Toni Reverter-Gomez

List of Publications by Year in Descending Order

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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.

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	Leveraging host-genetics and gut microbiota to determine immunocompetence in pigs. *Animal Microbiome*, **2021**, 3, 74	4.1	0
182	ImmuneDEX: a strategy for the genetic improvement of immune competence in Australian Angus cattle. *Journal of Animal Science*, **2021**, 99,	0.7	3
181	Network Analyses Predict Small RNAs That Might Modulate Gene Expression in the Testis and Epididymis of Bulls. *Frontiers in Genetics*, **2021**, 12, 610116	4.5	1
180	Development of Angus SteerSELECT: a genomic-based tool to identify performance differences of Australian Angus steers during feedlot finishing: Phase 1 validation. *Animal Production Science*, **2021**,	1.4	3
179	A gene co-association network regulating gut microbial communities in a Duroc pig population. *Microbiome*, **2021**, 9, 52	16.6	6
178	Identification of Predictor Genes for Feed Efficiency in Beef Cattle by Applying Machine Learning Methods to Multi-Tissue Transcriptome Data. *Frontiers in Genetics*, **2021**, 12, 619857	4.5	5
177	A conserved haplotype in Wagyu cattle contains RAB4A whose encoded protein regulates glucose trafficking in muscle and fat cells. *Animal Genetics*, **2021**, 52, 275-283	2.5	
176	Chromatin accessibility and regulatory vocabulary across indicine cattle tissues. *Genome Biology*, **2021**, 22, 273	18.3	4
175	Bias, dispersion, and accuracy of genomic predictions for feedlot and carcase traits in Australian Angus steers. *Genetics Selection Evolution*, **2021**, 53, 77	4.9	0
174	A systems biology framework integrating GWAS and RNA-seq to shed light on the molecular basis of sperm quality in swine. *Genetics Selection Evolution*, **2020**, 52, 72	4.9	4
173	Identification and Annotation of Potential Function of Regulatory Antisense Long Non-Coding RNAs Related to Feed Efficiency in Bulls. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	4
172	In silico validation of pooled genotyping strategies for genomic evaluation in Angus cattle. *Journal of Animal Science*, **2020**, 98,	0.7	2
171	Selection signatures in tropical cattle are enriched for promoter and coding regions and reveal missense mutations in the damage response gene HELB. *Genetics Selection Evolution*, **2020**, 52, 27	4.9	10
170	Gene regulation could be attributed to TCF3 and other key transcription factors in the muscle of pubertal heifers. *Veterinary Medicine and Science*, **2020**, 6, 695-710	2.1	2
169	Dynamics of Gene Co-expression Networks in Time-Series Data: A Case Study in Embryogenesis. *Frontiers in Genetics*, **2020**, 11, 517	4.5	3
168	Gene Networks Driving Genetic Variation in Milk and Cheese-Making Traits of Spanish Assaf Sheep. *Genes*, **2020**, 11,	4.2	6
167	Gene expression identifies metabolic and functional differences between intramuscular and subcutaneous adipocytes in cattle. *BMC Genomics*, **2020**, 21, 77	4.5	9

166	Genetic regulators of mineral amount in Nelore cattle muscle predicted by a new co-expression and regulatory impact factor approach. *Scientific Reports*, **2020**, 10, 8436	4.9	4
165	Genome-Wide Co-Expression Distributions as a Metric to Prioritize Genes of Functional Importance. *Genes*, **2020**, 11,	4.2	1
164	Unravelling student evaluations of courses and teachers. *Cogent Education*, **2020**, 7, 1771830	0.9	
163	Exploring the Regulatory Potential of Long Non-Coding RNA in Feed Efficiency of Indicine Cattle. *Genes*, **2020**, 11,	4.2	7
162	X chromosome variants are associated with male fertility traits in two bovine populations. *Genetics Selection Evolution*, **2020**, 52, 46	4.9	3
