

# Haja N Kadarmideen

## List of Publications by Citations

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127  
papers

2,950  
citations

27  
h-index

50  
g-index

148  
ext. papers

3,920  
ext. citations

3.8  
avg, IF

5.35  
L-index

#	Paper	IF	Citations
127	Genome-wide associations for birth weight and correlations with adult disease. <i>Nature</i> , <b>2016</b> , 538, 248-252.	52.4	266
126	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 389-403	5.6	202
125	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , <b>2019</b> , 51, 804-814	36.3	181
124	Linear and threshold model genetic parameters for disease, fertility and milk production in dairy cattle. <i>Animal Science</i> , <b>2000</b> , 71, 411-419		144
123	Genetic parameters and evaluations from single- and multiple-trait analysis of dairy cow fertility and milk production. <i>Livestock Science</i> , <b>2003</b> , 81, 183-195		97
122	Multi-omic data integration and analysis using systems genomics approaches: methods and applications in animal production, health and welfare. <i>Genetics Selection Evolution</i> , <b>2016</b> , 48, 38	4.9	96
121	Liver transcriptomic networks reveal main biological processes associated with feed efficiency in beef cattle. <i>BMC Genomics</i> , <b>2015</b> , 16, 1073	4.5	80
120	Genome-wide association and systems genetic analyses of residual feed intake, daily feed consumption, backfat and weight gain in pigs. <i>BMC Genetics</i> , <b>2014</b> , 15, 27	2.6	71
119	Identification of co-expression gene networks, regulatory genes and pathways for obesity based on adipose tissue RNA Sequencing in a porcine model. <i>BMC Medical Genomics</i> , <b>2014</b> , 7, 57	3.7	66
118	Genetic parameters for different measures of feed efficiency and related traits in boars of three pig breeds. <i>Journal of Animal Science</i> , <b>2013</b> , 91, 4069-79	0.7	64
117	PCIT: an R package for weighted gene co-expression networks based on partial correlation and information theory approaches. <i>Bioinformatics</i> , <b>2010</b> , 26, 411-3	7.2	63
116	From genetical genomics to systems genetics: potential applications in quantitative genomics and animal breeding. <i>Mammalian Genome</i> , <b>2006</b> , 17, 548-64	3.2	61
115	RNA-Seq transcriptomics and pathway analyses reveal potential regulatory genes and molecular mechanisms in high- and low-residual feed intake in Nordic dairy cattle. <i>BMC Genomics</i> , <b>2017</b> , 18, 258	4.5	57
114	Genome-wide association and pathway analysis of feed efficiency in pigs reveal candidate genes and pathways for residual feed intake. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 307	4.5	56
113	Genomics to systems biology in animal and veterinary sciences: Progress, lessons and opportunities. <i>Livestock Science</i> , <b>2014</b> , 166, 232-248	1.7	55
112	Genome-wide association study reveals genetic architecture of eating behavior in pigs and its implications for humans obesity by comparative mapping. <i>PLoS ONE</i> , <b>2013</b> , 8, e71509	3.7	52
111	Genetics of osteochondral disease and its relationship with meat quality and quantity, growth, and feed conversion traits in pigs. <i>Journal of Animal Science</i> , <b>2004</b> , 82, 3118-27	0.7	49

