

Heebal Kim

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

220
papers

5,565
citations

30
h-index

68
g-index

242
ext. papers

7,479
ext. citations

5.2
avg, IF

4.93
L-index

#	Paper	IF	Citations
220	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012 , 491, 393-8	50.4	928
219	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014 , 346, 1311-20	33.3	628
218	Multi-platform next-generation sequencing of the domestic turkey (<i>Meleagris gallopavo</i>): genome assembly and analysis. <i>PLoS Biology</i> , 2010 , 8, e1000475	9.7	311
217	Rhizosphere microbiome structure alters to enable wilt resistance in tomato. <i>Nature Biotechnology</i> , 2018 ,	44.5	244
216	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. <i>Nature Genetics</i> , 2013 , 45, 776-783	36.3	240
215	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015 , 16, 57	18.3	196
214	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746	36.4	161
213	The genome landscape of indigenous African cattle. <i>Genome Biology</i> , 2017 , 18, 34	18.3	123
212	Reproduction of wild birds via interspecies germ cell transplantation. <i>Biology of Reproduction</i> , 2008 , 79, 931-7	3.9	65
211	Estimating rates of alternative splicing in mammals and invertebrates. <i>Nature Genetics</i> , 2004 , 36, 915-6; author reply 916-7	36.3	65
210	Joint identification of multiple genetic variants via elastic-net variable selection in a genome-wide association analysis. <i>Annals of Human Genetics</i> , 2010 , 74, 416-28	2.2	64
209	Generation of transgenic quail through germ cell-mediated germline transmission. <i>FASEB Journal</i> , 2008 , 22, 2435-44	0.9	63
208	Genome sequence of pacific abalone (<i>Haliotis discus hannai</i>): the first draft genome in family Haliotidae. <i>GigaScience</i> , 2017 , 6, 1-8	7.6	58
207	Genome scanning for conditionally essential genes in <i>Salmonella enterica</i> Serotype Typhimurium. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 3098-107	4.8	58
206	Primed pluripotent cell lines derived from various embryonic origins and somatic cells in pig. <i>PLoS ONE</i> , 2013 , 8, e52481	3.7	57
205	Comparative Transcriptome Analysis of Adipose Tissues Reveals that ECM-Receptor Interaction Is Involved in the Depot-Specific Adipogenesis in Cattle. <i>PLoS ONE</i> , 2013 , 8, e66267	3.7	56
204	Ubiquitous polygenicity of human complex traits: genome-wide analysis of 49 traits in Koreans. <i>PLoS Genetics</i> , 2013 , 9, e1003355	6	50

203	Author Correction: Rhizosphere microbiome structure alters to enable wilt resistance in tomato. <i>Nature Biotechnology</i> , 2018 , 36, 1117	44.5	49
202	A genome-wide scan for signatures of directional selection in domesticated pigs. <i>BMC Genomics</i> , 2015 , 16, 130	4.5	47
201	Genome-wide SNP identification and QTL mapping for black rot resistance in cabbage. <i>BMC Plant Biology</i> , 2015 , 15, 32	5.3	45
200	Identification of genetic polymorphisms in FABP3 and FABP4 and putative association with back fat thickness in Korean native cattle. <i>BMB Reports</i> , 2008 , 41, 29-34	5.5	45
199	Genetic diversity, population structure and relationships in indigenous cattle populations of Ethiopia and Korean Hanwoo breeds using SNP markers. <i>Frontiers in Genetics</i> , 2013 , 4, 35	4.5	41
198	A consensus sequence for binding of SmcR, a <i>Vibrio vulnificus</i> LuxR homologue, and genome-wide identification of the SmcR regulon. <i>Journal of Biological Chemistry</i> , 2008 , 283, 23610-8	5.4	39
197	Neuronal genes for subcutaneous fat thickness in human and pig are identified by local genomic sequencing and combined SNP association study. <i>PLoS ONE</i> , 2011 , 6, e16356	3.7	39
196	Whole genome scan reveals the genetic signature of African Ankole cattle breed and potential for higher quality beef. <i>BMC Genetics</i> , 2017 , 18, 11	2.6	38
195	Towards complete and error-free genome assemblies of all vertebrate species		38
194	Gut microbiota Modulated by Probiotics and Garcinia cambogia Extract Correlate with Weight Gain and Adipocyte Sizes in High Fat-Fed Mice. <i>Scientific Reports</i> , 2016 , 6, 33566	4.9	32
193	Deleted copy number variation of Hanwoo and Holstein using next generation sequencing at the population level. <i>BMC Genomics</i> , 2014 , 15, 240	4.5	32
192	Sexually dimorphic gene expression in the chick brain before gonadal differentiation. <i>Poultry Science</i> , 2009 , 88, 1003-15	3.9	32
191	A double-screening method to identify reliable candidate non-synonymous SNPs from chicken EST data. <i>Animal Genetics</i> , 2003 , 34, 249-54	2.5	32
190	Exploring evidence of positive selection signatures in cattle breeds selected for different traits. <i>Mammalian Genome</i> , 2017 , 28, 528-541	3.2	30
189	Deciphering the genetic blueprint behind Holstein milk proteins and production. <i>Genome Biology and Evolution</i> , 2014 , 6, 1366-74	3.9	30
188	Revealing the combined effects of lactulose and probiotic enterococci on the swine faecal microbiota using 454 pyrosequencing. <i>Microbial Biotechnology</i> , 2016 , 9, 486-95	6.3	29
187	RNA-seq analysis for detecting quantitative trait-associated genes. <i>Scientific Reports</i> , 2016 , 6, 24375	4.9	28
186	Genetic markers and their application in poultry breeding. <i>Poultry Science</i> , 2003 , 82, 952-7	3.9	28

