

A Fast and Flexible Statistical Model for Large-Scale Population Applications to Inferring Missing Genotypes and Haplotypes

American Journal of Human Genetics

78, 629-644

DOI: [10.1086/502802](https://doi.org/10.1086/502802)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Multilocus Association Mapping Using Variable-Length Markov Chains. American Journal of Human Genetics, 2006, 78, 903-913.	2.6	119
2	A worldwide survey of haplotype variation and linkage disequilibrium in the human genome. Nature Genetics, 2006, 38, 1251-1260.	9.4	474
3	A tutorial on statistical methods for population association studies. Nature Reviews Genetics, 2006, 7, 781-791.	7.7	1,120
4	Modern computational approaches for analysing molecular genetic variation data. Nature Reviews Genetics, 2006, 7, 759-770.	7.7	172
5	Analytic methods for colorectal cancer. Current Colorectal Cancer Reports, 2006, 2, 206-210.	1.0	0
6	Whole genome association mapping by incompatibilities and local perfect phylogenies. BMC Bioinformatics, 2006, 7, 454.	1.2	41
7	HaploRec: efficient and accurate large-scale reconstruction of haplotypes. BMC Bioinformatics, 2006, 7, 542.	1.2	42
8	Testing Untyped Alleles (TUNA)â€™ applications to genome-wide association studies. Genetic Epidemiology, 2006, 30, 718-727.	0.6	112
9	Parkinson's disease due to the R1441G mutation in Dardarin: A founder effect in the basques. Movement Disorders, 2006, 21, 1954-1959.	2.2	84
10	EFFICIENT COMPUTATION OF MINIMUM RECOMBINATION WITH GENOTYPES (NOT HAPLOTYPES). , 2006, , .		3
11	A Map of Recent Positive Selection in the Human Genome. PLoS Biology, 2006, 4, e72.	2.6	2,329
12	Polymorphisms in the Gene for Lymphotoxinâ€™± Predispose to Chronic Chagas Cardiomyopathy. Journal of Infectious Diseases, 2007, 196, 1836-1843.	1.9	36
13	Molecular Phylogenetics of Candida albicans. Eukaryotic Cell, 2007, 6, 1041-1052.	3.4	285
14	EFFICIENT COMPUTATION OF MINIMUM RECOMBINATION WITH GENOTYPES (NOT HAPLOTYPES). Journal of Bioinformatics and Computational Biology, 2007, 05, 181-200.	0.3	2
15	Imputation-Based Analysis of Association Studies: Candidate Regions and Quantitative Traits. PLoS Genetics, 2007, 3, e114.	1.5	460
16	Computational identification of candidate loci for recessively inherited mutation using high-throughput SNP arrays. Bioinformatics, 2007, 23, 1952-1961.	1.8	2
17	The RANTES -28 g polymorphism is associated with primary sclerosing cholangitis. Gut, 2007, 56, 891-892.	6.1	4
18	Inferring missing genotypes in large SNP panels using fast nearest-neighbor searches over sliding windows. Bioinformatics, 2007, 23, i401-i407.	1.8	77

#	ARTICLE	IF	CITATIONS
19	Error detection in SNP data by considering the likelihood of recombinational history implied by three-site combinations. <i>Bioinformatics</i> , 2007, 23, 1807-1814.	1.8	11
20	Bayesian association of haplotypes and non-genetic factors to regulatory and phenotypic variation in human populations. <i>Bioinformatics</i> , 2007, 23, i212-i221.	1.8	4
21	Algorithms to Distinguish the Role of Gene-Conversion from Single-Crossover Recombination in the Derivation of SNP Sequences in Populations. <i>Journal of Computational Biology</i> , 2007, 14, 1273-1286.	0.8	14
22	A variant of mitochondrial protein LOC387715/ARMS2, not HTRA1, is strongly associated with age-related macular degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16227-16232.	3.3	398
23	Pattern-recognition techniques with haplotype analysis in pharmacogenomics. <i>Pharmacogenomics</i> , 2007, 8, 75-83.	0.6	38
24	Associations Between Sperm Competition and Natural Variation in Male Reproductive Genes on the Third Chromosome of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2007, 176, 1245-1260.	1.2	100
25	An insertion deletion polymorphism in the Interferon Regulatory Factor 5 (IRF5) gene confers risk of inflammatory bowel diseases. <i>Human Molecular Genetics</i> , 2007, 16, 3008-3016.	1.4	163
26	Three lectures on case control genetic association analysis. <i>Briefings in Bioinformatics</i> , 2007, 9, 1-13.	3.2	35
27	Variants in the Plasmacytoma Variant Translocation Gene (<i>PVT1</i>) Are Associated With End-Stage Renal Disease Attributed to Type 1 Diabetes. <i>Diabetes</i> , 2007, 56, 3027-3032.	0.3	89
28	A Bayesian Multilocus Association Method: Allowing for Higher-Order Interaction in Association Studies. <i>Genetics</i> , 2007, 176, 1197-1208.	1.2	12
29	Joint study of genetic regulators for expression traits related to breast cancer. <i>BMC Proceedings</i> , 2007, 1, S10.	1.8	3
30	Multilocus analysis of GAW15 NARAC chromosome 18 case-control data. <i>BMC Proceedings</i> , 2007, 1, S11.	1.8	2
31	Constructing gene association networks for rheumatoid arthritis using the backward genotype-trait association (BGTA) algorithm. <i>BMC Proceedings</i> , 2007, 1, S13.	1.8	13
33	Population-Based Case-Control Association Studies. <i>Current Protocols in Human Genetics</i> , 2007, 52, Unit 1.17.	3.5	6
34	Family-Based Association Tests for Genomewide Association Scans. <i>American Journal of Human Genetics</i> , 2007, 81, 913-926.	2.6	383
35	Rapid and Accurate Haplotype Phasing and Missing-Data Inference for Whole-Genome Association Studies By Use of Localized Haplotype Clustering. <i>American Journal of Human Genetics</i> , 2007, 81, 1084-1097.	2.6	2,845
36	Algorithms in Bioinformatics. <i>Lecture Notes in Computer Science</i> , 2007, , .	1.0	1
37	CYP1B1 Mutation Profile of Iranian Primary Congenital Glaucoma Patients and Associated Haplotypes. <i>Journal of Molecular Diagnostics</i> , 2007, 9, 382-393.	1.2	65

#	ARTICLE	IF	CITATIONS
38	HMMoCâ€™a compiler for hidden Markov models. <i>Bioinformatics</i> , 2007, 23, 2485-2487.	1.8	28
39	A Practical Genome Scan for Population-Specific Strong Selective Sweeps That Have Reached Fixation. <i>PLoS ONE</i> , 2007, 2, e286.	1.1	378
40	Cladistic analysis of genotype data-application to GAW15 Problem 3. <i>BMC Proceedings</i> , 2007, 1, S125.	1.8	2
41	Association mapping through heuristic evolutionary history reconstruction-application to GAW15 Problem 3. <i>BMC Proceedings</i> , 2007, 1, S131.	1.8	2
42	Comparison of haplotyping methods using families and unrelated individuals on simulated rheumatoid arthritis data. <i>BMC Proceedings</i> , 2007, 1, S55.	1.8	11
43	A Resampling-Based Approach to Multiple Testing with Uncertainty in Phase. <i>International Journal of Biostatistics</i> , 2007, 3, Article 2.	0.4	1
44	Understanding the accuracy of statistical haplotype inference with sequence data of known phase. <i>Genetic Epidemiology</i> , 2007, 31, 659-671.	0.6	64
45	Haplotype uncertainty in association studies. <i>Genetic Epidemiology</i> , 2007, 31, 348-357.	0.6	13
46	Efficient multilocus association testing for whole genome association studies using localized haplotype clustering. <i>Genetic Epidemiology</i> , 2007, 31, 365-375.	0.6	151
47	Sequential haplotype scan methods for association analysis. <i>Genetic Epidemiology</i> , 2007, 31, 553-564.	0.6	26
48	A novel method to express SNP-based genetic heterogeneity, \hat{f} , and its use to measure linkage disequilibrium for multiple SNPs, D_g , and to estimate absolute maximum of haplotype frequency. <i>Genetic Epidemiology</i> , 2007, 31, 709-726.	0.6	1
49	Haplotype inference using a Bayesian Hidden Markov model. <i>Genetic Epidemiology</i> , 2007, 31, 937-948.	0.6	25
51	Convergent adaptation of human lactase persistence in Africa and Europe. <i>Nature Genetics</i> , 2007, 39, 31-40.	9.4	1,375
52	A new multipoint method for genome-wide association studies by imputation of genotypes. <i>Nature Genetics</i> , 2007, 39, 906-913.	9.4	2,407
53	Large-scale genetic fine mapping and genotype-phenotype associations implicate polymorphism in the IL2RA region in type 1 diabetes. <i>Nature Genetics</i> , 2007, 39, 1074-1082.	9.4	380
54	ISHAPE: new rapid and accurate software for haplotyping. <i>BMC Bioinformatics</i> , 2007, 8, 205.	1.2	14
55	Direct maximum parsimony phylogeny reconstruction from genotype data. <i>BMC Bioinformatics</i> , 2007, 8, 472.	1.2	13
56	Constrained hidden Markov models for population-based haplotyping. <i>BMC Bioinformatics</i> , 2007, 8, S9.	1.2	9

#	ARTICLE	IF	CITATIONS
57	Methods to impute missing genotypes for population data. <i>Human Genetics</i> , 2007, 122, 495-504.	1.8	47
58	Association and Expression Study of PRKCH Gene in a French Caucasian Population with Rheumatoid Arthritis. <i>Journal of Clinical Immunology</i> , 2008, 28, 115-121.	2.0	6
59	Association between urokinase haplotypes and outcome from infection-associated acute lung injury. <i>Intensive Care Medicine</i> , 2008, 34, 300-307.	3.9	22
60	Reconstruction of N-acetyltransferase 2 haplotypes using PHASE. <i>Archives of Toxicology</i> , 2008, 82, 265-270.	1.9	12
61	An imputed genotype resource for the laboratory mouse. <i>Mammalian Genome</i> , 2008, 19, 199-208.	1.0	79
62	Grouping preprocess to accurately extend application of EM algorithm to haplotype inference. <i>Journal of Human Genetics</i> , 2008, 53, 747-756.	1.1	3
63	High-Throughput Multiplex Single-Nucleotide Polymorphism (SNP) Analysis in Genes Involved in Methionine Metabolism. <i>Biochemical Genetics</i> , 2008, 46, 406-423.	0.8	7
64	Fine-mapping the genetic basis of CRP regulation in African Americans: a Bayesian approach. <i>Human Genetics</i> , 2008, 123, 633-642.	1.8	9
65	Missing data imputation and haplotype phase inference for genome-wide association studies. <i>Human Genetics</i> , 2008, 124, 439-450.	1.8	142
66	Prevalence of common disease-associated variants in Asian Indians. <i>BMC Genetics</i> , 2008, 9, 13.	2.7	38
67	Mixed modeling and multiple imputation for unobservable genotype clusters. <i>Statistics in Medicine</i> , 2008, 27, 2784-2801.	0.8	8
68	Increasing the power of identifying gene-gene interactions in genome-wide association studies. <i>Genetic Epidemiology</i> , 2008, 32, 255-263.	0.6	175
69	Inference from genome-wide association studies using a novel Markov model. <i>Genetic Epidemiology</i> , 2008, 32, 497-504.	0.6	5
70	Exploring case-control genetic association tests using phase diagrams. <i>Computational Biology and Chemistry</i> , 2008, 32, 391-399.	1.1	4
71	A Powerful and Flexible Multilocus Association Test for Quantitative Traits. <i>American Journal of Human Genetics</i> , 2008, 82, 386-397.	2.6	206
72	Simple and Efficient Analysis of Disease Association with Missing Genotype Data. <i>American Journal of Human Genetics</i> , 2008, 82, 444-452.	2.6	87
73	Multipoint Approximations of Identity-by-Descent Probabilities for Accurate Linkage Analysis of Distantly Related Individuals. <i>American Journal of Human Genetics</i> , 2008, 82, 607-622.	2.6	9
74	Detection, Imputation, and Association Analysis of Small Deletions and Null Alleles on Oligonucleotide Arrays. <i>American Journal of Human Genetics</i> , 2008, 82, 1316-1333.	2.6	40

#	ARTICLE	IF	CITATIONS
75	Genotype, haplotype and copy-number variation in worldwide human populations. <i>Nature</i> , 2008, 451, 998-1003.	13.7	780
76	Detection of sharing by descent, long-range phasing and haplotype imputation. <i>Nature Genetics</i> , 2008, 40, 1068-1075.	9.4	409
77	Imputing missing genotypic data of single-nucleotide polymorphisms using neural networks. <i>European Journal of Human Genetics</i> , 2008, 16, 487-495.	1.4	31
78	Using Population Mixtures to Optimize the Utility of Genomic Databases: Linkage Disequilibrium and Association Study Design in India. <i>Annals of Human Genetics</i> , 2008, 72, 535-546.	0.3	31
79	Haplotype reconstruction for scnp DNA: a consensus vote approach with extensive sequence data from populations of the migratory locust (<i>Locusta migratoria</i>). <i>Molecular Ecology</i> , 2008, 17, 1930-1947.	2.0	16
80	Main pigmentary features and <i>melanocortin 1 receptor</i> (<i>MC1R</i>) gene polymorphisms in the population of the Canary Islands. <i>International Journal of Dermatology</i> , 2008, 47, 806-811.	0.5	5
81	Using an evolutionary algorithm and parallel computing for haplotyping in a general complex pedigree with multiple marker loci. <i>BMC Bioinformatics</i> , 2008, 9, 189.	1.2	3
82	Generating samples for association studies based on HapMap data. <i>BMC Bioinformatics</i> , 2008, 9, 44.	1.2	39
83	Inference of haplotypic phase and missing genotypes in polyploid organisms and variable copy number genomic regions. <i>BMC Bioinformatics</i> , 2008, 9, 513.	1.2	23
84	Shape-IT: new rapid and accurate algorithm for haplotype inference. <i>BMC Bioinformatics</i> , 2008, 9, 540.	1.2	156
85	Haplotype block partitioning as a tool for dimensionality reduction in SNP association studies. <i>BMC Genomics</i> , 2008, 9, 405.	1.2	22
86	The IBD process along four chromosomes. <i>Theoretical Population Biology</i> , 2008, 73, 369-373.	0.5	31
87	Haplotype Association Analysis. <i>Advances in Genetics</i> , 2008, 60, 335-405.	0.8	116
88	Does the Pain-Protective GTP Cyclohydrolase Haplotype Significantly Alter the Pattern or Severity of Pain in Humans with Chronic Pancreatitis?. <i>Molecular Pain</i> , 2008, 4, 1744-8069-4-58.	1.0	35
89	Variants in the promoter region of <i>IKBL/NFKBIL1</i> gene may mark susceptibility to the development of chronic Chagas™ cardiomyopathy among <i>Trypanosoma cruzi</i> -infected individuals. <i>Molecular Immunology</i> , 2008, 45, 283-288.	1.0	29
90	Variation in <i>NPC1</i> , the gene encoding Niemann-Pick C1, a protein involved in intracellular cholesterol transport, is associated with Alzheimer disease and/or aging in the Polish population. <i>Neuroscience Letters</i> , 2008, 447, 153-157.	1.0	29
91	Evidence for Natural Selection on Leukocyte Immunoglobulin-like Receptors for HLA Class I in Northeast Asians. <i>American Journal of Human Genetics</i> , 2008, 82, 1075-1083.	2.6	52
92	Glycogen synthase (<i>GYS1</i>) mutation causes a novel skeletal muscle glycogenosis. <i>Genomics</i> , 2008, 91, 458-466.	1.3	156

#	ARTICLE	IF	CITATIONS
93	A Statistical Method for Predicting Classical HLA Alleles from SNP Data. American Journal of Human Genetics, 2008, 82, 48-56.	2.6	159
94	Molecular phylogenetic analysis of <i>Candida tropicalis</i> isolates by multi-locus sequence typing. Fungal Genetics and Biology, 2008, 45, 1040-1042.	0.9	22
95	Highly Scalable Genotype Phasing by Entropy Minimization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 252-261.	1.9	17
96	Matrix Metalloproteinase 1 (<i>MMP1</i>) Is Associated with Early-Onset Lung Cancer. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1127-1135.	1.1	127
97	Genome-wide association studies: potential next steps on a genetic journey. Human Molecular Genetics, 2008, 17, R156-R165.	1.4	292
98	Fast and flexible simulation of DNA sequence data. Genome Research, 2009, 19, 136-142.	2.4	358
99	Penalized estimation of haplotype frequencies. Bioinformatics, 2008, 24, 1596-1602.	1.8	16
100	Disease association tests by inferring ancestral haplotypes using a hidden markov model. Bioinformatics, 2008, 24, 972-978.	1.8	22
101	Effect of genetic divergence in identifying ancestral origin using HAPAA. Genome Research, 2008, 18, 676-682.	2.4	66
102	HAPLOTYPE INFERENCE AND BLOCK PARTITIONING IN MIXED POPULATION SAMPLES. Journal of Bioinformatics and Computational Biology, 2008, 06, 1177-1192.	0.3	1
103	Genetic analysis of 56 polymorphisms in 17 genes involved in methionine metabolism in patients with abdominal aortic aneurysm. Journal of Medical Genetics, 2008, 45, 721-730.	1.5	63
104	Polymorphisms of the IL1-Receptor Antagonist Gene (<i>IL1RN</i>) Are Associated With Multiple Markers of Systemic Inflammation. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 1407-1412.	1.1	68
105	Population Genetic Analysis of the N-Acylsphingosine Amidohydrolase Gene Associated With Mental Activity in Humans. Genetics, 2008, 178, 1505-1515.	1.2	16
106	Gene Flow and Natural Selection in Oceanic Human Populations Inferred from Genome-Wide SNP Typing. Molecular Biology and Evolution, 2008, 25, 1750-1761.	3.5	47
107	Inferring Human Colonization History Using a Copying Model. PLoS Genetics, 2008, 4, e1000078.	1.5	83
108	A Candidate Gene Approach Identifies the CHRNA5-A3-B4 Region as a Risk Factor for Age-Dependent Nicotine Addiction. PLoS Genetics, 2008, 4, e1000125.	1.5	239
109	Practical Issues in Imputation-Based Association Mapping. PLoS Genetics, 2008, 4, e1000279.	1.5	155
110	Familial Aggregation of Common Sequence Variants on 15q24-25.1 in Lung Cancer. Journal of the National Cancer Institute, 2008, 100, 1326-1330.	3.0	141

#	ARTICLE	IF	CITATIONS
111	A better block partition and ligation strategy for individual haplotyping. <i>Bioinformatics</i> , 2008, 24, 2720-2725.	1.8	11
112	Genetic Variations in MicroRNA-Related Genes Are Novel Susceptibility Loci for Esophageal Cancer Risk. <i>Cancer Prevention Research</i> , 2008, 1, 460-469.	0.7	206
113	<i>G72</i> and Its Association With Major Depression and Neuroticism in Large Population-Based Groups From Germany. <i>American Journal of Psychiatry</i> , 2008, 165, 753-762.	4.0	50
114	Nonlinear Analysis of Time Series in Genome-Wide Linkage Disequilibrium Data. <i>AIP Conference Proceedings</i> , 2008, , .	0.3	1
115	Efficient whole-genome association mapping using local phylogenies for unphased genotype data. <i>Bioinformatics</i> , 2008, 24, 2215-2221.	1.8	11
116	Association studies for untyped markers with TUNA. <i>Bioinformatics</i> , 2008, 24, 435-437.	1.8	13
117	Algorithm for Disease Association Studies Using Functionally Informative Haplotype Motif. , 2008, , .		0
118	Genotype Error Detection Using Hidden Markov Models of Haplotype Diversity. <i>Journal of Computational Biology</i> , 2008, 15, 1155-1171.	0.8	16
119	Common statistical issues in genome-wide association studies: a review on power, data quality control, genotype calling and population structure. <i>Current Opinion in Lipidology</i> , 2008, 19, 133-143.	1.2	88
120	Linkage Disequilibrium-Based Quality Control for Large-Scale Genetic Studies. <i>PLoS Genetics</i> , 2008, 4, e1000147.	1.5	15
121	Small Deletion Variants Have Stable Breakpoints Commonly Associated with Alu Elements. <i>PLoS ONE</i> , 2008, 3, e3104.	1.1	52
122	Analyses and Comparison of Accuracy of Different Genotype Imputation Methods. <i>PLoS ONE</i> , 2008, 3, e3551.	1.1	117
123	Genome-wide gene-based analysis of rheumatoid arthritis-associated interaction with PTPN22 and HLA-DRB1. <i>BMC Proceedings</i> , 2009, 3, S132.	1.8	10
124	STrengthening the REporting of Genetic Association Studies (STREGA)â€™ An Extension of the STROBE Statement. <i>PLoS Medicine</i> , 2009, 6, e1000022.	3.9	411
125	A Validated Genome Wide Association Study to Breed Cattle Adapted to an Environment Altered by Climate Change. <i>PLoS ONE</i> , 2009, 4, e6676.	1.1	122
126	Clustering of SNPs by a Structural EM Algorithm. , 2009, , .		7
127	Big and Slow: Phylogenetic Estimates of Molecular Evolution in Baleen Whales (Suborder Mysticeti). <i>Molecular Biology and Evolution</i> , 2009, 26, 2427-2440.	3.5	73
128	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18644-18649.	3.3	196

#	ARTICLE	IF	CITATIONS
129	Candidate Gene Analysis Using Imputed Genotypes: Cell Cycle Single-Nucleotide Polymorphisms and Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 935-944.	1.1	37
130	Analysis of genomic diversity in Mexican Mestizo populations to develop genomic medicine in Mexico. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8611-8616.	3.3	341
131	ITERATIVE TWO-PASS ALGORITHM FOR MISSING DATA IMPUTATION IN SNP ARRAYS. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 833-852.	0.3	5
132	ERCC5 promoter polymorphisms at -763 and +25 predict the response to oxaliplatin-based chemotherapy in patients with advanced colorectal cancer. <i>Cancer Biology and Therapy</i> , 2009, 8, 1424-1430.	1.5	32
133	Functional polymorphisms, altered gene expression and genetic association link NRH:quinone oxidoreductase 2 to breast cancer with wild-type p53. <i>Human Molecular Genetics</i> , 2009, 18, 2502-2517.	1.4	31
134	Data Integration in Genetics and Genomics: Methods and Challenges. <i>Human Genomics and Proteomics</i> , 2009, 1, .	1.5	105
135	Genome-wide Interrogation of Germline Genetic Variation Associated With Treatment Response in Childhood Acute Lymphoblastic Leukemia. <i>JAMA - Journal of the American Medical Association</i> , 2009, 301, 393.	3.8	193
136	Interrogating 11 Fast-Evolving Genes for Signatures of Recent Positive Selection in Worldwide Human Populations. <i>Molecular Biology and Evolution</i> , 2009, 26, 2285-2297.	3.5	20
137	Integrated study of copy number states and genotype calls using high-density SNP arrays. <i>Nucleic Acids Research</i> , 2009, 37, 5365-5377.	6.5	99
138	Haplotype-Sharing Analysis Showing Uyghurs Are Unlikely Genetic Donors. <i>Molecular Biology and Evolution</i> , 2009, 26, 2197-2206.	3.5	34
139	Geographical structure and differential natural selection among North European populations. <i>Genome Research</i> , 2009, 19, 804-814.	2.4	75
140	X-Linked Variation in Immune Response in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2009, 183, 1477-1491.	1.2	43
141	Methods for Human Demographic Inference Using Haplotype Patterns From Genomewide Single-Nucleotide Polymorphism Data. <i>Genetics</i> , 2009, 182, 217-231.	1.2	53
142	Genotyping Error Detection in Samples of Unrelated Individuals without Replicate Genotyping. <i>Human Heredity</i> , 2009, 67, 154-162.	0.4	7
143	Evaluation of Potential Power Gain with Imputed Genotypes in Genome-Wide Association Studies. <i>Human Heredity</i> , 2009, 68, 23-34.	0.4	3
144	A Novel Method to Select High-risk Disease-Related Regions after a Genome Wide Haplotype-Based Association Study: An Application to Alcoholism. , 2009, , .		0
145	Singapore Genome Variation Project: A haplotype map of three Southeast Asian populations. <i>Genome Research</i> , 2009, 19, 2154-2162.	2.4	146
146	A Flexible and Accurate Genotype Imputation Method for the Next Generation of Genome-Wide Association Studies. <i>PLoS Genetics</i> , 2009, 5, e1000529.	1.5	3,526

