Haja N Kadarmideen

List of Publications by Year
in descending order

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137
papers

4,502
citations

136885
32
h-index

128225
60
g-index

148
all docs

148
docs citations

148
times ranked

6036
citing authors

#	Article	IF	Citations
1	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
2	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
3	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	1.4	275
4	Linear and threshold model genetic parameters for disease, fertility and milk production in dairy cattle. Animal Science, 2000, 71, 411-419.	1.3	175
5	Liver transcriptomic networks reveal main biological processes associated with feed efficiency in beef cattle. BMC Genomics, 2015, 16, 1073.	1.2	161
6	Multi-omic data integration and analysis using systems genomics approaches: methods and applications in animal production, health and welfare. Genetics Selection Evolution, 2016, 48, 38.	1.2	144
7	Genetic parameters and evaluations from single- and multiple-trait analysis of dairy cow fertility and milk production. Livestock Science, 2003, 81, 183-195.	1.2	130
8	Genetic parameters for different measures of feed efficiency and related traits in boars of three pig breeds1. Journal of Animal Science, 2013, 91, 4069-4079.	0.2	100
9	Genome-wide association and systems genetic analyses of residual feed intake, daily feed consumption, backfat and weight gain in pigs. BMC Genetics, 2014, 15, 27.	2.7	97
10	Identification of co-expression gene networks, regulatory genes and pathways for obesity based on adipose tissue RNA Sequencing in a porcine model. BMC Medical Genomics, 2014, 7, 57.	0.7	96
11	PCIT: an R package for weighted gene co-expression networks based on partial correlation and information theory approaches. Bioinformatics, 2010, 26, 411-413.	1.8	90
12	Genome-wide association and pathway analysis of feed efficiency in pigs reveal candidate genes and pathways for residual feed intake. Frontiers in Genetics, 2014, 5, 307.	1.1	84
13	Copy number variations and genome-wide associations reveal putative genes and metabolic pathways involved with the feed conversion ratio in beef cattle. Journal of Applied Genetics, 2016, 57, 495-504.	1.0	78
14	RNA-Seq transcriptomics and pathway analyses reveal potential regulatory genes and molecular mechanisms in high- and low-residual feed intake in Nordic dairy cattle. BMC Genomics, 2017, 18, 258.	1.2	76
15	Genome-Wide Association Study Reveals Genetic Architecture of Eating Behavior in Pigs and Its Implications for Humans Obesity by Comparative Mapping. PLoS ONE, 2013, 8, e71509.	1.1	73
16	From genetical genomics to systems genetics: potential applications in quantitative genomics and animal breeding. Mammalian Genome, 2006, 17, 548-564.	1.0	71
17	Genomics to systems biology in animal and veterinary sciences: Progress, lessons and opportunities. Livestock Science, 2014, 166, 232-248.	0.6	69
18	Systems biology of ovine intestinal parasite resistance: disease gene modules and biomarkers. Molecular BioSystems, 2011, 7, 235-246.	2.9	65