185	The mosaic genome of indigenous African cattle as a unique genetic resource for African pastoralism. <i>Nature Genetics</i> , 2020 , 52, 1099-1110	36.3	28
184	Whole genome detection of signature of positive selection in African cattle reveals selection for thermotolerance. <i>Animal Science Journal</i> , 2017 , 88, 1889-1901	1.8	27
183	Identification of candidate genes related to bovine marbling using protein-protein interaction networks. <i>International Journal of Biological Sciences</i> , 2011 , 7, 992-1002	11.2	27
182	Generation and analysis of large-scale expressed sequence tags (ESTs) from a full-length enriched cDNA library of porcine backfat tissue. <i>BMC Genomics</i> , 2006 , 7, 36	4.5	27
181	Gene Co-expression Analysis to Characterize Genes Related to Marbling Trait in Hanwoo (Korean) Cattle. <i>Asian-Australasian Journal of Animal Sciences</i> , 2013 , 26, 19-29	2.4	26
180	Comparative transcriptomic analysis to identify differentially expressed genes in fat tissue of adult Berkshire and Jeju Native Pig using RNA-seq. <i>Molecular Biology Reports</i> , 2014 , 41, 6305-15	2.8	25
179	Exploring the genetic signature of body size in Yucatan miniature pig. <i>PLoS ONE</i> , 2015 , 10, e0121732	3.7	25
178	A Genome-wide Scan for Selective Sweeps in Racing Horses. <i>Asian-Australasian Journal of Animal Sciences</i> , 2015 , 28, 1525-31	2.4	25
177	HGTree: database of horizontally transferred genes determined by tree reconciliation. <i>Nucleic Acids Research</i> , 2016 , 44, D610-9	20.1	24
176	Evidence of recombination in a new isolate of foot-and-mouth disease virus serotype Asia 1. <i>Virus Research</i> , 2009 , 139, 117-21	6.4	24
175	An integrated approach of comparative genomics and heritability analysis of pig and human on obesity trait: evidence for candidate genes on human chromosome 2. <i>BMC Genomics</i> , 2012 , 13, 711	4.5	23
174	An approach of orthology detection from homologous sequences under minimum evolution. <i>Nucleic Acids Research</i> , 2008 , 36, e110	20.1	23
173	Exploring evidence of positive selection reveals genetic basis of meat quality traits in Berkshire pigs through whole genome sequencing. <i>BMC Genetics</i> , 2015 , 16, 104	2.6	22
172	Gene expression profiling of chicken primordial germ cell ESTs. <i>BMC Genomics</i> , 2006 , 7, 220	4.5	22
171	Identification of genes related to intramuscular fat content of pigs using genome-wide association study. <i>Asian-Australasian Journal of Animal Sciences</i> , 2018 , 31, 157-162	2.4	22
170	Comparative genomic analysis of <i>Lactobacillus mucosae</i> LM1 identifies potential niche-specific genes and pathways for gastrointestinal adaptation. <i>Genomics</i> , 2019 , 111, 24-33	4.3	21
169	Gene expression profiling of the uterus with embryos cloned by somatic cell nuclear transfer on day 30 of pregnancy. <i>Animal Reproduction Science</i> , 2008 , 108, 79-91	2.1	20
168	Change in gene expression of mouse embryonic stem cells derived from parthenogenetic activation. <i>Human Reproduction</i> , 2009 , 24, 805-14	5.7	19