#	ARTICLE	IF	CITATIONS
147	Assessment of genotype imputation methods. BMC Proceedings, 2009, 3, S5.	1.8	29
148	Single versus multiple imputation for genotypic data. BMC Proceedings, 2009, 3, S7.	1.8	2
149	Sensitive Detection of Chromosomal Segments of Distinct Ancestry in Admixed Populations. PLoS Genetics, 2009, 5, e1000519.	1.5	475
150	Genome-wide association study of rheumatoid arthritis by a score test based on wavelet transformation. BMC Proceedings, 2009, 3, S8.	1.8	6
151	Rheumatoid arthritis-associated gene-gene interaction network for rheumatoid arthritis candidate genes. BMC Proceedings, 2009, 3, S75.	1.8	17
152	A method and program for estimating graphical models for linkage disequilibrium that scale linearly with the number of loci, and their application to gene drop simulation. Bioinformatics, 2009, 25, 1287-1292.	1.8	10
153	Designing Genome-Wide Association Studies: Sample Size, Power, Imputation, and the Choice of Genotyping Chip. PLoS Genetics, 2009, 5, e1000477.	1.5	499
154	HI: haplotype improver using paired-end short reads. Bioinformatics, 2009, 25, 2436-2437.	1.8	12
155	Evaluation of imputation-based association in and around the integrin- α -M (ITGAM) gene and replication of robust association between a non-synonymous functional variant within ITGAM and systemic lupus erythematosus (SLE). Human Molecular Genetics, 2009, 18, 1171-1180.	1.4	100
156	A novel predictor of multilocus haplotype homozygosity: comparison with existing predictors. Genetical Research, 2009, 91, 413-426.	0.3	31
157	Germline Genetic Variation in an Organic Anion Transporter Polypeptide Associated With Methotrexate Pharmacokinetics and Clinical Effects. Journal of Clinical Oncology, 2009, 27, 5972-5978.	0.8	305
158	The emergence of whole genome association scans in barley. Current Opinion in Plant Biology, 2009, 12, 218-222.	3.5	138
159	Accuracy of genomic breeding values in multi-breed dairy cattle populations. Genetics Selection Evolution, 2009, 41, 51.	1.2	371
160	Genotype determination for polymorphisms in linkage disequilibrium. BMC Bioinformatics, 2009, 10, 63.	1.2	7
161	Genetic diversity of canine olfactory receptors. BMC Genomics, 2009, 10, 21.	1.2	51
162	Decay of linkage disequilibrium within genes across HGDP-CEPH human samples: most population isolates do not show increased LD. BMC Genomics, 2009, 10, 338.	1.2	19
163	SNP_tools: A compact tool package for analysis and conversion of genotype data for MS-Excel. BMC Research Notes, 2009, 2, 214.	0.6	57
164	Fully non-homogeneous hidden Markov model double net: A generative model for haplotype reconstruction and block discovery. Artificial Intelligence in Medicine, 2009, 45, 135-150.	3.8	4

#	ARTICLE	IF	CITATIONS
165	Power consequences of linkage disequilibrium variation between populations. <i>Genetic Epidemiology</i> , 2009, 33, 128-135.	0.6	28
166	More powerful haplotype sharing by accounting for the mode of inheritance. <i>Genetic Epidemiology</i> , 2009, 33, 228-236.	0.6	4
167	Strengthening the Reporting of Genetic Association Studies (STREGA) – an extension of the STROBE statement. <i>Genetic Epidemiology</i> , 2009, 33, 581-598.	0.6	211
168	Identification of gene-gene interactions in the presence of missing data using the multifactor dimensionality reduction method. <i>Genetic Epidemiology</i> , 2009, 33, 646-656.	0.6	22
169	A novel method for haplotype clustering and visualization. <i>Genetic Epidemiology</i> , 2010, 34, 34-41.	0.6	6
170	Practical considerations for imputation of untyped markers in admixed populations. <i>Genetic Epidemiology</i> , 2010, 34, 258-265.	0.6	32
171	FcRL3 gene promoter variant is associated with peripheral arthritis in Crohn's disease. <i>Inflammatory Bowel Diseases</i> , 2009, 15, 1351-1357.	0.9	12
172	Haplotype Inference for Population Data with Genotyping Errors. <i>Biometrical Journal</i> , 2009, 51, 644-658.	0.6	1
173	Strengthening the reporting of genetic association studies (STREGA): an extension of the STROBE Statement. <i>Human Genetics</i> , 2009, 125, 131-151.	1.8	167
174	Strengthening the reporting of genetic association studies (STREGA): an extension of the STROBE statement. <i>European Journal of Epidemiology</i> , 2009, 24, 37-55.	2.5	41
175	Developments in statistical analysis in quantitative genetics. <i>Genetica</i> , 2009, 136, 319-332.	0.5	17
176	High-resolution haplotype block structure in the cattle genome. <i>BMC Genetics</i> , 2009, 10, 19.	2.7	141
177	Accuracy of genome-wide imputation of untyped markers and impacts on statistical power for association studies. <i>BMC Genetics</i> , 2009, 10, 27.	2.7	72
178	Haplotype frequencies in a sub-region of chromosome 19q13.3, related to risk and prognosis of cancer, differ dramatically between ethnic groups. <i>BMC Medical Genetics</i> , 2009, 10, 20.	2.1	16
179	Lack of association of TIM3 polymorphisms and allergic phenotypes. <i>BMC Medical Genetics</i> , 2009, 10, 62.	2.1	11
180	Strengthening the Reporting of Genetic Association studies (STREGA) – an extension of the STROBE statement. <i>European Journal of Clinical Investigation</i> , 2009, 39, 247-266.	1.7	216
181	A phylogenetic framework for wing pattern evolution in the mimetic Mocker Swallowtail <i>Papilio dardanus</i> . <i>Molecular Ecology</i> , 2009, 18, 3872-3884.	2.0	12
182	Variation in neighbouring genes of the dopaminergic and serotonergic systems affects feather pecking behaviour of laying hens. <i>Animal Genetics</i> , 2009, 40, 192-199.	0.6	65

#	ARTICLE	IF	CITATIONS
183	<i>Toll-like receptor 4</i> genetic diversity among pig populations. <i>Animal Genetics</i> , 2009, 40, 289-299.	0.6	23
184	The pattern of linkage disequilibrium in German Holstein cattle. <i>Animal Genetics</i> , 2010, 41, 346-356.	0.6	160
185	Global variation in CYP2C8 and CYP2C9 functional haplotypes. <i>Pharmacogenomics Journal</i> , 2009, 9, 283-290.	0.9	47
186	Replication of the BANK1 genetic association with systemic lupus erythematosus in a European-derived population. <i>Genes and Immunity</i> , 2009, 10, 531-538.	2.2	40
187	SNP imputation in association studies. <i>Nature Biotechnology</i> , 2009, 27, 349-351.	9.4	59
188	Experimental evolution reveals natural selection on standing genetic variation. <i>Nature Genetics</i> , 2009, 41, 251-257.	9.4	143
189	Genome-wide and fine-resolution association analysis of malaria in West Africa. <i>Nature Genetics</i> , 2009, 41, 657-665.	9.4	345
190	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. <i>Nature Genetics</i> , 2009, 41, 996-1000.	9.4	276
191	Mitochondrial introgression and replacement between yellowhammers (<i>Emberiza citrinella</i>) and pine buntings (<i>Emberiza leucocephalos</i>) (Aves: Passeriformes). <i>Biological Journal of the Linnean Society</i> , 0, 98, 422-438.	0.7	107
192	Detection of prion gene promoter and intron1 indel polymorphisms in Anatolian water buffalo (<i>Bubalus bubalis</i>). <i>Journal of Animal Breeding and Genetics</i> , 2009, 126, 463-467.	0.8	17
193	Multivariate Association Test Using Haplotype Trend Regression. <i>Annals of Human Genetics</i> , 2009, 73, 456-464.	0.3	14
194	Distribution of mutations distinguishing the most prevalent disease-causing <i>Candida albicans</i> genotype from other genotypes. <i>Infection, Genetics and Evolution</i> , 2009, 9, 493-500.	1.0	11
195	Estimation of graphical models whose conditional independence graphs are interval graphs and its application to modelling linkage disequilibrium. <i>Computational Statistics and Data Analysis</i> , 2009, 53, 1818-1828.	0.7	14
196	A Unified Approach to Genotype Imputation and Haplotype-Phase Inference for Large Data Sets of Trios and Unrelated Individuals. <i>American Journal of Human Genetics</i> , 2009, 84, 210-223.	2.6	1,441
197	Genotype-Imputation Accuracy across Worldwide Human Populations. <i>American Journal of Human Genetics</i> , 2009, 84, 235-250.	2.6	231
198	ATRIUM: Testing Untyped SNPs in Case-Control Association Studies with Related Individuals. <i>American Journal of Human Genetics</i> , 2009, 85, 667-678.	2.6	6
199	Gene-centric Association Signals for Lipids and Apolipoproteins Identified via the HumanCVD BeadChip. <i>American Journal of Human Genetics</i> , 2009, 85, 628-642.	2.6	183
200	Assessment of Chromosome 19 for Genetic Association in Severe Chronic Periodontitis. <i>Journal of Periodontology</i> , 2009, 80, 663-671.	1.7	6

#	ARTICLE	IF	CITATIONS
201	Evolutionary History of <i>GS3</i> , a Gene Conferring Grain Length in Rice. <i>Genetics</i> , 2009, 182, 1323-1334.	1.2	305
202	Is there still a need for candidate gene approaches in the era of genome-wide association studies?. <i>Genomics</i> , 2009, 93, 415-419.	1.3	73
203	Strengthening the reporting of genetic association studies (STREGA) – an extension of the strengthening the reporting of observational studies in epidemiology (STROBE) statement. <i>Journal of Clinical Epidemiology</i> , 2009, 62, 597-608.e4.	2.4	98
204	DnaSP v5: a software for comprehensive analysis of DNA polymorphism data. <i>Bioinformatics</i> , 2009, 25, 1451-1452.	1.8	13,645
205	Applied Statistical Genetics with R. , 2009, , .		66
206	Analysis of recently identified dyslipidemia alleles reveals two loci that contribute to risk for carotid artery disease. <i>Lipids in Health and Disease</i> , 2009, 8, 52.	1.2	31
207	Invited review: Genomic selection in dairy cattle: Progress and challenges. <i>Journal of Dairy Science</i> , 2009, 92, 433-443.	1.4	1,359
208	Haplotype Structure. , 2009, , 25-79.		3
209	Genotype Imputation. <i>Annual Review of Genomics and Human Genetics</i> , 2009, 10, 387-406.	2.5	920
210	Polymorphisms in innate immunity genes predispose to bacteremia and death in the medical intensive care unit*. <i>Critical Care Medicine</i> , 2009, 37, 192-e3.	0.4	130
211	A hierarchical Dirichlet process mixture model for haplotype reconstruction from multi-population data. <i>Annals of Applied Statistics</i> , 2009, 3, .	0.5	11
212	Molecular population genetics of SLC4A1 and Southeast Asian Ovalocytosis. <i>Journal of Human Genetics</i> , 2009, 54, 182-187.	1.1	20
213	STrengthening the REporting of Genetic Association Studies (STREGA): An Extension of the STROBE Statement. <i>Annals of Internal Medicine</i> , 2009, 150, 206.	2.0	105
214	Association tests and software for copy number variant data. <i>Human Genomics</i> , 2009, 3, 191.	1.4	6
215	Identifying positive selection candidate loci for high-altitude adaptation in Andean populations. <i>Human Genomics</i> , 2009, 4, 79-90.	1.4	195
216	Using linear predictors to impute allele frequencies from summary or pooled genotype data. <i>Annals of Applied Statistics</i> , 2010, 4, 1158-1182.	0.5	74
218	Marker Genotype Imputation in a Low-Marker-Density Panel with a High-Marker-Density Reference Panel: Accuracy Evaluation in Barley Breeding Lines. <i>Crop Science</i> , 2010, 50, 1269-1278.	0.8	23
219	Prioritizing GWAS Results: A Review of Statistical Methods and Recommendations for Their Application. <i>American Journal of Human Genetics</i> , 2010, 86, 6-22.	2.6	531

#	ARTICLE	IF	CITATIONS
220	The Distribution and Most Recent Common Ancestor of the 17q21 Inversion in Humans. <i>American Journal of Human Genetics</i> , 2010, 86, 161-171.	2.6	59
221	High-Resolution Detection of Identity by Descent in Unrelated Individuals. <i>American Journal of Human Genetics</i> , 2010, 86, 526-539.	2.6	196
222	Interpretation of Association Signals and Identification of Causal Variants from Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2010, 86, 730-742.	2.6	146
223	To Identify Associations with Rare Variants, Just WHaIT: Weighted Haplotype and Imputation-Based Tests. <i>American Journal of Human Genetics</i> , 2010, 87, 728-735.	2.6	86
224	Tag SNP selection based on clustering according to dominant sets found using replicator dynamics. <i>Advances in Data Analysis and Classification</i> , 2010, 4, 65-83.	0.9	16
225	Genetic contribution of GADD45A to susceptibility to sporadic and non-BRCA1/2 familial breast cancers: a systematic evaluation in Chinese populations. <i>Breast Cancer Research and Treatment</i> , 2010, 121, 157-167.	1.1	9
226	Association of IGF1 and IGFBP3 polymorphisms with colorectal polyps and colorectal cancer risk. <i>Cancer Causes and Control</i> , 2010, 21, 91-97.	0.8	51
227	Angiogenesis-associated sequence variants relative to breast cancer recurrence and survival. <i>Cancer Causes and Control</i> , 2010, 21, 1545-1557.	0.8	22
228	The impact of genetic relationship information on genomic breeding values in German Holstein cattle. <i>Genetics Selection Evolution</i> , 2010, 42, 5.	1.2	370
229	Spatial normalization improves the quality of genotype calling for Affymetrix SNP 6.0 arrays. <i>BMC Bioinformatics</i> , 2010, 11, 356.	1.2	6
230	Haplotype allelic classes for detecting ongoing positive selection. <i>BMC Bioinformatics</i> , 2010, 11, 65.	1.2	18
231	Detecting positive selection from genome scans of linkage disequilibrium. <i>BMC Genomics</i> , 2010, 11, 8.	1.2	19
232	Algorithm for haplotype resolution and block partitioning for partial XOR-genotype data. <i>Journal of Biomedical Informatics</i> , 2010, 43, 51-59.	2.5	11
233	Vascular endothelial growth factor gene polymorphisms and ovarian cancer survival. <i>Gynecologic Oncology</i> , 2010, 119, 479-483.	0.6	26
234	Methods for detecting interactions between genetic polymorphisms and prenatal environment exposure with a mother-child design. <i>Genetic Epidemiology</i> , 2010, 34, 125-132.	0.6	6
235	Detecting rare variants for complex traits using family and unrelated data. <i>Genetic Epidemiology</i> , 2010, 34, 171-187.	0.6	114
236	Sibship analysis of associations between SNP haplotypes and a continuous trait with application to mammographic density. <i>Genetic Epidemiology</i> , 2010, 34, 309-318.	0.6	10
237	MaCH: using sequence and genotype data to estimate haplotypes and unobserved genotypes. <i>Genetic Epidemiology</i> , 2010, 34, 816-834.	0.6	1,718

#	ARTICLE	IF	CITATIONS
238	Detailed haplotype analysis at the <i>TP53</i> locus in p.R337H mutation carriers in the population of Southern Brazil: evidence for a founder effect. <i>Human Mutation</i> , 2010, 31, 143-150.	1.1	116
239	β -N133p53 expression levels in relation to haplotypes of the TP53 internal promoter region. <i>Human Mutation</i> , 2010, 31, 456-465.	1.1	21
240	Prediction of haplotypes for ungenotyped animals and its effect on marker-assisted breeding value estimation. <i>Genetics Selection Evolution</i> , 2010, 42, 10.	1.2	15
241	Linkage disequilibrium reveals different demographic history in egg laying chickens. <i>BMC Genetics</i> , 2010, 11, 103.	2.7	48
242	Genetic evidence supports linguistic affinity of Mlabri - a hunter-gatherer group in Thailand. <i>BMC Genetics</i> , 2010, 11, 18.	2.7	30
243	Impact of reduced marker set estimation of genomic relationship matrices on genomic selection for feed efficiency in Angus cattle. <i>BMC Genetics</i> , 2010, 11, 24.	2.7	50
244	Age modifies the genotype-phenotype relationship for the bitter receptor TAS2R38. <i>BMC Genetics</i> , 2010, 11, 60.	2.7	156
245	ParaHaplo 2.0: a program package for haplotype-estimation and haplotype-based whole-genome association study using parallel computing. <i>Source Code for Biology and Medicine</i> , 2010, 5, 5.	1.7	1
246	Bayesian methods for meta-analysis of causal relationships estimated using genetic instrumental variables. <i>Statistics in Medicine</i> , 2010, 29, 1298-1311.	0.8	22
247	No association between chromosome 12p13 single nucleotide polymorphisms and early-onset ischemic stroke. <i>Journal of Thrombosis and Haemostasis</i> , 2010, 8, 1858-1860.	1.9	20
248	<i>APOE</i> is not Associated with Alzheimer Disease: a Cautionary tale of Genotype Imputation. <i>Annals of Human Genetics</i> , 2010, 74, 189-194.	0.3	13
249	<i>Cis</i> -acting Allelic Variation in <i>MUC5B</i> mRNA Expression is Associated with Different Promoter Haplotypes. <i>Annals of Human Genetics</i> , 2010, 74, 498-505.	0.3	6
250	A genome-wide scan for signatures of recent selection in Holstein cattle. <i>Animal Genetics</i> , 2010, 41, 377-389.	0.6	148
251	Segregation distortion in chicken and the evolutionary consequences of female meiotic drive in birds. <i>Heredity</i> , 2010, 105, 290-298.	1.2	33
252	Common variants at 7p21 are associated with frontotemporal lobar degeneration with TDP-43 inclusions. <i>Nature Genetics</i> , 2010, 42, 234-239.	9.4	479
253	Common variants at 19p13 are associated with susceptibility to ovarian cancer. <i>Nature Genetics</i> , 2010, 42, 880-884.	9.4	235
254	cnvHap: an integrative population and haplotype-based multiplatform model of SNPs and CNVs. <i>Nature Methods</i> , 2010, 7, 541-546.	9.0	44
255	Genotype imputation for genome-wide association studies. <i>Nature Reviews Genetics</i> , 2010, 11, 499-511.	7.7	1,408

#	ARTICLE	IF	CITATIONS
256	Genetic Architecture of Complex Traits and Accuracy of Genomic Prediction: Coat Colour, Milk-Fat Percentage, and Type in Holstein Cattle as Contrasting Model Traits. <i>PLoS Genetics</i> , 2010, 6, e1001139.	1.5	381
257	Analyses and Comparison of Imputation-Based Association Methods. <i>PLoS ONE</i> , 2010, 5, e10827.	1.1	34
258	Common Variation in ISL1 Confers Genetic Susceptibility for Human Congenital Heart Disease. <i>PLoS ONE</i> , 2010, 5, e10855.	1.1	74
259	A genome-wide association study for milk production traits in Danish Jersey cattle using a 50K single nucleotide polymorphism chip1. <i>Journal of Animal Science</i> , 2010, 88, 3522-3528.	0.2	55
260	A Hidden Markov Model Combining Linkage and Linkage Disequilibrium Information for Haplotype Reconstruction and Quantitative Trait Locus Fine Mapping. <i>Genetics</i> , 2010, 184, 789-798.	1.2	178
261	A Principled Approach to Deriving Approximate Conditional Sampling Distributions in Population Genetics Models with Recombination. <i>Genetics</i> , 2010, 186, 321-338.	1.2	30
262	<i>ANRIL</i> Expression Is Associated With Atherosclerosis Risk at Chromosome 9p21. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010, 30, 620-627.	1.1	402
263	Genetic Polymorphisms in Vitamin D Receptor <i>VDR/RXRA</i> Influence the Likelihood of Colon Adenoma Recurrence. <i>Cancer Research</i> , 2010, 70, 1496-1504.	0.4	46
264	Fine Mapping in 94 Inbred Mouse Strains Using a High-Density Haplotype Resource. <i>Genetics</i> , 2010, 185, 1081-1095.	1.2	95
265	The Use of Family Relationships and Linkage Disequilibrium to Impute Phase and Missing Genotypes in Up to Whole-Genome Sequence Density Genotypic Data. <i>Genetics</i> , 2010, 185, 1441-1449.	1.2	80
266	Natural Selection and the Distribution of Identity-by-Descent in the Human Genome. <i>Genetics</i> , 2010, 186, 295-308.	1.2	119
267	The conditional independences between variables derived from two independent identically distributed Markov random fields when pairwise order is ignored. <i>Mathematical Medicine and Biology</i> , 2010, 27, 283-288.	0.8	3
268	Identity-by-Descent Matrix Decomposition Using Latent Ancestral Allele Models. <i>Genetics</i> , 2010, 185, 1045-1057.	1.2	17
269	Inferring combined CNV/SNP haplotypes from genotype data. <i>Bioinformatics</i> , 2010, 26, 1437-1445.	1.8	31
270	Early-onset ischaemic stroke: Analysis of 58 polymorphisms in 17 genes involved in methionine metabolism. <i>Thrombosis and Haemostasis</i> , 2010, 104, 231-242.	1.8	35
271	EMINIM: An Adaptive and Memory-Efficient Algorithm for Genotype Imputation. <i>Journal of Computational Biology</i> , 2010, 17, 547-560.	0.8	16
272	Accurate Prediction of Genetic Values for Complex Traits by Whole-Genome Resequencing. <i>Genetics</i> , 2010, 185, 623-631.	1.2	334
273	Multi-objective tag SNPs selection using evolutionary algorithms. <i>Bioinformatics</i> , 2010, 26, 1446-1452.	1.8	17

#	ARTICLE	IF	CITATIONS
274	Common genetic variation in the sex hormone metabolic pathway and endometrial cancer risk: pathway-based evaluation of candidate genes. <i>Carcinogenesis</i> , 2010, 31, 827-833.	1.3	42
275	A New Method to Reconstruct Recombination Events at a Genomic Scale. <i>PLoS Computational Biology</i> , 2010, 6, e1001010.	1.5	14
276	A Simple Genetic Architecture Underlies Morphological Variation in Dogs. <i>PLoS Biology</i> , 2010, 8, e1000451.	2.6	429
277	Modeling associations between genetic markers using Bayesian networks. <i>Bioinformatics</i> , 2010, 26, i632-i637.	1.8	4
278	Population differentiation as a test for selective sweeps. <i>Genome Research</i> , 2010, 20, 393-402.	2.4	600
279	Localizing Putative Markers in Genetic Association Studies by Incorporating Linkage Disequilibrium into Bayesian Hierarchical Models. <i>Human Heredity</i> , 2010, 70, 63-73.	0.4	4
280	Population Structure With Localized Haplotype Clusters. <i>Genetics</i> , 2010, 185, 1337-1344.	1.2	28
281	ReFHap. , 2010, , .		38
282	SplittingHeirs. , 2010, , .		2
284	Using Population Genomics to Detect Selection in Natural Populations: Key Concepts and Methodological Considerations. <i>International Journal of Plant Sciences</i> , 2010, 171, 1059-1071.	0.6	165
285	Genetic Regulation of Serum Phytosterol Levels and Risk of Coronary Artery Disease. <i>Circulation: Cardiovascular Genetics</i> , 2010, 3, 331-339.	5.1	141
286	CVhaplot: a consensus tool for statistical haplotyping. <i>Molecular Ecology Resources</i> , 2010, 10, 1066-1070.	2.2	5
287	Application of single nucleotide polymorphisms to non-€model species: a technical review. <i>Molecular Ecology Resources</i> , 2010, 10, 915-934.	2.2	177
288	Genetic markers for lactation persistency in primiparous Australian dairy cows. <i>Journal of Dairy Science</i> , 2010, 93, 2202-2214.	1.4	23
289	Prediction of unobserved single nucleotide polymorphism genotypes of Jersey cattle using reference panels and population-based imputation algorithms. <i>Journal of Dairy Science</i> , 2010, 93, 2229-2238.	1.4	58
290	A validated genome-wide association study in 2 dairy cattle breeds for milk production and fertility traits using variable length haplotypes. <i>Journal of Dairy Science</i> , 2010, 93, 3331-3345.	1.4	135
291	Multivariate analysis of a genome-wide association study in dairy cattle. <i>Journal of Dairy Science</i> , 2010, 93, 3818-3833.	1.4	72
292	Using eigenvalues as variance priors in the prediction of genomic breeding values by principal component analysis. <i>Journal of Dairy Science</i> , 2010, 93, 2765-2774.	1.4	25

#	ARTICLE	IF	CITATIONS
293	Accuracy of direct genomic values derived from imputed single nucleotide polymorphism genotypes in Jersey cattle. <i>Journal of Dairy Science</i> , 2010, 93, 5423-5435.	1.4	85
294	Marker imputation with low-density marker panels in Dutch Holstein cattle. <i>Journal of Dairy Science</i> , 2010, 93, 5487-5494.	1.4	102
295	SDHAF2 mutations in familial and sporadic paraganglioma and pheochromocytoma. <i>Lancet Oncology</i> , The, 2010, 11, 366-372.	5.1	256
296	Handbook on Analyzing Human Genetic Data. , 2010, , .		7
297	Accuracy of estimated genomic breeding values for wool and meat traits in a multi-breed sheep population. <i>Animal Production Science</i> , 2010, 50, 1004.	0.6	94
299	Genetic diversity in India and the inference of Eurasian population expansion. <i>Genome Biology</i> , 2010, 11, R113.	3.8	60
300	Rapid haplotype inference for nuclear families. <i>Genome Biology</i> , 2010, 11, R108.	3.8	22
301	Characterization of X-Linked SNP genotypic variation in globally distributed human populations. <i>Genome Biology</i> , 2010, 11, R10.	13.9	32
302	An EM method based on entropy LD block partition for haplotype inference. , 2010, , .		0
303	Comprehensive Analysis of HLA-G: Implications for Recurrent Spontaneous Abortion. <i>Reproductive Sciences</i> , 2010, 17, 331-338.	1.1	41
304	CollHaps: A Heuristic Approach to Haplotype Inference by Parsimony. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 511-523.	1.9	15
305	Haplotype inference based on sparse dictionary selection. , 2011, , .		0
306	Associations of marker panel scores with feed intake and efficiency traits in beef cattle using preselected single nucleotide polymorphisms ¹ . <i>Journal of Animal Science</i> , 2011, 89, 3362-3371.	0.2	14
307	A Functional Single Nucleotide Polymorphism in Mucin 1, at Chromosome 1q22, Determines Susceptibility to Diffuse-Type Gastric Cancer. <i>Gastroenterology</i> , 2011, 140, 892-902.	0.6	114
308	Identification of ATPAF1 as a novel candidate gene for asthma in children. <i>Journal of Allergy and Clinical Immunology</i> , 2011, 128, 753-760.e11.	1.5	28
309	Association of WNK1 exon 1 polymorphisms with essential hypertension in Hani and Yi minorities of China. <i>Journal of Genetics and Genomics</i> , 2011, 38, 165-171.	1.7	11
310	Modeling of Identity-by-Descent Processes Along a Chromosome Between Haplotypes and Their Genotyped Ancestors. <i>Genetics</i> , 2011, 188, 409-419.	1.2	26
311	Genetic Epidemiology. <i>Methods in Molecular Biology</i> , 2011, , .	0.4	3