161	Networks of inbreeding coefficients in a selected population of rabbits. *Journal of Animal Breeding and Genetics*, **2020**, 137, 599-608	2.9	1
160	The Efficacy of Sunitinib Treatment of Renal Cancer Cells Is Associated with the Protein PHAX In Vitro. *Biology*, **2020**, 9,	4.9	1
159	Systems Biology Reveals and as Key Regulators of Feed Efficiency in Beef Cattle. *Frontiers in Genetics*, **2019**, 10, 230	4.5	15
158	Across-sex genomic-assisted genetic correlations for sex-influenced traits in Brahman cattle. *Genetics Selection Evolution*, **2019**, 51, 41	4.9	1
157	Pooled genotyping strategies for the rapid construction of genomic reference populations1. *Journal of Animal Science*, **2019**, 97, 4761-4769	0.7	8
156	Greenlip Abalone () Genome and Protein Analysis Provides Insights into Maturation and Spawning. *G3: Genes, Genomes, Genetics*, **2019**, 9, 3067-3078	3.2	5
155	Biological Network Approach for the Identification of Regulatory Long Non-Coding RNAs Associated With Metabolic Efficiency in Cattle. *Frontiers in Genetics*, **2019**, 10, 1130	4.5	18
154	Neuropeptidome of the Hypothalamus and Pituitary Gland of Indicine Taurine Heifers: Evidence of Differential Neuropeptide Processing in the Pituitary Gland before and after Puberty. *Journal of Proteome Research*, **2018**, 17, 1852-1865	5.6	8
153	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. *Nature Communications*, **2018**, 9, 859	17.4	61
152	Mammalian genomic regulatory regions predicted by utilizing human genomics, transcriptomics, and epigenetics data. *GigaScience*, **2018**, 7, 1-17	7.6	19
151	Weighting genomic and genealogical information for genetic parameter estimation and breeding value prediction in tropical beef cattle. *Journal of Animal Science*, **2018**, 96, 612-617	0.7	4
150	Convergent Evolution of Slick Coat in Cattle through Truncation Mutations in the Prolactin Receptor. *Frontiers in Genetics*, **2018**, 9, 57	4.5	32
149	, , and Emerge as Predicted Regulators of 452 Differentially Expressed Genes Associated With Puberty in Brahman Heifers. *Frontiers in Genetics*, **2018**, 9, 87	4.5	16

148	Evaluation of nonadditive effects in yearling weight of tropical beef cattle. *Journal of Animal Science*, **2018**, 96, 4028-4034	0.7	8
147	Genomic Prediction of Breeding Values Using a Subset of SNPs Identified by Three Machine Learning Methods. *Frontiers in Genetics*, **2018**, 9, 237	4.5	54
146	RAPID COMMUNICATION: A haplotype information theory method reveals genes of evolutionary interest in European vs. Asian pigs. *Journal of Animal Science*, **2018**, 96, 3064-3069	0.7	2
145	Semi-parametric estimates of population accuracy and bias of predictions of breeding values and future phenotypes using the LR method. *Genetics Selection Evolution*, **2018**, 50, 53	4.9	52
144	Dominance and epistatic genetic variances for litter size in pigs using genomic models. *Genetics Selection Evolution*, **2018**, 50, 71	4.9	19
143	Combining multi-OMICs information to identify key-regulator genes for pleiotropic effect on fertility and production traits in beef cattle. *PLoS ONE*, **2018**, 13, e0205295	3.7	22
142	Multi-Tissue Transcriptome Profiling of North American Derived Atlantic Salmon. *Frontiers in Genetics*, **2018**, 9, 369	4.5	6
141	Pre- and post-puberty expression of genes and proteins in the uterus of Bos indicus heifers: the luteal phase effect post-puberty. *Animal Genetics*, **2018**, 49, 539-549	2.5	8
140	Identification of differentially expressed reproductive and metabolic proteins in the female abalone (Haliotis laevigata) gonad following artificial induction of spawning. *Comparative Biochemistry and Physiology Part D: Genomics and Proteomics*, **2017**, 24, 127-138	2	3