167	Metagenome Analysis of Protein Domain Collocation within Cellulase Genes of Goat Rumen Microbes. <i>Asian-Australasian Journal of Animal Sciences</i> , 2013 , 26, 1144-51	2.4	19
166	Cetaceans evolution: insights from the genome sequences of common minke whales. <i>BMC Genomics</i> , 2015 , 16, 13	4.5	18
165	Comprehensive identification of sexually dimorphic genes in diverse cattle tissues using RNA-seq. <i>BMC Genomics</i> , 2016 , 17, 81	4.5	18
164	Association of SLC6A4 5-HTTLPR and TRPV1 945G>C with functional dyspepsia in Korea. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2014 , 29, 1770-7	4	18
163	Investigation of de novo unique differentially expressed genes related to evolution in exercise response during domestication in Thoroughbred race horses. <i>PLoS ONE</i> , 2014 , 9, e91418	3.7	18
162	Gene expression profile of human peripheral blood mononuclear cells induced by Staphylococcus aureus lipoteichoic acid. <i>International Immunopharmacology</i> , 2012 , 13, 454-60	5.8	18
161	Peeling back the evolutionary layers of molecular mechanisms responsive to exercise-stress in the skeletal muscle of the racing horse. <i>DNA Research</i> , 2013 , 20, 287-98	4.5	18
160	Improved establishment of autologous stem cells derived from preantral follicle culture and oocyte parthenogenesis. <i>Stem Cells and Development</i> , 2008 , 17, 695-712	4.4	18
159	Cattle genome-wide analysis reveals genetic signatures in trypanotolerant NQama. <i>BMC Genomics</i> , 2017 , 18, 371	4.5	17
158	Molecular epidemiology of foot-and-mouth disease virus serotypes A and O with emphasis on Korean isolates: temporal and spatial dynamics. <i>Archives of Virology</i> , 2011 , 156, 817-26	2.6	17
157	Identification and characterization of the peroxiredoxin gene family in chickens. <i>Poultry Science</i> , 2005 , 84, 1432-8	3.9	17
156	Characterizing Milk Production Related Genes in Holstein Using RNA-seq. <i>Asian-Australasian Journal of Animal Sciences</i> , 2016 , 29, 343-51	2.4	17
155	Gene expression profiling of bovine mammary gland epithelial cells stimulated with lipoteichoic acid plus peptidoglycan from Staphylococcus aureus. <i>International Immunopharmacology</i> , 2014 , 21, 231-40	5.8	16
154	Analyses of porcine public SNPs in coding-gene regions by re-sequencing and phenotypic association studies. <i>Molecular Biology Reports</i> , 2011 , 38, 3805-20	2.8	16
153	Phylogenomics and molecular evolution of foot-and-mouth disease virus. <i>Molecules and Cells</i> , 2011 , 31, 413-21	3.5	16
152	Sequence and gene organization of 24 circles from the Cotesia plutellae bracovirus genome. <i>Archives of Virology</i> , 2009 , 154, 1313-27	2.6	16
151	Complete genome sequence of Bifidobacterium longum subsp. longum KACC 91563. <i>Journal of Bacteriology</i> , 2011 , 193, 5044	3.5	16
150	Deciphering signature of selection affecting beef quality traits in Angus cattle. <i>Genes and Genomics</i> , 2018 , 40, 63-75	2.1	16