#	ARTICLE	IF	CITATIONS
312	Genome Variation: A Review of Web Resources. <i>Methods in Molecular Biology</i> , 2011, 713, 129-139.	0.4	2
313	No association of XRCC1 polymorphisms Arg194Trp and Arg399Gln with colorectal cancer risk. <i>Cancer Epidemiology</i> , 2011, 35, e38-e41.	0.8	32
314	Genetic structure and domestication history of the grape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3530-3535.	3.3	684
315	Genome-wide nested association mapping of quantitative resistance to northern leaf blight in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6893-6898.	3.3	350
316	Acceleration Genotype Imputation for Large Dataset on GPU. <i>Procedia Environmental Sciences</i> , 2011, 8, 457-463.	1.3	4
317	Genetic variation within IL18 is associated with insulin levels, insulin resistance and postprandial measures. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2011, 21, 476-484.	1.1	14
318	Application of SNPs for population genetics of nonmodel organisms: new opportunities and challenges. <i>Molecular Ecology Resources</i> , 2011, 11, 123-136.	2.2	391
319	Genomic breeding value estimation using genetic markers, inferred ancestral haplotypes, and the genomic relationship matrix. <i>Journal of Dairy Science</i> , 2011, 94, 4708-4714.	1.4	30
320	Effect of imputing markers from a low-density chip on the reliability of genomic breeding values in Holstein populations. <i>Journal of Dairy Science</i> , 2011, 94, 3679-3686.	1.4	69
321	Haplotype Methods for Population-based Association Studies. , 2011, , 177-195.		0
322	Genotype Imputation. , 2011, , 157-175.		0
323	SNPpattern: A Genetic Tool to Derive Haplotype Blocks and Measure Genomic Diversity in Populations Using SNP Genotypes. , 0, , .		1
324	Multisite haplotype on cattle chromosome 3 is associated with quantitative trait locus effects on lactation traits. <i>Physiological Genomics</i> , 2011, 43, 1185-1197.	1.0	12
325	Two Novel Polymorphisms in 5' Flanking Region of the Mesothelin Gene are Associated with Soluble Mesothelin-Related Peptide (SMRP) Levels. <i>International Journal of Biological Markers</i> , 2011, 26, 117-123.	0.7	13
326	Genome Partitioning of Genetic Variation for Milk Production and Composition Traits in Holstein Cattle. <i>Frontiers in Genetics</i> , 2011, 2, 19.	1.1	28
327	Accelerating Haplotype-Based Genome-Wide Association Study Using Perfect Phylogeny and Phase-Known Reference Data. <i>PLoS ONE</i> , 2011, 6, e22097.	1.1	11
328	No Evidence for Strong Recent Positive Selection Favoring the 7 Repeat Allele of VNTR in the DRD4 Gene. <i>PLoS ONE</i> , 2011, 6, e24410.	1.1	12
329	The Whereabouts of an Ancient Wanderer: Global Phylogeography of the Solitary Ascidian <i>Styela plicata</i> . <i>PLoS ONE</i> , 2011, 6, e25495.	1.1	72

#	ARTICLE	IF	CITATIONS
330	Local Genealogies in a Linear Mixed Model for Genome-Wide Association Mapping in Complex Pedigreed Populations. PLoS ONE, 2011, 6, e27061.	1.1	6
331	METU-SNP: An Integrated Software System for SNPComplex Disease Association Analysis. Journal of Integrative Bioinformatics, 2011, 8, 204-221.	1.0	3
332	Association of a common vitamin D-binding protein polymorphism with inflammatory bowel disease. Pharmacogenetics and Genomics, 2011, 21, 559-564.	0.7	66
333	Mixed Model Association Mapping for Fusarium Head Blight Resistance in Tunisian-Derived Durum Wheat Populations. G3: Genes, Genomes, Genetics, 2011, 1, 209-218.	0.8	72
334	The distribution of SNP marker effects for faecal worm egg count in sheep, and the feasibility of using these markers to predict genetic merit for resistance to worm infections. Genetical Research, 2011, 93, 203-219.	0.3	67
335	Estimating the correlation of non-allele descents along chromosomes. Genetical Research, 2011, 93, 23-32.	0.3	1
336	Genetic determinants of plasma von Willebrand factor antigen levels: a target gene SNP and haplotype analysis of ARIC cohort. Blood, 2011, 117, 5224-5230.	0.6	45
337	Bayesian variable selection regression for genome-wide association studies and other large-scale problems. Annals of Applied Statistics, 2011, 5, .	0.5	303
338	Genome-Wide Association Analysis Identifies Candidate Genes Associated with Iron Deficiency Chlorosis in Soybean. Plant Genome, 2011, 4, 154-164.	1.6	106
339	Using the genomic relationship matrix to predict the accuracy of genomic selection. Journal of Animal Breeding and Genetics, 2011, 128, 409-421.	0.8	262
340	Exploration of relationships between production and fertility traits in dairy cattle via association studies of SNPs within candidate genes derived by expression profiling. Animal Genetics, 2011, 42, 251-262.	0.6	60
341	A genome-wide association study of direct gestation length in US Holstein and Italian Brown populations. Animal Genetics, 2011, 42, 585-591.	0.6	28
342	Bridging the gap: western rock skinks (<i>Trachylepis sulcata</i>) have a short history in South Africa. Molecular Ecology, 2011, 20, 1744-1758.	2.0	36
343	The performance of phylogenetic algorithms in estimating haplotype genealogies with migration. Molecular Ecology, 2011, 20, 1952-1963.	2.0	316
344	Wolbachia-mediated persistence of mtDNA from a potentially extinct species. Molecular Ecology, 2011, 20, 2805-2817.	2.0	24
345	Footprints of selection in the ancestral admixture of a New World Creole cattle breed. Molecular Ecology, 2011, 20, 3128-3143.	2.0	130
346	Evolutionary and functional analyses of cytochrome P4501A promoter polymorphisms in natural populations. Molecular Ecology, 2011, 20, 5236-5247.	2.0	21
347	Genetic Variants Associated with von Willebrand Factor Levels in Healthy Men and Women Identified Using the HumanCVD BeadChip. Annals of Human Genetics, 2011, 75, 456-467.	0.3	28

#	ARTICLE	IF	CITATIONS
348	Chromosome-Wide Haplotype Sharing: A Measure Integrating Recombination Information to Reconstruct the Phylogeny of Human Populations. <i>Annals of Human Genetics</i> , 2011, 75, 694-706.	0.3	5
349	Genome-wide association study of leaf architecture in the maize nested association mapping population. <i>Nature Genetics</i> , 2011, 43, 159-162.	9.4	987
350	The importance of phase information for human genomics. <i>Nature Reviews Genetics</i> , 2011, 12, 215-223.	7.7	288
351	Genotype and SNP calling from next-generation sequencing data. <i>Nature Reviews Genetics</i> , 2011, 12, 443-451.	7.7	1,238
352	Haplotype phasing: existing methods and new developments. <i>Nature Reviews Genetics</i> , 2011, 12, 703-714.	7.7	537
353	Human-aided dispersal has altered but not erased the phylogeography of the tench. <i>Evolutionary Applications</i> , 2011, 4, 545-561.	1.5	19
354	Phred-Phrap package to analyses tools: a pipeline to facilitate population genetics re-sequencing studies. <i>Investigative Genetics</i> , 2011, 2, 3.	3.3	42
355	Haplotype inference with pseudo-Boolean optimization. <i>Annals of Operations Research</i> , 2011, 184, 137-162.	2.6	13
356	Identification of novel genomic regions associated with resistance to <i>Pyrenophora tritici-repentis</i> races 1 and 5 in spring wheat landraces using association analysis. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1029-1041.	1.8	58
357	Genetic variants in urinary bladder cancer: collective power of the "wimp SNPs". <i>Archives of Toxicology</i> , 2011, 85, 539-554.	1.9	65
358	Genetic mapping of the major histocompatibility complex in the zebra finch (<i>Taeniopygia guttata</i>). <i>Immunogenetics</i> , 2011, 63, 523-530.	1.2	35
359	Search for compound heterozygous effects in exome sequence of unrelated subjects. <i>BMC Proceedings</i> , 2011, 5, S95.	1.8	3
360	A Monte Carlo test of linkage disequilibrium for single nucleotide polymorphisms. <i>BMC Research Notes</i> , 2011, 4, 124.	0.6	1
361	A combined long-range phasing and long haplotype imputation method to impute phase for SNP genotypes. <i>Genetics Selection Evolution</i> , 2011, 43, 12.	1.2	133
362	Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. <i>Genetics Selection Evolution</i> , 2011, 43, 40.	1.2	174
363	SNIPlay: a web-based tool for detection, management and analysis of SNPs. Application to grapevine diversity projects. <i>BMC Bioinformatics</i> , 2011, 12, 134.	1.2	82
364	Enhancements to the ADMIXTURE algorithm for individual ancestry estimation. <i>BMC Bioinformatics</i> , 2011, 12, 246.	1.2	990
365	Application of site and haplotype-frequency based approaches for detecting selection signatures in cattle. <i>BMC Genomics</i> , 2011, 12, 318.	1.2	135

#	ARTICLE	IF	CITATIONS
366	Postassociation cleaning using linkage disequilibrium information. <i>Genetic Epidemiology</i> , 2011, 35, 1-10.	0.6	20
367	A comparison of approaches to account for uncertainty in analysis of imputed genotypes. <i>Genetic Epidemiology</i> , 2011, 35, 102-110.	0.6	98
368	Optimal methods for meta-analysis of genome-wide association studies. <i>Genetic Epidemiology</i> , 2011, 35, 581-591.	0.6	23
369	Haplotype variation and genotype imputation in African populations. <i>Genetic Epidemiology</i> , 2011, 35, 766-780.	0.6	39
370	Identity-by-descent based phasing and imputation in founder populations using graphical models. <i>Genetic Epidemiology</i> , 2011, 35, 853-860.	0.6	31
371	Genetic Variation in <i>LPAL2</i> , <i>LPA</i> , and <i>PLG</i> Predicts Plasma Lipoprotein(a) Level and Carotid Artery Disease Risk. <i>Stroke</i> , 2011, 42, 2-9.	1.0	46
372	Characterization of genetic variation and natural selection at the arylamine <i>N</i> -acetyltransferase genes in global human populations. <i>Pharmacogenomics</i> , 2011, 12, 1545-1558.	0.6	38
373	Genetic and Clinical Features of Progranulin-Associated Frontotemporal Lobar Degeneration. <i>Archives of Neurology</i> , 2011, 68, 488.	4.9	108
374	Accurate Single-Nucleotide Polymorphism Allele Assignment in Trisomic or Duplicated Regions by Using a Single Base Extension Assay with MALDI-TOF Mass Spectrometry. <i>Clinical Chemistry</i> , 2011, 57, 1188-1195.	1.5	10
375	A method for identifying haplotypes carrying the causative allele in positive natural selection and genome-wide association studies. <i>Bioinformatics</i> , 2011, 27, 822-828.	1.8	8
376	Inference of Population Mutation Rate and Detection of Segregating Sites from Next-Generation Sequence Data. <i>Genetics</i> , 2011, 189, 595-605.	1.2	8
377	BDNF Contributes to the Genetic Variance of Milk Fat Yield in German Holstein Cattle. <i>Frontiers in Genetics</i> , 2011, 2, 16.	1.1	13
378	Imputation of Missing Genotypes From Sparse to High Density Using Long-Range Phasing. <i>Genetics</i> , 2011, 189, 317-327.	1.2	79
379	Accuracy and Computational Efficiency of a Graphical Modeling Approach to Linkage Disequilibrium Estimation. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2011, 10, Article 5.	0.2	12
380	Integration of genomic and epigenomic DNA methylation data in common complex diseases by haplotype-specific methylation analysis. <i>Personalized Medicine</i> , 2011, 8, 243-251.	0.8	8
381	A Genome-Wide Search for Signals of High-Altitude Adaptation in Tibetans. <i>Molecular Biology and Evolution</i> , 2011, 28, 1003-1011.	3.5	311
382	Polymorphisms at the regulatory regions of the <i>CASR</i> gene influence stone risk in primary hyperparathyroidism. <i>European Journal of Endocrinology</i> , 2011, 164, 421-427.	1.9	42
383	Genome-Wide Association Study Identifies Two Major Loci Affecting Calving Ease and Growth-Related Traits in Cattle. <i>Genetics</i> , 2011, 187, 289-297.	1.2	96

#	ARTICLE	IF	CITATIONS
384	Psychophysical Dissection of Genotype Effects on Human Bitter Perception. <i>Chemical Senses</i> , 2011, 36, 161-167.	1.1	53
385	Global patterns of genetic diversity and signals of natural selection for human ADME genes. <i>Human Molecular Genetics</i> , 2011, 20, 528-540.	1.4	84
386	The Neuropeptide Galanin and Variants in the GalR1 Gene are Associated with Nicotine Dependence. <i>Neuropsychopharmacology</i> , 2011, 36, 2339-2348.	2.8	31
387	Missing Data Methods in Mendelian Randomization Studies With Multiple Instruments. <i>American Journal of Epidemiology</i> , 2011, 174, 1069-1076.	1.6	11
388	Bayesian Detection of Expression Quantitative Trait Loci Hot Spots. <i>Genetics</i> , 2011, 189, 1449-1459.	1.2	70
389	An Accurate Sequentially Markov Conditional Sampling Distribution for the Coalescent With Recombination. <i>Genetics</i> , 2011, 187, 1115-1128.	1.2	56
390	Association of the histidine-triad nucleotide-binding protein-1 (HINT1) gene variants with nicotine dependence. <i>Pharmacogenomics Journal</i> , 2011, 11, 251-257.	0.9	23
391	The Clark Phaseable Sample Size Problem: Long-Range Phasing and Loss of Heterozygosity in GWAS. <i>Journal of Computational Biology</i> , 2011, 18, 323-333.	0.8	16
392	HLA Type Inference via Haplotypes Identical by Descent. <i>Journal of Computational Biology</i> , 2011, 18, 483-493.	0.8	14
393	Inference from Samples of DNA Sequences Using a Two-Locus Model. <i>Journal of Computational Biology</i> , 2011, 18, 109-127.	0.8	19
394	Accuracy of Genomic Selection Prediction in Barley Breeding Programs: A Simulation Study Based On the Real Single Nucleotide Polymorphism Data of Barley Breeding Lines. <i>Crop Science</i> , 2011, 51, 1915-1927.	0.8	80
395	Diversity and Population Structure in a Geographic Sample of Tomato Accessions. <i>Crop Science</i> , 2011, 51, 1068-1079.	0.8	16
396	Imputation of missing single nucleotide polymorphism genotypes using a multivariate mixed model framework1. <i>Journal of Animal Science</i> , 2011, 89, 2042-2049.	0.2	19
397	Accuracy of genomic breeding values for residual feed intake in crossbred beef cattle1. <i>Journal of Animal Science</i> , 2011, 89, 3353-3361.	0.2	45
398	A comprehensively molecular haplotype-resolved genome of a European individual. <i>Genome Research</i> , 2011, 21, 1672-1685.	2.4	74
399	Integrating Rare-Variant Testing, Function Prediction, and Gene Network in Composite Resequencing-Based Genome-Wide Association Studies (CR-GWAS). <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 233-243.	0.8	16
400	Genotype Imputation with Thousands of Genomes. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 457-470.	0.8	869
401	DNA polymorphism in recombining and non-recombining mating-type-specific loci of the smut fungus <i>Microbotryum</i> . <i>Heredity</i> , 2011, 106, 936-944.	1.2	4

#	ARTICLE	IF	CITATIONS
402	Identification of Genomic Regions Associated with Phenotypic Variation between Dog Breeds using Selection Mapping. <i>PLoS Genetics</i> , 2011, 7, e1002316.	1.5	339
403	The History of African Gene Flow into Southern Europeans, Levantines, and Jews. <i>PLoS Genetics</i> , 2011, 7, e1001373.	1.5	224
404	Identification, Replication, and Functional Fine-Mapping of Expression Quantitative Trait Loci in Primary Human Liver Tissue. <i>PLoS Genetics</i> , 2011, 7, e1002078.	1.5	191
405	Detection of chromosome segments of zebu and taurine origin and their effect on beef production and growth1. <i>Journal of Animal Science</i> , 2011, 89, 2050-2060.	0.2	41
406	A Regression-Based Approach to Selection Mapping. <i>Journal of Heredity</i> , 2011, 102, 294-305.	1.0	11
407	A High Density SNP Array for the Domestic Horse and Extant Perissodactyla: Utility for Association Mapping, Genetic Diversity, and Phylogeny Studies. <i>PLoS Genetics</i> , 2012, 8, e1002451.	1.5	208
408	Variation of BMP3 Contributes to Dog Breed Skull Diversity. <i>PLoS Genetics</i> , 2012, 8, e1002849.	1.5	159
409	HTreeQA: Using Semi-Perfect Phylogeny Trees in Quantitative Trait Loci Study on Genotype Data. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 175-189.	0.8	16
410	Blockwise HMM computation for large-scale population genomic inference. <i>Bioinformatics</i> , 2012, 28, 2008-2015.	1.8	19
411	Crohn's Disease and Genetic Hitchhiking at IBD5. <i>Molecular Biology and Evolution</i> , 2012, 29, 101-111.	3.5	52
412	Genome-Wide Association Study Implicates Testis-Sperm Specific FKBP6 as a Susceptibility Locus for Impaired Acrosome Reaction in Stallions. <i>PLoS Genetics</i> , 2012, 8, e1003139.	1.5	28
413	Genome Patterns of Selection and Introgression of Haplotypes in Natural Populations of the House Mouse (<i>Mus musculus</i>). <i>PLoS Genetics</i> , 2012, 8, e1002891.	1.5	128
414	Potential and Optimization of Genomic Selection for Fusarium Head Blight Resistance in Six-Row Barley. <i>Crop Science</i> , 2012, 52, 1609-1621.	0.8	216
415	Inference of Population Structure using Dense Haplotype Data. <i>PLoS Genetics</i> , 2012, 8, e1002453.	1.5	983
416	Patterns of Ancestry, Signatures of Natural Selection, and Genetic Association with Stature in Western African Pygmies. <i>PLoS Genetics</i> , 2012, 8, e1002641.	1.5	118
417	The Contribution of RNA Decay Quantitative Trait Loci to Inter-Individual Variation in Steady-State Gene Expression Levels. <i>PLoS Genetics</i> , 2012, 8, e1003000.	1.5	104
418	Controls of Nucleosome Positioning in the Human Genome. <i>PLoS Genetics</i> , 2012, 8, e1003036.	1.5	255
419	A Two-Stage Random Forest-Based Pathway Analysis Method. <i>PLoS ONE</i> , 2012, 7, e36662.	1.1	22

#	ARTICLE	IF	CITATIONS
420	Systematic Detection of Epistatic Interactions Based on Allele Pair Frequencies. <i>PLoS Genetics</i> , 2012, 8, e1002463.	1.5	15
421	Historical genomics of North American maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12420-12425.	3.3	151
422	Ancestral haplotype-based association mapping with generalized linear mixed models accounting for stratification. <i>Bioinformatics</i> , 2012, 28, 2467-2473.	1.8	46
423	Interleukin-10 (IL-10) Polymorphisms Are Associated with IL-10 Production and Clinical Malaria in Young Children. <i>Infection and Immunity</i> , 2012, 80, 2316-2322.	1.0	36
424	A Fast and Efficient Approach for Genomic Selection with High-Density Markers. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1179-1184.	0.8	3
425	Genome-Wide Association Mapping of Quantitative Traits in Outbred Mice. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 167-174.	0.8	42
426	Integrating genetic and gene expression evidence into genome-wide association analysis of gene sets. <i>Genome Research</i> , 2012, 22, 386-397.	2.4	90
427	Calling amplified haplotypes in next generation tumor sequence data. <i>Genome Research</i> , 2012, 22, 362-374.	2.4	10
428	Death of <i>PRDM9</i> coincides with stabilization of the recombination landscape in the dog genome. <i>Genome Research</i> , 2012, 22, 51-63.	2.4	116
429	BLUP Genotype Imputation for Case-Control Association Testing with Related Individuals and Missing Data. <i>Journal of Computational Biology</i> , 2012, 19, 756-765.	0.8	11
430	Simultaneous Analysis of Multiple Data Types in Pharmacogenomic Studies Using Weighted Sparse Canonical Correlation Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 363-373.	1.0	17
431	Coalescent-Based DNA Barcoding: Multilocus Analysis and Robustness. <i>Journal of Computational Biology</i> , 2012, 19, 271-278.	0.8	7
432	Maximum-Parsimony Haplotype Inference Based on Sparse Representations of Genotypes. <i>IEEE Transactions on Signal Processing</i> , 2012, 60, 2013-2023.	3.2	6
433	Genome-wide meta-analyses of smoking behaviors in African Americans. <i>Translational Psychiatry</i> , 2012, 2, e119-e119.	2.4	94
434	Use of the gamma method for self-contained gene-set analysis of SNP data. <i>European Journal of Human Genetics</i> , 2012, 20, 565-571.	1.4	32
435	A Genome-Wide Association Study Identifies Novel Loci for Paclitaxel-Induced Sensory Peripheral Neuropathy in CALGB 40101. <i>Clinical Cancer Research</i> , 2012, 18, 5099-5109.	3.2	183
436	An ensemble-based approach to imputation of moderate-density genotypes for genomic selection with application to Angus cattle. <i>Genetical Research</i> , 2012, 94, 133-150.	0.3	40
437	Megabase-Scale Inversion Polymorphism in the Wild Ancestor of Maize. <i>Genetics</i> , 2012, 191, 883-894.	1.2	94

#	ARTICLE	IF	CITATIONS
438	Fosmid-based whole genome haplotyping of a HapMap trio child: evaluation of Single Individual Haplotyping techniques. <i>Nucleic Acids Research</i> , 2012, 40, 2041-2053.	6.5	105
439	Genic and nongenic contributions to natural variation of quantitative traits in maize. <i>Genome Research</i> , 2012, 22, 2436-2444.	2.4	125
440	Nonparametric low-rank tensor imputation. , 2012, , .		2
441	Network-Level and Population Genetics Analysis of the Insulin/TOR Signal Transduction Pathway Across Human Populations. <i>Molecular Biology and Evolution</i> , 2012, 29, 1379-1392.	3.5	24
442	Pediatric Biomedical Informatics. <i>Translational Bioinformatics</i> , 2012, , .	0.0	3
443	Differences in Selection Drive Olfactory Receptor Genes in Different Directions in Dogs and Wolf. <i>Molecular Biology and Evolution</i> , 2012, 29, 3475-3484.	3.5	30
444	Rare versus common variants in pharmacogenetics: <i>SLCO1B1</i> variation and methotrexate disposition. <i>Genome Research</i> , 2012, 22, 1-8.	2.4	232
445	Combining Markers into Haplotypes Can Improve Population Structure Inference. <i>Genetics</i> , 2012, 190, 159-174.	1.2	42
446	Robust Estimation of Local Genetic Ancestry in Admixed Populations Using a Nonparametric Bayesian Approach. <i>Genetics</i> , 2012, 191, 1295-1308.	1.2	20
447	Whole-genome scan for signatures of recent selection reveals loci associated with important traits in White Leghorn chickens. <i>Poultry Science</i> , 2012, 91, 1804-1812.	1.5	17
448	Probabilistic graphical models for genetic association studies. <i>Briefings in Bioinformatics</i> , 2012, 13, 20-33.	3.2	22
449	Genome-wide meta-analysis points to CTC1 and ZNF676 as genes regulating telomere homeostasis in humans. <i>Human Molecular Genetics</i> , 2012, 21, 5385-5394.	1.4	210
450	SNP Web Resources and Their Potential Applications in Personalized Medicine. <i>Current Drug Metabolism</i> , 2012, 13, 978-990.	0.7	31
451	Genetic Association Studies: An Information Content Perspective. <i>Current Genomics</i> , 2012, 13, 566-573.	0.7	18
452	A Coalescent Model for Genotype Imputation. <i>Genetics</i> , 2012, 191, 1239-1255.	1.2	24
453	Association Mapping for Grain Quality in a Diverse Sorghum Collection. <i>Plant Genome</i> , 2012, 5, .	1.6	113
454	Simultaneous SNP identification in association studies with missing data. <i>Annals of Applied Statistics</i> , 2012, 6, .	0.5	16
455	Influence of single nucleotide polymorphisms in factor VIII and von Willebrand factor genes on plasma factor VIII activity: the ARIC Study. <i>Blood</i> , 2012, 119, 1929-1934.	0.6	26

