

# John Browne

## List of Publications by Year in descending order

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Version: 2024-02-01

29  
papers

1,730  
citations

361296

20  
h-index

477173

29  
g-index

29  
all docs

29  
docs citations

29  
times ranked

2946  
citing authors

#	ARTICLE	IF	CITATIONS
1	Do differences in the endometrial transcriptome between uterine horns ipsilateral and contralateral to the corpus luteum influence conceptus growth to day 14 in cattle? <i>Biology of Reproduction</i> , 2019, 100, 86-100.	1.2	21
2	Expression of granulosa cell microRNAs, AVEN and ATRX are associated with human blastocyst development. <i>Molecular Reproduction and Development</i> , 2018, 85, 836-848.	1.0	6
3	RNA Sequencing (RNA-Seq) Reveals Extremely Low Levels of Reticulocyte-Derived Globin Gene Transcripts in Peripheral Blood From Horses ( <i>Equus caballus</i> ) and Cattle ( <i>Bos taurus</i> ). <i>Frontiers in Genetics</i> , 2018, 9, 278.	1.1	13
4	IL-10 suppression of IFN- $\gamma$ responses in tuberculin-stimulated whole blood from <i>Mycobacterium bovis</i> infected cattle. <i>Veterinary Immunology and Immunopathology</i> , 2017, 189, 36-42.	0.5	11
5	Circulating microRNAs as Potential Biomarkers of Infectious Disease. <i>Frontiers in Immunology</i> , 2017, 8, 118.	2.2	189
6	Network Analysis of the Systemic Response to <i>Fasciola hepatica</i> Infection in Sheep Reveals Changes in Fibrosis, Apoptosis, Toll-Like Receptors 3/4, and B Cell Function. <i>Frontiers in Immunology</i> , 2017, 8, 485.	2.2	15
7	Transcriptomic Study on Ovine Immune Responses to <i>Fasciola hepatica</i> Infection. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005015.	1.3	46
8	Analysis of the Bovine Monocyte-Derived Macrophage Response to <i>Mycobacterium avium</i> Subspecies Paratuberculosis Infection Using RNA-seq. <i>Frontiers in Immunology</i> , 2015, 6, 23.	2.2	61
9	MicroRNA profiling of the bovine alveolar macrophage response to <i>Mycobacterium bovis</i> infection suggests pathogen survival is enhanced by microRNA regulation of endocytosis and lysosome trafficking. <i>Tuberculosis</i> , 2015, 95, 60-67.	0.8	64
10	Identity of rumen fluke in deer. <i>Parasitology Research</i> , 2014, 113, 4097-4103.	0.6	35
11	Improvements in growth performance, bone mineral status and nutrient digestibility in pigs following the dietary inclusion of phytase are accompanied by modifications in intestinal nutrient transporter gene expression. <i>British Journal of Nutrition</i> , 2014, 112, 688-697.	1.2	28
12	RNA-seq Transcriptional Profiling of Peripheral Blood Leukocytes from Cattle Infected with <i>Mycobacterium bovis</i> . <i>Frontiers in Immunology</i> , 2014, 5, 396.	2.2	65
13	Key Hub and Bottleneck Genes Differentiate the Macrophage Response to Virulent and Attenuated <i>Mycobacterium bovis</i> . <i>Frontiers in Immunology</i> , 2014, 5, 422.	2.2	29
14	Innate cytokine profiling of bovine alveolar macrophages reveals commonalities and divergence in the response to <i>Mycobacterium bovis</i> and <i>Mycobacterium tuberculosis</i> infection. <i>Tuberculosis</i> , 2014, 94, 441-450.	0.8	38
15	Profiling microRNA expression in bovine alveolar macrophages using RNA-seq. <i>Veterinary Immunology and Immunopathology</i> , 2013, 155, 238-244.	0.5	44
16	The need for transparency and good practices in the qPCR literature. <i>Nature Methods</i> , 2013, 10, 1063-1067.	9.0	251
17	Network analysis of adipose tissue gene expression highlights altered metabolic and regulatory transcriptomic activity in high-fat-diet-fed IL-1RI knockout mice. <i>Journal of Nutritional Biochemistry</i> , 2013, 24, 788-795.	1.9	16
18	Molecular aspects of mucin biosynthesis and mucus formation in the bovine cervix during the periestrous period. <i>Physiological Genomics</i> , 2012, 44, 1165-1178.	1.0	45

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19	Impact of delayed processing of bovine peripheral blood on differential gene expression. <i>Veterinary Immunology and Immunopathology</i> , 2012, 145, 199-205.	0.5	6
20	Global Gene Expression and Systems Biology Analysis of Bovine Monocyte-Derived Macrophages in Response to In Vitro Challenge with <i>Mycobacterium bovis</i> . <i>PLoS ONE</i> , 2012, 7, e32034.	1.1	45
21	<i>MSTN</i> genotypes in Thoroughbred horses influence skeletal muscle gene expression and racetrack performance. <i>Animal Genetics</i> , 2012, 43, 810-812.	0.6	42
22	Transcriptional profiling of immune genes in bovine monocyte-derived macrophages exposed to bacterial antigens. <i>Veterinary Immunology and Immunopathology</i> , 2011, 140, 130-139.	0.5	309
23	Early proteomic analysis may allow noninvasive identification of hepatitis C response to treatment with pegylated interferon $\alpha$ -2b and ribavirin. <i>European Journal of Gastroenterology and Hepatology</i> , 2011, 23, 177-183.	0.8	14
24	Early viral and peripheral blood mononuclear cell responses to pegylated interferon and ribavirin treatment: the first 24h. <i>European Journal of Gastroenterology and Hepatology</i> , 2010, 22, 1211-1220.	0.8	5
25	Circadian regulation of locomotor activity and skeletal muscle gene expression in the horse. <i>Journal of Applied Physiology</i> , 2010, 109, 1328-1336.	1.2	34
26	Gene induction by desiccation stress in the entomopathogenic nematode <i>Steinernema carpocapsae</i> reveals parallels with drought tolerance mechanisms in plants. <i>International Journal for Parasitology</i> , 2007, 37, 763-776.	1.3	33
27	The anhydrobiotic potential and molecular phylogenetics of species and strains of <i>Panagrolaimus</i> (Nematoda, Panagrolaimidae). <i>Journal of Experimental Biology</i> , 2005, 208, 2433-2445.	0.8	60
28	Molecular Anhydrobiology: Identifying Molecules Implicated in Invertebrate Anhydrobiosis. <i>Integrative and Comparative Biology</i> , 2005, 45, 702-709.	0.9	88
29	Dehydration-Specific Induction of Hydrophilic Protein Genes in the Anhydrobiotic Nematode <i>Aphelenchus avenae</i> . <i>Eukaryotic Cell</i> , 2004, 3, 966-975.	3.4	117