139	A Pathway-Centered Analysis of Pig Domestication and Breeding in Eurasia. *G3: Genes, Genomes, Genetics*, **2017**, 7, 2171-2184	3.2	6
138	Gonadal reproductive and metabolic proteins of male abalone Haliotis laevigata (Donovan, 1808) assessed by targeted mass spectrometry after artificial induction of spawning. *Aquaculture Research*, **2017**, 48, 6009-6015	1.9	
137	Mitochondrial metabolism: a driver of energy utilisation and product quality?. *Animal Production Science*, **2017**, 57, 2204	1.4	7
136	Chicken muscle mitochondrial content appears co-ordinately regulated and is associated with performance phenotypes. *Biology Open*, **2017**, 6, 50-58	2.2	12
135	Molecular regulation of high muscle mass in developing Blonde d'Aquitaine cattle foetuses. *Biology Open*, **2017**, 6, 1483-1492	2.2	8
134	Data compression can discriminate broilers by selection line, detect haplotypes, and estimate genetic potential for complex phenotypes. *Poultry Science*, **2017**, 96, 3031-3038	3.9	4
133	Progesterone signalling in broiler skeletal muscle is associated with divergent feed efficiency. *BMC Systems Biology*, **2017**, 11, 29	3.5	21
132	Evaluation of non-additive genetic variation in feed-related traits of broiler chickens. *Poultry Science*, **2017**, 96, 754-763	3.9	4
131	The 'heritability' of domestication and its functional partitioning in the pig. *Heredity*, **2017**, 118, 160-168	3.6	5

130	Proteogenomics Reveals Enriched Ribosome Assembly and Protein Translation in of High Feed Efficiency Pedigree Broiler Males. *Frontiers in Physiology*, **2017**, 8, 306	4.6	17
129	The Bos taurus-Bos indicus balance in fertility and milk related genes. *PLoS ONE*, **2017**, 12, e0181930	3.7	9
128	Global differential gene expression in the pituitary gland and the ovaries of pre- and postpubertal Brahman heifers. *Journal of Animal Science*, **2017**, 95, 599	0.7	10
127	Genomic inbreeding depression for climatic adaptation of tropical beef cattle. *Journal of Animal Science*, **2017**, 95, 3809-3821	0.7	18
126	Genomic analyses of tropical beef cattle fertility based on genotyping pools of Brahman cows with unknown pedigree. *Journal of Animal Science*, **2016**, 94, 4096-4108	0.7	18
125	Polymorphisms and genes associated with puberty in heifers. *Theriogenology*, **2016**, 86, 333-9	2.8	8
124	Identification of Gene Networks for Residual Feed Intake in Angus Cattle Using Genomic Prediction and RNA-seq. *PLoS ONE*, **2016**, 11, e0152274	3.7	50
123	Proteomics of Breast Muscle Tissue Associated with the Phenotypic Expression of Feed Efficiency within a Pedigree Male Broiler Line: I. Highlight on Mitochondria. *PLoS ONE*, **2016**, 11, e0155679	3.7	28
122	Transcriptome analyses identify five transcription factors differentially expressed in the hypothalamus of post- versus prepubertal Brahman heifers. *Journal of Animal Science*, **2016**, 94, 3693-3702	0.7	16
121	Genomic structure and marker-derived gene networks for growth and meat quality traits of Brazilian Nelore beef cattle. *BMC Genomics*, **2016**, 17, 235	4.5	21
120	A regulatory gene network related to the porcine umami taste receptor (TAS1R1/TAS1R3). *Animal Genetics*, **2016**, 47, 114-9	2.5	5
119	Non-additive genetic variation in growth, carcass and fertility traits of beef cattle. *Genetics Selection Evolution*, **2015**, 47, 26	4.9	40
118	Longitudinal muscle gene expression patterns associated with differential intramuscular fat in cattle. *Animal*, **2015**, 9, 650-9	3.1	32
117	Genome-wide association for the outcome of fixed-time artificial insemination of Brahman heifers in northern Australia. *Journal of Animal Science*, **2015**, 93, 5119-27	0.7	8