110	Systems biology of ovine intestinal parasite resistance: disease gene modules and biomarkers. <i>Molecular BioSystems</i> , <b>2011</b> , 7, 235-46		45
109	Genetic parameters for body condition score and its relationship with type and production traits in Swiss Holsteins. <i>Journal of Dairy Science</i> , <b>2003</b> , 86, 3685-93	4	44
108	Genetic and phenotypic parameters for conformation and yield traits in three Swiss dairy cattle breeds. <i>Journal of Animal Breeding and Genetics</i> , <b>2007</b> , 124, 12-9	2.9	36
107	Genetic correlations among body condition score, somatic cell score, milk production, fertility and conformation traits in dairy cows. <i>Animal Science</i> , <b>2004</b> , 79, 191-201		35
106	Copy number variations and genome-wide associations reveal putative genes and metabolic pathways involved with the feed conversion ratio in beef cattle. <i>Journal of Applied Genetics</i> , <b>2016</b> , 57, 495-504	2.5	34
105	Polymorphisms of the SLC11A1 gene and resistance to bovine tuberculosis in African Zebu cattle. <i>Animal Genetics</i> , <b>2011</b> , 42, 656-8	2.5	33
104	Evolutionary process of <i>Bos taurus</i> cattle in favourable versus unfavourable environments and its implications for genetic selection. <i>Evolutionary Applications</i> , <b>2010</b> , 3, 422-33	4.8	31
103	Power of quantitative trait locus mapping for polygenic binary traits using generalized and regression interval mapping in multi-family half-sib designs. <i>Genetical Research</i> , <b>2000</b> , 76, 305-17	1.1	31
102	An f2 pig resource population as a model for genetic studies of obesity and obesity-related diseases in humans: design and genetic parameters. <i>Frontiers in Genetics</i> , <b>2013</b> , 4, 29	4.5	30
101	SNP annotation-based whole genomic prediction and selection: an application to feed efficiency and its component traits in pigs. <i>Journal of Animal Science</i> , <b>2015</b> , 93, 2056-63	0.7	28
100	Genetic and economic relationships between somatic cell count and clinical mastitis and their use in selection for mastitis resistance in dairy cattle. <i>Animal Science</i> , <b>2001</b> , 73, 19-28		27
99	Genetic parameters for clinical mastitis in Holstein-Friesians in the United Kingdom: a Bayesian analysis. <i>Animal Science</i> , <b>2001</b> , 73, 229-240		27
98	An integrative systems genetics approach reveals potential causal genes and pathways related to obesity. <i>Genome Medicine</i> , <b>2015</b> , 7, 105	14.4	26
97	Population and systems genetics analyses of cortisol in pigs divergently selected for stress. <i>Physiological Genomics</i> , <b>2007</b> , 29, 57-65	3.6	26
96	Genetic parameters for functional traits in dairy cattle from daily random regression models. <i>Journal of Dairy Science</i> , <b>2006</b> , 89, 791-8	4	26
95	Evidence of a major gene from Bayesian segregation analyses of liability to osteochondral diseases in pigs. <i>Genetics</i> , <b>2005</b> , 171, 1195-206	4	26
94	Gene co-expression networks from RNA sequencing of dairy cattle identifies genes and pathways affecting feed efficiency. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 513	3.6	25
93	Weighted Interaction SNP Hub (WISH) network method for building genetic networks for complex diseases and traits using whole genome genotype data. <i>BMC Systems Biology</i> , <b>2014</b> , 8 Suppl 2, S5	3.5	24

