

Heebal Kim

List of Publications by Year in Descending Order

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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	Positive Effect of <i>Lactobacillus acidophilus</i> EG004 on Cognitive Ability of Healthy Mice by Fecal Microbiome Analysis Using Full-Length 16S-23S rRNA Metagenome Sequencing.. <i>Microbiology Spectrum</i> , 2022 , e0181521	8.9	0
219	Mitochondrial incompatibility as a hidden driver behind the genome ancestry of African admixed cattle.. <i>BMC Biology</i> , 2022 , 20, 20	7.3	1
218	Chicken blastoderms and primordial germ cells possess a higher expression of DNA repair genes and lower expression of apoptosis genes to preserve their genome stability.. <i>Scientific Reports</i> , 2022 , 12, 49	4.9	3
217	Immunogenic Epitope-Based Vaccine Prediction from Surface Glycoprotein of MERS-CoV by Deploying Immunoinformatics Approach.. <i>International Journal of Peptide Research and Therapeutics</i> , 2022 , 28, 77	2.1	1
216	Microbial Identification Using rRNA Operon Region: Database and Tool for Metataxonomics with Long-Read Sequence.. <i>Microbiology Spectrum</i> , 2022 , e0201721	8.9	0
215	Shared genetic etiology and antagonistic relationship of plasma renin activity and systolic blood pressure in a Korean cohorts.. <i>Genomics</i> , 2022 , 110334	4.3	
214	Selection and evaluation of bi-allelic autosomal SNP markers for paternity testing in Koreans. <i>International Journal of Legal Medicine</i> , 2021 , 135, 1369-1374	3.1	1
213	Genotyping-by-Sequencing of the regional Pacific abalone (<i>Haliotis discus</i>) genomes reveals population structures and patterns of gene flow. <i>PLoS ONE</i> , 2021 , 16, e0247815	3.7	2
212	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746	46.4	161
211	Population differentiated copy number variation of <i>Bos taurus</i> , <i>Bos indicus</i> and their African hybrids. <i>BMC Genomics</i> , 2021 , 22, 531	4.5	2
210	Phylogenetic and evolutionary analysis of foot-and-mouth disease virus A/ASIA/Sea-97 lineage. <i>Virus Genes</i> , 2021 , 57, 443-447	2.3	
209	The transcriptomic blueprint of molt in rooster using various tissues from Ginkkoridak (Korean long-tailed chicken). <i>BMC Genomics</i> , 2021 , 22, 594	4.5	0
208	Taxonomic profiling of skin microbiome and correlation with clinical skin parameters in healthy Koreans. <i>Scientific Reports</i> , 2021 , 11, 16269	4.9	3
207	Complete Genome Sequence of the Newly Developed Strain With Improved Thermal Adaptability. <i>Frontiers in Microbiology</i> , 2021 , 12, 697351	5.7	1
206	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
205	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
204	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

203	Is Gram-Positive? A Case Study of. <i>Microorganisms</i> , 2020 , 8,	4.9	4
202	Changes in Cell Membrane Fatty Acid Composition of in Response to Gradually Increasing Heat Temperature. <i>Journal of Microbiology and Biotechnology</i> , 2020 , 30, 739-748	3.3	1
201	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
200	Complete Genomic Analysis of Heat-Resistant Strain Developed by Two-Step Adaptation Laboratory Evolution Method. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 828	5.8	3
199	Synergistic Antibacterial Effects of Probiotic Lactic Acid Bacteria with Curcuma longa Rhizome Extract as Synbiotic against Cutibacterium acnes. <i>Applied Sciences (Switzerland)</i> , 2020 , 10, 8955	2.6	2
198	Enhanced Symbiotic Characteristics in Bacterial Genomes with the Disruption of rRNA Operon. <i>Biology</i> , 2020 , 9,	4.9	3
197	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
196	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
195	Bayesian evolutionary hypernetworks for interpretable learning from high-dimensional data. <i>Applied Soft Computing Journal</i> , 2019 , 81, 105477	7.5	2
194	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
193	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
192	Sensitivity and specificity evaluation of multiple neurodegenerative proteins for Creutzfeldt-Jakob disease diagnosis using a deep-learning approach. <i>Prion</i> , 2019 , 13, 141-150	2.3	1
191	Identification of Copy Number Variation in Domestic Chicken Using Whole-Genome Sequencing Reveals Evidence of Selection in the Genome. <i>Animals</i> , 2019 , 9,	3.1	3
190	Expression and Purification of Extracellular Solute-Binding Protein (ESBP) in , the Extracellular Protein Derived from KACC 91563. <i>Food Science of Animal Resources</i> , 2019 , 39, 601-609	3.2	3
189	Multi-tissue observation of the long non-coding RNA effects on sexually biased gene expression in cattle. <i>Asian-Australasian Journal of Animal Sciences</i> , 2019 , 32, 1044-1051	2.4	1
188	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
187	THERPA v2: an update of a small molecule database related to prion protein regulation and prion disease progression. <i>Prion</i> , 2019 , 13, 197-198	2.3	1
186	Comparative genomic analysis of Lactobacillus mucosae LM1 identifies potential niche-specific genes and pathways for gastrointestinal adaptation. <i>Genomics</i> , 2019 , 111, 24-33	4.3	21

