

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	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
2	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
3	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
4	Proteome and Nutritional Shifts Observed in Hordein Double-Mutant Barley Lines. <i>Frontiers in Plant Science</i> , 2021, 12, 718504.	3.6	4
5	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
6	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
7	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
8	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
9	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
10	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
11	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
12	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
13	Efficient Extraction and Digestion of Gluten Proteins. <i>Methods in Molecular Biology</i> , 2019, 1871, 405-412.	0.9	1
14	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
15	Oat of this world: Defining peptide markers for detection of oats in processed food. <i>Peptide Science</i> , 2018, 110, e24045.	1.8	21
16	Food for thought: Selecting the right enzyme for the digestion of gluten. <i>Food Chemistry</i> , 2017, 234, 389-397.	8.2	30
17	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
18	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

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19	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
20	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
21	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
22	Impacts of the Callipyge Mutation on Ovine Plasma Metabolites and Muscle Fibre Type. <i>PLoS ONE</i> , 2014, 9, e99726.	2.5	3
23	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
24	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
25	Comprehensive mapping of the bull sperm surface proteome. <i>Proteomics</i> , 2012, 12, 3559-3579.	2.2	81
26	An Always Correlated gene expression landscape for ovine skeletal muscle, lessons learnt from comparison with an α -equivalent β -bovine landscape. <i>BMC Research Notes</i> , 2012, 5, 632.	1.4	4
27	Genetic architecture of gene expression in ovine skeletal muscle. <i>BMC Genomics</i> , 2011, 12, 607.	2.8	18
28	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
29	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
30	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
31	Identification of a gene network contributing to hypertrophy in callipyge skeletal muscle. <i>Physiological Genomics</i> , 2007, 28, 253-272.	2.3	66
32	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
33	Analysis of gene expression during the onset of muscle hypertrophy in callipyge lambs. <i>Animal Genetics</i> , 2007, 38, 28-36.	1.7	44
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	A gene coexpression network for bovine skeletal muscle inferred from microarray data. <i>Physiological Genomics</i> , 2006, 28, 76-83.	2.3	38
36	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, 3239-3250.	0.5	60

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37	Gene expression profiling of bovine in vitro adipogenesis using a cDNA microarray. Functional and Integrative Genomics, 2006, 6, 235-249.	3.5	53
38	Gene expression profiling of muscle tissue in Brahman steers during nutritional restriction1. Journal of Animal Science, 2005, 83, 1-12.	0.5	109
39	Construction and validation of a Bovine Innate Immune Microarray. BMC Genomics, 2005, 6, 135.	2.8	75
40	Transcriptional profiling of skeletal muscle tissue from two breeds of cattle. Mammalian Genome, 2005, 16, 201-210.	2.2	135
41	Validation of alternative methods of data normalization in gene co-expression studies. Bioinformatics, 2005, 21, 1112-1120.	4.1	80
42	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.	1.0	37
43	Joint analysis of multiple cDNA microarray studies via multivariate mixed models applied to genetic improvement of beef cattle1. Journal of Animal Science, 2004, 82, 3430-3439.	0.5	40
44	Development and application of a bovine cDNA microarray for expression profiling of muscle and adipose tissue. Australian Journal of Experimental Agriculture, 2004, 44, 1127.	1.0	39
45	Genetic mapping of the kuruma prawn <i>Penaeus japonicus</i> using AFLP markers. Aquaculture, 2003, 219, 143-156.	3.5	124
46	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. Journal of Animal Science, 2003, 81, 1900-1910.	0.5	47
47	Development of polymorphic EST markers in <i>Penaeus monodon</i> : applications in penaeid genetics. Aquaculture, 2002, 208, 69-79.	3.5	17
48	Genetic mapping of the black tiger shrimp <i>Penaeus monodon</i> with amplified fragment length polymorphism. Aquaculture, 2002, 204, 297-309.	3.5	205
49	CSY234 : a SINE-associated genetic and physical marker on bovine chromosome X. Animal Genetics, 2002, 33, 163-164.	1.7	0
50	Physical mapping of <i>CSF2RA</i> , <i>ANT3</i> and <i>STS</i> on the pseudoautosomal region of bovine chromosome X. Animal Genetics, 2001, 32, 102-104.	1.7	10
51	Tissue-Specific Expressed Sequence Tags from the Black Tiger Shrimp <i>Penaeus monodon</i> . Marine Biotechnology, 1999, 1, 465-476.	2.4	55
52	Isolation of a cDNA encoding a putative cellulase in the red claw crayfish <i>Cherax quadricarinatus</i> . Gene, 1999, 239, 317-324.	2.2	92
53	The development and application of genetic markers for the Kuruma prawn <i>Penaeus japonicus</i> . Aquaculture, 1999, 173, 19-32.	3.5	138
54	NCAM: a polymorphic microsatellite locus conserved across eutherian mammal species. Animal Genetics, 1998, 29, 33-36.	1.7	19

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55	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
56	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
57	A medium-density genetic linkage map of the bovine genome. <i>Mammalian Genome</i> , 1997, 8, 21-28.	2.2	313
58	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
59	The genome of bovine ephemeral fever rhabdovirus contains two related glycoprotein genes. <i>Virology</i> , 1992, 191, 49-61.	2.4	80