92	Genetic parameters for androstenone and skatole as indicators of boar taint and their relationship to production and litter size traits in Danish Landrace. <i>Journal of Animal Science</i> , <b>2013</b> , 91, 2587-95	0.7	24
91	Building gene co-expression networks using transcriptomics data for systems biology investigations: Comparison of methods using microarray data. <i>Bioinformatics</i> , <b>2012</b> , 8, 855-61	1.1	24
90	Genetic parameters for male fertility and its relationship to skatole and androstenone in Danish Landrace boars. <i>Journal of Animal Science</i> , <b>2013</b> , 91, 4659-68	0.7	21
89	Genomic study and Medical Subject Headings enrichment analysis of early pregnancy rate and antral follicle numbers in Nelore heifers. <i>Journal of Animal Science</i> , <b>2017</b> , 95, 4796-4812	0.7	20
88	Potential role of lncRNA cyp2c91-protein interactions on diseases of the immune system. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 255	4.5	20
87	Differential expression and co-expression gene networks reveal candidate biomarkers of boar taint in non-castrated pigs. <i>Scientific Reports</i> , <b>2017</b> , 7, 12205	4.9	19
86	FunctSNP: an R package to link SNPs to functional knowledge and dbAutoMaker: a suite of Perl scripts to build SNP databases. <i>BMC Bioinformatics</i> , <b>2010</b> , 11, 311	3.6	19
85	Genetic correlations between body condition scores and fertility in dairy cattle using bivariate random regression models. <i>Journal of Animal Breeding and Genetics</i> , <b>2007</b> , 124, 277-85	2.9	19
84	Expression studies of six human obesity-related genes in seven tissues from divergent pig breeds. <i>Animal Genetics</i> , <b>2014</b> , 45, 59-66	2.5	18
83	Inter-Tissue Gene Co-Expression Networks between Metabolically Healthy and Unhealthy Obese Individuals. <i>PLoS ONE</i> , <b>2016</b> , 11, e0167519	3.7	18
82	Genetic architecture of gene expression in ovine skeletal muscle. <i>BMC Genomics</i> , <b>2011</b> , 12, 607	4.5	16
81	Bayesian segregation analysis of milk flow in Swiss dairy cattle using Gibbs sampling. <i>Genetics Selection Evolution</i> , <b>2004</b> , 36, 563-76	4.9	16
80	Assessment of genetic diversity and population structure of Vietnamese indigenous cattle populations by microsatellites. <i>Livestock Science</i> , <b>2013</b> , 155, 17-22	1.7	15
79	Validation of genome-wide intervertebral disk calcification associations in dachshund and further investigation of the chromosome 12 susceptibility locus. <i>Frontiers in Genetics</i> , <b>2012</b> , 3, 225	4.5	15
78	Genetical systems biology in livestock: application to gonadotrophin releasing hormone and reproduction. <i>IET Systems Biology</i> , <b>2008</b> , 2, 423-41	1.4	15
77	Comparative Analyses of QTLs Influencing Obesity and Metabolic Phenotypes in Pigs and Humans. <i>PLoS ONE</i> , <b>2015</b> , 10, e0137356	3.7	15
76	Detection of Co-expressed Pathway Modules Associated With Mineral Concentration and Meat Quality in Nelore Cattle. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 210	4.5	14
75	Gene co-expression networks in liver and muscle transcriptome reveal sex-specific gene expression in lambs fed with a mix of essential oils. <i>BMC Genomics</i> , <b>2018</b> , 19, 236	4.5	14

74	Systems genetics of obesity in an F2 pig model by genome-wide association, genetic network, and pathway analyses. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 214	4.5	14
73	Molecular genetic diversity and genetic structure of Vietnamese indigenous pig populations. <i>Journal of Animal Breeding and Genetics</i> , <b>2014</b> , 131, 379-86	2.9	14
72	Selection on multiple QTL with control of gene diversity and inbreeding for long-term benefit. <i>Journal of Animal Breeding and Genetics</i> , <b>2008</b> , 125, 320-9	2.9	14
71	A genome-wide association study of thyroid stimulating hormone and free thyroxine in Danish children and adolescents. <i>PLoS ONE</i> , <b>2017</b> , 12, e0174204	3.7	14
70	An Epigenome-Wide DNA Methylation Map of Testis in Pigs for Study of Complex Traits. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 405	4.5	13
69	Metabolomics Analyses in High-Low Feed Efficient Dairy Cows Reveal Novel Biochemical Mechanisms and Predictive Biomarkers. <i>Metabolites</i> , <b>2019</b> , 9,	5.6	13
68	Genetics of parity-dependant production increase and its relationship with health, fertility, longevity, and conformation in swiss holsteins. <i>Journal of Dairy Science</i> , <b>2005</b> , 88, 1540-51	4	13
67	Genome-Wide Epistatic Interaction Networks Affecting Feed Efficiency in Duroc and Landrace Pigs. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 121	4.5	12
66	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. <i>Acta Physiologica</i> , <b>2015</b> , 213, 519-36	5.6	12
65	Systematic in vitro and in vivo characterization of Leukemia-inhibiting factor- and Fibroblast growth factor-derived porcine induced pluripotent stem cells. <i>Molecular Reproduction and Development</i> , <b>2017</b> , 84, 229-245	2.6	11
64	Metabolomic networks and pathways associated with feed efficiency and related-traits in Duroc and Landrace pigs. <i>Scientific Reports</i> , <b>2020</b> , 10, 255	4.9	11
63	Generalized marker regression and interval QTL mapping methods for binary traits in half-sib family designs. <i>Journal of Animal Breeding and Genetics</i> , <b>2001</b> , 118, 297-309	2.9	11
62	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. <i>PLoS ONE</i> , <b>2013</b> , 8, e65452	3.7	10
61	Biochemical, ECF18R, and RYR1 gene polymorphisms and their associations with osteochondral diseases and production traits in pigs. <i>Biochemical Genetics</i> , <b>2008</b> , 46, 41-53	2.4	10
60	Single Nucleotide Polymorphism Discovery in Bovine Pituitary Gland Using RNA-Seq Technology. <i>PLoS ONE</i> , <b>2016</b> , 11, e0161370	3.7	10
59	Genome-wide DNA methylation analysis using next-generation sequencing to reveal candidate genes responsible for boar taint in pigs. <i>Animal Genetics</i> , <b>2019</b> , 50, 644-659	2.5	9
58	Systems genomics study reveals expression quantitative trait loci, regulator genes and pathways associated with boar taint in pigs. <i>PLoS ONE</i> , <b>2018</b> , 13, e0192673	3.7	9
57	Additive and epistatic genome-wide association for growth and ultrasound scan measures of carcass-related traits in Brahman cattle. <i>Journal of Animal Breeding and Genetics</i> , <b>2015</b> , 132, 187-97	2.9	8