149	Methanobrevibacter attenuation via probiotic intervention reduces flatulence in adult human: A non-randomised paired-design clinical trial of efficacy. <i>PLoS ONE</i> , 2017 , 12, e0184547	3.7	15
148	Establishment and evaluation of prediction model for multiple disease classification based on gut microbial data. <i>Scientific Reports</i> , 2019 , 9, 10189	4.9	15
147	Genome-wide Association Study of Integrated Meat Quality-related Traits of the Duroc Pig Breed. <i>Asian-Australasian Journal of Animal Sciences</i> , 2014 , 27, 303-9	2.4	15
146	Identification of BoLA-DRB3.2 alleles in Korean native cattle (Hanwoo) and Holstein populations using a next generation sequencer. <i>Animal Genetics</i> , 2012 , 43, 438-41	2.5	15
145	Testis-specific novel transcripts in chicken: in situ localization and expression pattern profiling during sexual development. <i>Biology of Reproduction</i> , 2008 , 79, 413-20	3.9	15
144	A set of stage-specific gene transcripts identified in EK stage X and HH stage 3 chick embryos. <i>BMC Developmental Biology</i> , 2007 , 7, 60	3.1	15
143	A set of testis-specific novel genes collected from a collection of Korean Native Chicken ESTs. <i>Animal Genetics</i> , 2005 , 36, 346-8	2.5	15
142	Accurate estimation of effective population size in the Korean dairy cattle based on linkage disequilibrium corrected by genomic relationship matrix. <i>Asian-Australasian Journal of Animal Sciences</i> , 2013 , 26, 1672-9	2.4	15
141	RNA-seq analysis of the kidneys of broiler chickens fed diets containing different concentrations of calcium. <i>Scientific Reports</i> , 2017 , 7, 11740	4.9	14
140	Microarray Analysis of Gene Expression in the Uterine Endometrium during the Implantation Period in Pigs. <i>Asian-Australasian Journal of Animal Sciences</i> , 2012 , 25, 1102-16	2.4	14
139	Accurate and Strict Identification of Probiotic Species Based on Coverage of Whole-Metagenome Shotgun Sequencing Data. <i>Frontiers in Microbiology</i> , 2019 , 10, 1683	5.7	13
138	Complete genome analysis of <i>Lactobacillus fermentum</i> SK152 from kimchi reveals genes associated with its antimicrobial activity. <i>FEMS Microbiology Letters</i> , 2017 , 364,	2.9	13
137	Analysis of Stage-Specific Gene Expression Profiles in the Uterine Endometrium during Pregnancy in Pigs. <i>PLoS ONE</i> , 2015 , 10, e0143436	3.7	13
136	Multiple Genes Related to Muscle Identified through a Joint Analysis of a Two-stage Genome-wide Association Study for Racing Performance of 1,156 Thoroughbreds. <i>Asian-Australasian Journal of Animal Sciences</i> , 2015 , 28, 771-81	2.4	13
135	Genome-wide association study of copy number variations associated with pulmonary function measures in Korea Associated Resource (KARE) cohorts. <i>Genomics</i> , 2011 , 97, 101-5	4.3	13
134	The Pig Genome Database (PiGenome): an integrated database for pig genome research. <i>Mammalian Genome</i> , 2009 , 20, 60-6	3.2	13
133	Genetic diversity at the major histocompatibility complex (B) and microsatellite loci in three commercial broiler pure lines. <i>Poultry Science</i> , 2002 , 81, 1609-17	3.9	13
132	The transcriptome of early chicken embryos reveals signaling pathways governing rapid asymmetric cellularization and lineage segregation. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	12