#	ARTICLE	IF	CITATIONS
456	Improving the Prediction of Clinical Outcomes from Genomic Data Using Multiresolution Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1442-1450.	1.9	4
457	Fast and accurate inference of local ancestry in Latino populations. Bioinformatics, 2012, 28, 1359-1367.	1.8	205
458	An assessment of linkage disequilibrium in Holstein cattle using a Bayesian network. Journal of Animal Breeding and Genetics, 2012, 129, 474-487.	0.8	14
459	Validation of single nucleotide polymorphisms associated with milk production traits in dairy cattle. Journal of Dairy Science, 2012, 95, 864-875.	1.4	40
460	Novel strategies to minimize progeny inbreeding while maximizing genetic gain using genomic information. Journal of Dairy Science, 2012, 95, 377-388.	1.4	107
461	Imputation of genotypes with low-density chips and its effect on reliability of direct genomic values in Dutch Holstein cattle. Journal of Dairy Science, 2012, 95, 876-889.	1.4	86
462	Different methods to calculate genomic predictions—Comparisons of BLUP at the single nucleotide polymorphism level (SNP-BLUP), BLUP at the individual level (G-BLUP), and the one-step approach (H-BLUP). Journal of Dairy Science, 2012, 95, 4065-4073.	1.4	41
463	<i>rehh</i> : an R package to detect footprints of selection in genome-wide SNP data from haplotype structure. Bioinformatics, 2012, 28, 1176-1177.	1.8	434
464	Inferring the History of Population Size Change from Genome-Wide SNP Data. Molecular Biology and Evolution, 2012, 29, 3653-3667.	3.5	20
465	Fast computation for genome-wide association studies using boosted one-step statistics. Bioinformatics, 2012, 28, 1818-1822.	1.8	12
466	Genetic adaptation to high altitude in the Ethiopian highlands. Genome Biology, 2012, 13, R1.	13.9	327
467	Dissecting the regulatory architecture of gene expression QTLs. Genome Biology, 2012, 13, R7.	13.9	188
468	Multiple ant colony algorithm method for selecting tag SNPs. Journal of Biomedical Informatics, 2012, 45, 931-937.	2.5	14
469	TNF-alpha gene (TNFA) variants increase risk for multi-organ dysfunction syndrome (MODS) in acute pancreatitis. Pancreatology, 2012, 12, 113-118.	0.5	42
470	Untangling the complex: molecular patterns in <i>Trachylepis variegata</i> and <i>T. punctulata</i> (Reptilia: Scincidae). African Journal of Herpetology, 2012, 61, 128-142.	0.3	7
471	Genomic Variation in Seven Khoe-San Groups Reveals Adaptation and Complex African History. Science, 2012, 338, 374-379.	6.0	364
472	Simpute: A Simple Genotype Imputation Method. , 2012, , .		0
473	Genetic polymorphisms of antioxidant enzymes as risk factors for oxidative stress-associated complications in preterm infants. Free Radical Research, 2012, 46, 1130-1139.	1.5	43

#	ARTICLE	IF	CITATIONS
474	Accurate prediction of error in Haplotype Inference methods through neural networks. , 2012, , .		1
475	Turkish Population Structure and Genetic Ancestry Reveal Relatedness among Eurasian Populations. <i>Annals of Human Genetics</i> , 2012, 76, 128-141.	0.3	53
476	The association between two single nucleotide polymorphisms within the insulin-degrading enzyme gene and Alzheimerâ€™s disease in a Chinese Han population. <i>Journal of Clinical Neuroscience</i> , 2012, 19, 745-749.	0.8	8
477	Length Distributions of Identity by Descent Reveal Fine-Scale Demographic History. <i>American Journal of Human Genetics</i> , 2012, 91, 809-822.	2.6	240
478	Assessment of gene-by-sex interaction effect on bone mineral density. <i>Journal of Bone and Mineral Research</i> , 2012, 27, 2051-2064.	3.1	47
479	Assessment of alternative genotyping strategies to maximize imputation accuracy at minimal cost. <i>Genetics Selection Evolution</i> , 2012, 44, 25.	1.2	73
480	Accuracy of pedigree and genomic predictions of carcass and novel meat quality traits in multi-breed sheep data assessed by cross-validation. <i>Genetics Selection Evolution</i> , 2012, 44, 33.	1.2	96
481	A phasing and imputation method for pedigreed populations that results in a single-stage genomic evaluation. <i>Genetics Selection Evolution</i> , 2012, 44, 9.	1.2	135
482	Identifying mutation regions for closely related individuals without a known pedigree. <i>BMC Bioinformatics</i> , 2012, 13, 146.	1.2	3
483	SNP interaction detection with Random Forests in high-dimensional genetic data. <i>BMC Bioinformatics</i> , 2012, 13, 164.	1.2	83
484	Identification of polymorphic inversions from genotypes. <i>BMC Bioinformatics</i> , 2012, 13, 28.	1.2	46
485	Distribution of events of positive selection and population differentiation in a metabolic pathway: the case of asparagine N-glycosylation. <i>BMC Evolutionary Biology</i> , 2012, 12, 98.	3.2	19
486	Genomic scan of selective sweeps in thin and fat tail sheep breeds for identifying of candidate regions associated with fat deposition. <i>BMC Genetics</i> , 2012, 13, 10.	2.7	236
487	Combining evidence of selection with association analysis increases power to detect regions influencing complex traits in dairy cattle. <i>BMC Genomics</i> , 2012, 13, 48.	1.2	31
488	Strategies and utility of imputed SNP genotypes for genomic analysis in dairy cattle. <i>BMC Genomics</i> , 2012, 13, 538.	1.2	68
489	A genome-wide scan of selective sweeps in two broiler chicken lines divergently selected for abdominal fat content. <i>BMC Genomics</i> , 2012, 13, 704.	1.2	48
490	Evaluation of the imputation performance of the program IMPUTE in an admixed sample from Mexico City using several model designs. <i>BMC Medical Genomics</i> , 2012, 5, 12.	0.7	9
491	Fast accurate missing SNP genotype local imputation. <i>BMC Research Notes</i> , 2012, 5, 404.	0.6	23

#	ARTICLE	IF	CITATIONS
492	Multi-SNP Haplotype Analysis Methods for Association Analysis. <i>Methods in Molecular Biology</i> , 2012, 850, 423-452.	0.4	17
493	Fast and accurate genotype imputation in genome-wide association studies through pre-phasing. <i>Nature Genetics</i> , 2012, 44, 955-959.	9.4	1,592
494	Population-Based Case-Control Association Studies. <i>Current Protocols in Human Genetics</i> , 2012, 74, Unit1.17.	3.5	9
495	Reliability of genomic prediction for German Holsteins using imputed genotypes from low-density chips. <i>Journal of Dairy Science</i> , 2012, 95, 5403-5411.	1.4	43
496	Comparative genomics between fly, mouse, and cattle identifies genes associated with sire conception rate. <i>Journal of Dairy Science</i> , 2012, 95, 6122-6129.	1.4	21
497	Haplotype Inference. <i>Methods in Molecular Biology</i> , 2012, 888, 177-196.	0.4	16
498	Phasing of Many Thousands of Genotyped Samples. <i>American Journal of Human Genetics</i> , 2012, 91, 238-251.	2.6	115
499	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. <i>American Journal of Human Genetics</i> , 2012, 91, 823-838.	2.6	227
500	Exploring Population Admixture Dynamics via Empirical and Simulated Genome-wide Distribution of Ancestral Chromosomal Segments. <i>American Journal of Human Genetics</i> , 2012, 91, 849-862.	2.6	36
501	Functional analysis of HapMap SNPs. <i>Gene</i> , 2012, 511, 358-363.	1.0	5
502	Solutions for biomedical grid computing—Case studies from the D-Grid project Services@MediGRID. <i>Journal of Computational Science</i> , 2012, 3, 280-297.	1.5	8
503	Association Mapping and Disease: Evolutionary Perspectives. <i>Methods in Molecular Biology</i> , 2012, 856, 275-291.	0.4	2
504	Extensive linkage disequilibrium and parallel adaptive divergence across threespine stickleback genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 395-408.	1.8	190
505	Application of imputation methods to genomic selection in Chinese Holstein cattle. <i>Journal of Animal Science and Biotechnology</i> , 2012, 3, 6.	2.1	10
506	A linear complexity phasing method for thousands of genomes. <i>Nature Methods</i> , 2012, 9, 179-181.	9.0	1,611
507	Advances in Bioinformatics and Computational Biology. <i>Lecture Notes in Computer Science</i> , 2012, , .	1.0	1
508	Detecting Rare Variants. <i>Methods in Molecular Biology</i> , 2012, 850, 453-464.	0.4	7
509	Statistical Human Genetics. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	13

#	ARTICLE	IF	CITATIONS
513	Genetic effects and correlations between production and fertility traits and their dependency on the lactation-stage in Holstein Friesians. <i>BMC Genetics</i> , 2012, 13, 108.	2.7	27
514	A novel analytical method, Birth Date Selection Mapping, detects response of the Angus (<i>Bos taurus</i>) genome to selection on complex traits. <i>BMC Genomics</i> , 2012, 13, 606.	1.2	37
515	Phenotype prediction from genome-wide association studies: application to smoking behaviors. <i>BMC Systems Biology</i> , 2012, 6, S11.	3.0	7
516	Exon-Specific QTLs Skew the Inferred Distribution of Expression QTLs Detected Using Gene Expression Array Data. <i>PLoS ONE</i> , 2012, 7, e30629.	1.1	18
517	Haplotype Analyses of Haemoglobin C and Haemoglobin S and the Dynamics of the Evolutionary Response to Malaria in Kassena-Nankana District of Ghana. <i>PLoS ONE</i> , 2012, 7, e34565.	1.1	16
518	A Quasi-Exclusive European Ancestry in the Senepol Tropical Cattle Breed Highlights the Importance of the slick Locus in Tropical Adaptation. <i>PLoS ONE</i> , 2012, 7, e36133.	1.1	48
519	WinHAP: An Efficient Haplotype Phasing Algorithm Based on Scalable Sliding Windows. <i>PLoS ONE</i> , 2012, 7, e43163.	1.1	6
520	Gene-Wide Characterization of Common Quantitative Trait Loci for ABCB1 mRNA Expression in Normal Liver Tissues in the Chinese Population. <i>PLoS ONE</i> , 2012, 7, e46295.	1.1	11
521	Genetic Markers Enhance Coronary Risk Prediction in Men: The MORGAM Prospective Cohorts. <i>PLoS ONE</i> , 2012, 7, e40922.	1.1	81
522	Nicotine Reward and Affective Nicotine Withdrawal Signs Are Attenuated in Calcium/Calmodulin-Dependent Protein Kinase IV Knockout Mice. <i>PLoS ONE</i> , 2012, 7, e51154.	1.1	11
523	Positive Selection in the Chromosome 16 VKORC1 Genomic Region Has Contributed to the Variability of Anticoagulant Response in Humans. <i>PLoS ONE</i> , 2012, 7, e53049.	1.1	9
524	Genotype Imputation for Latinos Using the HapMap and 1000 Genomes Project Reference Panels. <i>Frontiers in Genetics</i> , 2012, 3, 117.	1.1	20
525	Xenobiotic Metabolizing Gene Variants and Renal Cell Cancer: A Multicenter Study. <i>Frontiers in Oncology</i> , 2012, 2, 16.	1.3	8
526	Application of multiple shrinkage methods to genomic predictions ¹ . <i>Journal of Animal Science</i> , 2012, 90, 1777-1787.	0.2	8
527	Pharmacogenetics and Metabolism: Past, Present and Future. , 0, , .		2
528	Genome-Wide Approaches for the Study of Dog Domestication. , 0, , 275-298.		2
529	Components of the accuracy of genomic prediction in a multi-breed sheep population ¹ . <i>Journal of Animal Science</i> , 2012, 90, 3375-3384.	0.2	137
530	The accuracies of DNA-based estimates of genetic merit derived from Angus or multibreed beef cattle training populations ^{1,2,3} . <i>Journal of Animal Science</i> , 2012, 90, 4191-4202.	0.2	8

#	ARTICLE	IF	CITATIONS
531	Origins and Genetic Legacy of Neolithic Farmers and Hunter-Gatherers in Europe. <i>Science</i> , 2012, 336, 466-469.	6.0	507
532	Association of genetic variants of human telomerase with colorectal polyps and colorectal cancer risk. <i>Molecular Carcinogenesis</i> , 2012, 51, E176-82.	1.3	34
533	A Bayesian Integrative Genomic Model for Pathway Analysis of Complex Traits. <i>Genetic Epidemiology</i> , 2012, 36, 352-359.	0.6	40
534	DIVERGENOME: A Bioinformatics Platform to Assist Population Genetics and Genetic Epidemiology Studies. <i>Genetic Epidemiology</i> , 2012, 36, 360-367.	0.6	6
535	A Two-Platform Design for Next Generation Genome-Wide Association Studies. <i>Genetic Epidemiology</i> , 2012, 36, 401-409.	0.6	14
536	Reprioritizing Genetic Associations in Hit Regions Using LASSO-Based Resample Model Averaging. <i>Genetic Epidemiology</i> , 2012, 36, 451-462.	0.6	22
537	Genotype Imputation for African Americans Using Data From the Phase III Versus 1000 Genomes Projects. <i>Genetic Epidemiology</i> , 2012, 36, 508-516.	0.6	13
538	Detecting Association of Rare and Common Variants by Testing an Optimally Weighted Combination of Variants. <i>Genetic Epidemiology</i> , 2012, 36, 561-571.	0.6	74
539	Combined effects of different interleukin-28B gene variants on the outcome of dual combination therapy in chronic hepatitis C virus type 1 infection. <i>Hepatology</i> , 2012, 55, 1700-1710.	3.6	75
540	Association of serum bilirubin and promoter variations in <i>HMOX1</i> and <i>UGT1A1</i> genes with sporadic colorectal cancer. <i>International Journal of Cancer</i> , 2012, 131, 1549-1555.	2.3	70
541	Common variants near <i>MBNL1</i> and <i>NKX2-5</i> are associated with infantile hypertrophic pyloric stenosis. <i>Nature Genetics</i> , 2012, 44, 334-337.	9.4	40
542	Recombination networks as genetic markers in a human variation study of the Old World. <i>Human Genetics</i> , 2012, 131, 601-613.	1.8	7
543	Population Identification Using Genetic Data. <i>Annual Review of Genomics and Human Genetics</i> , 2012, 13, 337-361.	2.5	76
544	Population structure and linkage disequilibrium in <i>Lupinus albus</i> L. germplasm and its implication for association mapping. <i>Theoretical and Applied Genetics</i> , 2012, 125, 517-530.	1.8	21
545	The <i>RIPK2</i> gene: a positional candidate for tick burden supported by genetic associations in cattle and immunological response of knockout mouse. <i>Immunogenetics</i> , 2012, 64, 379-388.	1.2	9
546	A global view of the <i>OCA2-HERC2</i> region and pigmentation. <i>Human Genetics</i> , 2012, 131, 683-696.	1.8	113
547	Genetic Adaptation of Fatty-Acid Metabolism: A Human-Specific Haplotype Increasing the Biosynthesis of Long-Chain Omega-3 and Omega-6 Fatty Acids. <i>American Journal of Human Genetics</i> , 2012, 90, 809-820.	2.6	205
548	Accuracy of genotype imputation in sheep breeds. <i>Animal Genetics</i> , 2012, 43, 72-80.	0.6	98

#	ARTICLE	IF	CITATIONS
549	Comparison of penalty functions for sparse canonical correlation analysis. <i>Computational Statistics and Data Analysis</i> , 2012, 56, 245-254.	0.7	22
550	EVIDENCE OF ADAPTATION FROM ANCESTRAL VARIATION IN YOUNG POPULATIONS OF BEACH MICE. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 3209-3223.	1.1	64
551	Imputation of missing SNP genotypes using low density panels. <i>Livestock Science</i> , 2012, 146, 80-83.	0.6	4
552	Genome-wide association analysis for feed efficiency in Angus cattle. <i>Animal Genetics</i> , 2012, 43, 367-374.	0.6	110
553	Genome-wide association analysis for quantitative trait loci influencing <i>W</i> <i>B</i> ratzler shear force in five taurine cattle breeds. <i>Animal Genetics</i> , 2012, 43, 662-673.	0.6	76
554	Genetic mapping of recurrent exertional rhabdomyolysis in a population of <i>N</i> orth <i>A</i> <i>T</i> thoroughbreds. <i>Animal Genetics</i> , 2012, 43, 730-738.	0.6	16
555	Cytosuclear equilibrium following interspecific introgression in a turtle lacking sex chromosomes. <i>Biological Journal of the Linnean Society</i> , 2012, 106, 405-417.	0.7	3
556	Effects of vicariant barriers, habitat stability, population isolation and environmental features on species divergence in the south-western Australian coastal reptile community. <i>Molecular Ecology</i> , 2012, 21, 3809-3822.	2.0	34
557	Pedigree- and marker-based methods in the estimation of genetic diversity in small groups of Holstein cattle. <i>Journal of Animal Breeding and Genetics</i> , 2012, 129, 195-205.	0.8	20
558	The importance of information on relatives for the prediction of genomic breeding values and the implications for the makeup of reference data sets in livestock breeding schemes. <i>Genetics Selection Evolution</i> , 2012, 44, 4.	1.2	249
559	Haplotype reconstruction using perfect phylogeny and sequence data. <i>BMC Bioinformatics</i> , 2012, 13, S3.	1.2	8
560	A novel method to identify high order gene-gene interactions in genome-wide association studies: Gene-based MDR. <i>BMC Bioinformatics</i> , 2012, 13, S5.	1.2	66
561	Comparison of linear mixed model analysis and genealogy-based haplotype clustering with a Bayesian approach for association mapping in a pedigreed population. <i>BMC Proceedings</i> , 2012, 6, S4.	1.8	5
562	Haploscope: a tool for the graphical display of haplotype structure in populations. <i>Genetic Epidemiology</i> , 2012, 36, 17-21.	0.6	10
563	The same ELA class II risk factors confer equine insect bite hypersensitivity in two distinct populations. <i>Immunogenetics</i> , 2012, 64, 201-208.	1.2	40
564	Breed-specific ancestry studies and genome-wide association analysis highlight an association between the MYH9 gene and heat tolerance in Alaskan sprint racing sled dogs. <i>Mammalian Genome</i> , 2012, 23, 178-194.	1.0	14
565	Association of B3GNT5 Polymorphisms with Susceptibility to ETEC F4ab/ac in the White Duroc \times Erhualian Intercross and 15 Outbred Pig Breeds. <i>Biochemical Genetics</i> , 2012, 50, 19-33.	0.8	4
566	A unique genome-wide association analysis in extended Utah high-risk pedigrees identifies a novel melanoma risk variant on chromosome arm 10q. <i>Human Genetics</i> , 2012, 131, 77-85.	1.8	24

#	ARTICLE	IF	CITATIONS
567	Genetic variants in a lipid regulatory pathway as potential tools for improving the nutritional quality of grass-fed beef. <i>Animal Genetics</i> , 2013, 44, 121-129.	0.6	12
568	Identifying a predictive model for response to atypical antipsychotic monotherapy treatment in south Indian schizophrenia patients. <i>Genomics</i> , 2013, 102, 131-135.	1.3	10
569	Genotype Imputation in Genome-Wide Association Studies. <i>Current Protocols in Human Genetics</i> , 2013, 78, Unit 1.25.	3.5	34
570	Use of partial least squares regression to impute SNP genotypes in Italian Cattle breeds. <i>Genetics Selection Evolution</i> , 2013, 45, 15.	1.2	8
571	iXora: exact haplotype inferencing and trait association. <i>BMC Genetics</i> , 2013, 14, 48.	2.7	23
572	Variants in the 3' UTR of General Transcription Factor IIF, polypeptide 2 affect female calving efficiency in Japanese Black cattle. <i>BMC Genetics</i> , 2013, 14, 41.	2.7	15
573	Assessment of the genomic variation in a cattle population by re-sequencing of key animals at low to medium coverage. <i>BMC Genomics</i> , 2013, 14, 446.	1.2	64
574	A genome-wide integrative study of microRNAs in human liver. <i>BMC Genomics</i> , 2013, 14, 395.	1.2	39
575	A candidate gene based approach validates Md-PG1 as the main responsible for a QTL impacting fruit texture in apple (<i>Malus x domestica</i> Borkh). <i>BMC Plant Biology</i> , 2013, 13, 37.	1.6	70
576	Association of surfactant protein B gene polymorphisms (C/A-18, C/T1580, intron 4 and A/G9306) and haplotypes with bronchopulmonary dysplasia in chinese han population. <i>Journal of Huazhong University of Science and Technology [Medical Sciences]</i> , 2013, 33, 323-328.	1.0	10
577	Probabilistic Inference of Viral Quasispecies Subject to Recombination. <i>Journal of Computational Biology</i> , 2013, 20, 113-123.	0.8	123
578	A block-based imputation approach with adaptive LD blocks for fast genotype imputation. <i>Biochip Journal</i> , 2013, 7, 63-67.	2.5	1
579	Analyses of genetic ancestry enable key insights for molecular ecology. <i>Molecular Ecology</i> , 2013, 22, 5278-5294.	2.0	31
580	Short communication: A missense mutation in the PROP1 (prophet of Pit 1) gene affects male fertility and milk production traits in the US Holstein population. <i>Journal of Dairy Science</i> , 2013, 96, 1255-1257.	1.4	35
582	Artificial Selection on Brain-Expressed Genes during the Domestication of Dog. <i>Molecular Biology and Evolution</i> , 2013, 30, 1867-1876.	3.5	74
583	Adaptive Evolution of Multiple Traits Through Multiple Mutations at a Single Gene. <i>Science</i> , 2013, 339, 1312-1316.	6.0	277
584	Genomic prediction of trait segregation in a progeny population: a case study of Japanese pear (<i>Pyrus</i> Tj ETQq0 0 0 rgBT /Overlock 10 T	2.7	31
585	High-density marker imputation accuracy in sixteen French cattle breeds. <i>Genetics Selection Evolution</i> , 2013, 45, 33.	1.2	93

#	ARTICLE	IF	CITATIONS
586	Haplotype phasing after joint estimation of recombination and linkage disequilibrium in breeding populations. <i>Journal of Animal Science and Biotechnology</i> , 2013, 4, 30.	2.1	14
587	Genomic selection using low density marker panels with application to a sire line in pigs. <i>Genetics Selection Evolution</i> , 2013, 45, 28.	1.2	58
588	The estimation of genomic relationships using breedwise allele frequencies among animals in multibreed populations. <i>Journal of Dairy Science</i> , 2013, 96, 5364-5375.	1.4	31
589	Assets of imputation to ultra-high density for productive and functional traits. <i>Journal of Dairy Science</i> , 2013, 96, 6047-6058.	1.4	12
590	An evaluation of a novel estimator of linkage disequilibrium. <i>Heredity</i> , 2013, 111, 275-285.	1.2	6
591	Genome-wide association analysis to identify genotype × environment interaction for milk protein yield and level of somatic cell score as environmental descriptors in German Holsteins. <i>Journal of Dairy Science</i> , 2013, 96, 7318-7324.	1.4	17
592	Performance analysis & improvement of SNP-HAP on Multi-core CPUs. , 2013, , .		2
593	Accuracy of genomic prediction using an evenly spaced, low-density single nucleotide polymorphism panel in broiler chickens. <i>Poultry Science</i> , 2013, 92, 1712-1723.	1.5	27
594	Confirmation and fine-mapping of clinical mastitis and somatic cell score QTL in Nordic Holstein cattle. <i>Animal Genetics</i> , 2013, 44, 620-626.	0.6	39
595	Malaria haplotype frequency estimation. <i>Statistics in Medicine</i> , 2013, 32, 3737-3751.	0.8	10
596	Admixture Patterns and Genetic Differentiation in Negrito Groups from West Malaysia Estimated from Genome-wide SNP Data. <i>Human Biology</i> , 2013, 85, 173-188.	0.4	21
597	Genomic Divergence during Speciation Driven by Adaptation to Altitude. <i>Molecular Biology and Evolution</i> , 2013, 30, 2553-2567.	3.5	91
598	Association analysis for feed efficiency traits in beef cattle using preserved haplotypes. <i>Genome</i> , 2013, 56, 586-591.	0.9	1
599	Genotype imputation via matrix completion. <i>Genome Research</i> , 2013, 23, 509-518.	2.4	50
600	Common variants in the HLA-DRB1-HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis. <i>Nature Genetics</i> , 2013, 45, 208-213.	9.4	86
601	An integrative variant analysis pipeline for accurate genotype/haplotype inference in population NGS data. <i>Genome Research</i> , 2013, 23, 833-842.	2.4	93
602	Improved whole-chromosome phasing for disease and population genetic studies. <i>Nature Methods</i> , 2013, 10, 5-6.	9.0	1,153
603	THE OPPORTUNITY FOR BALANCING SELECTION IN EXPERIMENTAL POPULATIONS OF <i>CAENORHABDITIS ELEGANS</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 142-156.	1.1	38