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19	Gene co-expression networks from RNA sequencing of dairy cattle identifies genes and pathways affecting feed efficiency. BMC Bioinformatics, 2018, 19, 513.	1.2	59
20	Genetic Parameters for Body Condition Score and its Relationship with Type and Production Traits in Swiss Holsteins. Journal of Dairy Science, 2003, 86, 3685-3693.	1.4	57
21	Genetics of osteochondral disease and its relationship with meat quality and quantity, growth, and feed conversion traits in pigs1. Journal of Animal Science, 2004, 82, 3118-3127.	0.2	56
22	Genetic and phenotypic parameters for conformation and yield traits in three Swiss dairy cattle breeds. Journal of Animal Breeding and Genetics, 2007, 124, 12-19.	0.8	55
23	Genetic correlations among body condition score, somatic cell score, milk production, fertility and conformation traits in dairy cows. Animal Science, 2004, 79, 191-201.	1.3	53
24	Differential expression and co-expression gene networks reveal candidate biomarkers of boar taint in non-castrated pigs. Scientific Reports, 2017, 7, 12205.	1.6	46
25	Polymorphisms of the SLC11A1 gene and resistance to bovine tuberculosis in African Zebu cattle. Animal Genetics, 2011, 42, 656-658.	0.6	44
26	Evolutionary process of <i>Bos taurus</i> cattle in favourable versus unfavourable environments and its implications for genetic selection. Evolutionary Applications, 2010, 3, 422-433.	1.5	42
27	An F2 Pig Resource Population as a Model for Genetic Studies of Obesity and Obesity-Related Diseases in Humans: Design and Genetic Parameters. Frontiers in Genetics, 2013, 4, 29.	1.1	42
28	Weighted Interaction SNP Hub (WISH) network method for building genetic networks for complex diseases and traits using whole genome genotype data. BMC Systems Biology, 2014, 8, S5.	3.0	42
29	Genetic Parameters for Functional Traits in Dairy Cattle from Daily Random Regression Models. Journal of Dairy Science, 2006, 89, 791-798.	1.4	36
30	SNP annotation-based whole genomic prediction and selection: An application to feed efficiency and its component traits in pigs1. Journal of Animal Science, 2015, 93, 2056-2063.	0.2	35
31	Building gene co-expression networks using transcriptomics data for systems biology investigations: Comparison of methods using microarray data. Bioinformation, 2012, 8, 855-861.	0.2	35
32	Power of quantitative trait locus mapping for polygenic binary traits using generalized and regression interval mapping in multi-family half-sib designs. Genetical Research, 2000, 76, 305-317.	0.3	34
33	Genetic and economic relationships between somatic cell count and clinical mastitis and their use in selection for mastitis resistance in dairy cattle. Animal Science, 2001, 73, 19-28.	1.3	32
34	Genetic parameters for clinical mastitis in Holstein-Friesians in the United Kingdom: a Bayesian analysis. Animal Science, 2001, 73, 229-240.	1.3	31
35	Genomic study and Medical Subject Headings enrichment analysis of early pregnancy rate and antral follicle numbers in Nelore heifers1,2. Journal of Animal Science, 2017, 95, 4796-4812.	0.2	31
36	Population and systems genetics analyses of cortisol in pigs divergently selected for stress. Physiological Genomics, 2007, 29, 57-65.	1.0	30

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37	An integrative systems genetics approach reveals potential causal genes and pathways related to obesity. Genome Medicine, 2015, 7, 105.	3.6	30
38	Potential role of lncRNA cyp2c91â€"protein interactions on diseases of the immune system. Frontiers in Genetics, 2015, 6, 255.	1.1	30
39	Genetic parameters for androstenone and skatole as indicators of boar taint and their relationship to production and litter size traits in Danish Landrace1. Journal of Animal Science, 2013, 91, 2587-2595.	0.2	29
40	Evidence of a Major Gene From Bayesian Segregation Analyses of Liability to Osteochondral Diseases in Pigs. Genetics, 2005, 171, 1195-1206.	1.2	28
41	An Epigenome-Wide DNA Methylation Map of Testis in Pigs for Study of Complex Traits. Frontiers in Genetics, 2019, 10, 405.	1.1	27
42	Detection of Co-expressed Pathway Modules Associated With Mineral Concentration and Meat Quality in Nelore Cattle. Frontiers in Genetics, 2019, 10, 210.	1.1	27
43	Metabolomics Analyses in High-Low Feed Efficient Dairy Cows Reveal Novel Biochemical Mechanisms and Predictive Biomarkers. Metabolites, 2019, 9, 151.	1.3	26
44	Genome-Wide Epistatic Interaction Networks Affecting Feed Efficiency in Duroc and Landrace Pigs. Frontiers in Genetics, 2020, 11, 121.	1.1	26
45	FunctSNP: an R package to link SNPs to functional knowledge and dbAutoMaker: a suite of Perl scripts to build SNP databases. BMC Bioinformatics, 2010, 11, 311.	1.2	25
46	Systems genetics of obesity in an F2 pig model by genome-wide association, genetic network, and pathway analyses. Frontiers in Genetics, 2014, 5, 214.	1.1	25
47	Bayesian segregation analysis of milk flow in Swiss dairy cattle using Gibbs sampling. Genetics Selection Evolution, 2004, 36, 563-76.	1.2	23
48	Metabolomic networks and pathways associated with feed efficiency and related-traits in Duroc and Landrace pigs. Scientific Reports, 2020, 10, 255.	1.6	23
49	Genetic parameters for male fertility and its relationship to skatole and androstenone in Danish Landrace boars1. Journal of Animal Science, 2013, 91, 4659-4668.	0.2	22
50	Systems genomics study reveals expression quantitative trait loci, regulator genes and pathways associated with boar taint in pigs. PLoS ONE, 2018, 13, e0192673.	1.1	22
51	Assessment of genetic diversity and population structure of Vietnamese indigenous cattle populations by microsatellites. Livestock Science, 2013, 155, 17-22.	0.6	21
52	Expression studies of six human obesityâ€related genes in seven tissues from divergent pig breeds. Animal Genetics, 2014, 45, 59-66.	0.6	21
53	Inter-Tissue Gene Co-Expression Networks between Metabolically Healthy and Unhealthy Obese Individuals. PLoS ONE, 2016, 11, e0167519.	1.1	21
54	Comparative Analyses of QTLs Influencing Obesity and Metabolic Phenotypes in Pigs and Humans. PLoS ONE, 2015, 10, e0137356.	1.1	21