185	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
184	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
183	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
182	THERPA: A small molecule database related to prion protein regulation and prion diseases progression. <i>Prion</i> , 2018 , 12, 138-142	2.3	2
181	Selective pressure on the protein-coding genes of the pufferfish is correlated with phenotypic traits. <i>Marine Genomics</i> , 2018 , 37, 182-186	1.9	1
180	Coelacanth-specific adaptive genes give insights into primitive evolution for water-to-land transition of tetrapods. <i>Marine Genomics</i> , 2018 , 38, 89-95	1.9	1
179	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
178	Comparative genomic analysis of GB-LP4 and identification of evolutionarily divergent genes in high-osmolarity environment. <i>Genes and Genomics</i> , 2018 , 40, 217-223	2.1	1
177	Horizontal gene transfer of Chlamydia: Novel insights from tree reconciliation. <i>PLoS ONE</i> , 2018 , 13, e0195139	3.7	5
176	Potential Survival and Pathogenesis of a Novel Strain, FORC_022, Isolated From a Soy Sauce Marinated Crab by Genome and Transcriptome Analyses. <i>Frontiers in Microbiology</i> , 2018 , 9, 1504	5.7	3
175	Genome sequencing and protein domain annotations of Korean Hanwoo cattle identify Hanwoo-specific immunity-related and other novel genes. <i>BMC Genetics</i> , 2018 , 19, 37	2.6	0
174	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
173	Analysis of cross-population differentiation between Thoroughbred and Jeju horses. <i>Asian-Australasian Journal of Animal Sciences</i> , 2018 , 31, 1110-1118	2.4	3
172	Deciphering signature of selection affecting beef quality traits in Angus cattle. <i>Genes and Genomics</i> , 2018 , 40, 63-75	2.1	16
171	Transcriptional and translational dynamics during maternal-to-zygotic transition in early chicken development. <i>FASEB Journal</i> , 2018 , 32, 2004-2011	0.9	7
170	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
169	Author Correction: Rhizosphere microbiome structure alters to enable wilt resistance in tomato. <i>Nature Biotechnology</i> , 2018 , 36, 1117	44.5	49
168	Deciphering the evolutionary signatures of pinnipeds using novel genome sequences: The first genomes of <i>Phoca largha</i> , <i>Callorhinus ursinus</i> , and <i>Eumetopias jubatus</i> . <i>Scientific Reports</i> , 2018 , 8, 16877	4.9	5

167	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
166	Rhizosphere microbiome structure alters to enable wilt resistance in tomato. <i>Nature Biotechnology</i> , 2018 ,	44.5	244
165	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
164	Origin and spread of Thoroughbred racehorses inferred from complete mitochondrial genome sequences: Phylogenomic and Bayesian coalescent perspectives. <i>PLoS ONE</i> , 2018 , 13, e0203917	3.7	3
163	Effects of road transportation on metabolic and immunological responses in Holstein heifers. <i>Animal Science Journal</i> , 2017 , 88, 140-148	1.8	8
162	The genome landscape of indigenous African cattle. <i>Genome Biology</i> , 2017 , 18, 34	18.3	123
161	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
160	Complete mitochondrial genome sequences of Korean native horse from Jeju Island: uncovering the spatio-temporal dynamics. <i>Molecular Biology Reports</i> , 2017 , 44, 233-242	2.8	1
159	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
158	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
157	Identifying candidate positive selection genes in Korean imported pig breeds. <i>Genes and Genomics</i> , 2017 , 39, 557-565	2.1	2
156	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
155	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
154	Exploring evidence of positive selection signatures in cattle breeds selected for different traits. <i>Mammalian Genome</i> , 2017 , 28, 528-541	3.2	30
153	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
152	The Genetic Origin of Short Tail in Endangered Korean Dog, DongGyeonggi. <i>Scientific Reports</i> , 2017 , 7, 10048	4.9	5
151	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
150	Tracing the spatio-temporal dynamics of endangered fin whales (<i>Balaenoptera physalus</i>) within baleen whale (Mysticeti) lineages: a mitogenomic perspective. <i>Genetica</i> , 2017 , 145, 603-612	1.5	1