116	Prospecting major genes in dairy buffaloes. *BMC Genomics*, **2015**, 16, 872	4.5	56
115	Compression distance can discriminate animals by genetic profile, build relationship matrices and estimate breeding values. *Genetics Selection Evolution*, **2015**, 47, 78	4.9	6
114	Genomic correlation: harnessing the benefit of combining two unrelated populations for genomic selection. *Genetics Selection Evolution*, **2015**, 47, 84	4.9	24
113	Low frequency of Y anomaly detected in Australian Brahman cow-herds. *Meta Gene*, **2015**, 3, 59-61	0.7	2

112	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. *PLoS ONE*, **2015**, 10, e0124574	3.7	26
111	RNF14 is a regulator of mitochondrial and immune function in muscle. *BMC Systems Biology*, **2014**, 8, 10	3.5	3
110	Post-partum anoestrus in tropical beef cattle: A systems approach combining gene expression and genome-wide association results. *Livestock Science*, **2014**, 166, 158-166	1.7	7
109	The extent of linkage disequilibrium in beef cattle breeds using high-density SNP genotypes. *Genetics Selection Evolution*, **2014**, 46, 22	4.9	73
108	Information compression exploits patterns of genome composition to discriminate populations and highlight regions of evolutionary interest. *BMC Bioinformatics*, **2014**, 15, 66	3.6	12
107	From SNP co-association to RNA co-expression: novel insights into gene networks for intramuscular fatty acid composition in porcine. *BMC Genomics*, **2014**, 15, 232	4.5	31
106	A marker-derived gene network reveals the regulatory role of PPARGC1A, HNF4G, and FOXP3 in intramuscular fat deposition of beef cattle. *Journal of Animal Science*, **2014**, 92, 2832-45	0.7	45
105	Multi-tissue omics analyses reveal molecular regulatory networks for puberty in composite beef cattle. *PLoS ONE*, **2014**, 9, e102551	3.7	71
104	The genetic architecture of climatic adaptation of tropical cattle. *PLoS ONE*, **2014**, 9, e113284	3.7	68
103	Numerical analysis of intensity signals resulting from genotyping pooled DNA samples in beef cattle and broiler chicken. *Journal of Animal Science*, **2014**, 92, 1874-85	0.7	7
102	A multi-trait, meta-analysis for detecting pleiotropic polymorphisms for stature, fatness and reproduction in beef cattle. *PLoS Genetics*, **2014**, 10, e1004198	6	139
101	Linkage disequilibrium over short physical distances measured in sheep using a high-density SNP chip. *Animal Genetics*, **2014**, 45, 754-7	2.5	65
100	Variation in genes involved in epigenetic processes offers insights into tropically adapted cattle diversity. *Frontiers in Genetics*, **2014**, 5, 89	4.5	1
99	Characterization of the porcine nutrient and taste receptor gene repertoire in domestic and wild populations across the globe. *BMC Genomics*, **2014**, 15, 1057	4.5	20
98	Sensory rewiring in an echolocator: genome-wide modification of retinogenic and auditory genes in the bat Myotis davidii. *G3: Genes, Genomes, Genetics*, **2014**, 4, 1825-35	3.2	5
97	INsPeCT: INtegrative Platform for Cancer Transcriptomics. *Cancer Informatics*, **2014**, 13, 59-66	2.4	7
96	Evidence for pleiotropism and recent selection in the PLAG1 region in Australian Beef cattle. *Animal Genetics*, **2013**, 44, 636-47	2.5	72
95	Genomic regions associated with fertility traits in male and female cattle: advances from microsatellites to high-density chips and beyond. *Animal Reproduction Science*, **2013**, 141, 1-19	2.1	35

94	Inferring the in vivo cellular program of developing bovine skeletal muscle from expression data. *Gene Expression Patterns*, **2013**, 13, 109-25	1.5	11
93	A systems biology approach using metabolomic data reveals genes and pathways interacting to modulate divergent growth in cattle. *BMC Genomics*, **2013**, 14, 798	4.5	42
