

Brian P Dalrymple

List of Publications by Year in descending order

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97
papers

9,844
citations

94415

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37202

96
g-index

99
all docs

99
docs citations

99
times ranked

12709
citing authors

#	ARTICLE	IF	CITATIONS
1	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
2	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
3	Genome-Wide Analysis of the World's Sheep Breeds Reveals High Levels of Historic Mixture and Strong Recent Selection. <i>PLoS Biology</i> , 2012, 10, e1001258.	5.6	719
4	The sheep genome illuminates biology of the rumen and lipid metabolism. <i>Science</i> , 2014, 344, 1168-1173.	12.6	436
5	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015, 16, 57.	8.8	331
6	A microRNA catalog of the developing chicken embryo identified by a deep sequencing approach. <i>Genome Research</i> , 2008, 18, 957-964.	5.5	282
7	A Genome Wide Survey of SNP Variation Reveals the Genetic Structure of Sheep Breeds. <i>PLoS ONE</i> , 2009, 4, e4668.	2.5	269
8	A Differential Wiring Analysis of Expression Data Correctly Identifies the Gene Containing the Causal Mutation. <i>PLoS Computational Biology</i> , 2009, 5, e1000382.	3.2	211
9	Regulatory impact factors: unraveling the transcriptional regulation of complex traits from expression data. <i>Bioinformatics</i> , 2010, 26, 896-904.	4.1	193
10	High osmolarity improves the electro-transformation efficiency of the gram-positive bacteria <i>Bacillus subtilis</i> and <i>Bacillus licheniformis</i> . <i>Journal of Microbiological Methods</i> , 1999, 34, 183-191.	1.6	179
11	The sheep genome reference sequence: a work in progress. <i>Animal Genetics</i> , 2010, 41, 449-453.	1.7	173
12	Origin, Evolution, and Biological Role of miRNA Cluster in DLK-DIO3 Genomic Region in Placental Mammals. <i>Molecular Biology and Evolution</i> , 2008, 25, 939-948.	8.9	127
13	An analysis of the organization and evolution of type 4 fimbrial (MePhe) subunit proteins. <i>Journal of Molecular Evolution</i> , 1987, 25, 261-269.	1.8	102
14	Beyond differential expression: the quest for causal mutations and effector molecules. <i>BMC Genomics</i> , 2012, 13, 356.	2.8	93
15	16S rDNA sequencing of <i>Ruminococcus albus</i> and <i>Ruminococcus flavefaciens</i> : design of a signature probe and its application in adult sheep. <i>Microbiology (United Kingdom)</i> , 1999, 145, 1797-1807.	1.8	89
16	Three <i>Neocallimastix patriciarum</i> esterases associated with the degradation of complex polysaccharides are members of a new family of hydrolases. <i>Microbiology (United Kingdom)</i> , 1997, 143, 2605-2614.	1.8	87
17	Epithelial, metabolic and innate immunity transcriptomic signatures differentiating the rumen from other sheep and mammalian gastrointestinal tract tissues. <i>PeerJ</i> , 2016, 4, e1762.	2.0	87
18	Validation of alternative methods of data normalization in gene co-expression studies. <i>Bioinformatics</i> , 2005, 21, 1112-1120.	4.1	80