131	Characterization of genes for beef marbling based on applying gene coexpression network. <i>International Journal of Genomics</i> , 2014 , 2014, 708562	2.5	12
130	Identification of breed-specific DNA polymorphisms for a simple and unambiguous screening system in germline chimeric chickens. <i>Journal of Experimental Zoology</i> , 2007 , 307, 241-8		12
129	Genome-wide detection and characterization of positive selection in Korean Native Black Pig from Jeju Island. <i>BMC Genetics</i> , 2015 , 16, 3	2.6	11
128	Application of LogitBoost Classifier for Traceability Using SNP Chip Data. <i>PLoS ONE</i> , 2015 , 10, e0139685	3.7	11
127	Genome-wide Association Study of Chicken Plumage Pigmentation. <i>Asian-Australasian Journal of Animal Sciences</i> , 2013 , 26, 1523-8	2.4	11
126	Proteome analysis of chicken embryonic gonads: identification of major proteins from cultured gonadal primordial germ cells. <i>Molecular Reproduction and Development</i> , 2005 , 72, 521-9	2.6	11
125	Time-calibrated phylogenomics of the classical swine fever viruses: genome-wide bayesian coalescent approach. <i>PLoS ONE</i> , 2015 , 10, e0121578	3.7	11
124	Genetic variants and signatures of selective sweep of Hanwoo population (Korean native cattle). <i>BMB Reports</i> , 2013 , 46, 346-51	5.5	11
123	Genome-association analysis of Korean Holstein milk traits using genomic estimated breeding value. <i>Asian-Australasian Journal of Animal Sciences</i> , 2017 , 30, 309-319	2.4	11
122	Complete genome sequence of <i>Vibrio vulnificus</i> FORC_017 isolated from a patient with a hemorrhagic rash after consuming raw dotted gizzard shad. <i>Gut Pathogens</i> , 2016 , 8, 22	5.4	10
121	Identification and gene expression profiling of the Pum1 and Pum2 members of the Pumilio family in the chicken. <i>Molecular Reproduction and Development</i> , 2008 , 75, 184-90	2.6	10
120	Developmental Dynamic Analysis of the Excreted Microbiome of Chickens Using Next-Generation Sequencing. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2015 , 25, 262-8	0.9	9
119	Genomic Prediction Accuracy Using Haplotypes Defined by Size and Hierarchical Clustering Based on Linkage Disequilibrium. <i>Frontiers in Genetics</i> , 2020 , 11, 134	4.5	9
118	Complete genome sequences of porcine reproductive and respiratory syndrome viruses: perspectives on their temporal and spatial dynamics. <i>Molecular Biology Reports</i> , 2013 , 40, 6843	2.8	9
117	Comprehensive Identification of Sexual Dimorphism-Associated Differentially Expressed Genes in Two-Way Factorial Designed RNA-Seq Data on Japanese Quail (<i>Coturnix coturnix japonica</i>). <i>PLoS ONE</i> , 2015 , 10, e0139324	3.7	9
116	ASePCR: alternative splicing electronic RT-PCR in multiple tissues and organs. <i>Nucleic Acids Research</i> , 2005 , 33, W681-5	20.1	9
115	Genomic sequence analysis of a potential QTL region for fat trait on pig chromosome 6. <i>Genomics</i> , 2006 , 87, 218-24	4.3	9
114	ChickGCE: a novel germ cell EST database for studying the early developmental stage in chickens. <i>Genomics</i> , 2006 , 88, 252-7	4.3	9