92	Association weight matrix: a network-based approach towards functional genome-wide association studies. *Methods in Molecular Biology*, **2013**, 1019, 437-47	1.4	14
91	Detection of quantitative trait loci in Bos indicus and Bos taurus cattle using genome-wide association studies. *Genetics Selection Evolution*, **2013**, 45, 43	4.9	33
90	Accuracy of prediction of genomic breeding values for residual feed intake and carcass and meat quality traits in Bos taurus, Bos indicus, and composite beef cattle. *Journal of Animal Science*, **2013**, 91, 3088-104	0.7	111
89	Gene expression phenotypes for lipid metabolism and intramuscular fat in skeletal muscle of cattle. *Journal of Animal Science*, **2013**, 91, 1112-28	0.7	35
88	Genome-wide association study for inhibin, luteinizing hormone, insulin-like growth factor 1, testicular size and semen traits in bovine species. *Andrology*, **2013**, 1, 644-50	4.2	62
87	Breeding and Genetics Symposium: networks and pathways to guide genomic selection. *Journal of Animal Science*, **2013**, 91, 537-52	0.7	46
86	Breeding and Genetics Symposium: building single nucleotide polymorphism-derived gene regulatory networks: Towards functional genomewide association studies. *Journal of Animal Science*, **2013**, 91, 530-6	0.7	27
85	The integrity of sperm chromatin in young tropical composite bulls. *Theriogenology*, **2012**, 78, 326-33, 333.e1-4	2.8	20
84	Proteomic analysis of the abomasal mucosal response following infection by the nematode, Haemonchus contortus, in genetically resistant and susceptible sheep. *Journal of Proteomics*, **2012**, 75, 2141-52	3.9	21
83	Beyond differential expression: the quest for causal mutations and effector molecules. *BMC Genomics*, **2012**, 13, 356	4.5	73
82	An Always Correlated gene expression landscape for ovine skeletal muscle, lessons learnt from comparison with an "equivalent" bovine landscape. *BMC Research Notes*, **2012**, 5, 632	2.3	4
81	Gene network analyses of first service conception in Brangus heifers: use of genome and trait associations, hypothalamic-transcriptome information, and transcription factors. *Journal of Animal Science*, **2012**, 90, 2894-906	0.7	50
80	Finding genes for economically important traits: Brahman cattle puberty. *Animal Production Science* , **2012**, 52, 143	1.4	75
79	Gene regulatory network inference: evaluation and application to ovarian cancer allows the prioritization of drug targets. *Genome Medicine*, **2012**, 4, 41	14.4	104
78	Porcine tissue-specific regulatory networks derived from meta-analysis of the transcriptome. *PLoS ONE*, **2012**, 7, e46159	3.7	13
77	Muscle-specific gene expression is underscored by differential stressor responses and coexpression changes. *Functional and Integrative Genomics*, **2012**, 12, 93-103	3.8	3

76	Physiology and Endocrinology Symposium: How single nucleotide polymorphism chips will advance our knowledge of factors controlling puberty and aid in selecting replacement beef females. *Journal of Animal Science*, **2012**, 90, 1152-65	0.7	36
75	Genome-wide association studies of female reproduction in tropically adapted beef cattle. *Journal of Animal Science*, **2012**, 90, 1398-410	0.7	106
74	Candidate genes associated with testicular development, sperm quality, and hormone levels of inhibin, luteinizing hormone, and insulin-like growth factor 1 in Brahman bulls. *Biology of Reproduction*, **2012**, 87, 58	3.9	59
73	Divergent ghrelin expression patterns in sheep genetically resistant or susceptible to gastrointestinal nematodes. *Veterinary Parasitology*, **2011**, 181, 194-202	2.8	8
72	A Boolean-based systems biology approach to predict novel genes associated with cancer: Application to colorectal cancer. *BMC Systems Biology*, **2011**, 5, 35	3.5	50
