

Keren A Byrne

List of Publications by Year in descending order

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59
papers

3,245
citations

109321

35
h-index

144013

57
g-index

59
all docs

59
docs citations

59
times ranked

3069
citing authors

#	ARTICLE	IF	CITATIONS
1	A medium-density genetic linkage map of the bovine genome. <i>Mammalian Genome</i> , 1997, 8, 21-28.	2.2	313
2	Genetic mapping of the black tiger shrimp <i>Penaeus monodon</i> with amplified fragment length polymorphism. <i>Aquaculture</i> , 2002, 204, 297-309.	3.5	205
3	Genetic diversity of Asian water buffalo (<i>Bubalus bubalis</i>): microsatellite variation and a comparison with protein-coding loci. <i>Animal Genetics</i> , 1997, 28, 103-115.	1.7	164
4	Microsatellite evolution--a reciprocal study of repeat lengths at homologous loci in cattle and sheep. <i>Molecular Biology and Evolution</i> , 1997, 14, 854-860.	8.9	150
5	The development and application of genetic markers for the Kuruma prawn <i>Penaeus japonicus</i> . <i>Aquaculture</i> , 1999, 173, 19-32.	3.5	138
6	Transcriptional profiling of skeletal muscle tissue from two breeds of cattle. <i>Mammalian Genome</i> , 2005, 16, 201-210.	2.2	135
7	Genetic mapping of the kuruma prawn <i>Penaeus japonicus</i> using AFLP markers. <i>Aquaculture</i> , 2003, 219, 143-156.	3.5	124
8	Gene expression studies of developing bovine longissimus muscle from two different beef cattle breeds. <i>BMC Developmental Biology</i> , 2007, 7, 95.	2.1	115
9	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.	1.9	113
10	Gene expression profiling of muscle tissue in Brahman steers during nutritional restriction1. <i>Journal of Animal Science</i> , 2005, 83, 1-12.	0.5	109
11	Isolation of a cDNA encoding a putative cellulase in the red claw crayfish <i>Cherax quadricarinatus</i> . <i>Gene</i> , 1999, 239, 317-324.	2.2	92
12	Proteomic Profiling of 16 Cereal Grains and the Application of Targeted Proteomics To Detect Wheat Contamination. <i>Journal of Proteome Research</i> , 2015, 14, 2659-2668.	3.7	85
13	Comprehensive mapping of the bull sperm surface proteome. <i>Proteomics</i> , 2012, 12, 3559-3579.	2.2	81
14	The genome of bovine ephemeral fever rhabdovirus contains two related glycoprotein genes. <i>Virology</i> , 1992, 191, 49-61.	2.4	80
15	Validation of alternative methods of data normalization in gene co-expression studies. <i>Bioinformatics</i> , 2005, 21, 1112-1120.	4.1	80
16	Construction and validation of a Bovine Innate Immune Microarray. <i>BMC Genomics</i> , 2005, 6, 135.	2.8	75
17	Identification of a gene network contributing to hypertrophy in callipyge skeletal muscle. <i>Physiological Genomics</i> , 2007, 28, 253-272.	2.3	66
18	Gene expression profiling of bovine skeletal muscle in response to and during recovery from chronic and severe undernutrition1. <i>Journal of Animal Science</i> , 2006, 84, 3239-3250.	0.5	60

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19	Genome organization and transcription strategy in the complex GNS-L intergenic region of bovine ephemeral fever rhabdovirus.. <i>Journal of General Virology</i> , 1997, 78, 1309-1317.	2.9	56
20	Tissue-Specific Expressed Sequence Tags from the Black Tiger Shrimp <i>Penaeus monodon</i> . <i>Marine Biotechnology</i> , 1999, 1, 465-476.	2.4	55
21	Gene expression profiling of bovine in vitro adipogenesis using a cDNA microarray. <i>Functional and Integrative Genomics</i> , 2006, 6, 235-249.	3.5	53
22	Engineering α -amylase levels in wheat grain suggests a highly sophisticated level of carbohydrate regulation during development. <i>Journal of Experimental Botany</i> , 2014, 65, 5443-5457.	4.8	48
23	A mixture model-based cluster analysis of DNA microarray gene expression data on Brahman and Brahman composite steers fed high-, medium-, and low-quality diets1. <i>Journal of Animal Science</i> , 2003, 81, 1900-1910.	0.5	47
24	Identification of barley-specific peptide markers that persist in processed foods and are capable of detecting barley contamination by LC-MS/MS. <i>Journal of Proteomics</i> , 2016, 147, 169-176.	2.4	45
25	Analysis of gene expression during the onset of muscle hypertrophy in callipyge lambs. <i>Animal Genetics</i> , 2007, 38, 28-36.	1.7	44
26	Optimisation of protein extraction for in-depth profiling of the cereal grain proteome. <i>Journal of Proteomics</i> , 2019, 197, 23-33.	2.4	44
27	Joint analysis of multiple cDNA microarray studies via multivariate mixed models applied to genetic improvement of beef cattle1. <i>Journal of Animal Science</i> , 2004, 82, 3430-3439.	0.5	40
28	Comparing Multiple Reaction Monitoring and Sequential Window Acquisition of All Theoretical Mass Spectra for the Relative Quantification of Barley Gluten in Selectively Bred Barley Lines. <i>Analytical Chemistry</i> , 2016, 88, 9127-9135.	6.5	40
29	Development and application of a bovine cDNA microarray for expression profiling of muscle and adipose tissue. <i>Australian Journal of Experimental Agriculture</i> , 2004, 44, 1127.	1.0	39
30	A gene coexpression network for bovine skeletal muscle inferred from microarray data. <i>Physiological Genomics</i> , 2006, 28, 76-83.	2.3	38
31	Comparison of Gluten Extraction Protocols Assessed by LC-MS/MS Analysis. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 2857-2866.	5.2	38
32	The Imprinted Retrotransposon-Like Gene PEG11 (RTL1) Is Expressed as a Full-Length Protein in Skeletal Muscle from Callipyge Sheep. <i>PLoS ONE</i> , 2010, 5, e8638.	2.5	38
33	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.	1.0	37
34	QTL detection of production traits for the Kuruma prawn <i>Penaeus japonicus</i> (Bate) using AFLP markers. <i>Aquaculture</i> , 2006, 258, 198-210.	3.5	37
35	Liquid Chromatography–Mass Spectrometry Analysis Reveals Hydrolyzed Gluten in Beers Crafted To Remove Gluten. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 9715-9725.	5.2	36
36	Food for thought: Selecting the right enzyme for the digestion of gluten. <i>Food Chemistry</i> , 2017, 234, 389-397.	8.2	30