56	WISH-R- a fast and efficient tool for construction of epistatic networks for complex traits and diseases. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 277	3.6	8
55	Characterization of eQTLs associated with androstenone by RNA sequencing in porcine testis. <i>Physiological Genomics</i> , <b>2019</b> , 51, 488-499	3.6	8
54	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. <i>Diabetologia</i> , <b>2018</b> , 61, 1769-1779	10.3	8
53	Characterization of the endometrial transcriptome in early diestrus influencing pregnancy status in dairy cattle after transfer of in vitro-produced embryos. <i>Physiological Genomics</i> , <b>2020</b> , 52, 269-279	3.6	7
52	Genomic analyses suggest adaptive differentiation of northern European native cattle breeds. <i>Evolutionary Applications</i> , <b>2019</b> , 12, 1096-1113	4.8	7
51	Gene-environment interactions in complex diseases: genetic models and methods for QTL mapping in multiple half-sib populations. <i>Genetical Research</i> , <b>2006</b> , 88, 119-31	1.1	7
50	Arthrogyrosis multiplex congenita (AMC), a hereditary disease in swine, maps to chromosome 5 by linkage analysis. <i>Mammalian Genome</i> , <b>2004</b> , 15, 935-41	3.2	7
49	Genetic Parameters and Genome-Wide Association Studies for Anti-Müllerian Hormone Levels and Antral Follicle Populations Measured After Estrus Synchronization in Nellore Cattle. <i>Animals</i> , <b>2020</b> , 10,	3.1	7
48	Genetic Susceptibility for Childhood BMI has no Impact on Weight Loss Following Lifestyle Intervention in Danish Children. <i>Obesity</i> , <b>2018</b> , 26, 1915-1922	8	7
47	Transcriptomic changes in bovine skeletal muscle cells after resveratrol treatment. <i>Gene</i> , <b>2020</b> , 754, 144849	3.8	6
46	Identification of potential biomarkers in donor cows for in vitro embryo production by granulosa cell transcriptomics. <i>PLoS ONE</i> , <b>2017</b> , 12, e0175464	3.7	6
45	Prediction of transcription factor binding sites using genetical genomics methods. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2007</b> , 5, 773-93	1	6
44	Regression on markers with uncertain allele transmission for QTL mapping in half-sib designs. <i>Genetics Selection Evolution</i> , <b>1999</b> , 31, 437	4.9	6
43	Single nucleotide polymorphism discovery in bovine liver using RNA-seq technology. <i>PLoS ONE</i> , <b>2017</b> , 12, e0172687	3.7	6
42	Transient treatment of pregnant Merino ewes with modulators of cortisol biosynthesis coinciding with primary wool follicle initiation alters lifetime wool growth. <i>Animal Production Science</i> , <b>2013</b> , 53, 1101	1.4	6
41	Simulated physiological oocyte maturation has side effects on bovine oocytes and embryos. <i>Journal of Assisted Reproduction and Genetics</i> , <b>2019</b> , 36, 413-424	3.4	6
40	Genome Regulation and Gene Interaction Networks Inferred From Muscle Transcriptome Underlying Feed Efficiency in Pigs. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 650	4.5	5
39	Characterization of Global DNA Methylation in Different Gene Regions Reveals Candidate Biomarkers in Pigs with High and Low Levels of Boar Taint. <i>Veterinary Sciences</i> , <b>2020</b> , 7,	2.4	5