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19	Using comparative genomics to reorder the human genome sequence into a virtual sheep genome. <i>Genome Biology</i> , 2007, 8, R152.	9.6	77
20	Inhibition of Protein Interactions with the β Sliding Clamp of <i>Escherichia coli</i> DNA Polymerase III by Peptides from β -Binding Proteins. <i>Biochemistry</i> , 2004, 43, 5661-5671.	2.5	76
21	Characterisation of a family of multi-copy genes encoding rhostry protein homologues in <i>Babesia bovis</i> , <i>Babesia ovis</i> and <i>Babesia canis</i> . <i>Molecular and Biochemical Parasitology</i> , 1993, 57, 181-192.	1.1	73
22	A physical map of the bovine genome. <i>Genome Biology</i> , 2007, 8, R165.	9.6	73
23	Transcriptome analysis of cattle muscle identifies potential markers for skeletal muscle growth rate and major cell types. <i>BMC Genomics</i> , 2015, 16, 177.	2.8	69
24	Gene network analysis identifies rumen epithelial cell proliferation, differentiation and metabolic pathways perturbed by diet and correlated with methane production. <i>Scientific Reports</i> , 2016, 6, 39022.	3.3	68
25	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, 467-478.	2.3	67
26	Simultaneous identification of differential gene expression and connectivity in inflammation, adipogenesis and cancer. <i>Bioinformatics</i> , 2006, 22, 2396-2404.	4.1	66
27	IS30, a new insertion sequence of <i>Escherichia coli</i> K12. <i>Molecular Genetics and Genomics</i> , 1984, 196, 68-73.	2.4	64
28	Inferring the Transcriptional Landscape of Bovine Skeletal Muscle by Integrating Co-Expression Networks. <i>PLoS ONE</i> , 2009, 4, e7249.	2.5	63
29	Ribosomal DNA sequence comparison of <i>Babesia</i> and <i>Theileria</i> . <i>Molecular and Biochemical Parasitology</i> , 1992, 54, 87-95.	1.1	62
30	An interactive bovine in silico SNP database (IBISS). <i>Mammalian Genome</i> , 2004, 15, 819-827.	2.2	60
31	Cloning and characterization of the rRNA genes and flanking regions from <i>Babesia bovis</i> : use of the genes as strain discriminating probes. <i>Molecular and Biochemical Parasitology</i> , 1990, 43, 117-124.	1.1	58
32	Longitudinal muscle gene expression patterns associated with differential intramuscular fat in cattle. <i>Animal</i> , 2015, 9, 650-659.	3.3	56
33	Expression of a <i>Butyrivibrio fibrisolvens</i> E14 gene (cinB) encoding an enzyme with cinnamoyl ester hydrolase activity is negatively regulated by the product of an adjacent gene (cinR). <i>Microbiology (United Kingdom)</i> , 1997, 143, 1203-1210.	1.8	53
34	Cloning of a gene encoding cinnamoyl ester hydrolase from the ruminant bacterium <i>Butyrivibrio fibrisolvens</i> E14 by a novel method. <i>FEMS Microbiology Letters</i> , 1996, 143, 115-120.	1.8	51
35	Interaction of the Sliding Clamp β -Subunit and Hda, a DnaA-Related Protein. <i>Journal of Bacteriology</i> , 2004, 186, 3508-3515.	2.2	51
36	Novel rearrangements of IS30 carrying plasmids leading to the reactivation of gene expression. <i>Molecular Genetics and Genomics</i> , 1987, 207, 413-420.	2.4	47

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37	A gene expression estimator of intramuscular fat percentage for use in both cattle and sheep. <i>Journal of Animal Science and Biotechnology</i> , 2014, 5, 35.	5.3	47
38	A gene coexpression network for bovine skeletal muscle inferred from microarray data. <i>Physiological Genomics</i> , 2006, 28, 76-83.	2.3	38
39	Binding Inhibitors of the Bacterial Sliding Clamp by Design. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 4831-4838.	6.4	38
40	Molecular variation and diversity in candidate vaccine antigens from <i>Babesia</i> . <i>Acta Tropica</i> , 1993, 53, 227-238.	2.0	35
41	Modification of the substrate specificity of porcine pepsin for the enzymatic production of bovine hide gelatin. <i>Protein Science</i> , 2000, 9, 1947-1959.	7.6	33
42	Conservation of Eubacterial Replicases. <i>IUBMB Life</i> , 2005, 57, 413-419.	3.4	32
43	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.	4.0	32
44	Transcription profiling provides insights into gene pathways involved in horn and scurs development in cattle. <i>BMC Genomics</i> , 2010, 11, 370.	2.8	32
45	Phosphoinositide 3-Kinase (PI3K(p110 \pm)) Directly Regulates Key Components of the Z-disc and Cardiac Structure*. <i>Journal of Biological Chemistry</i> , 2011, 286, 30837-30846.	3.4	32
46	Cloning and characterisation of cDNA clones encoding two <i>Babesia bovis</i> proteins with homologous amino- and carboxy-terminal domains. <i>Molecular and Biochemical Parasitology</i> , 1993, 59, 181-189.	1.1	31
47	PCR methods for the discrimination of <i>Babesia bovis</i> isolates. <i>Veterinary Parasitology</i> , 1997, 71, 223-237.	1.8	28
48	A rapid method for computationally inferring transcriptome coverage and microarray sensitivity. <i>Bioinformatics</i> , 2005, 21, 80-89.	4.1	28
49	The Plasmid RK2 Replication Initiator Protein (TrfA) Binds to the Sliding Clamp $\hat{2}$ Subunit of DNA Polymerase III: Implication for the Toxicity of a Peptide Derived from the Amino-Terminal Portion of 33-Kilodalton TrfA. <i>Journal of Bacteriology</i> , 2006, 188, 5501-5509.	2.2	28
50	Genetic Testing for TMEM154 Mutations Associated with Lentivirus Susceptibility in Sheep. <i>PLoS ONE</i> , 2013, 8, e55490.	2.5	28
51	Mammalian genomic regulatory regions predicted by utilizing human genomics, transcriptomics, and epigenetics data. <i>GigaScience</i> , 2018, 7, 1-17.	6.4	27
52	Characterisation and application of a bovine U6 promoter for expression of short hairpin RNAs. <i>BMC Biotechnology</i> , 2005, 5, 13.	3.3	26
53	Improvement of expression and secretion of a fungal xylanase in the rumen bacterium <i>Butyrivibrio fibrisolvens</i> OB156 by manipulation of promoter and signal sequences. <i>Journal of Biotechnology</i> , 1997, 54, 139-148.	3.8	24
54	Porcine Tissue-Specific Regulatory Networks Derived from Meta-Analysis of the Transcriptome. <i>PLoS ONE</i> , 2012, 7, e46159.	2.5	23