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55	Genetic correlations between body condition scores and fertility in dairy cattle using bivariate random regression models. Journal of Animal Breeding and Genetics, 2007, 124, 277-285.	0.8	19
56	Gene co-expression networks in liver and muscle transcriptome reveal sex-specific gene expression in lambs fed with a mix of essential oils. BMC Genomics, 2018, 19, 236.	1.2	19
57	Genomeâ€wide <scp>DNA</scp> methylation analysis using nextâ€generation sequencing to reveal candidate genes responsible for boar taint in pigs. Animal Genetics, 2019, 50, 644-659.	0.6	19
58	Genetical systems biology in livestock: application to gonadotrophin releasing hormone and reproduction. IET Systems Biology, 2008, 2, 423-441.	0.8	18
59	Genetic architecture of gene expression in ovine skeletal muscle. BMC Genomics, 2011, 12, 607.	1.2	18
60	Validation of Genome-Wide Intervertebral Disk Calcification Associations in Dachshund and Further Investigation of the Chromosome 12 Susceptibility Locus. Frontiers in Genetics, 2012, 3, 225.	1.1	18
61	Genetics of Parity-Dependant Production Increase and its Relationship with Health, Fertility, Longevity, and Conformation in Swiss Holsteins. Journal of Dairy Science, 2005, 88, 1540-1551.	1.4	17
62	Selection on multiple QTL with control of gene diversity and inbreeding for longâ€term benefit. Journal of Animal Breeding and Genetics, 2008, 125, 320-329.	0.8	17
63	Late gestation under- and overnutrition have differential impacts when combined with a post-natal obesogenic diet on glucose-lactate-insulin adaptations during metabolic challenges in adolescent sheep. Acta Physiologica, 2015, 213, 519-536.	1.8	17
64	A genome-wide association study of thyroid stimulating hormone and free thyroxine in Danish children and adolescents. PLoS ONE, 2017, 12, e0174204.	1.1	17
65	Molecular genetic diversity and genetic structure of <scp>V</scp>ietnamese indigenous pig populations. Journal of Animal Breeding and Genetics, 2014, 131, 379-386.	0.8	16
66	Characterization of Global DNA Methylation in Different Gene Regions Reveals Candidate Biomarkers in Pigs with High and Low Levels of Boar Taint. Veterinary Sciences, 2020, 7, 77.	0.6	16
67	Biochemical, ECF18R, and RYR1 Gene Polymorphisms and Their Associations with Osteochondral Diseases and Production Traits in Pigs. Biochemical Genetics, 2008, 46, 41-53.	0.8	15
68	Genetic Parameters and Genome-Wide Association Studies for Anti-MÃ¼llerian Hormone Levels and Antral Follicle Populations Measured After Estrus Synchronization in Nellore Cattle. Animals, 2020, 10, 1185.	1.0	15
69	Generalized marker regression and interval QTL mapping methods for binary traits in half-sib family designs. Journal of Animal Breeding and Genetics, 2001, 118, 297-309.	0.8	14
70	WISH-Râ€“ a fast and efficient tool for construction of epistatic networks for complex traits and diseases. BMC Bioinformatics, 2018, 19, 277.	1.2	14
71	Characterization of eQTLs associated with androstenone by RNA sequencing in porcine testis. Physiological Genomics, 2019, 51, 488-499.	1.0	14
72	Characterization of the endometrial transcriptome in early diestrus influencing pregnancy status in dairy cattle after transfer of in vitro-produced embryos. Physiological Genomics, 2020, 52, 269-279.	1.0	14