38	Comparisons of improved genomic predictions generated by different imputation methods for genotyping by sequencing data in livestock populations. <i>Journal of Animal Science and Biotechnology</i> , <b>2020</b> , 11, 3	6	5
37	Combined genetic, genomic and transcriptomic methods in the analysis of animal traits.. <i>CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources</i> , <b>2007</b> , 2,	3.2	5
36	Systems genetics and genome-wide association approaches for analysis of feed intake, feed efficiency, and performance in beef cattle. <i>Genetics and Molecular Research</i> , <b>2016</b> , 15,	1.2	5
35	Improving genomic predictions by correction of genotypes from genotyping by sequencing in livestock populations. <i>Journal of Animal Science and Biotechnology</i> , <b>2019</b> , 10, 8	6	4
34	Metabolite Genome-Wide Association Study (mGWAS) and Gene-Metabolite Interaction Network Analysis Reveal Potential Biomarkers for Feed Efficiency in Pigs. <i>Metabolites</i> , <b>2020</b> , 10,	5.6	4
33	Differential impacts of late gestational over-and undernutrition on adipose tissue traits and associated visceral obesity risk upon exposure to a postnatal high-fat diet in adolescent sheep. <i>Physiological Reports</i> , <b>2020</b> , 8, e14359	2.6	4
32	Genetic parameters of infectious bovine keratoconjunctivitis and its relationship with weight and parasite infestations in Australian tropical Bos taurus cattle. <i>Genetics Selection Evolution</i> , <b>2012</b> , 44, 22	4.9	4
31	Bayesian inference on major loci in related multigeneration selection lines of laying hens. <i>Poultry Science</i> , <b>2004</b> , 83, 1932-9	3.9	4
30	Impact of IL-17F 7488T/C Functional Polymorphism on Progressive Rheumatoid Arthritis: Novel Insight from the Molecular Dynamic Simulations. <i>Immunological Investigations</i> , <b>2021</b> , 50, 416-426	2.9	4
29	Transcription Factor Co-expression Networks of Adipose RNA-Seq Data Reveal Regulatory Mechanisms of Obesity. <i>Current Genomics</i> , <b>2018</b> , 19, 289-299	2.6	4
28	Systems genetics analysis of pharmacogenomics variation during antidepressant treatment. <i>Pharmacogenomics Journal</i> , <b>2018</b> , 18, 144-152	3.5	3
27	Applications of Systems Genetics and Biology for Obesity Using Pig Models <b>2016</b> , 25-42		3
26	Investigation of gut microbiome association with inflammatory bowel disease and depression: a machine learning approach. <i>F1000Research</i> , <b>7</b> , 702	3.6	3
25	Machine learning approach to integrated endometrial transcriptomic datasets reveals biomarkers predicting uterine receptivity in cattle at seven days after estrous. <i>Scientific Reports</i> , <b>2020</b> , 10, 16981	4.9	3
24	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. <i>PLoS ONE</i> , <b>2021</b> , 16, e0252096	3.7	3
23	Transcriptomics-genomics data integration and expression quantitative trait loci analyses in oocyte donors and embryo recipients for improving invitro production of dairy cattle embryos. <i>Reproduction, Fertility and Development</i> , <b>2018</b> , 31, 55-67	1.8	2
22	Computational Methods for Quality Check, Preprocessing and Normalization of RNA-Seq Data for Systems Biology and Analysis <b>2016</b> , 61-77		2
21	Systems Biology in Animal Production and Health, Vol. 2 <b>2016</b> ,		2