113	Effects of road transportation on metabolic and immunological responses in Holstein heifers. <i>Animal Science Journal</i> , 2017 , 88, 140-148	1.8	8
112	The first whole transcriptomic exploration of pre-oviposited early chicken embryos using single and bulked embryonic RNA-sequencing. <i>GigaScience</i> , 2018 , 7, 1-9	7.6	8
111	Estimating effective population size of thoroughbred horses using linkage disequilibrium and theta (4N _e) value. <i>Livestock Science</i> , 2014 , 168, 32-37	1.7	8
110	Powerful usage of phylogenetically diverse <i>Staphylococcus aureus</i> control strains for detecting multidrug resistance genes in transcriptomics studies. <i>Molecules and Cells</i> , 2010 , 30, 71-6	3.5	8
109	MPSS profiling of embryonic gonad and primordial germ cells in chicken. <i>Physiological Genomics</i> , 2007 , 29, 253-9	3.6	8
108	Comparative genomic analysis of <i>Staphylococcus aureus</i> FORC_001 and <i>S. aureus</i> MRSA252 reveals the characteristics of antibiotic resistance and virulence factors for human infection. <i>Journal of Microbiology and Biotechnology</i> , 2015 , 25, 98-108	3.3	8
107	Comparative Analysis of the Complete Genome of <i>Lactobacillus plantarum</i> GB-LP2 and Potential Candidate Genes for Host Immune System Enhancement. <i>Journal of Microbiology and Biotechnology</i> , 2016 , 26, 684-92	3.3	8
106	Analysis of copy number variation in 8,842 Korean individuals reveals 39 genes associated with hepatic biomarkers AST and ALT. <i>BMB Reports</i> , 2010 , 43, 547-53	5.5	8
105	Zygotic gene activation in the chicken occurs in two waves, the first involving only maternally derived genes. <i>ELife</i> , 2018 , 7,	8.9	8
104	Bovine Genome-wide Association Study for Genetic Elements to Resist the Infection of Foot-and-mouth Disease in the Field. <i>Asian-Australasian Journal of Animal Sciences</i> , 2015 , 28, 166-70	2.4	7
103	Direct typing and molecular evolutionary analysis of field samples of foot-and-mouth disease virus collected in Viet Nam between 2006 and 2007. <i>Veterinary Microbiology</i> , 2011 , 147, 244-52	3.3	7
102	Native Pig and Chicken Breed Database: NPCDB. <i>Asian-Australasian Journal of Animal Sciences</i> , 2014 , 27, 1394-8	2.4	7
101	Comprehensive genome and transcriptome analyses reveal genetic relationship, selection signature, and transcriptome landscape of small-sized Korean native Jeju horse. <i>Scientific Reports</i> , 2019 , 9, 16672	4.9	7
100	Transcriptional and translational dynamics during maternal-to-zygotic transition in early chicken development. <i>FASEB Journal</i> , 2018 , 32, 2004-2011	0.9	7
99	Complete Genome of KY Using Flongle Provides Insight Into the Genetic Background of Optimal Adaption to Vaginal Ecniche. <i>Frontiers in Microbiology</i> , 2020 , 11, 1048	5.7	6
98	Uncovering genomic features and maternal origin of korean native chicken by whole genome sequencing. <i>PLoS ONE</i> , 2014 , 9, e114763	3.7	6
97	Genome-wide analysis of copy number variations reveals that aging processes influence body fat distribution in Korea Associated Resource (KARE) cohorts. <i>Human Genetics</i> , 2012 , 131, 1795-804	6.3	6
96	Transcript profiling of expressed sequence tags from intramuscular fat, longissimus dorsi muscle and liver in Korean cattle (Hanwoo). <i>BMB Reports</i> , 2010 , 43, 115-21	5.5	6

95	Horizontal gene transfer of Chlamydia: Novel insights from tree reconciliation. <i>PLoS ONE</i> , 2018 , 13, e0195139	5.1	5
94	Genotype-environment interactions for quantitative traits in Korea Associated Resource (KARE) cohorts. <i>BMC Genetics</i> , 2014 , 15, 18	2.6	5
93	The Genetic Origin of Short Tail in Endangered Korean Dog, DongGyeonggi. <i>Scientific Reports</i> , 2017 , 7, 10048	4.9	5
92	Genome-wide DNA Methylation Profiles of Small Intestine and Liver in Fast-growing and Slow-growing Weaning Piglets. <i>Asian-Australasian Journal of Animal Sciences</i> , 2014 , 27, 1532-9	2.4	5
91	Differential Evolution between Monotocous and Polytocous Species. <i>Asian-Australasian Journal of Animal Sciences</i> , 2014 , 27, 464-70	2.4	5
90	Tracing the genetic history of porcine reproductive and respiratory syndrome viruses derived from the complete ORF 5-7 sequences: a Bayesian coalescent approach. <i>Archives of Virology</i> , 2012 , 157, 2143-51	2.6	5
89	Principal components analysis applied to genetic evaluation of racing performance of Thoroughbred race horses in Korea. <i>Livestock Science</i> , 2011 , 135, 293-299	1.7	5
88	A genome-wide identification of genes potentially associated with host specificity of Brucella species. <i>Journal of Microbiology</i> , 2011 , 49, 768-75	3	5
87	Genetic Variation in Susceptibility to Marek's Disease in a Commercial Broiler Population. <i>Avian Diseases</i> , 2001 , 45, 400	1.6	5
86	Detecting Positive Selection of Korean Native Goat Populations Using Next-Generation Sequencing. <i>Molecules and Cells</i> , 2016 , 39, 862-868	3.5	5
85	Comparative Genomic Analysis of GB-LP1 Isolated from Traditional Korean Fermented Food. <i>Journal of Microbiology and Biotechnology</i> , 2017 , 27, 1419-1427	3.3	5
84	A replication study of genome-wide CNV association for hepatic biomarkers identifies nine genes associated with liver function. <i>BMB Reports</i> , 2011 , 44, 578-83	5.5	5
83	Deciphering the evolutionary signatures of pinnipeds using novel genome sequences: The first genomes of Phoca largha, Callorhinus ursinus, and Eumetopias jubatus. <i>Scientific Reports</i> , 2018 , 8, 16877	4.9	5
82	Microbial community and functions associated with digestion of algal polysaccharides in the visceral tract of <i>Haliotis discus hannai</i> : Insights from metagenome and metatranscriptome analysis. <i>PLoS ONE</i> , 2018 , 13, e0205594	3.7	5
81	Is Gram-Positive? A Case Study of. <i>Microorganisms</i> , 2020 , 8,	4.9	4
80	Multivariate genome-wide association studies on tenderness of Berkshire and Duroc pig breeds. <i>Genes and Genomics</i> , 2018 , 40, 701-705	2.1	4
79	Complete genome of FORC014 isolated from the toothfish. <i>Gut Pathogens</i> , 2016 , 8, 59	5.4	4
78	Comparative genomic analysis reveals genetic features related to the virulence of FORC_013. <i>Gut Pathogens</i> , 2017 , 9, 29	5.4	4