#	ARTICLE	IF	CITATIONS
604	Positive natural selection of TRIB2, a novel gene that influences visceral fat accumulation, in East Asia. <i>Human Genetics</i> , 2013, 132, 201-217.	1.8	19
605	Modeling Recent Human Evolution in Mice by Expression of a Selected EDAR Variant. <i>Cell</i> , 2013, 152, 691-702.	13.5	250
606	GIGI: An Approach to Effective Imputation of Dense Genotypes on Large Pedigrees. <i>American Journal of Human Genetics</i> , 2013, 92, 504-516.	2.6	57
607	Genomic evaluations using similarity between haplotypes. <i>Journal of Animal Breeding and Genetics</i> , 2013, 130, 259-269.	0.8	31
608	Kernel methods and haplotypes used in selection of sparse DNA markers for protein yield in dairy cattle. <i>Mathematical Biosciences</i> , 2013, 243, 57-66.	0.9	1
609	Porcine colonization of the Americas: a 60k SNP story. <i>Heredity</i> , 2013, 110, 321-330.	1.2	58
610	THE GENETIC ARCHITECTURE OF REPRODUCTIVE ISOLATION DURING SPECIATION-WITH-GENE-FLOW IN LAKE WHITEFISH SPECIES PAIRS ASSESSED BY RAD SEQUENCING. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 2483-2497.	1.1	187
611	The genomic signature of dog domestication reveals adaptation to a starch-rich diet. <i>Nature</i> , 2013, 495, 360-364.	13.7	805
612	Microsatellite variation in the equine <sc>MHC</sc>. <i>Animal Genetics</i> , 2013, 44, 267-275.	0.6	16
613	Positive selection of protective variants for type 2 diabetes from the Neolithic onward: a case study in Central Asia. <i>European Journal of Human Genetics</i> , 2013, 21, 1146-1151.	1.4	35
614	Detecting Signatures of Selection Through Haplotype Differentiation Among Hierarchically Structured Populations. <i>Genetics</i> , 2013, 193, 929-941.	1.2	340
615	Genetic structure and association mapping of adaptive and selective traits in the east Texas loblolly pine (<i>Pinus taeda</i> L.) breeding populations. <i>Tree Genetics and Genomes</i> , 2013, 9, 1161-1178.	0.6	40
616	Identifying Darwinian Selection Acting on Different Human APOL1 Variants among Diverse African Populations. <i>American Journal of Human Genetics</i> , 2013, 93, 54-66.	2.6	91
617	Identity by Descent: Variation in Meiosis, Across Genomes, and in Populations. <i>Genetics</i> , 2013, 194, 301-326.	1.2	279
618	Introgression and the fate of domesticated genes in a wild mammal population. <i>Molecular Ecology</i> , 2013, 22, 4210-4221.	2.0	53
619	Use of Ancestral Haplotypes in Genome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2013, 1019, 347-380.	0.4	2
620	Genotype Phasing in Populations of Closely Related Individuals. <i>Methods in Molecular Biology</i> , 2013, 1019, 381-394.	0.4	0
621	Genotype Imputation to Increase Sample Size in Pedigreed Populations. <i>Methods in Molecular Biology</i> , 2013, 1019, 395-410.	0.4	8

#	ARTICLE	IF	CITATIONS
622	Genome-Wide Association Studies and Genomic Prediction. <i>Methods in Molecular Biology</i> , 2013, , .	0.4	53
623	INTEGRATIVE TESTING OF HOW ENVIRONMENTS FROM THE PAST TO THE PRESENT SHAPE GENETIC STRUCTURE ACROSS LANDSCAPES. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3386-3402.	1.1	110
624	The genomics of selection in dogs and the parallel evolution between dogs and humans. <i>Nature Communications</i> , 2013, 4, 1860.	5.8	275
625	Genome-wide association study for backfat thickness in Canchim beef cattle using Random Forest approach. <i>BMC Genetics</i> , 2013, 14, 47.	2.7	32
626	Rank Regularization and Bayesian Inference for Tensor Completion and Extrapolation. <i>IEEE Transactions on Signal Processing</i> , 2013, 61, 5689-5703.	3.2	55
627	FNphasing: A Novel Fast Heuristic Algorithm for Haplotype Phasing Based on Flow Network Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 372-382.	1.9	0
628	The Use of Imputed Sibling Genotypes in Sibship-Based Association Analysis: On Modeling Alternatives, Power and Model Misspecification. <i>Behavior Genetics</i> , 2013, 43, 254-266.	1.4	6
629	HapBoost: A Fast Approach to Boosting Haplotype Association Analyses in Genome-Wide Association Studies. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 207-212.	1.9	2
630	RNA sequencing reveals the complex regulatory network in the maize kernel. <i>Nature Communications</i> , 2013, 4, 2832.	5.8	252
631	Systems-level approaches reveal conservation of trans-regulated genes in the rat and genetic determinants of blood pressure in humans. <i>Cardiovascular Research</i> , 2013, 97, 653-665.	1.8	31
632	Genome-wide meta-analysis of observational studies shows common genetic variants associated with macronutrient intake. <i>American Journal of Clinical Nutrition</i> , 2013, 97, 1395-1402.	2.2	210
633	The Population Genomics of Repeated Evolution in the Blind Cavefish <i>Astyanax mexicanus</i> . <i>Molecular Biology and Evolution</i> , 2013, 30, 2383-2400.	3.5	87
634	Improving the Accuracy and Efficiency of Identity-by-Descent Detection in Population Data. <i>Genetics</i> , 2013, 194, 459-471.	1.2	536
635	A dynamic Bayesian Markov model for phasing and characterizing haplotypes in next-generation sequencing. <i>Bioinformatics</i> , 2013, 29, 878-885.	1.8	11
636	Genotype calling and haplotyping in parent-offspring trios. <i>Genome Research</i> , 2013, 23, 142-151.	2.4	46
637	Adaptive clustering and adaptive weighting methods to detect disease associated rare variants. <i>European Journal of Human Genetics</i> , 2013, 21, 332-337.	1.4	13
638	Genome-Wide Analysis Reveals Selection for Important Traits in Domestic Horse Breeds. <i>PLoS Genetics</i> , 2013, 9, e1003211.	1.5	240
639	Simpute: An Efficient Solution for Dense Genotypic Data. <i>BioMed Research International</i> , 2013, 2013, 1-7.	0.9	0

#	ARTICLE	IF	CITATIONS
640	Comparative Polygenic Analysis of Maximal Ethanol Accumulation Capacity and Tolerance to High Ethanol Levels of Cell Proliferation in Yeast. <i>PLoS Genetics</i> , 2013, 9, e1003548.	1.5	88
641	Gene Copy-Number Polymorphism Caused by Retrotransposition in Humans. <i>PLoS Genetics</i> , 2013, 9, e1003242.	1.5	88
642	Admixture Mapping in Lupus Identifies Multiple Functional Variants within <i>IFIH1</i> Associated with Apoptosis, Inflammation, and Autoantibody Production. <i>PLoS Genetics</i> , 2013, 9, e1003222.	1.5	107
643	GUESS-ing Polygenic Associations with Multiple Phenotypes Using a GPU-Based Evolutionary Stochastic Search Algorithm. <i>PLoS Genetics</i> , 2013, 9, e1003657.	1.5	58
644	The Genomic Signature of Crop-Wild Introgression in Maize. <i>PLoS Genetics</i> , 2013, 9, e1003477.	1.5	291
645	Enlarging a training set for genomic selection by imputation of un-genotyped animals in populations of varying genetic architecture. <i>Genetics Selection Evolution</i> , 2013, 45, 12.	1.2	29
646	Inferring Selection Intensity and Allele Age from Multilocus Haplotype Structure. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1429-1442.	0.8	26
647	Complex Patterns of Local Adaptation in Teosinte. <i>Genome Biology and Evolution</i> , 2013, 5, 1594-1609.	1.1	139
648	Variants in the 15q25 gene cluster are associated with risk for schizophrenia and bipolar disorder. <i>Psychiatric Genetics</i> , 2013, 23, 20-28.	0.6	35
649	Genetic Structure and Linkage Disequilibrium in a Diverse, Representative Collection of the C4 Model Plant, <i>Sorghum bicolor</i> . <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 783-793.	0.8	58
650	OATP1B1-related drug-drug and drug-gene interactions as potential risk factors for cerivastatin-induced rhabdomyolysis. <i>Pharmacogenetics and Genomics</i> , 2013, 23, 355-364.	0.7	47
651	HapFABIA: Identification of very short segments of identity by descent characterized by rare variants in large sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, e202-e202.	6.5	21
652	Integrative Modeling of eQTLs and Cis-Regulatory Elements Suggests Mechanisms Underlying Cell Type Specificity of eQTLs. <i>PLoS Genetics</i> , 2013, 9, e1003649.	1.5	151
653	Genomic architecture of adaptive color pattern divergence and convergence in <i>Heliconius</i> butterflies. <i>Genome Research</i> , 2013, 23, 1248-1257.	2.4	72
654	Detecting Association of Rare Variants by Testing an Optimally Weighted Combination of Variants for Quantitative Traits in General Families. <i>Annals of Human Genetics</i> , 2013, 77, 524-534.	0.3	7
655	EMLasso: logistic lasso with missing data. <i>Statistics in Medicine</i> , 2013, 32, 3143-3157.	0.8	18
656	Testing the genetic predictions of a biogeographical model in a dominant endemic Eastern Pacific coral (<i>Porites panamensis</i>) using a genetic seascape approach. <i>Ecology and Evolution</i> , 2013, 3, 4070-4091.	0.8	25
657	Andean and Tibetan patterns of adaptation to high altitude. <i>American Journal of Human Biology</i> , 2013, 25, 190-197.	0.8	115

#	ARTICLE	IF	CITATIONS
658	Haplotype-based profiling of subtle allelic imbalance with SNP arrays. <i>Genome Research</i> , 2013, 23, 152-158.	2.4	47
659	Identification of QTL in Spring Wheat Associated with Resistance to a Novel Isolate of <i>Pyrenophora tritici-repentis</i> . <i>Crop Science</i> , 2013, 53, 842-852.	0.8	32
660	Using Genome-Wide Association Analysis to Characterize Environmental Sensitivity of Milk Traits in Dairy Cattle. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1085-1093.	0.8	16
661	WHOLE GENOME IDENTITY-BY-DESCENT DETERMINATION. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1350002.	0.3	10
662	New World cattle show ancestry from multiple independent domestication events. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1398-406.	3.3	126
663	Admixture Patterns and Genetic Differentiation in Negrito Groups from West Malaysia Estimated from Genome-wide SNP Data. <i>Human Biology</i> , 2013, 85, 173.	0.4	3
664	Methods of tagSNP selection and other variables affecting imputation accuracy in swine. <i>BMC Genetics</i> , 2013, 14, 8.	2.7	36
665	Comparison of different imputation methods from low- to high-density panels using Chinese Holstein cattle. <i>Animal</i> , 2013, 7, 729-735.	1.3	13
666	The genome sequence of the most widely cultivated cacao type and its use to identify candidate genes regulating pod color. <i>Genome Biology</i> , 2013, 14, r53.	3.8	225
667	Pharmacogenetics in American Indian populations. <i>Pharmacogenetics and Genomics</i> , 2013, 23, 403-414.	0.7	54
669	The admixed population structure in Danish Jersey dairy cattle challenges accurate genomic predictions ¹ . <i>Journal of Animal Science</i> , 2013, 91, 3105-3112.	0.2	23
670	Identification of single nucleotide polymorphisms in genes involved in digestive and metabolic processes associated with feed efficiency and performance traits in beef cattle ^{1,2} . <i>Journal of Animal Science</i> , 2013, 91, 2512-2529.	0.2	24
671	Clarifying haplotype ambiguity of NAT2 in multi-national cohorts. <i>Frontiers in Bioscience - Scholar</i> , 2013, S5, 672-684.	0.8	10
672	On Combining Reference Data to Improve Imputation Accuracy. <i>PLoS ONE</i> , 2013, 8, e55600.	1.1	8
673	Breakdown of Methods for Phasing and Imputation in the Presence of Double Genotype Sharing. <i>PLoS ONE</i> , 2013, 8, e60354.	1.1	3
674	Detecting Loci under Recent Positive Selection in Dairy and Beef Cattle by Combining Different Genome-Wide Scan Methods. <i>PLoS ONE</i> , 2013, 8, e64280.	1.1	84
675	Adaptation of Maize to Temperate Climates: Mid-Density Genome-Wide Association Genetics and Diversity Patterns Reveal Key Genomic Regions, with a Major Contribution of the Vgt2 (ZCN8) Locus. <i>PLoS ONE</i> , 2013, 8, e71377.	1.1	83
676	A Large Animal Model for CNGB1 Autosomal Recessive Retinitis Pigmentosa. <i>PLoS ONE</i> , 2013, 8, e72229.	1.1	53

#	ARTICLE	IF	CITATIONS
677	Effect of Artificial Selection on Runs of Homozygosity in U.S. Holstein Cattle. PLoS ONE, 2013, 8, e80813.	1.1	165
678	A Post-GWAS Replication Study Confirming the PTK2 Gene Associated with Milk Production Traits in Chinese Holstein. PLoS ONE, 2013, 8, e83625.	1.1	14
679	Imputation of microsatellite alleles from dense SNP genotypes for parentage verification across multiple Bos taurus and Bos indicus breeds. Frontiers in Genetics, 2013, 4, 176.	1.1	29
680	A genome-wide association scan in pig identifies novel regions associated with feed efficiency trait1. Journal of Animal Science, 2013, 91, 1041-1050.	0.2	54
681	Rapid Identification of Alleles at the Soybean Maturity Gene E3 using genotyping by Sequencing and a Haplotype-Based Approach. Plant Genome, 2014, 7, plantgenome2013.10.0034.	1.6	45
682	Genome-Wide Association Scan for Variants Associated with Early-Onset Prostate Cancer. PLoS ONE, 2014, 9, e93436.	1.1	25
683	Assessing Accuracy of Genotype Imputation in American Indians. PLoS ONE, 2014, 9, e102544.	1.1	9
684	Genome-Wide Association Study Reveals Novel Quantitative Trait Loci Associated with Resistance to Multiple Leaf Spot Diseases of Spring Wheat. PLoS ONE, 2014, 9, e108179.	1.1	189
685	Accelerating the Switchgrass (Panicum virgatum L.) Breeding Cycle Using Genomic Selection Approaches. PLoS ONE, 2014, 9, e112227.	1.1	65
686	Genome-wide association study and ancestral origins of the slick-hair coat in tropically adapted cattle. Frontiers in Genetics, 2014, 5, 101.	1.1	51
687	Genome Wide Association Mapping of <i>Sclerotinia sclerotiorum</i> Resistance in Soybean with a Genotyping-by-Sequencing Approach. Plant Genome, 2014, 7, plantgenome2013.10.0030.	1.6	135
688	Statistic and Analytical Strategies for HLA Data. , 2014, , .		0
690	A genome-wide scan for selection signatures in Yorkshire and Landrace pigs based on sequencing data. Animal Genetics, 2014, 45, 808-816.	0.6	19
691	Human-induced evolution caught in action: SNP-array reveals rapid amphi-atlantic spread of pesticide resistance in the salmon ectoparasite Lepeophtheirus salmonis. BMC Genomics, 2014, 15, 937.	1.2	74
692	Groupwise registration of brain magnetic resonance images: A review. Journal of Shanghai Jiaotong University (Science), 2014, 19, 755-762.	0.5	4
693	The genetic basis and experimental evolution of inbreeding depression in Caenorhabditis elegans. Heredity, 2014, 112, 248-254.	1.2	18
694	HIBAG-HLA genotype imputation with attribute bagging. Pharmacogenomics Journal, 2014, 14, 192-200.	0.9	339
695	Privacy preserving protocol for detecting genetic relatives using rare variants. Bioinformatics, 2014, 30, i204-i211.	1.8	10

#	ARTICLE	IF	CITATIONS
696	A set-based association test identifies sex-specific gene sets associated with type 2 diabetes. <i>Frontiers in Genetics</i> , 2014, 5, 395.	1.1	9
697	HapTree: A Novel Bayesian Framework for Single Individual Polyplotyping Using NGS Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003502.	1.5	75
698	Genome-Wide Inference of Ancestral Recombination Graphs. <i>PLoS Genetics</i> , 2014, 10, e1004342.	1.5	323
699	A hidden Markov model for haplotype inference for present-absent data of clustered genes using identified haplotypes and haplotype patterns. <i>Frontiers in Genetics</i> , 2014, 5, 267.	1.1	1
700	An HMM-Based Comparative Genomic Framework for Detecting Introgression in Eukaryotes. <i>PLoS Computational Biology</i> , 2014, 10, e1003649.	1.5	50
701	Introgression from Domestic Goat Generated Variation at the Major Histocompatibility Complex of Alpine Ibex. <i>PLoS Genetics</i> , 2014, 10, e1004438.	1.5	87
702	Decreased Nucleotide and Expression Diversity and Modified Coexpression Patterns Characterize Domestication in the Common Bean. <i>Plant Cell</i> , 2014, 26, 1901-1912.	3.1	103
703	Analysis of Deep Sequencing Data. <i>Comprehensive Analytical Chemistry</i> , 2014, , 325-354.	0.7	0
704	Joint Identification of Genetic Variants for Physical Activity in Korean Population. <i>International Journal of Molecular Sciences</i> , 2014, 15, 12407-12421.	1.8	16
705	A Population Genetic Signal of Polygenic Adaptation. <i>PLoS Genetics</i> , 2014, 10, e1004412.	1.5	447
706	Identification of Allelic Imbalance with a Statistical Model for Subtle Genomic Mosaicism. <i>PLoS Computational Biology</i> , 2014, 10, e1003765.	1.5	6
707	A General Approach for Haplotype Phasing across the Full Spectrum of Relatedness. <i>PLoS Genetics</i> , 2014, 10, e1004234.	1.5	553
708	Early Back-to-Africa Migration into the Horn of Africa. <i>PLoS Genetics</i> , 2014, 10, e1004393.	1.5	87
709	A Genomic Approach for Distinguishing between Recent and Ancient Admixture as Applied to Cattle. <i>Journal of Heredity</i> , 2014, 105, 445-456.	1.0	15
710	Detecting Local Haplotype Sharing and Haplotype Association. <i>Genetics</i> , 2014, 197, 823-838.	1.2	51
711	Multiple <i>FLC</i> haplotypes defined by independent <i>cis</i> -regulatory variation underpin life history diversity in <i>Arabidopsis thaliana</i> . <i>Genes and Development</i> , 2014, 28, 1635-1640.	2.7	122
712	Haplotype-centered mapping for improved alignments and genetic association studies. , 2014, , .		1
713	Maternal <i>PRKAA1</i> and <i>EDNRA</i> genotypes are associated with birth weight, and <i>PRKAA1</i> with uterine artery diameter and metabolic homeostasis at high altitude. <i>Physiological Genomics</i> , 2014, 46, 687-697.	1.0	83

#	ARTICLE	IF	CITATIONS
714	Insights into the Maize Pan-Genome and Pan-Transcriptome. <i>Plant Cell</i> , 2014, 26, 121-135.	3.1	498
715	A Novel Test for Testing the Optimally Weighted Combination of Rare and Common Variants Based on Data of Parents and Affected Children. <i>Genetic Epidemiology</i> , 2014, 38, 135-143.	0.6	5
716	PedBLIMP: Extending Linear Predictors to Impute Genotypes in Pedigrees. <i>Genetic Epidemiology</i> , 2014, 38, 531-541.	0.6	5
717	Multiple haplotype-resolved genomes reveal population patterns of gene and protein diplotypes. <i>Nature Communications</i> , 2014, 5, 5569.	5.8	27
718	Footprints of recent selection and variability in breed composition in the Göttingen Minipig genome. <i>Animal Genetics</i> , 2014, 45, 381-391.	0.6	7
719	A Rare Variant Association Test Based on Combinations of Single-Variant Tests. <i>Genetic Epidemiology</i> , 2014, 38, 494-501.	0.6	7
720	Navigating the mitochondrial DNA road map out of the morphological maze: interpreting morphological variation in the diverse <i>Monomorium rothsteini</i> (<i>F</i>) complex (<i>Hymenoptera: Formicidae</i>). <i>Systematic Entomology</i> , 2014, 39, 264-278.	1.7	8
721	Local and Global Ancestry Inference and Applications to Genetic Association Analysis for Admixed Populations. <i>Genetic Epidemiology</i> , 2014, 38, S5-S12.	0.6	40
722	Genome-wide association analysis for growth, muscularity and meat quality in Pietrain pigs. <i>Animal Genetics</i> , 2014, 45, 350-356.	0.6	15
723	Haplotype diversity in the equine <i>myostatin</i> gene with focus on variants associated with race distance propensity and muscle fiber type proportions. <i>Animal Genetics</i> , 2014, 45, 827-835.	0.6	44
724	Repeated landmass reformation limits diversification in the widespread littoral zone mosquito <i>Anopheles sundaicus</i> sensu lato in the Indo-Oriental region. <i>Molecular Ecology</i> , 2014, 23, 2573-2589.	2.0	6
725	Imputing genotypes using regularized generalized linear regression models. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 519-29.	0.2	7
726	Genetic architectures of ADME genes in five Eurasian admixed populations and implications for drug safety and efficacy. <i>Journal of Medical Genetics</i> , 2014, 51, 614-622.	1.5	22
727	Exon expression QTL (eeQTL) analysis highlights distant genomic variations associated with splicing regulation. <i>Quantitative Biology</i> , 2014, 2, 71-79.	0.3	6
728	Recombination locations and rates in beef cattle assessed from parent-offspring pairs. <i>Genetics Selection Evolution</i> , 2014, 46, 34.	1.2	52
729	Single nucleotide polymorphism and haplotype effects associated with somatic cell score in German Holstein cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 35.	1.2	43
730	Inactive alleles of cytochrome P450 2C19 may be positively selected in human evolution. <i>BMC Evolutionary Biology</i> , 2014, 14, 71.	3.2	15
731	Private haplotypes can reveal local adaptation. <i>BMC Genetics</i> , 2014, 15, 61.	2.7	26

#	ARTICLE	IF	CITATIONS
732	Copy number polymorphisms near SLC2A9 are associated with serum uric acid concentrations. BMC Genetics, 2014, 15, 81.	2.7	16
733	Flexible and scalable genotyping-by-sequencing strategies for population studies. BMC Genomics, 2014, 15, 979.	1.2	45
734	A genome wide pattern of population structure and admixture in peninsular Malaysia Malays. The HUGO Journal, 2014, 8, 5.	4.1	14
735	Genetic determinants of glucose-6-phosphate dehydrogenase activity in Kenya. BMC Medical Genetics, 2014, 15, 93.	2.1	24
736	Selection Signatures in Worldwide Sheep Populations. PLoS ONE, 2014, 9, e103813.	1.1	197
737	Investigations on the pattern of linkage disequilibrium and selection signatures in the genomes of German PiÅ©train pigs. Journal of Animal Breeding and Genetics, 2014, 131, 473-482.	0.8	10
738	FISH: fast and accurate diploid genotype imputation via segmental hidden Markov model. Bioinformatics, 2014, 30, 1876-1883.	1.8	27
739	Two Functional Lupus-Associated BLK Promoter Variants Control Cell-Type- and Developmental-Stage-Specific Transcription. American Journal of Human Genetics, 2014, 94, 586-598.	2.6	59
740	Efficiency of haplotype-based methods to fine-map QTLs and embryonic lethal variants affecting fertility: Illustration with a deletion segregating in Nordic Red cattle. Livestock Science, 2014, 166, 167-175.	0.6	1
741	Exonic single nucleotide polymorphisms within TLR3 associated with infant responses to serogroup C meningococcal conjugate vaccine. Vaccine, 2014, 32, 3424-3430.	1.7	3
742	A Genetic Atlas of Human Admixture History. Science, 2014, 343, 747-751.	6.0	691
743	An independent validation association study of carcass quality, shear force, intramuscular fat percentage and omega-3 polyunsaturated fatty acid content with gene markers in Australian lamb. Meat Science, 2014, 96, 1025-1033.	2.7	18
744	The utility of low-density genotyping for imputation in the Thoroughbred horse. Genetics Selection Evolution, 2014, 46, 9.	1.2	34
745	Single nucleotide polymorphisms for feed efficiency and performance in crossbred beef cattle. BMC Genetics, 2014, 15, 14.	2.7	47
746	Identification of a major locus interacting with MC1R and modifying black coat color in an F2 Nellore-Angus population. Genetics Selection Evolution, 2014, 46, 4.	1.2	29
747	Genetic Origins of Lactase Persistence and the Spread of Pastoralism in Africa. American Journal of Human Genetics, 2014, 94, 496-510.	2.6	174
748	Next-Generation Statistical Genetics: Modeling, Penalization, and Optimization in High-Dimensional Data. Annual Review of Statistics and Its Application, 2014, 1, 279-300.	4.1	40
749	Population Variation Revealed High-Altitude Adaptation of Tibetan Mastiffs. Molecular Biology and Evolution, 2014, 31, 1200-1205.	3.5	130