149	Cattle genome-wide analysis reveals genetic signatures in trypanotolerant NQama. <i>BMC Genomics</i> , 2017 , 18, 371	4.5	17
148	Comparative genomic analysis reveals genetic features related to the virulence of FORC_013. <i>Gut Pathogens</i> , 2017 , 9, 29	5.4	4
147	Genomic Insights and Its Comparative Analysis with Reveals the Potential Virulence Determinants and Further Pathogenicity for Foodborne Outbreaks. <i>Journal of Microbiology and Biotechnology</i> , 2017 , 27, 262-270	3.3	3
146	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
145	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
144	Tracing the breeding farm of domesticated pig using feature selection (<i>Sus scrofa</i>). <i>Asian-Australasian Journal of Animal Sciences</i> , 2017 , 30, 1540-1549	2.4	3
143	Complete genome sequence and SNPs of <i>Raja pulchra</i> (Rajiformes, Rajidae) mitochondria. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 2975-7	1.3	0
142	RNA-seq analysis for detecting quantitative trait-associated genes. <i>Scientific Reports</i> , 2016 , 6, 24375	4.9	28
141	Gut microbiota Modulated by Probiotics and <i>Garcinia cambogia</i> Extract Correlate with Weight Gain and Adipocyte Sizes in High Fat-Fed Mice. <i>Scientific Reports</i> , 2016 , 6, 33566	4.9	32
140	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
139	Complete genome of FORC014 isolated from the toothfish. <i>Gut Pathogens</i> , 2016 , 8, 59	5.4	4
138	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
137	Comprehensive identification of sexually dimorphic genes in diverse cattle tissues using RNA-seq. <i>BMC Genomics</i> , 2016 , 17, 81	4.5	18
136	HGTtree: database of horizontally transferred genes determined by tree reconciliation. <i>Nucleic Acids Research</i> , 2016 , 44, D610-9	20.1	24
135	Genomic Characteristics of Genetic Creutzfeldt-Jakob Disease Patients with V180I Mutation and Associations with Other Neurodegenerative Disorders. <i>PLoS ONE</i> , 2016 , 11, e0157540	3.7	2
134	Detecting Positive Selection of Korean Native Goat Populations Using Next-Generation Sequencing. <i>Molecules and Cells</i> , 2016 , 39, 862-868	3.5	5
133	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
132	Genome Sequence of FORC_021, a Food-Borne Pathogen Isolated from a Knife at a Sashimi Restaurant. <i>Journal of Microbiology and Biotechnology</i> , 2016 , 26, 2030-2035	3.3	3

131	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
130	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
129	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
128	Status of dosage compensation of X chromosome in bovine genome. <i>Genetica</i> , 2016 , 144, 435-44	1.5	3
127	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
126	Complete genome sequence of <i>Vibrio parahaemolyticus</i> strain FORC_008, a foodborne pathogen from a flounder fish in South Korea. <i>Pathogens and Disease</i> , 2016 , 74,	4.2	3
125	Complete genome sequence of <i>Vibrio parahaemolyticus</i> FORC_023 isolated from raw fish storage water. <i>Pathogens and Disease</i> , 2016 , 74, ftw032	4.2	1
124	A novel genetic variant database for Korean native cattle (Hanwoo): HanwooGDB. <i>Genes and Genomics</i> , 2015 , 37, 15-22	2.1	3
123	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
122	Cetaceans evolution: insights from the genome sequences of common minke whales. <i>BMC Genomics</i> , 2015 , 16, 13	4.5	18
121	A genome-wide scan for signatures of directional selection in domesticated pigs. <i>BMC Genomics</i> , 2015 , 16, 130	4.5	47
120	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
119	Genome-wide SNP identification and QTL mapping for black rot resistance in cabbage. <i>BMC Plant Biology</i> , 2015 , 15, 32	5.3	45
118	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
117	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
116	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
115	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
114	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