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73	Single Nucleotide Polymorphism Discovery in Bovine Pituitary Gland Using RNA-Seq Technology. PLoS ONE, 2016, 11, e0161370.	1.1	14
74	Systematic in vitro and in vivo characterization of Leukemiaâ€•inhibiting factorâ€•and Fibroblast growth factorâ€•derived porcine induced pluripotent stem cells. Molecular Reproduction and Development, 2017, 84, 229-245.	1.0	13
75	Identification of potential biomarkers in donor cows for in vitro embryo production by granulosa cell transcriptomics. PLoS ONE, 2017, 12, e0175464.	1.1	13
76	Metabolite Genome-Wide Association Study (mGWAS) and Gene-Metabolite Interaction Network Analysis Reveal Potential Biomarkers for Feed Efficiency in Pigs. Metabolites, 2020, 10, 201.	1.3	13
77	Additive and epistatic genomeâ€•wide association for growth and ultrasound scan measures of carcassâ€•related traits in <scp>B</scp>rahman cattle. Journal of Animal Breeding and Genetics, 2015, 132, 187-197.	0.8	12
78	Systems genetics and genome-wide association approaches for analysis of feed intake, feed efficiency, and performance in beef cattle. Genetics and Molecular Research, 2016, 15, .	0.3	12
79	Genetic Susceptibility for Childhood BMI has no Impact on Weight Loss Following Lifestyle Intervention in Danish Children. Obesity, 2018, 26, 1915-1922.	1.5	12
80	Genomic analyses suggest adaptive differentiation of northern European native cattle breeds. Evolutionary Applications, 2019, 12, 1096-1113.	1.5	12
81	An adult-based insulin resistance genetic risk score associates with insulin resistance, metabolic traits and altered fat distribution in Danish children and adolescents who are overweight or obese. Diabetologia, 2018, 61, 1769-1779.	2.9	11
82	Machine learning approach to integrated endometrial transcriptomic datasets reveals biomarkers predicting uterine receptivity in cattle at seven days after estrous. Scientific Reports, 2020, 10, 16981.	1.6	11
83	Differential impacts of late gestational overâ€“and undernutrition on adipose tissue traits and associated visceral obesity risk upon exposure to a postnatal highâ€•fat diet in adolescent sheep. Physiological Reports, 2020, 8, e14359.	0.7	11
84	Comparisons of improved genomic predictions generated by different imputation methods for genotyping by sequencing data in livestock populations. Journal of Animal Science and Biotechnology, 2020, 11, 3.	2.1	11
85	Impact of IL-17F 7488T/C Functional Polymorphism on Progressive Rheumatoid Arthritis: Novel Insight from the Molecular Dynamic Simulations. Immunological Investigations, 2021, 50, 416-426.	1.0	11
86	Application of multi-omics data integration and machine learning approaches to identify epigenetic and transcriptomic differences between in vitro and in vivo produced bovine embryos. PLoS ONE, 2021, 16, e0252096.	1.1	11
87	Single nucleotide polymorphism discovery in bovine liver using RNA-seq technology. PLoS ONE, 2017, 12, e0172687.	1.1	11
88	Pre- and Early-Postnatal Nutrition Modify Gene and Protein Expressions of Muscle Energy Metabolism Markers and Phospholipid Fatty Acid Composition in a Muscle Type Specific Manner in Sheep. PLoS ONE, 2013, 8, e65452.	1.1	10
89	Simulated physiological oocyte maturation has side effects on bovine oocytes and embryos. Journal of Assisted Reproduction and Genetics, 2019, 36, 413-424.	1.2	10
90	Integrative Analysis of Metabolomic and Transcriptomic Profiles Uncovers Biological Pathways of Feed Efficiency in Pigs. Metabolites, 2020, 10, 275.	1.3	10