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37	Protein extraction protocols for optimal proteome measurement and arginine kinase quantitation from cricket <i>Acheta domesticus</i> for food safety assessment. <i>Food Chemistry</i> , 2021, 348, 129110.	8.2	29
38	A gene network switch enhances the oxidative capacity of ovine skeletal muscle during late fetal development. <i>BMC Genomics</i> , 2010, 11, 378.	2.8	27
39	Identification and Quantitation of Amylase Trypsin Inhibitors Across Cultivars Representing the Diversity of Bread Wheat. <i>Journal of Proteome Research</i> , 2020, 19, 2136-2148.	3.7	24
40	Oat of this world: Defining peptide markers for detection of oats in processed food. <i>Peptide Science</i> , 2018, 110, e24045.	1.8	21
41	Using LC-MS to examine the fermented food products vinegar and soy sauce for the presence of gluten. <i>Food Chemistry</i> , 2018, 254, 302-308.	8.2	20
42	NCAM: a polymorphic microsatellite locus conserved across eutherian mammal species. <i>Animal Genetics</i> , 1998, 29, 33-36.	1.7	19
43	Plant expression of NifD protein variants resistant to mitochondrial degradation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23165-23173.	7.1	19
44	Genetic architecture of gene expression in ovine skeletal muscle. <i>BMC Genomics</i> , 2011, 12, 607.	2.8	18
45	Development of polymorphic EST markers in <i>Penaeus monodon</i> : applications in penaeid genetics. <i>Aquaculture</i> , 2002, 208, 69-79.	3.5	17
46	Targeted proteomics to monitor the extraction efficiency and levels of barley α -amylase trypsin inhibitors that are implicated in non-coeliac gluten sensitivity. <i>Journal of Chromatography A</i> , 2019, 1600, 55-64.	3.7	15
47	A Synthetic Biology Workflow Reveals Variation in Processing and Solubility of Nitrogenase Proteins Targeted to Plant Mitochondria, and Differing Tolerance of Targeting Sequences in a Bacterial Nitrogenase Assay. <i>Frontiers in Plant Science</i> , 2020, 11, 552160.	3.6	14
48	Proteome Analysis of Hordein-Null Barley Lines Reveals Storage Protein Synthesis and Compensation Mechanisms. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 5763-5775.	5.2	13
49	Quantitation of seven transmembrane proteins from the DHA biosynthesis pathway in genetically engineered canola by targeted mass spectrometry. <i>Food and Chemical Toxicology</i> , 2019, 126, 313-321.	3.6	11
50	Physical mapping of <i>CSF2RA</i> , <i>ANT3</i> and <i>STS</i> on the pseudoautosomal region of bovine chromosome X. <i>Animal Genetics</i> , 2001, 32, 102-104.	1.7	10
51	Proteomics reveals the in vitro protein digestibility of seven transmembrane enzymes from the docosahexaenoic acid biosynthesis pathway. <i>Food and Chemical Toxicology</i> , 2019, 130, 89-98.	3.6	10
52	Genomic architecture of histone 3 lysine 27 trimethylation during late ovine skeletal muscle development. <i>Animal Genetics</i> , 2014, 45, 427-438.	1.7	8
53	Overexpression of a wheat α -amylase type 2 impact on starch metabolism and abscisic acid sensitivity during grain germination. <i>Plant Journal</i> , 2021, 108, 378-393.	5.7	6
54	An Always Correlated gene expression landscape for ovine skeletal muscle, lessons learnt from comparison with an α -equivalent bovine landscape. <i>BMC Research Notes</i> , 2012, 5, 632.	1.4	4

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55	Proteome and Nutritional Shifts Observed in Hordein Double-Mutant Barley Lines. <i>Frontiers in Plant Science</i> , 2021, 12, 718504.	3.6	4
56	Impacts of the Callipyge Mutation on Ovine Plasma Metabolites and Muscle Fibre Type. <i>PLoS ONE</i> , 2014, 9, e99726.	2.5	3
57	Over-Expression of a Wheat Late Maturity Alpha-Amylase Type 1 Impact on Starch Properties During Grain Development and Germination. <i>Frontiers in Plant Science</i> , 2022, 13, 811728.	3.6	2
58	Efficient Extraction and Digestion of Gluten Proteins. <i>Methods in Molecular Biology</i> , 2019, 1871, 405-412.	0.9	1
59	CSY234 : a SINE-associated genetic and physical marker on bovine chromosome X. <i>Animal Genetics</i> , 2002, 33, 163-164.	1.7	0