113	Application of LogitBoost Classifier for Traceability Using SNP Chip Data. <i>PLoS ONE</i> , 2015 , 10, e0139685	3.7	11
112	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
111	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
110	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
109	Time-calibrated phylogenomics of the classical swine fever viruses: genome-wide bayesian coalescent approach. <i>PLoS ONE</i> , 2015 , 10, e0121578	3.7	11
108	Exploring the genetic signature of body size in Yucatan miniature pig. <i>PLoS ONE</i> , 2015 , 10, e0121732	3.7	25
107	Comparative genomic analysis of Staphylococcus aureus FORC_001 and S. aureus 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
106	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
105	Prediction of Genes Related to Positive Selection Using Whole-Genome Resequencing in Three Commercial Pig Breeds. <i>Genomics and Informatics</i> , 2015 , 13, 137-45	1.9	1
104	Heritability Estimated Using 50K SNPs Indicates Missing Heritability Problem in Holstein Breeding. <i>Genomics and Informatics</i> , 2015 , 13, 146-51	1.9	1
103	Genome Wide Association Studies Using Multiple-lactation Breeding Value in Holsteins. <i>Asian-Australasian Journal of Animal Sciences</i> , 2015 , 28, 328-33	2.4	
102	Genotype-environment interactions for quantitative traits in Korea Associated Resource (KARE) cohorts. <i>BMC Genetics</i> , 2014 , 15, 18	2.6	5
101	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
100	Estimating effective population size of thoroughbred horses using linkage disequilibrium and theta (4 N _e) value. <i>Livestock Science</i> , 2014 , 168, 32-37	1.7	8
99	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
98	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
97	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
96	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

95	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
94	Uncovering genomic features and maternal origin of Korean native chicken by whole genome sequencing. <i>PLoS ONE</i> , 2014 , 9, e114763	3.7	6
93	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
92	Differential Evolution between Monotocous and Polytocous Species. <i>Asian-Australasian Journal of Animal Sciences</i> , 2014 , 27, 464-70	2.4	5
91	Characterization of genes for beef marbling based on applying gene coexpression network. <i>International Journal of Genomics</i> , 2014 , 2014, 708562	2.5	12
90	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014 , 346, 1311-20	33.3	628
89	Deciphering the genetic blueprint behind Holstein milk proteins and production. <i>Genome Biology and Evolution</i> , 2014 , 6, 1366-74	3.9	30
88	Thoroughbred Horse Single Nucleotide Polymorphism and Expression Database: HSDB. <i>Asian-Australasian Journal of Animal Sciences</i> , 2014 , 27, 1236-43	2.4	2
87	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
86	Native Pig and Chicken Breed Database: NPCDB. <i>Asian-Australasian Journal of Animal Sciences</i> , 2014 , 27, 1394-8	2.4	7
85	VCS: Tool for Visualizing Copy Number Variation and Single Nucleotide Polymorphism. <i>Asian-Australasian Journal of Animal Sciences</i> , 2014 , 27, 1691-4	2.4	1
84	Genomic selection for adjacent genetic markers of Yorkshire pigs using regularized regression approaches. <i>Asian-Australasian Journal of Animal Sciences</i> , 2014 , 27, 1678-83	2.4	1
83	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
82	Semantic Modeling for SNPs Associated with Ethnic Disparities in HapMap Samples. <i>Genomics and Informatics</i> , 2014 , 12, 35-41	1.9	
81	Semantic networks for genome-wide CNV associated with AST and ALT in Korean cohorts. <i>Molecular and Cellular Toxicology</i> , 2013 , 9, 103-111	1.6	1
80	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
79	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
78	Ubiquitous polygenicity of human complex traits: genome-wide analysis of 49 traits in Koreans. <i>PLoS Genetics</i> , 2013 , 9, e1003355	6	50

77	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
76	Identification of differentially evolved genes: an alternative approach to detection of accelerated molecular evolution from genome-wide comparative data. <i>Evolutionary Bioinformatics</i> , 2013 , 9, 285-99	1.9	
75	Genome-wide Association Study of Chicken Plumage Pigmentation. <i>Asian-Australasian Journal of Animal Sciences</i> , 2013 , 26, 1523-8	2.4	11
74	Primed pluripotent cell lines derived from various embryonic origins and somatic cells in pig. <i>PLoS ONE</i> , 2013 , 8, e52481	3.7	57
73	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
72	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
71	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
70	Acceleration of X-chromosome gene order evolution in the cattle lineage. <i>BMB Reports</i> , 2013 , 46, 310-5	5.5	1
69	Genetic variants and signatures of selective sweep of Hanwoo population (Korean native cattle). <i>BMB Reports</i> , 2013 , 46, 346-51	5.5	11
68	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
67	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
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