77	Complete genome sequence of <i>Bacillus cereus</i> FORC_005, a food-borne pathogen from the soy sauce braised fish-cake with quail-egg. <i>Standards in Genomic Sciences</i> , 2015 , 10, 97		4
76	Development of an in silico coding gene SNP map in pigs. <i>Animal Genetics</i> , 2008 , 39, 446-50	2.5	4
75	Artificial selection increased body weight but induced increase of runs of homozygosity in Hanwoo cattle. <i>PLoS ONE</i> , 2018 , 13, e0193701	3.7	4
74	De Novo assembly and comparative analysis of the <i>Enterococcus faecalis</i> genome (KACC 91532) from a Korean Neonate. <i>Journal of Microbiology and Biotechnology</i> , 2013 , 23, 966-73	3.3	4
73	The Prediction of the Expected Current Selection Coefficient of Single Nucleotide Polymorphism Associated with Holstein Milk Yield, Fat and Protein Contents. <i>Asian-Australasian Journal of Animal Sciences</i> , 2016 , 29, 36-42	2.4	4
72	Copy number deletion has little impact on gene expression levels in racehorses. <i>Asian-Australasian Journal of Animal Sciences</i> , 2014 , 27, 1345-54	2.4	4
71	The Usage of an SNP-SNP Relationship Matrix for Best Linear Unbiased Prediction (BLUP) Analysis Using a Community-Based Cohort Study. <i>Genomics and Informatics</i> , 2014 , 12, 254-60	1.9	4
70	Whole genome sequencing of Gyeongbuk Araucana, a newly developed blue-egg laying chicken breed, reveals its origin and genetic characteristics. <i>Scientific Reports</i> , 2016 , 6, 26484	4.9	4
69	Comparative genome analysis of <i>Lactobacillus plantarum</i> GB-LP3 provides candidates of survival-related genetic factors. <i>Infection, Genetics and Evolution</i> , 2017 , 53, 218-226	4.5	3
68	Whole genome sequencing reveals the impact of recent artificial selection on red sea bream reared in fish farms. <i>Scientific Reports</i> , 2019 , 9, 6487	4.9	3
67	De novo emergence and potential function of human-specific tandem repeats in brain-related loci. <i>Human Genetics</i> , 2019 , 138, 661-672	6.3	3
66	A novel genetic variant database for Korean native cattle (Hanwoo): HanwooGDB. <i>Genes and Genomics</i> , 2015 , 37, 15-22	2.1	3
65	Comparative genomic analysis of mitochondrial protein-coding genes in Veneroida clams: Analysis of superfamily-specific genomic and evolutionary features. <i>Marine Genomics</i> , 2015 , 24 Pt 3, 329-34	1.9	3
64	Whole-Transcriptome Sequencing-Based Analysis of and Its Interacting Genes during Germ Cells Specification and Zygotic Genome Activation in Chickens. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	3
63	Time-calibrated phylogenomics of the porcine epidemic diarrhea virus: genome-wide insights into the spatio-temporal dynamics. <i>Genes and Genomics</i> , 2018 , 40, 825-834	2.1	3
62	Evolutionary constraints over microsatellite abundance in larger mammals as a potential mechanism against carcinogenic burden. <i>Scientific Reports</i> , 2016 , 6, 25246	4.9	3
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