i>) gonad following artificial induction of spawning. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017 , 24, 127-138	2	3
28	Dynamics of Gene Co-expression Networks in Time-Series Data: A Case Study in Embryogenesis. <i>Frontiers in Genetics</i> , 2020 , 11, 517	4.5	3
27	RNF14 is a regulator of mitochondrial and immune function in muscle. <i>BMC Systems Biology</i> , 2014 , 8, 10	3.5	3
26	Muscle-specific gene expression is underscored by differential stressor responses and coexpression changes. <i>Functional and Integrative Genomics</i> , 2012 , 12, 93-103	3.8	3
25	X chromosome variants are associated with male fertility traits in two bovine populations. <i>Genetics Selection Evolution</i> , 2020 , 52, 46	4.9	3
24	ImmuneDEX: a strategy for the genetic improvement of immune competence in Australian Angus cattle. <i>Journal of Animal Science</i> , 2021 , 99,	0.7	3
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