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91	Bayesian inference on major loci in related multigeneration selection lines of laying hens. Poultry Science, 2004, 83, 1932-1939.	1.5	9
92	Transcription Factor Co-expression Networks of Adipose RNA-Seq Data Reveal Regulatory Mechanisms of Obesity. Current Genomics, 2018, 19, 289-299.	0.7	9
93	Genome Regulation and Gene Interaction Networks Inferred From Muscle Transcriptome Underlying Feed Efficiency in Pigs. Frontiers in Genetics, 2020, 11, 650.	1.1	9
94	Regression on markers with uncertain allele transmission for QTL mapping in half-sib designs. Genetics Selection Evolution, 1999, 31, 1.	1.2	8
95	Arthrogryposis multiplex congenita (AMC), a hereditary disease in swine, maps to Chromosome 5 by linkage analysis. Mammalian Genome, 2004, 15, 935-941.	1.0	8
96	PREDICTION OF TRANSCRIPTION FACTOR BINDING SITES USING GENETICAL GENOMICS METHODS. Journal of Bioinformatics and Computational Biology, 2007, 05, 773-793.	0.3	8
97	Improving genomic predictions by correction of genotypes from genotyping by sequencing in livestock populations. Journal of Animal Science and Biotechnology, 2019, 10, 8.	2.1	8
98	Transcriptomic changes in bovine skeletal muscle cells after resveratrol treatment. Gene, 2020, 754, 144849.	1.0	8
99	Transient treatment of pregnant Merino ewes with modulators of cortisol biosynthesis coinciding with primary wool follicle initiation alters lifetime wool growth. Animal Production Science, 2013, 53, 1101.	0.6	8
100	Geneâ€“environment interactions in complex diseases: genetic models and methods for QTL mapping in multiple half-sib populations. Genetical Research, 2006, 88, 119-131.	0.3	7
101	Applications of Systems Genetics and Biology for Obesity Using Pig Models. , 2016, , 25-42.		7
102	Epigenomic and transcriptomic analyses reveal early activation of the HPG axis in in vitroâ€produced male dairy calves. FASEB Journal, 2021, 35, e21882.	0.2	7
103	Genetic parameters of infectious bovine keratoconjunctivitis and its relationship with weight and parasite infestations in Australian tropical Bos taurus cattle. Genetics Selection Evolution, 2012, 44, 22.	1.2	6
104	Systems genetics analysis of pharmacogenomics variation during antidepressant treatment. Pharmacogenomics Journal, 2018, 18, 144-152.	0.9	6
105	Transcriptomicsâ€“genomics data integration and expression quantitative trait loci analyses in oocyte donors and embryo recipients for improving invitro production of dairy cattle embryos. Reproduction, Fertility and Development, 2019, 31, 55.	0.1	6
106	GeneDMRs: An R Package for Gene-Based Differentially Methylated Regions Analysis. Journal of Computational Biology, 2021, 28, 304-316.	0.8	6
107	Combined genetic, genomic and transcriptomic methods in the analysis of animal traits.. CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources, 0, , .	0.6	6
108	Systems Genetics of Complex Diseases Using RNA-Sequencing Methods. International Journal of Bioscience, Biochemistry, Bioinformatics (IJBBB), 2015, 5, 264-279.	0.2	6