71	Genome-wide patterns of promoter sharing and co-expression in bovine skeletal muscle. *BMC Genomics*, **2011**, 12, 23	4.5	12
70	Chronic exposure to anabolic steroids induces the muscle expression of oxytocin and a more than fiftyfold increase in circulating oxytocin in cattle. *Physiological Genomics*, **2011**, 43, 467-78	3.6	38
69	Detection of chromosome segments of zebu and taurine origin and their effect on beef production and growth. *Journal of Animal Science*, **2011**, 89, 2050-60	0.7	27
68	A single nucleotide polymorphism-derived regulatory gene network underlying puberty in 2 tropical breeds of beef cattle. *Journal of Animal Science*, **2011**, 89, 1669-83	0.7	79
67	Using regulatory and epistatic networks to extend the findings of a genome scan: identifying the gene drivers of pigmentation in merino sheep. *PLoS ONE*, **2011**, 6, e21158	3.7	27
66	Eukaryotic evolutionary transitions are associated with extreme codon bias in functionally-related proteins. *PLoS ONE*, **2011**, 6, e25457	3.7	11
65	The evolution of tropical adaptation: comparing taurine and zebu cattle. *Animal Genetics*, **2010**, 41, 467-77	2.5	53
64	Nematode challenge induces differential expression of oxidant, antioxidant and mucous genes down the longitudinal axis of the sheep gut. *Parasite Immunology*, **2010**, 32, 36-46	2.2	29
63	PCIT: an R package for weighted gene co-expression networks based on partial correlation and information theory approaches. *Bioinformatics*, **2010**, 26, 411-3	7.2	63
62	Regulatory impact factors: unraveling the transcriptional regulation of complex traits from expression data. *Bioinformatics*, **2010**, 26, 896-904	7.2	116
61	Association weight matrix for the genetic dissection of puberty in beef cattle. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 13642-7	11.5	104
60	Skeletal muscle specific genes networks in cattle. *Functional and Integrative Genomics*, **2010**, 10, 609-18	3.8	21
59	Transcription profiling provides insights into gene pathways involved in horn and scurs development in cattle. *BMC Genomics*, **2010**, 11, 370	4.5	29

58	The interplay between evolution, regulation and tissue specificity in the Human Hereditary Diseasome. *BMC Genomics*, **2010**, 11 Suppl 4, S23	4.5	5
57	A genomics-informed, SNP association study reveals FBLN1 and FABP4 as contributing to resistance to fleece rot in Australian Merino sheep. *BMC Veterinary Research*, **2010**, 6, 27	2.7	18
56	Model selection in a global analysis of a microarray experiment. *Journal of Animal Science*, **2009**, 87, 88-98	0.7	4
55	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. *Animal Production Science*, **2009**, 49, 239	1.4	5
54	A differential wiring analysis of expression data correctly identifies the gene containing the causal mutation. *PLoS Computational Biology*, **2009**, 5, e1000382	5	150
53	Microarray-based detection of viruses causing vesicular or vesicular-like lesions in livestock animals. *Veterinary Microbiology*, **2009**, 133, 145-53	3.3	23
52	The combined effect of SNP-marker and phenotype attributes in genome-wide association studies. *Animal Genetics*, **2009**, 40, 149-56	2.5	19
51	Gene expression patterns during intramuscular fat development in cattle. *Journal of Animal Science* , **2009**, 87, 119-30	0.7	137
50	Inferring the transcriptional landscape of bovine skeletal muscle by integrating co-expression networks. *PLoS ONE*, **2009**, 4, e7249	3.7	51
49	Using a 3D virtual muscle model to link gene expression changes during myogenesis to protein spatial location in muscle. *BMC Systems Biology*, **2008**, 2, 88	3.5	4