#	ARTICLE	IF	CITATIONS
750	Whole-genome sequencing of six dog breeds from continuous altitudes reveals adaptation to high-altitude hypoxia. <i>Genome Research</i> , 2014, 24, 1308-1315.	2.4	235
751	Land subsidence susceptibility mapping at Kinta Valley (Malaysia) using the evidential belief function model in GIS. <i>Natural Hazards</i> , 2014, 73, 1019-1042.	1.6	190
752	Detecting and Measuring Selection from Gene Frequency Data. <i>Genetics</i> , 2014, 196, 799-817.	1.2	64
753	Kernel canonical correlation analysis for assessing gene-gene interactions and application to ovarian cancer. <i>European Journal of Human Genetics</i> , 2014, 22, 126-131.	1.4	33
754	Origin and Differential Selection of Allelic Variation at TAS2R16 Associated with Salicin Bitter Taste Sensitivity in Africa. <i>Molecular Biology and Evolution</i> , 2014, 31, 288-302.	3.5	43
755	Whole-genome haplotyping approaches and genomic medicine. <i>Genome Medicine</i> , 2014, 6, 73.	3.6	66
756	How to Include Chromosome X in Your Genome-Wide Association Study. <i>Genetic Epidemiology</i> , 2014, 38, 97-103.	0.6	91
757	Recent Selection on the Y-to-Dot Translocation in <i>Drosophila pseudoobscura</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 846-856.	3.5	8
758	Genome-Wide Estimation of Linkage Disequilibrium from Population-Level High-Throughput Sequencing Data. <i>Genetics</i> , 2014, 197, 1303-1313.	1.2	27
759	Genome-wide scans to detect positive selection in Large White and Tongcheng pigs. <i>Animal Genetics</i> , 2014, 45, 329-339.	0.6	51
760	Two Genomic Regions Contribute Disproportionately to Geographic Differentiation in Wild Barley. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1193-1203.	0.8	38
761	Exome resequencing reveals signatures of demographic and adaptive processes across the genome and range of black cottonwood (<i>Populus trichocarpa</i>). <i>Molecular Ecology</i> , 2014, 23, 2486-2499.	2.0	54
762	Comparative genomics of the mimicry switch in <i>Papilio dardanus</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140465.	1.2	40
763	Imputation of non-genotyped individuals using genotyped progeny in Nellore, a <i>Bos indicus</i> cattle breed. <i>Livestock Science</i> , 2014, 166, 176-189.	0.6	10
764	Genome-wide signatures of population bottlenecks and diversifying selection in European wolves. <i>Heredity</i> , 2014, 112, 428-442.	1.2	87
765	A new approach for efficient genotype imputation using information from relatives. <i>BMC Genomics</i> , 2014, 15, 478.	1.2	760
766	Signatures of selection in sheep bred for resistance or susceptibility to gastrointestinal nematodes. <i>BMC Genomics</i> , 2014, 15, 637.	1.2	109
767	Impact of pre-imputation SNP-filtering on genotype imputation results. <i>BMC Genetics</i> , 2014, 15, 88.	2.7	36

#	ARTICLE	IF	CITATIONS
768	THE EVOLUTIONARY HISTORY OF DARWIN'S FINCHES: SPECIATION, GENE FLOW, AND INTROGRESSION IN A FRAGMENTED LANDSCAPE. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 2932-2944.	1.1	53
769	A transposable element insertion disturbed starch synthase gene <i>SSIIb</i> in maize. <i>Molecular Breeding</i> , 2014, 34, 1159-1171.	1.0	4
770	The American Quarter Horse: Population Structure and Relationship to the Thoroughbred. <i>Journal of Heredity</i> , 2014, 105, 148-162.	1.0	51
771	A genome-wide association study of production traits in a commercial population of Large White pigs: evidence of haplotypes affecting meat quality. <i>Genetics Selection Evolution</i> , 2014, 46, 12.	1.2	71
772	IGENT: efficient entropy based algorithm for genome-wide gene-gene interaction analysis. <i>BMC Medical Genomics</i> , 2014, 7, S6.	0.7	22
773	Evidence of Positive Selection for a Glycogen Synthase (<i>GYS1</i>) Mutation in Domestic Horse Populations. <i>Journal of Heredity</i> , 2014, 105, 163-172.	1.0	40
774	The SLICK hair locus derived from Senepol cattle confers thermotolerance to intensively managed lactating Holstein cows. <i>Journal of Dairy Science</i> , 2014, 97, 5508-5520.	1.4	112
775	Adaptive admixture in the West African bovine hybrid zone: insight from the Borgou population. <i>Molecular Ecology</i> , 2014, 23, 3241-3257.	2.0	60
776	Using the unified relationship matrix adjusted by breed-wise allele frequencies in genomic evaluation of a multibreed population. <i>Journal of Dairy Science</i> , 2014, 97, 1117-1127.	1.4	25
777	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713.	9.4	1,159
778	Detecting Structure of Haplotypes and Local Ancestry. <i>Genetics</i> , 2014, 196, 625-642.	1.2	171
779	Admixture facilitates genetic adaptations to high altitude in Tibet. <i>Nature Communications</i> , 2014, 5, 3281.	5.8	172
780	The development of genomics applied to dairy breeding. <i>Livestock Science</i> , 2014, 166, 66-75.	0.6	19
781	Genomic Signature of Adaptation to Climate in <i>Medicago truncatula</i> . <i>Genetics</i> , 2014, 196, 1263-1275.	1.2	160
782	Genomewide Prediction Accuracy within 969 Maize Biparental Populations. <i>Crop Science</i> , 2014, 54, 1514-1522.	0.8	78
783	Integrative analysis of gene-environment interactions under a multi-response partially linear varying coefficient model. <i>Statistics in Medicine</i> , 2014, 33, 4988-4998.	0.8	23
784	A community assessment of privacy preserving techniques for human genomes. <i>BMC Medical Informatics and Decision Making</i> , 2014, 14, S1.	1.5	44
785	Evaluation of measures of correctness of genotype imputation in the context of genomic prediction: a review of livestock applications. <i>Animal</i> , 2014, 8, 1743-1753.	1.3	68

#	ARTICLE	IF	CITATIONS
786	Genomic basis of the differences between cider and dessert apple varieties. <i>Evolutionary Applications</i> , 2015, 8, 650-661.	1.5	33
787	Signatures of positive selection in East African Shorthorn Zebu: A genome-wide single nucleotide polymorphism analysis. <i>Scientific Reports</i> , 2015, 5, 11729.	1.6	114
788	Genetics of glucocorticoid-associated osteonecrosis in children with acute lymphoblastic leukemia. <i>Blood</i> , 2015, 126, 1770-1776.	0.6	102
789	The genomics of ecological vicariance in threespine stickleback fish. <i>Nature Communications</i> , 2015, 6, 8767.	5.8	115
790	The genetics of feed conversion efficiency traits in a commercial broiler line. <i>Scientific Reports</i> , 2015, 5, 16387.	1.6	60
791	Whole genome SNP genotype piecemeal imputation. <i>BMC Bioinformatics</i> , 2015, 16, 340.	1.2	3
792	Merino and Merino-derived sheep breeds: a genome-wide intercontinental study. <i>Genetics Selection Evolution</i> , 2015, 47, 64.	1.2	97
793	Design of a low-density SNP chip for the main Australian sheep breeds and its effect on imputation and genomic prediction accuracy. <i>Animal Genetics</i> , 2015, 46, 544-556.	0.6	38
794	TACR1 gene polymorphism and sex differences in postoperative nausea and vomiting. <i>Anaesthesia</i> , 2015, 70, 1148-1159.	1.8	15
795	Accuracy of genotype imputation based on random and selected reference sets in purebred and crossbred sheep populations and its effect on accuracy of genomic prediction. <i>Genetics Selection Evolution</i> , 2015, 47, 97.	1.2	28
796	Characterization of the biological processes shaping the genetic structure of the Italian population. <i>BMC Genetics</i> , 2015, 16, 132.	2.7	10
797	Multi-allelic haplotype model based on genetic partition for genomic prediction and variance component estimation using SNP markers. <i>BMC Genetics</i> , 2015, 16, 144.	2.7	34
798	Prediction of Genetic Variance in Biparental Maize Populations: Genomewide Marker Effects versus Mean Genetic Variance in Prior Populations. <i>Crop Science</i> , 2015, 55, 1181-1188.	0.8	24
799	Detection of functional polymorphisms influencing the promoter activity of the SAA2 gene and their association with milk production traits in Chinese Holstein cows. <i>Animal Genetics</i> , 2015, 46, 591-598.	0.6	9
800	LinkImpute: Fast and Accurate Genotype Imputation for Nonmodel Organisms. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2383-2390.	0.8	407
801	Study of lipid metabolism-related genes as candidate genes of sexual precocity in Nellore cattle. <i>Genetics and Molecular Research</i> , 2015, 14, 234-243.	0.3	21
802	Revisiting demographic processes in cattle with genome-wide population genetic analysis. <i>Frontiers in Genetics</i> , 2015, 6, 191.	1.1	45
803	Genome-Wide Scan of Gastrointestinal Nematode Resistance in Closed Angus Population Selected for Minimized Influence of MHC. <i>PLoS ONE</i> , 2015, 10, e0119380.	1.1	37

#	ARTICLE	IF	CITATIONS
804	Genomic Prediction of Biological Shape: Elliptic Fourier Analysis and Kernel Partial Least Squares (PLS) Regression Applied to Grain Shape Prediction in Rice (<i>Oryza sativa</i> L.). PLoS ONE, 2015, 10, e0120610.	1.1	43
805	Scanning and Filling: Ultra-Dense SNP Genotyping Combining Genotyping-By-Sequencing, SNP Array and Whole-Genome Resequencing Data. PLoS ONE, 2015, 10, e0131533.	1.1	60
806	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. PLoS ONE, 2015, 10, e0136803.	1.1	98
807	Variable-Selection Emerges on Top in Empirical Comparison of Whole-Genome Complex-Trait Prediction Methods. PLoS ONE, 2015, 10, e0138903.	1.1	15
808	Marker Imputation Before Genomewide Selection in Biparental Maize Populations. Plant Genome, 2015, 8, eplantgenome2014.10.0078.	1.6	35
809	Inference of Gorilla Demographic and Selective History from Whole-Genome Sequence Data. Molecular Biology and Evolution, 2015, 32, 600-612.	3.5	55
810	Recent artificial selection in U.S. Jersey cattle impacts autozygosity levels of specific genomic regions. BMC Genomics, 2015, 16, 302.	1.2	21
811	Association Mapping of Seedling Resistance to Spot Form Net Blotch in a Worldwide Collection of Barley. Phytopathology, 2015, 105, 500-508.	1.1	47
812	Fine-mapping Additive and Dominant SNP Effects Using Group-LASSO and Fractional Resample Model Averaging. Genetic Epidemiology, 2015, 39, 77-88.	0.6	18
813	Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of <i>Ficedula</i> flycatchers. Genome Research, 2015, 25, 1656-1665.	2.4	385
814	A Comparison of Optimality Measures for Estimating Untyped SNP Using the Allele Frequencies of Neighboring SNPs. , 2015, , .		0
815	Combined QTL and Selective Sweep Mappings with Coding SNP Annotation and cis-eQTL Analysis Revealed <i>PARK2</i> and <i>JAG2</i> as New Candidate Genes for Adiposity Regulation. G3: Genes, Genomes, Genetics, 2015, 5, 517-529.	0.8	17
816	Significant association of full-thickness rotator cuff tears and estrogen-related receptor- β (ESRRB). Journal of Shoulder and Elbow Surgery, 2015, 24, e31-e35.	1.2	48
817	Genotype-by-sequencing of the plant pathogenic fungi <i>Pyrenophora teres</i> and <i>Sclerotinia phaeocephala</i> utilizing Ion Torrent sequencing technology. Molecular Plant Pathology, 2015, 16, 623-632.	2.0	36
818	Long-Term Balancing Selection in LAD1 Maintains a Missense Trans-Species Polymorphism in Humans, Chimpanzees, and Bonobos. Molecular Biology and Evolution, 2015, 32, 1186-1196.	3.5	70
819	Genome-wide association mapping of salinity tolerance in rice (<i>Oryza sativa</i>). DNA Research, 2015, 22, 133-145.	1.5	292
820	Genome-wide association studies in elite varieties of German winter barley using single-marker and haplotype-based methods. Plant Breeding, 2015, 134, 28-39.	1.0	59
821	Single-nucleotide polymorphisms in CD8A and their associations with T lymphocyte subpopulations in pig. Molecular Genetics and Genomics, 2015, 290, 1447-1456.	1.0	2

#	ARTICLE	IF	CITATIONS
822	Association mapping of QTLs for sclerotinia stem rot resistance in a collection of soybean plant introductions using a genotyping by sequencing (GBS) approach. <i>BMC Plant Biology</i> , 2015, 15, 5.	1.6	98
823	Characterizing Male-Female Interactions Using Natural Genetic Variation in <i>Drosophila melanogaster</i> . <i>Journal of Heredity</i> , 2015, 106, 67-79.	1.0	29
824	Breeding patterns and cultivated beets origins by genetic diversity and linkage disequilibrium analyses. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2255-2271.	1.8	12
825	Prospection of genomic regions divergently selected in cutting line of Quarter Horses in relation to racing line. <i>Livestock Science</i> , 2015, 174, 1-9.	0.6	24
826	Test of rare variant association based on affected sib-pairs. <i>European Journal of Human Genetics</i> , 2015, 23, 229-237.	1.4	6
827	A Genomic Portrait of Haplotype Diversity and Signatures of Selection in Indigenous Southern African Populations. <i>PLoS Genetics</i> , 2015, 11, e1005052.	1.5	42
828	SNP imputation bias reduces effect size determination. <i>Frontiers in Genetics</i> , 2015, 6, 30.	1.1	7
829	Genomic data as the "hitchhiker's guide" to cattle adaptation: tracking the milestones of past selection in the bovine genome. <i>Frontiers in Genetics</i> , 2015, 6, 36.	1.1	23
830	Establishment of a 100-seed weight quantitative trait locus "allele matrix of the germplasm population for optimal recombination design in soybean breeding programmes. <i>Journal of Experimental Botany</i> , 2015, 66, 6311-6325.	2.4	91
831	Unique characteristics of the Ainu population in Northern Japan. <i>Journal of Human Genetics</i> , 2015, 60, 565-571.	1.1	26
832	Resolving Evolutionary Relationships in Closely Related Species with Whole-Genome Sequencing Data. <i>Systematic Biology</i> , 2015, 64, 1000-1017.	2.7	102
833	Evolutionary analysis of the female-specific avian W chromosome. <i>Nature Communications</i> , 2015, 6, 7330.	5.8	121
834	Association of THBS1 rs1478605 T>C in 5'-untranslated regions with the development and progression of gastric cancer. <i>Biomedical Reports</i> , 2015, 3, 207-214.	0.9	10
835	Association of polymorphisms and haplotypes in the cytochrome P450 1B1 gene with uterine leiomyoma: A case control study. <i>Biomedical Reports</i> , 2015, 3, 201-206.	0.9	7
836	Integration of Random Forest with population-based outlier analyses provides insight on the genomic basis and evolution of run timing in Chinook salmon (<i>Oncorhynchus tshawytscha</i>). <i>Molecular Ecology</i> , 2015, 24, 2729-2746.	2.0	76
837	Genome-wide association analyses reveal significant loci and strong candidate genes for growth and fatness traits in two pig populations. <i>Genetics Selection Evolution</i> , 2015, 47, 17.	1.2	57
838	Predicting haplotype carriers from SNP genotypes in <i>Bos taurus</i> through linear discriminant analysis. <i>Genetics Selection Evolution</i> , 2015, 47, 4.	1.2	15
839	Comparison of Bayesian models to estimate direct genomic values in multi-breed commercial beef cattle. <i>Genetics Selection Evolution</i> , 2015, 47, 23.	1.2	38

#	ARTICLE	IF	CITATIONS
840	Low levels of taurine introgression in the current Brazilian Nelore and Gir indicine cattle populations. <i>Genetics Selection Evolution</i> , 2015, 47, 31.	1.2	29
841	Relative extended haplotype homozygosity signals across breeds reveal dairy and beef specific signatures of selection. <i>Genetics Selection Evolution</i> , 2015, 47, 25.	1.2	49
842	The genetic architecture of local adaptation I: the genomic landscape of foxtail pine (<i>Pinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 667 To 2015, 11, 1.	0.6	22
843	Phylogeographic Analyses of American Black Bears (<i>Ursus americanus</i>) Suggest Four Glacial Refugia and Complex Patterns of Postglacial Admixture. <i>Molecular Biology and Evolution</i> , 2015, 32, 2338-2350.	3.5	90
844	Genome-wide analysis reveals population structure and selection in Chinese indigenous sheep breeds. <i>BMC Genomics</i> , 2015, 16, 194.	1.2	161
845	Association between vitamin D receptor polymorphisms and haplotypes with pulmonary tuberculosis. <i>Biomedical Reports</i> , 2015, 3, 189-194.	0.9	36
846	Genome-wide association study of body weight in Australian Merino sheep reveals an orthologous region on OAR6 to human and bovine genomic regions affecting height and weight. <i>Genetics Selection Evolution</i> , 2015, 47, 66.	1.2	105
847	Seed filling in domesticated maize and rice depends on SWEET-mediated hexose transport. <i>Nature Genetics</i> , 2015, 47, 1489-1493.	9.4	360
849	W<sc>hats</sc>H<sc>ap</sc>: Weighted Haplotype Assembly for Future-Generation Sequencing Reads. <i>Journal of Computational Biology</i> , 2015, 22, 498-509.	0.8	337
850	Jackknife-based gene-gene interaction tests for untyped SNPs. <i>BMC Genetics</i> , 2015, 16, 85.	2.7	0
851	HaploPOP: a software that improves population assignment by combining markers into haplotypes. <i>BMC Bioinformatics</i> , 2015, 16, 242.	1.2	8
852	Genome-wide association study identifies HLA 8.1 ancestral haplotype alleles as major genetic risk factors for myositis phenotypes. <i>Genes and Immunity</i> , 2015, 16, 470-480.	2.2	103
853	Independent Molecular Basis of Convergent Highland Adaptation in Maize. <i>Genetics</i> , 2015, 200, 1297-1312.	1.2	67
854	Genome- and exome-wide association study of serum lipoprotein (a) in the Jackson Heart Study. <i>Journal of Human Genetics</i> , 2015, 60, 755-761.	1.1	42
855	A multivariate Bernoulli model to predict DNaseI hypersensitivity status from haplotype data. <i>Bioinformatics</i> , 2015, 31, 3514-3521.	1.8	2
856	The Genomic Impacts of Drift and Selection for Hybrid Performance in Maize. <i>Genetics</i> , 2015, 201, 1201-1211.	1.2	56
857	Ecological Divergence, Adaptive Diversification, and the Evolution of Social Signaling Traits: An Empirical Study in Arid Australian Lizards. <i>American Naturalist</i> , 2015, 186, E144-E161.	1.0	19
858	Impact of regulatory variation from RNA to protein. <i>Science</i> , 2015, 347, 664-667.	6.0	399

#	ARTICLE	IF	CITATIONS
859	A hidden Markov model for investigating recent positive selection through haplotype structure. <i>Theoretical Population Biology</i> , 2015, 99, 18-30.	0.5	41
860	Novel genomic signals of recent selection in an Ethiopian population. <i>European Journal of Human Genetics</i> , 2015, 23, 1085-1092.	1.4	25
861	Relatedness in the post-genomic era: is it still useful?. <i>Nature Reviews Genetics</i> , 2015, 16, 33-44.	7.7	228
862	Identification of loci governing eight agronomic traits using a GBS GWAS approach and validation by QTL mapping in soya bean. <i>Plant Biotechnology Journal</i> , 2015, 13, 211-221.	4.1	340
864	Characterizing Two Inter-specific Bin Maps for the Exploration of the QTLs/Genes that Confer Three Soybean Evolutionary Traits. <i>Frontiers in Plant Science</i> , 2016, 7, 1248.	1.7	18
865	Application of computational methods in genetic study of inflammatory bowel disease. <i>World Journal of Gastroenterology</i> , 2016, 22, 949.	1.4	6
866	Ascertainment bias from imputation methods evaluation in wheat. <i>BMC Genomics</i> , 2016, 17, 773.	1.2	5
867	Genome-wide analysis reveals signatures of selection for important traits in domestic sheep from different ecoregions. <i>BMC Genomics</i> , 2016, 17, 863.	1.2	67
868	Sequence-Based Introgression Mapping Identifies Candidate White Mold Tolerance Genes in Common Bean. <i>Plant Genome</i> , 2016, 9, plantgenome2015.09.0092.	1.6	10
869	Genome-Wide Association Study Identifies Candidate Loci Underlying Agronomic Traits in a Middle American Diversity Panel of Common Bean. <i>Plant Genome</i> , 2016, 9, plantgenome2016.02.0012.	1.6	136
870	Genome-wide association mapping of partial resistance to <i>Phytophthora sojae</i> in soybean plant introductions from the Republic of Korea. <i>BMC Genomics</i> , 2016, 17, 607.	1.2	46
871	The <i>Arabidopsis thaliana</i> mobilome and its impact at the species level. <i>ELife</i> , 2016, 5, .	2.8	271
872	A practical approach to detect ancestral haplotypes in livestock populations. <i>BMC Genetics</i> , 2016, 17, 91.	2.7	2
873	Adaptation to Temporally Fluctuating Environments by the Evolution of Maternal Effects. <i>PLoS Biology</i> , 2016, 14, e1002388.	2.6	96
874	Combining Image Analysis, Genome Wide Association Studies and Different Field Trials to Reveal Stable Genetic Regions Related to Panicle Architecture and the Number of Spikelets per Panicle in Rice. <i>Frontiers in Plant Science</i> , 2016, 7, 1384.	1.7	68
875	A genome-wide association study of copy number variations with umbilical hernia in swine. <i>Animal Genetics</i> , 2016, 47, 298-305.	0.6	36
876	GWAS-identified schizophrenia risk SNPs at <i>TSPAN18</i> are highly diverged between Europeans and East Asians. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 1032-1040.	1.1	9
877	A haplotype method detects diverse scenarios of local adaptation from genomic sequence variation. <i>Molecular Ecology</i> , 2016, 25, 3081-3100.	2.0	19

#	ARTICLE	IF	CITATIONS
878	Evidence for extensive parallelism but divergent genomic architecture of adaptation along altitudinal and latitudinal gradients in <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2016, 209, 1240-1251.	3.5	81
879	Rapid genotype imputation from sequence without reference panels. <i>Nature Genetics</i> , 2016, 48, 965-969.	9.4	172
880	Genome-wide association of multiple complex traits in outbred mice by ultra-low-coverage sequencing. <i>Nature Genetics</i> , 2016, 48, 912-918.	9.4	124
881	The Effects of Both Recent and Long-Term Selection and Genetic Drift Are Readily Evident in North American Barley Breeding Populations. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 609-622.	0.8	21
882	Identification of genome-wide selection signatures in the Limousin beef cattle breed. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 264-276.	0.8	27
883	Modeling X Chromosome Data Using Random Forests: Conquering Sex Bias. <i>Genetic Epidemiology</i> , 2016, 40, 123-132.	0.6	5
884	Long-term selection for litter size in swine results in shifts in allelic frequency in regions involved in reproductive processes. <i>Animal Genetics</i> , 2016, 47, 534-542.	0.6	13
885	Genomic and functional approaches reveal a case of adaptive introgression from <i>Populus balsamifera</i> (balsam poplar) in <i>P. trichocarpa</i> (black cottonwood). <i>Molecular Ecology</i> , 2016, 25, 2427-2442.	2.0	85
886	Stripes, jewels and spines: further investigations into the evolution of defensive strategies in a chemically defended gecko radiation (<i>Strophurus</i> , Diplodactylidae). <i>Zoologica Scripta</i> , 2016, 45, 481-493.	0.7	13
887	HAPI-Gen., 2016, , .		2
888	Protecting genomic data analytics in the cloud: state of the art and opportunities. <i>BMC Medical Genomics</i> , 2016, 9, 63.	0.7	43
889	Genome-Wide Association Studies of Grain Yield Components in Diverse Sorghum Germplasm. <i>Plant Genome</i> , 2016, 9, plantgenome2015.09.0091.	1.6	78
890	Population structure of eleven Spanish ovine breeds and detection of selective sweeps with BayeScan and hapFLK. <i>Scientific Reports</i> , 2016, 6, 27296.	1.6	52
891	Genomic selection in pigs: state of the art and perspectives. <i>Italian Journal of Animal Science</i> , 2016, 15, 211-232.	0.8	56
892	Uncovering Adaptation from Sequence Data: Lessons from Genome Resequencing of Four Cattle Breeds. <i>Genetics</i> , 2016, 203, 433-450.	1.2	93
893	Whole-genome sequencing reveals small genomic regions of introgression in an introduced crater lake population of threespine stickleback. <i>Ecology and Evolution</i> , 2016, 6, 2190-2204.	0.8	17
894	Genomic Landscape Established by Allelic Imbalance in the Cancerization Field of a Normal Appearing Airway. <i>Cancer Research</i> , 2016, 76, 3676-3683.	0.4	35
895	Detecting the QTL-allele system of seed isoflavone content in Chinese soybean landrace population for optimal cross design and gene system exploration. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1557-1576.	1.8	70