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109	Genetic variations (eQTLs) in muscle transcriptome and mitochondrial genes, and trans-eQTL molecular pathways in feed efficiency from Danish breeding pigs. PLoS ONE, 2020, 15, e0239143.	1.1	5
110	Identification of Differentially Expressed Gene Transcripts in Porcine Endometrium during Early Stages of Pregnancy. Life, 2020, 10, 68.	1.1	5
111	Investigation of gut microbiome association with inflammatory bowel disease and depression: a machine learning approach. F1000Research, 0, 7, 702.	0.8	5
112	Basic and practical aspects of pregnancy establishment in cattle. Animal Reproduction, 2017, 14, 581-588.	0.4	4
113	Host Genomeâ€"Metagenome Analyses Using Combinatorial Network Methods Reveal Key Metagenomic and Host Genetic Features for Methane Emission and Feed Efficiency in Cattle. Frontiers in Genetics, 2022, 13, 795717.	1.1	4
114	Investigation of major gene for milk yield, milking speed, dry matter intake, and body weight in dairy cattle. Journal of Applied Genetics, 2006, 47, 337-343.	1.0	3
115	Copy Number Variations and Expression Levels of Guanylate-Binding Protein 6 Gene Associated with Growth Traits of Chinese Cattle. Animals, 2020, 10, 566.	1.0	3
116	In vitro production of bovine embryos: cumulus/granulosa cell gene expression patterns point to early atresia as beneficial for oocyte competence. Animal Reproduction, 2017, 14, 482-489.	0.4	3
117	In vitro and in vivo-produced male dairy calves show molecular differences in the hepatic and muscular energy regulation. Biology of Reproduction, 0, , .	1.2	3
118	Genetic evaluations and parameter estimates for dairy cow fertility in the United Kingdom. Proceedings of the British Society of Animal Science, 2001, 2001, 36-36.	0.0	2
119	Proximity loggers: data handling and classification for quality Control. IEEE Sensors Journal, 2011, , .	2.4	2
120	Computational Methods for Quality Check, Preprocessing and Normalization of RNA-Seq Data for Systems Biology and Analysis. , 2016, , 61-77.		2
121	Bovine in-vitro produced embryos: Development of embryo proper and associated membranes from day 26 to 47 of gestation. Reproductive Biology, 2020, 20, 595-599.	0.9	2
122	Application of integrative genomics and systems biology to conventional and in vitro reproductive traits in cattle. Animal Reproduction, 2017, 14, 507-513.	0.4	2
123	Association between microsatellite markers and bovine tuberculosis in Chadian Zebu cattle. Open Journal of Animal Sciences, 2013, 03, 27-35.	0.2	2
124	Interplay among miR-29 family, mineral metabolism, and gene regulation in Bos indicus muscle. Molecular Genetics and Genomics, 2020, 295, 1113-1127.	1.0	2
125	Effect of relationship between mastitis and somatic cell count on genetic selection for mastitis resistance in dairy cattle. Proceedings of the British Society of Animal Science, 2000, 2000, 113-113.	0.0	1
126	Protocol for Construction of Genome-Wide Epistatic SNP Networks Using WISH-R Package. Methods in Molecular Biology, 2021, 2212, 155-168.	0.4	1

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127	Complex Segregation Analysis of Categorical Traits in Farm Animals: Comparison of Linear and Threshold Models. Asian-Australasian Journal of Animal Sciences, 2005, 18, 1088-1097.	2.4	1
128	Predicting Breeding Values in Animals by Kalman Filter: Application to Body Condition Scores in Dairy Cattle. Kafkas Universitesi Veteriner Fakultesi Dergisi, 2012, , .	0.0	1
129	192 PREMATURATION OF BOVINE CUMULUS-OOCYTE COMPLEXES WITH CYCLIC ADENOSINE MONOPHOSPHATE MODULATORS AFFECTS BOTH OOCYTE AND BLASTOCYST ULTRASTRUCTURE. Reproduction, Fertility and Development, 2016, 28, 227.	0.1	1
130	Linear and threshold model genetic parameters for disease, fertility and milk production in dairy cattle. BSAP Occasional Publication, 2000, 27, 83-84.	0.0	0
131	Bayesian segregation analysis of osteochondral diseases in pigs to determine major gene role. Proceedings of the British Society of Animal Science, 2005, 2005, 51-51.	0.0	0
132	Systems Biology in Animal Production and Health, Vol. 1. , 2016, , .		0
133	PHARMACOGENOMICS OF METHYLPHENIDATE TREATMENT OF DANISH CHILDREN WITH ADHD. European Neuropsychopharmacology, 2019, 29, S868.	0.3	0
134	Analysis of SNP rs1800796 Association with Risk of Rheumatoid Arthritis in Pakistani Population: A Case Control Study. Pakistan Journal of Zoology, 2021, 53, .	0.1	0
135	78 Effects of invitro production on the epigenome and transcriptome of bovine embryos determined through a multi-omics data integration approach. Reproduction, Fertility and Development, 2021, 33, 147.	0.1	0
136	Genetic factors affecting feed efficiency, feeding behaviour and related traits in pigs. Burleigh Dodds Series in Agricultural Science, 2017, , 75-96.	0.1	0
137	Investigation of gut microbiome association with inflammatory bowel disease and depression: a machine learning approach. F1000Research, 0, 7, 702.	0.8	0