48	Gastrointestinal nematode challenge induces some conserved gene expression changes in the gut mucosa of genetically resistant sheep. *International Journal for Parasitology*, **2008**, 38, 431-42	4.3	78
47	Gene expression profiling of porcine peripheral blood leukocytes after infection with Actinobacillus pleuropneumoniae. *Veterinary Immunology and Immunopathology*, **2008**, 121, 260-74	2	12
46	Combining partial correlation and an information theory approach to the reversed engineering of gene co-expression networks. *Bioinformatics*, **2008**, 24, 2491-7	7.2	212
45	Dissection of beef quality phenotypes using a myogenin network-anchored systems biology approach. *Australian Journal of Experimental Agriculture*, **2008**, 48, 1053		1
44	Identification of immune genes and proteins involved in the response of bovine mammary tissue to Staphylococcus aureus infection. *BMC Veterinary Research*, **2008**, 4, 18	2.7	85
43	Mining tissue specificity, gene connectivity and disease association to reveal a set of genes that modify the action of disease causing genes. *BioData Mining*, **2008**, 1, 8	4.3	28
42	A validated whole-genome association study of efficient food conversion in cattle. *Genetics*, **2007**, 176, 1893-905	4	138
41	Gene expression studies of developing bovine longissimus muscle from two different beef cattle breeds. *BMC Developmental Biology*, **2007**, 7, 95	3.1	102

40	Identification of a gene network contributing to hypertrophy in callipyge skeletal muscle. *Physiological Genomics*, **2007**, 28, 253-72	3.6	60
39	Stress-induced gene expression profiling in the black tiger shrimp Penaeus monodon. *Physiological Genomics*, **2007**, 31, 126-38	3.6	55
38	Gene expression profiling of Hereford Shorthorn cattle following challenge with Boophilus microplus tick larvae. *Australian Journal of Experimental Agriculture*, **2007**, 47, 1397		38
37	Simultaneous identification of differential gene expression and connectivity in inflammation, adipogenesis and cancer. *Bioinformatics*, **2006**, 22, 2396-404	7.2	56
36	Gene expression-based approaches to beef quality research. *Australian Journal of Experimental Agriculture*, **2006**, 46, 165		15
35	Parasitic castration by the digenian trematode Allopodocotyle sp. alters gene expression in the brain of the host mollusc Haliotis asinina. *FEBS Letters*, **2006**, 580, 3769-74	3.8	9
34	A gene coexpression network for bovine skeletal muscle inferred from microarray data. *Physiological Genomics*, **2006**, 28, 76-83	3.6	26
33	Gene expression profiling of bovine skeletal muscle in response to and during recovery from chronic and severe undernutrition. *Journal of Animal Science*, **2006**, 84, 3239-50	0.7	54
32	Differential gene expression of wheat progeny with contrasting levels of transpiration efficiency. *Plant Molecular Biology*, **2006**, 61, 863-81	4.6	42
31	Gene expression profiling of bovine in vitro adipogenesis using a cDNA microarray. *Functional and Integrative Genomics*, **2006**, 6, 235-49	3.8	50
30	Transcriptional response of sugarcane roots to methyl jasmonate. *Plant Science*, **2005**, 168, 761-772	5.3	50
29	Gene expression profiling of muscle tissue in Brahman steers during nutritional restriction. *Journal of Animal Science*, **2005**, 83, 1-12	0.7	96
28	Gene expression profiling of ovine skin and wool follicle development using a combined ovine - bovine skin cDNA microarray. *Australian Journal of Experimental Agriculture*, **2005**, 45, 867		15
27	Potential for recombinant Babesia bovis antigens to protect against a highly virulent isolate. *Parasite Immunology*, **2005**, 27, 439-45	2.2	17
26	Construction and validation of a Bovine Innate Immune Microarray. *BMC Genomics*, **2005**, 6, 135	4.5	53