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55	Biochemical and molecular characterization of serine proteases from larvae of <i>Chrysomya bezziana</i> , the Old World Screwworm fly. <i>Insect Biochemistry and Molecular Biology</i> , 2001, 31, 1029-1040.	2.7	21
56	Analysis of the complement and molecular evolution of tRNA genes in cow. <i>BMC Genomics</i> , 2009, 10, 188.	2.8	21
57	Transcription of the fimbrial subunit gene and an associated transfer RNA gene of <i>Pseudomonas aeruginosa</i> . <i>Gene</i> , 1988, 62, 219-227.	2.2	20
58	The <i>Neocallimastix patriciarum</i> cellulase, CelD, contains three almost identical catalytic domains with high specific activities on Avicel. <i>Enzyme and Microbial Technology</i> , 1999, 24, 609-614.	3.2	19
59	Genome-wide patterns of promoter sharing and co-expression in bovine skeletal muscle. <i>BMC Genomics</i> , 2011, 12, 23.	2.8	19
60	Modes of genetic adaptations underlying functional innovations in the rumen. <i>Science China Life Sciences</i> , 2021, 64, 1-21.	4.9	19
61	The characterization of terminators of RNA transcription on IS30 and an analysis of their role in IS element-mediated polarity. <i>Gene</i> , 1986, 44, 1-10.	2.2	17
62	Distribution and Evolution of the Xylanase Genes <i>xynA</i> and <i>xynB</i> and Their Homologues in Strains of <i>Butyrivibrio fibrisolvens</i> . <i>Applied and Environmental Microbiology</i> , 1999, 65, 3660-3667.	3.1	17
63	A Polymerase Chain Reaction Method for the Identification of Genes Encoding Members of the Bv60/p58 Family of Rhoptry Protein Homologues in the Genus <i>Babesia</i> . <i>Experimental Parasitology</i> , 1996, 84, 96-100.	1.2	16
64	Molecular Cytogenetics and Gene Mapping in Sheep (<i>Ovis aries</i> , 2n = 54). <i>Cytogenetic and Genome Research</i> , 2009, 126, 63-76.	1.1	15
65	A Divergent Artiodactyl MYADM-like Repeat Is Associated with Erythrocyte Traits and Weight of Lamb Weaned in Domestic Sheep. <i>PLoS ONE</i> , 2013, 8, e74700.	2.5	15
66	Sequence of a putative glutathione synthetase II gene and flanking regions from <i>Anaplasma centrale</i> . <i>Biochemical and Biophysical Research Communications</i> , 1992, 182, 1040-1046.	2.1	14
67	The effect of combination treatment with trenbolone acetate and estradiol-17 β on skeletal muscle expression and plasma concentrations of oxytocin in sheep. <i>Domestic Animal Endocrinology</i> , 2012, 43, 67-73.	1.6	14
68	A comparison of transcriptomic patterns measured in the skin of Chinese fine and coarse wool sheep breeds. <i>Scientific Reports</i> , 2017, 7, 14301.	3.3	14
69	A high-resolution comparative radiation hybrid map of ovine chromosomal regions that are homologous to human chromosome 6 (HSA6). <i>Animal Genetics</i> , 2008, 39, 459-467.	1.7	13
70	Across-Experiment Transcriptomics of Sheep Rumen Identifies Expression of Lipid/Oxo-Acid Metabolism and Muscle Cell Junction Genes Associated With Variation in Methane-Related Phenotypes. <i>Frontiers in Genetics</i> , 2018, 9, 330.	2.3	13
71	Construction of gene interaction and regulatory networks in bovine skeletal muscle from expression data. <i>Australian Journal of Experimental Agriculture</i> , 2005, 45, 821.	1.0	12
72	Inferring the in vivo cellular program of developing bovine skeletal muscle from expression data. <i>Gene Expression Patterns</i> , 2013, 13, 109-125.	0.8	12