20	Investigation of major gene for milk yield, milking speed, dry matter intake, and body weight in dairy cattle. <i>Journal of Applied Genetics</i> , <b>2006</b> , 47, 337-43	2.5	2
19	Genetic evaluations and parameter estimates for dairy cow fertility in the United Kingdom. <i>Proceedings of the British Society of Animal Science</i> , <b>2001</b> , 2001, 36-36		2
18	Systems Genetics of Complex Diseases Using RNA-Sequencing Methods. <i>International Journal of Bioscience, Biochemistry, Bioinformatics (IJBBB)</i> , <b>2015</b> , 5, 264-279	0.3	2
17	In vitro production of bovine embryos: cumulus/granulosa cell gene expression patterns point to early atresia as beneficial for oocyte competence. <i>Animal Reproduction</i> , <b>2017</b> , 14, 482-489	1.7	2
16	Association between microsatellite markers and bovine tuberculosis in Chadian Zebu cattle. <i>Open Journal of Animal Sciences</i> , <b>2013</b> , 03, 27-35	0.5	2
15	Identification of Differentially Expressed Gene Transcripts in Porcine Endometrium during Early Stages of Pregnancy. <i>Life</i> , <b>2020</b> , 10,	3	1
14	Copy Number Variations and Expression Levels of Guanylate-Binding Protein 6 Gene Associated with Growth Traits of Chinese Cattle. <i>Animals</i> , <b>2020</b> , 10,	3.1	1
13	Proximity Loggers: Data Handling and Classification for Quality Control. <i>IEEE Sensors Journal</i> , <b>2011</b> ,	4	1
12	Effect of relationship between mastitis and somatic cell count on genetic selection for mastitis resistance in dairy cattle. <i>Proceedings of the British Society of Animal Science</i> , <b>2000</b> , 2000, 113-113		1
11	Interplay among miR-29 family, mineral metabolism, and gene regulation in <i>Bos indicus</i> muscle. <i>Molecular Genetics and Genomics</i> , <b>2020</b> , 295, 1113-1127	3.1	1
10	Integrative Analysis of Metabolomic and Transcriptomic Profiles Uncover Biological Pathways of Feed Efficiency in Pigs. <i>Metabolites</i> , <b>2020</b> , 10,	5.6	1
9	Genetic variations (eQTLs) in muscle transcriptome and mitochondrial genes, and trans-eQTL molecular pathways in feed efficiency from Danish breeding pigs. <i>PLoS ONE</i> , <b>2020</b> , 15, e0239143	3.7	1
8	Bovine in-vitro produced embryos: Development of embryo proper and associated membranes from day 26 to 47 of gestation. <i>Reproductive Biology</i> , <b>2020</b> , 20, 595-599	2.3	0
7	GeneDMRs: An R Package for Gene-Based Differentially Methylated Regions Analysis. <i>Journal of Computational Biology</i> , <b>2021</b> , 28, 304-316	1.7	0
6	Epigenomic and transcriptomic analyses reveal early activation of the HPG axis in in vitro-produced male dairy calves. <i>FASEB Journal</i> , <b>2021</b> , 35, e21882	0.9	0
5	Host Genome-Metagenome Analyses Using Combinatorial Network Methods Reveal Key Metagenomic and Host Genetic Features for Methane Emission and Feed Efficiency in Cattle.. <i>Frontiers in Genetics</i> , <b>2022</b> , 13, 795717	4.5	0
4	Bayesian segregation analysis of osteochondral diseases in pigs to determine major gene role. <i>Proceedings of the British Society of Animal Science</i> , <b>2005</b> , 2005, 51-51		
3	Linear and threshold model genetic parameters for disease, fertility and milk production in dairy cattle. <i>BSAP Occasional Publication</i> , <b>2000</b> , 27, 83-84		

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| 2 | Investigation of gut microbiome association with inflammatory bowel disease and depression: a machine learning approach. <i>F1000Research</i> ,7, 702   | 3.6 |
| 1 | Protocol for Construction of Genome-Wide Epistatic SNP Networks Using WISH-R Package. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2212, 155-168 | 1.4 |