25	Transcriptional profiling of skeletal muscle tissue from two breeds of cattle. *Mammalian Genome*, **2005**, 16, 201-10	3.2	124
24	A rapid method for computationally inferring transcriptome coverage and microarray sensitivity. *Bioinformatics*, **2005**, 21, 80-9	7.2	27
23	Validation of alternative methods of data normalization in gene co-expression studies. *Bioinformatics*, **2005**, 21, 1112-20	7.2	46

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22	Transcriptional profiling of muscle tissue in growing Japanese Black cattle to identify genes involved with the development of intramuscular fat. *Australian Journal of Experimental Agriculture*, **2005**, 45, 809		31
21	Construction of gene interaction and regulatory networks in bovine skeletal muscle from expression data. *Australian Journal of Experimental Agriculture*, **2005**, 45, 821		11
20	A mixed-model approach for the analysis of cDNA microarray gene expression data from extreme-performing pigs after infection with Actinobacillus pleuropneumoniae. *Journal of Animal Science*, **2004**, 82, 1261-71	0.7	34
19	Genetic and phenotypic characterisation of animal, carcass, and meat quality traits from temperate and tropically adapted beef breeds. 2. Abattoir carcass traits. *Australian Journal of Agricultural Research*, **2003**, 54, 119		47
18	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. *Australian Journal of Agricultural Research*, **2003**, 54, 149		82
17	Genetic and phenotypic characterisation of animal, carcass, and meat quality traits from temperate and tropically adapted beef breeds.. *Australian Journal of Agricultural Research*, **2003**, 54, 107		34
16	Genetic and phenotypic characterisation of animal, carcass, and meat quality traits from temperate and tropically adapted beef breeds. 3. Meat quality traits. *Australian Journal of Agricultural Research*, **2003**, 54, 135		60
15	A comparison of methods to pre-adjust data for systematic environmental effects in genetic evaluation of sheep. *Livestock Science*, **2002**, 75, 281-291		2
14	Purebred-crossbred performance and genetic evaluation of postweaning growth and carcass traits in Bos indicus x Bos taurus crosses in Australia. *Journal of Animal Science*, **2002**, 80, 1801-8	0.7	30
13	Estimation of genetic covariances with method R. *Journal of Animal Science*, **2001**, 79, 605-15	0.7	7
12	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. *Australian Journal of Experimental Agriculture*, **2001**, 41, 991		25
11	Genetic analyses of live-animal ultrasound and abattoir carcass traits in Australian Angus and Hereford cattle. *Journal of Animal Science*, **2000**, 78, 1786-95	0.7	71
10	Assessing the efficiency of multiplicative mixed model equations to account for heterogeneous variance across herds in carcass scan traits from beef cattle. *Journal of Animal Science*, **1997**, 75, 1477-85	0.7	7
9	Approximate confidence intervals for heritability from method R estimates. *Journal of Animal Science*, **1997**, 75, 2041-6	0.7	10
8	The role of different pedigree structures on the sampling variance of heritability estimates. *Journal of Animal Science*, **1997**, 75, 2355-61	0.7	1
7	The rate of L-lactate production: a feasible parameter for the fresh diluted boar semen quality analysis. *Animal Reproduction Science*, **1996**, 43, 161-172	2.1	15
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3	Integrated transcriptome, DNA methylome and chromatin state accessibility landscapes reveal regulators of Atlantic salmon maturation		2
2	Association analysis of loci implied in “buffering” epistasis		1
1	Genetic regulators of mineral amount in Nelore cattle muscle predicted by a new co-expression and regulatory impact factor approach		1