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73	Eukaryotic Evolutionary Transitions Are Associated with Extreme Codon Bias in Functionally-Related Proteins. PLoS ONE, 2011, 6, e25457.	2.5	11
74	Characterization of a cDNA clone from the haemoparasite Babesia bovis encoding a protein containing and "HMG-Box". Biochemical and Biophysical Research Communications, 1992, 184, 31-35.	2.1	10
75	A High-Resolution Radiation Hybrid Map of Sheep Chromosome X and Comparison with Human and Cattle. Cytogenetic and Genome Research, 2009, 125, 40-45.	1.1	9
76	Evolutionary Relevance of Genetic Rearrangements Involving Plasmids. , 1985, 30, 21-31.		9
77	Identification of L10e/L12e ribosomal protein gene in Babesia bovis. Nucleic Acids Research, 1992, 20, 2376-2376.	14.5	7
78	Identification of putative DnaN-binding motifs in plasmid replication initiation proteins. Plasmid, 2007, 57, 82-88.	1.4	7
79	A comparative radiation hybrid map of sheep chromosome 10. Cytogenetic and Genome Research, 2008, 121, 35-40.	1.1	7
80	A radiation hybrid comparative map of ovine chromosome 1 aligned to the virtual sheep genome. Animal Genetics, 2009, 40, 435-455.	1.7	6
81	Quality control of the sheep bacterial artificial chromosome library, CHORI-243. BMC Research Notes, 2010, 3, 334.	1.4	6
82	RNF14 is a regulator of mitochondrial and immune function in muscle. BMC Systems Biology, 2014, 8, 10.	3.0	6
83	Molecular Biology of the Fimbriae of Dichelobacter (Previously Bacteroides) nodosus. Brock/Springer Series in Contemporary Bioscience, 1993, , 517-545.	0.3	6
84	The phage Mu repressor c and IS30 transposase proteins are significantly related. FEBS Letters, 1986, 208, 7-10.	2.8	5
85	Cloning and characterisation of members of a family of Babesia bigemina antigen genes containing repeated sequences. Molecular and Biochemical Parasitology, 1992, 55, 29-38.	1.1	5
86	Using muscle gene expression to estimate triacylglyceride deposition, and relative contributions of fatty acid synthesis and fatty acid import in intramuscular fat in cattle. Animal Production Science, 2014, 54, 1436.	1.3	5
87	Beta-globin gene evolution in the ruminants: evidence for an ancient origin of sheep haplotype <i>B</i>. Animal Genetics, 2015, 46, 506-514.	1.7	5
88	Analysis of the R16 plasmid primase gene. Plasmid, 1984, 12, 206-210.	1.4	4
89	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.	3.0	4
90	A multiway analysis for identifying high integrity bovine BACs. BMC Genomics, 2009, 10, 46.	2.8	4

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91	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.	1.4	4
92	Manipulation of Rumen Function by the Inoculation of Novel Microorganisms. Outlook on Agriculture, 1998, 27, 107-113.	3.4	3
93	Using paired-end sequences to optimise parameters for alignment of sequence reads against related genomes. BMC Genomics, 2010, 11, 458.	2.8	3
94	Sequencing and expression of the aroA gene from Dichelobacter nodosus. Gene, 1994, 145, 97-101.	2.2	2
95	Harnessing the bovine genome sequence for the Australian cattle and sheep industries. Australian Journal of Experimental Agriculture, 2005, 45, 1011.	1.0	2
96	Dissection of beef quality phenotypes using a myogenin network-anchored systems biology approach. Australian Journal of Experimental Agriculture, 2008, 48, 1053.	1.0	1
97	Cellular localisation of the clamp protein during DNA replication. FEMS Microbiology Letters, 2002, 216, 255-262.	1.8	1