#	ARTICLE	IF	CITATIONS
896	Extensive Hidden Genomic Mosaicism Revealed in Normal Tissue. <i>American Journal of Human Genetics</i> , 2016, 98, 571-578.	2.6	59
897	Assessing and comparison of different machine learning methods in parent-offspring trios for genotype imputation. <i>Journal of Theoretical Biology</i> , 2016, 399, 148-158.	0.8	6
898	Genetic subdivision and candidate genes under selection in North American grey wolves. <i>Molecular Ecology</i> , 2016, 25, 380-402.	2.0	100
899	Variation in Linked Selection and Recombination Drive Genomic Divergence during Allopatric Speciation of European and American Aspens. <i>Molecular Biology and Evolution</i> , 2016, 33, 1754-1767.	3.5	83
900	Combining genetic and distributional approaches to sourcing introduced species: a case study on the Nile monitor (<i>Varanus niloticus</i>) in Florida. <i>Royal Society Open Science</i> , 2016, 3, 150619.	1.1	4
901	Characteristics of runs of homozygosity in selected cattle breeds maintained in Poland. <i>Livestock Science</i> , 2016, 188, 72-80.	0.6	79
902	Deep kernel dimensionality reduction for scalable data integration. <i>International Journal of Approximate Reasoning</i> , 2016, 74, 121-132.	1.9	3
903	Demographic inference under a spatially continuous coalescent model. <i>Heredity</i> , 2016, 117, 94-99.	1.2	11
904	Bioinformatic analysis of genotype by sequencing (GBS) data with NGSEP. <i>BMC Genomics</i> , 2016, 17, 498.	1.2	49
905	Toward Pediatric Precision Medicine: Examples of Genomics-Based Stratification Strategies. <i>Translational Bioinformatics</i> , 2016, , 339-361.	0.0	0
906	Plant adaptation or acclimation to rising CO ₂ ? Insight from first multigenerational RNA-Seq transcriptome. <i>Global Change Biology</i> , 2016, 22, 3760-3773.	4.2	47
908	Reference-based phasing using the Haplotype Reference Consortium panel. <i>Nature Genetics</i> , 2016, 48, 1443-1448.	9.4	1,357
909	Genome wide association study (GWAS) for grain yield in rice cultivated under water deficit. <i>Genetica</i> , 2016, 144, 651-664.	0.5	57
911	Identification and validation of a major cadmium accumulation locus and closely associated SNP markers in North Dakota durum wheat cultivars. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	25
912	Detection of selection signatures of population-specific genomic regions selected during domestication process in Jinhua pigs. <i>Animal Genetics</i> , 2016, 47, 672-681.	0.6	17
913	Genomic signatures among <i>Oncorhynchus nerka</i> ecotypes to inform conservation and management of endangered Sockeye Salmon. <i>Evolutionary Applications</i> , 2016, 9, 1285-1300.	1.5	47
914	A Genomic Resource for the Development, Improvement, and Exploitation of Sorghum for Bioenergy. <i>Genetics</i> , 2016, 204, 21-33.	1.2	115
915	Coding and noncoding variants in <i>HFM1</i> , <i>MLH3</i> , <i>MSH4</i> , <i>MSH5</i> , <i>RNF212</i> , and <i>RNF212B</i> affect recombination rate in cattle. <i>Genome Research</i> , 2016, 26, 1323-1332.	2.4	77

#	ARTICLE	IF	CITATIONS
916	A genome-wide association study identifies a region strongly associated with symmetrical onychomadesis on chromosome 12 in dogs. <i>Animal Genetics</i> , 2016, 47, 708-716.	0.6	5
917	Occasional recombination of a selfish X-chromosome may permit its persistence at high frequencies in the wild. <i>Journal of Evolutionary Biology</i> , 2016, 29, 2229-2241.	0.8	18
918	Genomic analysis of Ugandan and Rwandan chicken ecotypes using a 600k genotyping array. <i>BMC Genomics</i> , 2016, 17, 407.	1.2	37
919	Rapid evolutionary response to a transmissible cancer in Tasmanian devils. <i>Nature Communications</i> , 2016, 7, 12684.	5.8	162
920	SparRec: An effective matrix completion framework of missing data imputation for GWAS. <i>Scientific Reports</i> , 2016, 6, 35534.	1.6	9
921	Evolution of heterogeneous genome differentiation across multiple contact zones in a crow species complex. <i>Nature Communications</i> , 2016, 7, 13195.	5.8	156
922	Genome-wide analysis reveals adaptation to high altitudes in Tibetan sheep. <i>Scientific Reports</i> , 2016, 6, 26770.	1.6	110
923	Global population divergence and admixture of the brown rat (<i>Rattus norvegicus</i>). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161762.	1.2	119
924	Genomic prediction contributing to a promising global strategy to turbocharge gene banks. <i>Nature Plants</i> , 2016, 2, 16150.	4.7	179
925	Emergence and evolution of inter-specific segregating retrocopies in cynomolgus monkey (<i>Macaca</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.6	2
927	Assessing accuracy of imputation using different SNP panel densities in a multi-breed sheep population. <i>Genetics Selection Evolution</i> , 2016, 48, 71.	1.2	48
928	Genome-wide association studies of immune, disease and production traits in indigenous chicken ecotypes. <i>Genetics Selection Evolution</i> , 2016, 48, 74.	1.2	36
929	Genotype Imputation Methods and Their Effects on Genomic Predictions in Cattle. <i>Springer Science Reviews</i> , 2016, 4, 79-98.	1.3	25
930	PWHATSHAP: efficient haplotyping for future generation sequencing. <i>BMC Bioinformatics</i> , 2016, 17, 342.	1.2	11
931	Multi-generational imputation of single nucleotide polymorphism marker genotypes and accuracy of genomic selection. <i>Animal</i> , 2016, 10, 1077-1085.	1.3	10
932	MODEM: multi-omics data envelopment and mining in maize. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw117.	1.4	39
933	Reproductive isolation and introgression between sympatric <i>Mimulus</i> species. <i>Molecular Ecology</i> , 2016, 25, 2499-2517.	2.0	70
934	A computational method for genotype calling in family-based sequencing data. <i>BMC Bioinformatics</i> , 2016, 17, 37.	1.2	8

#	ARTICLE	IF	CITATIONS
935	Haplotype estimation for biobank-scale data sets. <i>Nature Genetics</i> , 2016, 48, 817-820.	9.4	192
936	Fast and accurate long-range phasing in a UK Biobank cohort. <i>Nature Genetics</i> , 2016, 48, 811-816.	9.4	290
937	Impact of imputation methods on the amount of genetic variation captured by a single-nucleotide polymorphism panel in soybeans. <i>BMC Bioinformatics</i> , 2016, 17, 55.	1.2	21
938	Identification of candidate genes involved in Witchesâ€™ broom disease resistance in a segregating mapping population of <i>Theobroma cacao</i> L. in Brazil. <i>BMC Genomics</i> , 2016, 17, 107.	1.2	53
939	Genome-wide view of genetic diversity reveals paths of selection and cultivar differentiation in peach domestication. <i>DNA Research</i> , 2016, 23, 271-282.	1.5	64
940	Genomic Profiles of Diversification and Genotypeâ€“Phenotype Association in Island Nematode Lineages. <i>Molecular Biology and Evolution</i> , 2016, 33, 2257-2272.	3.5	31
941	Genomic selection for wheat traits and trait stability. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1697-1710.	1.8	73
942	Selection against recombinant hybrids maintains reproductive isolation in hybridizing <i>Populus</i> species despite F_1 fertility and recurrent gene flow. <i>Molecular Ecology</i> , 2016, 25, 2482-2498.	2.0	95
943	Polymorphisms in CAMKK2 may predict sensory neuropathy in African HIV patients. <i>Journal of NeuroVirology</i> , 2016, 22, 508-517.	1.0	25
944	Imputing Genotypes in Biallelic Populations from Low-Coverage Sequence Data. <i>Genetics</i> , 2016, 202, 487-495.	1.2	59
945	Population Variation Reveals Independent Selection toward Small Body Size in Chinese Debao Pony. <i>Genome Biology and Evolution</i> , 2016, 8, 42-50.	1.1	57
946	Analytical and Decision Support Tools for Genomics-Assisted Breeding. <i>Trends in Plant Science</i> , 2016, 21, 354-363.	4.3	70
947	<i>R2d2</i> Drives Selfish Sweeps in the House Mouse. <i>Molecular Biology and Evolution</i> , 2016, 33, 1381-1395.	3.5	55
948	Phasing for medical sequencing using rare variants and large haplotype reference panels. <i>Bioinformatics</i> , 2016, 32, 1974-1980.	1.8	21
949	SMILE: A novel dissimilarity-based procedure for detecting sparse-specific profiles in sparse contingency tables. <i>Computational Statistics and Data Analysis</i> , 2016, 99, 171-188.	0.7	0
950	Statistical Analysis of GWAS. <i>Computational Biology</i> , 2016, , 105-161.	0.1	0
951	Adaptive evolution of interleukin-3 (IL3), a gene associated with brain volume variation in general human populations. <i>Human Genetics</i> , 2016, 135, 377-392.	1.8	10
952	A study of common Mendelian disease carriers across ageing British cohorts: meta-analyses reveal heterozygosity for alpha 1-antitrypsin deficiency increases respiratory capacity and height. <i>Journal of Medical Genetics</i> , 2016, 53, 280-288.	1.5	9

#	ARTICLE	IF	CITATIONS
953	Phenotypes and Genotypes. Computational Biology, 2016, , .	0.1	11
954	A Primer in Genetics. Computational Biology, 2016, , 9-30.	0.1	0
955	Loci and candidate gene identification for resistance to Phytophthora sojae via association analysis in soybean [Glycine max (L.) Merr.]. Molecular Genetics and Genomics, 2016, 291, 1095-1103.	1.0	29
956	Paradigm Shifts in the Phylogeographic Analysis of Seaweeds. , 2016, , 23-62.		7
957	The Time Scale of Recombination Rate Evolution in Great Apes. Molecular Biology and Evolution, 2016, 33, 928-945.	3.5	92
958	A Genetic Mechanism for Convergent Skin Lightening during Recent Human Evolution. Molecular Biology and Evolution, 2016, 33, 1177-1187.	3.5	43
959	Association of Amine-Receptor DNA Sequence Variants with Associative Learning in the Honeybee. Behavior Genetics, 2016, 46, 242-251.	1.4	4
960	Molecular data from contemporary and historical collections reveal a complex story of cryptic diversification in the Varanus (Polydaedalus) niloticus Species Group. Molecular Phylogenetics and Evolution, 2016, 94, 591-604.	1.2	21
961	Survey of computational haplotype determination methods for single individual. Genes and Genomics, 2016, 38, 1-12.	0.5	29
962	Structured Matrix Completion with Applications to Genomic Data Integration. Journal of the American Statistical Association, 2016, 111, 621-633.	1.8	42
963	Genetic characterization of the Asian clam species complex (Corbicula) invasion in the Iberian Peninsula. Hydrobiologia, 2017, 784, 349-365.	1.0	16
964	Genome-wide search for signatures of selection in three major Brazilian locally adapted sheep breeds. Livestock Science, 2017, 197, 36-45.	0.6	57
965	Computational Haplotype Inference from Pooled Samples. Methods in Molecular Biology, 2017, 1551, 309-319.	0.4	3
966	A haplotype spanning P2X7R, P2X4R and CAMKK2 may mark susceptibility to pulmonary non-tuberculous mycobacterial disease. Immunogenetics, 2017, 69, 287-293.	1.2	8
967	New multilocus linkage disequilibrium measure for tag SNP selection. Journal of Bioinformatics and Computational Biology, 2017, 15, 1750001.	0.3	6
968	Genetic regulation of differentially methylated genes in visceral adipose tissue of severely obese men discordant for the metabolic syndrome. Translational Research, 2017, 184, 1-11.e2.	2.2	20
969	Signatures of local adaptation in lowland and highland teosintes from whole-genome sequencing of pooled samples. Molecular Ecology, 2017, 26, 2738-2756.	2.0	65
970	A Guide to Genome-Wide Association Mapping in Plants. Current Protocols in Plant Biology, 2017, 2, 22-38.	2.8	75

#	ARTICLE	IF	CITATIONS
971	Polymorphisms in IL10 may alter CD4 T-cell counts in Indonesian HIV patients beginning antiretroviral therapy. <i>Human Immunology</i> , 2017, 78, 387-390.	1.2	5
972	Use of modern tomato breeding germplasm for deciphering the genetic control of agronomical traits by Genome Wide Association study. <i>Theoretical and Applied Genetics</i> , 2017, 130, 875-889.	1.8	46
973	Association mapping utilizing diverse barley lines reveals net form net blotch seedling resistance/susceptibility loci. <i>Theoretical and Applied Genetics</i> , 2017, 130, 915-927.	1.8	37
974	Genomic Comparison of Indigenous African and Northern European Chickens Reveals Putative Mechanisms of Stress Tolerance Related to Environmental Selection Pressure. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1525-1537.	0.8	38
975	The Molecular Revolution in Cutaneous Biology: The Era of Genome-Wide Association Studies and Statistical, Big Data, and Computational Topics. <i>Journal of Investigative Dermatology</i> , 2017, 137, e113-e118.	0.3	14
976	Domestication rewired gene expression and nucleotide diversity patterns in tomato. <i>Plant Journal</i> , 2017, 91, 631-645.	2.8	34
977	Exploring the genetics of feed efficiency and feeding behaviour traits in a pig line highly selected for performance characteristics. <i>Molecular Genetics and Genomics</i> , 2017, 292, 1001-1011.	1.0	56
978	GenImp: Fast Imputation to Large Reference Panels Using Genotype Likelihoods from Ultralow Coverage Sequencing. <i>Genetics</i> , 2017, 206, 91-104.	1.2	38
979	Genetic diversity of tropical maize inbred lines combining resistance to <i>Striga hermonthica</i> with drought tolerance using SNP markers. <i>Plant Breeding</i> , 2017, 136, 338-343.	1.0	24
980	Fast admixture analysis and population tree estimation for SNP and NGS data. <i>Bioinformatics</i> , 2017, 33, 2148-2155.	1.8	40
981	Whole-genome patterns of linkage disequilibrium across flycatcher populations clarify the causes and consequences of fine-scale recombination rate variation in birds. <i>Molecular Ecology</i> , 2017, 26, 4158-4172.	2.0	87
982	Identification of major loci and genomic regions controlling acid and volatile content in tomato fruit: implications for flavor improvement. <i>New Phytologist</i> , 2017, 215, 624-641.	3.5	65
983	Genome-enabled predictions for fruit weight and quality from repeated records in European peach progenies. <i>BMC Genomics</i> , 2017, 18, 432.	1.2	44
984	Natural allelic variation of FRO2 modulates Arabidopsis root growth under iron deficiency. <i>Nature Communications</i> , 2017, 8, 15603.	5.8	73
985	The buffering capacity of stems: genetic architecture of nonstructural carbohydrates in cultivated Asian rice, <i>Oryza sativa</i> . <i>New Phytologist</i> , 2017, 215, 658-671.	3.5	31
986	Revealing allele-specific gene expression by single-cell transcriptomics. <i>International Journal of Biochemistry and Cell Biology</i> , 2017, 90, 155-160.	1.2	17
987	Genomewide patterns of variation in genetic diversity are shared among populations, species and higher-order taxa. <i>Molecular Ecology</i> , 2017, 26, 4284-4295.	2.0	75
988	Genetic Control of Plasticity in Root Morphology and Anatomy of Rice in Response to Water Deficit. <i>Plant Physiology</i> , 2017, 174, 2302-2315.	2.3	112

#	ARTICLE	IF	CITATIONS
989	Genome-wide association mapping for phenotypic plasticity in rice. <i>Plant, Cell and Environment</i> , 2017, 40, 1565-1575.	2.8	45
990	Caprine and ovine Greek dairy products: The official German method generates false-positive results due to β -casein gene polymorphism. <i>Journal of Dairy Science</i> , 2017, 100, 3539-3547.	1.4	3
991	Genotype Calling from Population-Genomic Sequencing Data. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1393-1404.	0.8	84
992	Invited review: Phenotypes to genetically reduce greenhouse gas emissions in dairying. <i>Journal of Dairy Science</i> , 2017, 100, 855-870.	1.4	80
993	<i>SERPINA</i> and <i>MAN1B1</i> polymorphisms are not linked to severe liver disease in a French cohort of α -1 antitrypsin deficiency children. <i>Liver International</i> , 2017, 37, 1608-1611.	1.9	9
994	Haplotype Inference. <i>Methods in Molecular Biology</i> , 2017, 1666, 469-484.	0.4	0
995	Multi-SNP Haplotype Analysis Methods for Association Analysis. <i>Methods in Molecular Biology</i> , 2017, 1666, 485-504.	0.4	19
996	Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago. <i>Science</i> , 2017, 358, 652-655.	6.0	351
997	Soil erosion susceptibility mapping for current and 2100 climate conditions using evidential belief function and frequency ratio. <i>Geomatics, Natural Hazards and Risk</i> , 2017, 8, 1695-1714.	2.0	28
998	The evolutionary basis of premature migration in Pacific salmon highlights the utility of genomics for informing conservation. <i>Science Advances</i> , 2017, 3, e1603198.	4.7	188
999	An innovative procedure of genome-wide association analysis fits studies on germplasm population and plant breeding. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2327-2343.	1.8	121
1000	Imputing Missing Genotypes. , 2017, , 287-309.		0
1001	Genomic signatures of adaptive introgression from European mouflon into domestic sheep. <i>Scientific Reports</i> , 2017, 7, 7623.	1.6	92
1002	Genetics of body fat mass and related traits in a pig population selected for leanness. <i>Scientific Reports</i> , 2017, 7, 9118.	1.6	17
1003	Intermediate degrees of synergistic pleiotropy drive adaptive evolution in ecological time. <i>Nature Ecology and Evolution</i> , 2017, 1, 1551-1561.	3.4	89
1004	Artificial Selection Response due to Polygenic Adaptation from a Multilocus, Multiallelic Genetic Architecture. <i>Molecular Biology and Evolution</i> , 2017, 34, 2678-2689.	3.5	27
1005	Mixture model-based association analysis with case-control data in genome wide association studies. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2017, 16, 173-187.	0.2	2
1006	Population genomics reveals a candidate gene involved in bumble bee pigmentation. <i>Ecology and Evolution</i> , 2017, 7, 3406-3413.	0.8	13

#	ARTICLE	IF	CITATIONS
1007	Patterns of genomic and phenomic diversity in wine and table grapes. <i>Horticulture Research</i> , 2017, 4, 17035.	2.9	87
1008	Reappraisal of the genetic diversity and pharmacogenetic assessment of <i>CES1</i> . <i>Pharmacogenomics</i> , 2017, 18, 1241-1257.	0.6	4
1009	Variation in Recombination Rate and Its Genetic Determinism in Sheep Populations. <i>Genetics</i> , 2017, 207, 767-784.	1.2	55
1010	Capturing haplotypes in germplasm core collections using bioinformatics. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 1821-1828.	0.8	8
1011	Genome-wide association study for resistance to the southern root-knot nematode (<i>Meloidogyne</i>) Tj ETQq0 0 0 rgBT/Overlogk 10 Tf 50	1.0	35
1012	Fine-scale population structure of common bottlenose dolphins (<i>Tursiops truncatus</i>) in offshore and coastal waters of the US Gulf of Mexico. <i>Marine Biology</i> , 2017, 164, 1.	0.7	9
1013	A hybrid method for the imputation of genomic data in livestock populations. <i>Genetics Selection Evolution</i> , 2017, 49, 30.	1.2	34
1014	Evaluation of the accuracy of imputed sequence variant genotypes and their utility for causal variant detection in cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 24.	1.2	94
1015	A strategy to improve phasing of whole-genome sequenced individuals through integration of familial information from dense genotype panels. <i>Genetics Selection Evolution</i> , 2017, 49, 46.	1.2	6
1016	Evolutionary history of the thicket rats (genus <i>Grammomys</i>) mirrors the evolution of African forests since late Miocene. <i>Journal of Biogeography</i> , 2017, 44, 182-194.	1.4	47
1017	Regional selection of the brain size regulating gene <i>CASC5</i> provides new insight into human brain evolution. <i>Human Genetics</i> , 2017, 136, 193-204.	1.8	14
1018	Association mapping for phenology and plant architecture in maize shows higher power for developmental traits compared with growth influenced traits. <i>Heredity</i> , 2017, 118, 249-259.	1.2	45
1019	Evolution of the Human Genome I. <i>Evolutionary Studies</i> , 2017, , .	0.2	1
1020	Human Leukocyte Antigen (HLA) Region in Human Population Studies. <i>Evolutionary Studies</i> , 2017, , 173-179.	0.2	3
1021	Association mapping of agronomic traits of canola (<i>Brassica napus</i> L.) subject to heat stress under field conditions. <i>Australian Journal of Crop Science</i> , 2017, 11, 1094-1105.	0.1	8
1022	Exploiting Wild Relatives for Genomics-assisted Breeding of Perennial Crops. <i>Frontiers in Plant Science</i> , 2017, 8, 460.	1.7	116
1023	A GJA9 frameshift variant is associated with polyneuropathy in Leonberger dogs. <i>BMC Genomics</i> , 2017, 18, 662.	1.2	20
1024	Signatures of Selection for Environmental Adaptation and Zebu \bar{A} —Taurine Hybrid Fitness in East African Shorthorn Zebu. <i>Frontiers in Genetics</i> , 2017, 8, 68.	1.1	133

#	ARTICLE	IF	CITATIONS
1025	Analysis of Complement C3 Gene Reveals Susceptibility to Severe Preeclampsia. <i>Frontiers in Immunology</i> , 2017, 8, 589.	2.2	50
1026	LinkImputeR: user-guided genotype calling and imputation for non-model organisms. <i>BMC Genomics</i> , 2017, 18, 523.	1.2	48
1027	Assessing the degree of stratification between closely related Holstein-Friesian populations. <i>Journal of Applied Genetics</i> , 2017, 58, 521-526.	1.0	4
1028	Identifying and mitigating batch effects in whole genome sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 351.	1.2	46
1029	Evaluation of MC1R high-throughput nucleotide sequencing data generated by the 1000 Genomes Project. <i>Genetics and Molecular Biology</i> , 2017, 40, 530-539.	0.6	5
1030	Inbred Strain Variant Database (ISVdb): A Repository for Probabilistically Informed Sequence Differences Among the Collaborative Cross Strains and Their Founders. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1623-1630.	0.8	26
1031	Genetic variation of world soybean maturity date and geographic distribution of maturity groups. <i>Breeding Science</i> , 2017, 67, 221-232.	0.9	43
1032	Genomic signatures reveal selection of characteristics within and between Meishan pig populations. <i>Animal Genetics</i> , 2018, 49, 119-126.	0.6	19
1033	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018, 9, 813.	5.8	220
1034	Homo sapiens-Specific Binding Site Variants within Brain Exclusive Enhancers Are Subject to Accelerated Divergence across Human Population. <i>Genome Biology and Evolution</i> , 2018, 10, 956-966.	1.1	10
1035	A practical introduction to Random Forest for genetic association studies in ecology and evolution. <i>Molecular Ecology Resources</i> , 2018, 18, 755-766.	2.2	87
1036	Genomic signatures of fine-scale local selection in Atlantic salmon suggest involvement of sexual maturation, energy homeostasis and immune defence-related genes. <i>Molecular Ecology</i> , 2018, 27, 2560-2575.	2.0	50
1037	Genomic analyses identify multiple Asian origins and deeply diverged mitochondrial clades in inbred brown rats (<i>Rattus norvegicus</i>). <i>Evolutionary Applications</i> , 2018, 11, 718-726.	1.5	12
1038	Genomewide association analyses of fitness traits in captive-reared Chinook salmon: Applications in evaluating conservation strategies. <i>Evolutionary Applications</i> , 2018, 11, 853-868.	1.5	23
1039	Canine NAPEPLD-associated models of human myelin disorders. <i>Scientific Reports</i> , 2018, 8, 5818.	1.6	14
1040	Detecting signatures of positive selection in non-model species using genomic data. <i>Zoological Journal of the Linnean Society</i> , 2018, 184, 528-583.	1.0	67
1041	Scale and direction of adaptive introgression between black cottonwood (<i>Populus trichocarpa</i>) and European larch (<i>Larix laricina</i>). <i>Evolutionary Applications</i> , 2018, 11, 1021-1028.	2.0	25
1042	Localization of adaptive variants in human genomes using averaged one-dependence estimation. <i>Nature Communications</i> , 2018, 9, 703.	5.8	83

#	ARTICLE	IF	CITATIONS
1043	Patterns of shared signatures of recent positive selection across human populations. <i>Nature Ecology and Evolution</i> , 2018, 2, 713-720.	3.4	63
1044	Polymorphisms in P2X4R and CAMKK2 may affect TNF α production: Implications for a role in HIV-associated sensory neuropathy. <i>Human Immunology</i> , 2018, 79, 224-227.	1.2	11
1045	Genotyping and Sequencing Technologies in Population Genetics and Genomics. <i>Population Genomics</i> , 2018, , 83-125.	0.2	12
1046	Widespread, long-term admixture between grey wolves and domestic dogs across Eurasia and its implications for the conservation status of hybrids. <i>Evolutionary Applications</i> , 2018, 11, 662-680.	1.5	64
1047	Complex signatures of natural selection at GYPA. <i>Human Genetics</i> , 2018, 137, 151-160.	1.8	20
1048	Loss of SNP genetic diversity following population collapse in a recreational walleye (<i>Sander</i>) Tj ETQq1 1 0.784314 rgBT / Q9lock	0.7	9
1049	Identifying Genetic Differences Between Dongxiang Blue-Shelled and White Leghorn Chickens Using Sequencing Data. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 469-476.	0.8	11
1050	Selection on Expected Maximum Haploid Breeding Values Can Increase Genetic Gain in Recurrent Genomic Selection. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1173-1181.	0.8	42
1051	Genomics of Parallel Ecological Speciation in Lake Victoria Cichlids. <i>Molecular Biology and Evolution</i> , 2018, 35, 1489-1506.	3.5	103
1052	Genomic Prediction and Association Mapping of Curd-Related Traits in Gene Bank Accessions of Cauliflower. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 707-718.	0.8	29
1053	Linkage Disequilibrium Estimation in Low Coverage High-Throughput Sequencing Data. <i>Genetics</i> , 2018, 209, 389-400.	1.2	26
1054	Whole-genome sequences of 89 Chinese sheep suggest role of RXFP2 in the development of unique horn phenotype as response to semi-feralization. <i>GigaScience</i> , 2018, 7, .	3.3	90
1055	Genome-wide association study of heat stress-tolerance traits in spring-type <i>Brassica napus</i> L. under controlled conditions. <i>Crop Journal</i> , 2018, 6, 115-125.	2.3	45
1056	Spatial population genomics of the brown rat (<i>Rattus norvegicus</i>) in New York City. <i>Molecular Ecology</i> , 2018, 27, 83-98.	2.0	81
1057	Introgression from <i>Populus balsamifera</i> underlies adaptively significant variation and range boundaries in <i>P. trichocarpa</i> . <i>New Phytologist</i> , 2018, 217, 416-427.	3.5	36
1058	Evolutionary significance of selected EDAR variants in Tibetan high-altitude adaptations. <i>Science China Life Sciences</i> , 2018, 61, 68-78.	2.3	1
1059	Selection Signatures Underlying Dramatic Male Inflorescence Transformation During Modern Hybrid Maize Breeding. <i>Genetics</i> , 2018, 210, 1125-1138.	1.2	45
1060	Noisy Epistasis Using Deep Learning. , 2018, , .		2

#	ARTICLE	IF	CITATIONS
1061	Methods to evaluate rare variants gene-age interaction for triglycerides. BMC Proceedings, 2018, 12, 49.	1.8	1
1062	Comparing Genome-Wide Association Study Results from Different Measurements of an Underlying Phenotype. G3: Genes, Genomes, Genetics, 2018, 8, 3715-3722.	0.8	16
1063	Slower environmental change hinders adaptation from standing genetic variation. PLoS Genetics, 2018, 14, e1007731.	1.5	20
1064	Signatures of selection and environmental adaptation across the goat genome post-domestication. Genetics Selection Evolution, 2018, 50, 57.	1.2	114
1065	Drepa-Opia: A Pilot Study to Determine the Predictive Factors of Morphine Use and Consumption in Hospitalized Adult Patients with Sickle Cell Disease. Hemoglobin, 2018, 42, 217-224.	0.4	1
1066	Four Parent Maize (FPM) Population: Effects of Mating Designs on Linkage Disequilibrium and Mapping Quantitative Traits. Plant Genome, 2018, 11, 170102.	1.6	21
1067	A genome-wide detection of selection signatures in conserved and commercial pig breeds maintained in Poland. BMC Genetics, 2018, 19, 95.	2.7	31
1068	Signatures of Selection in Admixed Dairy Cattle in Tanzania. Frontiers in Genetics, 2018, 9, 607.	1.1	58
1069	Recent Selection on a Class I ADH Locus Distinguishes Southwest Asian Populations Including Ashkenazi Jews. Genes, 2018, 9, 452.	1.0	9
1070	Turning Vice into Virtue: Using Batch-Effects to Detect Errors in Large Genomic Data Sets. Genome Biology and Evolution, 2018, 10, 2697-2708.	1.1	7
1071	Genomic signatures of adaptive introgression and environmental adaptation in the Sheko cattle of southwest Ethiopia. PLoS ONE, 2018, 13, e0202479.	1.1	30
1072	Genome-wide SNP-based association mapping of resistance to <i>Phytophthora sojae</i> in soybean (Glycine) Tj ETQq1 1,0,784314,rgBT /Ole	0.6	9
1073	Genetic Analysis of <i>Sugarcane mosaic virus</i> Resistance in the Wisconsin Diversity Panel of Maize. Crop Science, 2018, 58, 1853-1865.	0.8	20
1074	Assessment of the performance of hidden Markov models for imputation in animal breeding. Genetics Selection Evolution, 2018, 50, 44.	1.2	14
1075	Synaptogyrin-2 influences replication of Porcine circovirus 2. PLoS Genetics, 2018, 14, e1007750.	1.5	28
1076	Genome-wide association study for electrolyte leakage in rapeseed/canola (<i>Brassica napus</i> L.). Molecular Breeding, 2018, 38, 1.	1.0	9
1077	Polygenic Basis and Variable Genetic Architectures Contribute to the Complex Nature of Body Weight â€” A Genome-Wide Study in Four Chinese Indigenous Chicken Breeds. Frontiers in Genetics, 2018, 9, 229.	1.1	7
1078	User considerations in assessing pharmacogenomic tests and their clinical support tools. Npj Genomic Medicine, 2018, 3, 26.	1.7	38

#	ARTICLE	IF	CITATIONS
1079	Genomic analysis reveals genes affecting distinct phenotypes among different Chinese and western pig breeds. <i>Scientific Reports</i> , 2018, 8, 13352.	1.6	37
1080	The Accuracy of Genomic Prediction between Environments and Populations for Soft Wheat Traits. <i>Crop Science</i> , 2018, 58, 2274-2288.	0.8	15
1081	Scans for signatures of selection in Russian cattle breed genomes reveal new candidate genes for environmental adaptation and acclimation. <i>Scientific Reports</i> , 2018, 8, 12984.	1.6	85
1082	A locus on chromosome 5 shows African ancestryâ€‘limited association with alloimmunization in sickle cell disease. <i>Blood Advances</i> , 2018, 2, 3637-3647.	2.5	18
1083	Genotype Imputation from Large Reference Panels. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 73-96.	2.5	158
1084	Using Gene Genealogies to Localize Rare Variants Associated with Complex Traits in Diploid Populations. <i>Human Heredity</i> , 2018, 83, 30-39.	0.4	4
1085	Effect of complement component 5 polymorphisms on mastitis resistance in Egyptian buffalo and cattle. <i>Research in Veterinary Science</i> , 2018, 119, 45-51.	0.9	4
1086	Multilocus phylogenetics in a widespread African anuran lineage (<i>Brevicipitidae</i> : <i>Breviceps</i>) reveals patterns of diversity reflecting geoclimatic change. <i>Journal of Biogeography</i> , 2018, 45, 2067-2079.	1.4	14
1087	Darwinian Positive Selection on the Pleiotropic Effects of KITLG Explain Skin Pigmentation and Winter Temperature Adaptation in Eurasians. <i>Molecular Biology and Evolution</i> , 2018, 35, 2272-2283.	3.5	27
1088	Selecting microhaplotypes optimized for different purposes. <i>Electrophoresis</i> , 2018, 39, 2815-2823.	1.3	39
1089	Loter: A Software Package to Infer Local Ancestry for a Wide Range of Species. <i>Molecular Biology and Evolution</i> , 2018, 35, 2318-2326.	3.5	70
1090	A genome-wide scan for signatures of selection in Azeri and Khuzestani buffalo breeds. <i>BMC Genomics</i> , 2018, 19, 449.	1.2	40
1091	Identification of recombination events in outbred species with next-generation sequencing data. <i>BMC Genomics</i> , 2018, 19, 398.	1.2	5
1092	Mapping of a Major QTL for Ceratocystis Wilt Disease in an F1 Population of <i>Theobroma cacao</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 155.	1.7	12
1093	PolyCluster: Minimum Fragment Disagreement Clustering for Polyploid Phasing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	1.9	6
1094	Analysis of QTLâ€‘allele system conferring drought tolerance at seedling stage in a nested association mapping population of soybean [<i>Glycine max</i> (L.) Merr.] using a novel GWAS procedure. <i>Planta</i> , 2018, 248, 947-962.	1.6	34
1095	Ethylene-gibberellin signaling underlies adaptation of rice to periodic flooding. <i>Science</i> , 2018, 361, 181-186.	6.0	188
1096	LPCAT1 controls phosphate homeostasis in a zinc-dependent manner. <i>ELife</i> , 2018, 7, .	2.8	63

#	ARTICLE	IF	CITATIONS
1097	Identification of genomic regions and candidate genes for chicken meat ultimate pH by combined detection of selection signatures and QTL. BMC Genomics, 2018, 19, 294.	1.2	18
1098	A method combining a random forest-based technique with the modeling of linkage disequilibrium through latent variables, to run multilocus genome-wide association studies. BMC Bioinformatics, 2018, 19, 106.	1.2	6
1099	Bioinformatics in Toxicology: Statistical Methods for Supervised Learning in High-Dimensional Omics Data. , 2018, , 447-472.		0
1100	Revealing the selection history of adaptive loci using genome-wide scans for selection: an example from domestic sheep. BMC Genomics, 2018, 19, 71.	1.2	95
1101	A comprehensive analysis of <i>SNCA</i> -related genetic risk in sporadic parkinson disease. Annals of Neurology, 2018, 84, 117-129.	2.8	50
1102	A novel genetic marker of decreased inflammation and improved survival after acute myocardial infarction. Basic Research in Cardiology, 2018, 113, 38.	2.5	58
1103	A Genome-Wide Association Study of Apple Quality and Scab Resistance. Plant Genome, 2018, 11, 170075.	1.6	61
1104	Biases induced by using geography and environment to guide ex situ conservation. Conservation Genetics, 2018, 19, 1281-1293.	0.8	6
1105	Polymorphism analysis in genes associated with meat tenderness in Nelore cattle. Meta Gene, 2018, 18, 73-78.	0.3	3
1106	Urban rat races: spatial population genomics of brown rats (<i>Rattus norvegicus</i>) compared across multiple cities. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20180245.	1.2	48
1107	Demographic expansion and genetic load of the halophyte model plant <i>Eutrema salsugineum</i> . Molecular Ecology, 2018, 27, 2943-2955.	2.0	11
1108	Genomic association for sexual precocity in beef heifers using pre-selection of genes and haplotype reconstruction. PLoS ONE, 2018, 13, e0190197.	1.1	20
1109	A genome scan for selection signatures in Taihu pig breeds using next-generation sequencing. Animal, 2019, 13, 683-693.	1.3	15
1110	Genetics and Population Analysis. , 2019, , 363-378.		0
1111	Gene hunting with hidden Markov model knockoffs. Biometrika, 2019, 106, 1-18.	1.3	78
1112	Genome-Wide Haplotype Association Study. , 2019, , 441-446.		0
1113	Genome-wide association study for frost tolerance in canola (<i>Brassica napus</i> L.) under field conditions. Journal of Plant Biochemistry and Biotechnology, 2019, 28, 211-222.	0.9	7
1114	Inherited and De Novo Genetic Risk for Autism Impacts Shared Networks. Cell, 2019, 178, 850-866.e26.	13.5	326

#	ARTICLE	IF	CITATIONS
1115	Population Genomics Analysis Revealed Origin and High-altitude Adaptation of Tibetan Pigs. <i>Scientific Reports</i> , 2019, 9, 11463.	1.6	44
1116	Challenges in funding and developing genomic software: roots and remedies. <i>Genome Biology</i> , 2019, 20, 147.	3.8	21
1119	Complex interplay of evolutionary forces shaping population genomic structure of invasive <i>Aedes albopictus</i> in southern Europe. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007554.	1.3	25
1120	Genomic Analysis Reveals Pleiotropic Alleles at EDN3 and BMP7 Involved in Chicken Comb Color and Egg Production. <i>Frontiers in Genetics</i> , 2019, 10, 612.	1.1	20
1121	A complex structural variant at the <i>KIT</i> locus in cattle with the Pinzgauer spotting pattern. <i>Animal Genetics</i> , 2019, 50, 423-429.	0.6	12
1122	Multiple Maize Reference Genomes Impact the Identification of Variants by Genome-Wide Association Study in a Diverse Inbred Panel. <i>Plant Genome</i> , 2019, 12, 180069.	1.6	37
1123	Association Mapping for 24 Traits Related to Protein Content, Gluten Strength, Color, Cooking, and Milling Quality Using Balanced and Unbalanced Data in Durum Wheat [<i>Triticum turgidum</i> L. var. durum (Desf.)]. <i>Frontiers in Genetics</i> , 2019, 10, 717.	1.1	24
1124	Whole-genome SNP data unravel population structure and signatures of selection for black plumage of indigenous chicken breeds from Jiangxi province, China. <i>Animal Genetics</i> , 2019, 50, 475-483.	0.6	10
1125	Genetic Affinities among Southern Africa Hunter-Gatherers and the Impact of Admixing Farmer and Herder Populations. <i>Molecular Biology and Evolution</i> , 2019, 36, 1849-1861.	3.5	21
1126	Root System Depth in <i>Arabidopsis</i> Is Shaped by EXOCYST70A3 via the Dynamic Modulation of Auxin Transport. <i>Cell</i> , 2019, 178, 400-412.e16.	13.5	116
1127	Polymorphisms in CAMKK2 associate with susceptibility to sensory neuropathy in HIV patients treated without stavudine. <i>Journal of NeuroVirology</i> , 2019, 25, 814-824.	1.0	8
1128	Genetic control of male production in <i>Daphnia pulex</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15602-15609.	3.3	24
1129	A Random Forests Framework for Modeling Haplotypes as Mosaics of Reference Haplotypes. <i>Frontiers in Genetics</i> , 2019, 10, 562.	1.1	4
1130	Genetic Contribution to Variation in Blood Calcium, Phosphorus, and Alkaline Phosphatase Activity in Pigs. <i>Frontiers in Genetics</i> , 2019, 10, 590.	1.1	25
1131	Fluctuating and Geographically Specific Selection Characterize Rapid Evolution of the Human KIR Region. <i>Frontiers in Immunology</i> , 2019, 10, 989.	2.2	18
1132	Dissecting the Genetic Architecture of Seed Protein and Oil Content in Soybean from the Yangtze and Huaihe River Valleys Using Multi-Locus Genome-Wide Association Studies. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3041.	1.8	22
1133	Influence of single nucleotide polymorphisms in some candidate genes related to the performance traits in Italian beef cattle breeds. <i>Livestock Science</i> , 2019, 230, 103834.	0.6	4
1134	Identification of two <i>TYRP1</i> loss-of-function alleles in Valais Red sheep. <i>Animal Genetics</i> , 2019, 50, 778-782.	0.6	12

#	ARTICLE	IF	CITATIONS
1135	Exploring effective approaches for haplotype block phasing. BMC Bioinformatics, 2019, 20, 540.	1.2	24
1136	Association mapping of a locus that confers southern stem canker resistance in soybean and SNP marker development. BMC Genomics, 2019, 20, 798.	1.2	13
1137	A RAPGEF6 variant constitutes a major risk factor for laryngeal paralysis in dogs. PLoS Genetics, 2019, 15, e1008416.	1.5	5
1138	CSHAP: efficient haplotype frequency estimation based on sparse representation. Bioinformatics, 2019, 35, 2827-2833.	1.8	1
1139	Searching for Signatures of Cold Climate Adaptation in TRPM8 Gene in Populations of East Asian Ancestry. Frontiers in Genetics, 2019, 10, 759.	1.1	9
1140	Sparse Convolutional Denoising Autoencoders for Genotype Imputation. Genes, 2019, 10, 652.	1.0	28
1141	Selection, Linkage, and Population Structure Interact To Shape Genetic Variation Among Threespine Stickleback Genomes. Genetics, 2019, 212, 1367-1382.	1.2	6
1142	Genotype imputation as a cost-saving genomic strategy for South African Sanga cattle: A review. South African Journal of Animal Sciences, 2019, 49, 262.	0.2	8
1143	A Mutation in the Mitochondrial Aspartate/Glutamate Carrier Leads to a More Oxidizing Intramitochondrial Environment and an Inflammatory Myopathy in Dutch Shepherd Dogs. Journal of Neuromuscular Diseases, 2019, 6, 485-501.	1.1	11
1144	Exploring the Structure of Haplotype Blocks and Genetic Diversity in Chinese Indigenous Pig Populations for Conservation Purpose. Evolutionary Bioinformatics, 2019, 15, 117693431882508.	0.6	20
1145	Genome-wide association analysis of stalk biomass and anatomical traits in maize. BMC Plant Biology, 2019, 19, 45.	1.6	77
1146	Genotype Imputation in Genome-wide Association Studies. Current Protocols in Human Genetics, 2019, 102, e84.	3.5	22
1147	Combined approaches to identify genomic regions involved in phenotypic differentiation between low divergent breeds: Application in Sardinian sheep populations. Journal of Animal Breeding and Genetics, 2019, 136, 526-534.	0.8	11
1148	Selection signatures in candidate genes and QTL for reproductive traits in Nellore heifers. Animal Reproduction Science, 2019, 207, 1-8.	0.5	4
1149	Using the RTM-GWAS procedure to detect the drought tolerance QTL-allele system at the seedling stage under sand culture in a half-sib population of soybean [<i>Glycine max</i> (L.) Merr.]. Canadian Journal of Plant Science, 2019, 99, 801-814.	0.3	7
1150	Admixture mapping in interspecific <i>Populus</i> hybrids identifies classes of genomic architectures for phytochemical, morphological and growth traits. New Phytologist, 2019, 223, 2076-2089.	3.5	21
1151	Sequence imputation from low density single nucleotide polymorphism panel in a black poplar breeding population. BMC Genomics, 2019, 20, 302.	1.2	6
1152	Widespread gene duplication and adaptive evolution in the RNA interference pathways of the <i>Drosophila obscura</i> group. BMC Evolutionary Biology, 2019, 19, 99.	3.2	15

#	ARTICLE	IF	CITATIONS
1153	High-density genotyping reveals signatures of selection related to acclimation and economically important traits in 15 local sheep breeds from Russia. <i>BMC Genomics</i> , 2019, 20, 294.	1.2	57
1154	Genome-Wide Signatures of Selection Detection in Three South China Indigenous Pigs. <i>Genes</i> , 2019, 10, 346.	1.0	29
1155	Assessment of Autozygosity Derived From Runs of Homozygosity in Jinhua Pigs Disclosed by Sequencing Data. <i>Frontiers in Genetics</i> , 2019, 10, 274.	1.1	50
1156	Genome-Wide Association Mapping of Grain Mold Resistance in the US Sorghum Association Panel. <i>Plant Genome</i> , 2019, 12, 180070.	1.6	19
1157	Genome-wide nucleotide patterns and potential mechanisms of genome divergence following domestication in maize and soybean. <i>Genome Biology</i> , 2019, 20, 74.	3.8	13
1158	Brown rat demography reveals pre-commensal structure in eastern Asia before expansion into Southeast Asia. <i>Genome Research</i> , 2019, 29, 762-770.	2.4	24
1159	Genome-wide association study and scan for signatures of selection point to candidate genes for body temperature maintenance under the cold stress in Siberian cattle populations. <i>BMC Genetics</i> , 2019, 20, 26.	2.7	25
1160	A New Fast Phasing Method Based On Haplotype Subtraction. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 427-436.	1.2	1
1161	Detection of Quantitative Trait Loci From Genome-Wide Association Studies. <i>Handbook of Statistics</i> , 2019, 40, 287-353.	0.4	0
1162	Shovelomics for phenotyping root architectural traits of rapeseed/canola (<i>Brassica napus</i> L.) and genome-wide association mapping. <i>Molecular Genetics and Genomics</i> , 2019, 294, 985-1000.	1.0	27
1163	Morphology and genome of a snailfish from the Mariana Trench provide insights into deep-sea adaptation. <i>Nature Ecology and Evolution</i> , 2019, 3, 823-833.	3.4	99
1164	Linkage Mapping and Genome-Wide Association Studies of the Rf Gene Cluster in Sunflower (<i>Helianthus annuus</i> L.) and Their Distribution in World Sunflower Collections. <i>Frontiers in Genetics</i> , 2019, 10, 216.	1.1	34
1165	Discussion of "Gene hunting with hidden Markov model knockoffs"™. <i>Biometrika</i> , 2019, 106, 19-22.	1.3	3
1166	Accuracy of imputation to whole-genome sequence in sheep. <i>Genetics Selection Evolution</i> , 2019, 51, 1.	1.2	63
1167	Detection of Selection Signatures Among Brazilian, Sri Lankan, and Egyptian Chicken Populations Under Different Environmental Conditions. <i>Frontiers in Genetics</i> , 2018, 9, 737.	1.1	46
1168	Rejoinder: "Gene hunting with hidden Markov model knockoffs"™. <i>Biometrika</i> , 2019, 106, 35-45.	1.3	15
1169	High imputation accuracy from informative low-to-medium density single nucleotide polymorphism genotypes is achievable in sheep. <i>Journal of Animal Science</i> , 2019, 97, 1550-1567.	0.2	17
1170	An ensemble strategy for Haplotype Inference based on the internal variability of algorithms. , 2019, , .		1

#	ARTICLE	IF	CITATIONS
1171	Identification of QTN and Candidate Gene for Seed-flooding Tolerance in Soybean [<i>Glycine max</i> (L.) Merr.] using Genome-Wide Association Study (GWAS). <i>Genes</i> , 2019, 10, 957.	1.0	32
1172	Hepatocyte gene expression and DNA methylation as ancestry-dependent mechanisms in African Americans. <i>Npj Genomic Medicine</i> , 2019, 4, 29.	1.7	8
1173	perfectphyloR: An R package for reconstructing perfect phylogenies. <i>BMC Bioinformatics</i> , 2019, 20, 729.	1.2	2
1174	The population genomics of multiple tsetse fly (<i>Glossina fuscipes fuscipes</i>) admixture zones in Uganda. <i>Molecular Ecology</i> , 2019, 28, 66-85.	2.0	11
1175	Comparison and assessment of family- and population-based genotype imputation methods in large pedigrees. <i>Genome Research</i> , 2019, 29, 125-134.	2.4	16
1176	Genetic diversity analysis of French goat populations reveals selective sweeps involved in their differentiation. <i>Animal Genetics</i> , 2019, 50, 54-63.	0.6	22
1177	Imputation accuracy of wheat genotyping-by-sequencing (GBS) data using barley and wheat genome references. <i>PLoS ONE</i> , 2019, 14, e0208614.	1.1	48
1178	Statistical methods for genome-wide association studies. <i>Seminars in Cancer Biology</i> , 2019, 55, 53-60.	4.3	59
1179	Highly Accurate and Efficient Data-Driven Methods for Genotype Imputation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1107-1116.	1.9	6
1180	Achieving Privacy-Friendly Storage and Secure Statistics for Smart Meter Data on Outsourced Clouds. <i>IEEE Transactions on Cloud Computing</i> , 2019, 7, 638-649.	3.1	23
1181	Discovery and Characterization of Cancer Genetic Susceptibility Alleles. , 2020, , 323-336.e3.		1
1182	Natural variation and selection in <i>GmSWEET39</i> affect soybean seed oil content. <i>New Phytologist</i> , 2020, 225, 1651-1666.	3.5	73
1183	Genomic analyses reveal three independent introductions of the invasive brown rat (<i>Rattus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262 T	1.2	12
1184	MC1R and KIT Haplotypes Associate With Pigmentation Phenotypes of North American Yak (<i>Bos</i>) Tj ETQq1 1 0.7843 14 rgBT /Overlock 1	1.0	8
1185	Genome-wide association study for frost tolerance in rapeseed/canola (<i>Brassica napus</i>) under simulating freezing conditions. <i>Plant Breeding</i> , 2020, 139, 356-367.	1.0	11
1186	Improving Imputation Quality in BEAGLE for Crop and Livestock Data. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 177-188.	0.8	43
1187	Do different rates of gene flow underlie variation in phenotypic and phenological clines in a montane grasshopper community?. <i>Ecology and Evolution</i> , 2020, 10, 980-997.	0.8	4
1188	Association mapping and genetic dissection of drought-induced canopy temperature differences in rice. <i>Journal of Experimental Botany</i> , 2020, 71, 1614-1627.	2.4	33

#	ARTICLE	IF	CITATIONS
1189	Geographic differentiation and phylogeographic relationships among world soybean populations. <i>Crop Journal</i> , 2020, 8, 260-272.	2.3	16
1190	Whole genome detection of recent selection signatures in Sarabi cattle: a unique Iranian taurine breed. <i>Genes and Genomics</i> , 2020, 42, 203-215.	0.5	25
1191	Rapid homoploid hybrid speciation in British gardens: The origin of Oxford ragwort (<i>Senecio</i>). <i>Journal of Evolutionary Biology</i> , 2020, 33, 1075-1084.	2.0	22
1192	Inference of Chromosome-Length Haplotypes Using Genomic Data of Three or a Few More Single Gametes. <i>Molecular Biology and Evolution</i> , 2020, 37, 3684-3698.	3.5	11
1193	Genetic architecture of individual variation in recombination rate on the X chromosome in cattle. <i>Heredity</i> , 2020, 125, 304-316.	1.2	10
1194	Comprehensive Identification of Drought Tolerance QTL-Allele and Candidate Gene Systems in Chinese Cultivated Soybean Population. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4830.	1.8	14
1195	Detecting the QTL-allele system controlling seed-flooding tolerance in a nested association mapping population of soybean. <i>Crop Journal</i> , 2020, 8, 781-792.	2.3	19
1196	Genome-wide scan for selection signatures reveals novel insights into the adaptive capacity in local North African cattle. <i>Scientific Reports</i> , 2020, 10, 19466.	1.6	24
1197	Genome-Wide Association Studies Detect Multiple QTLs for Productivity in Mesoamerican Diversity Panel of Common Bean Under Drought Stress. <i>Frontiers in Plant Science</i> , 2020, 11, 574674.	1.7	24
1198	Genome-wide association studies of callus differentiation for the desert tree, <i>Populus euphratica</i> . <i>Tree Physiology</i> , 2020, 40, 1762-1777.	1.4	18
1199	imputeqc: an R package for assessing imputation quality of genotypes and optimizing imputation parameters. <i>BMC Bioinformatics</i> , 2020, 21, 304.	1.2	9
1200	Large-scale mutation in the evolution of a gene complex for cryptic coloration. <i>Science</i> , 2020, 369, 460-466.	6.0	43
1201	Alopecia areata susceptibility variant in MHC region impacts expressions of genes contributing to hair keratinization and is involved in hair loss. <i>EBioMedicine</i> , 2020, 57, 102810.	2.7	19
1202	Genetic Diversity and Selection Signatures Within Diannan Small-Ear Pigs Revealed by Next-Generation Sequencing. <i>Frontiers in Genetics</i> , 2020, 11, 733.	1.1	25
1203	The impact of transposable elements on tomato diversity. <i>Nature Communications</i> , 2020, 11, 4058.	5.8	92
1204	Unsupervised detection of ancestry tracks with the GHap package. <i>Methods in Ecology and Evolution</i> , 2020, 11, 1448-1454.	2.2	6
1205	Molecular characterization of QTL-allele system for drought tolerance at seedling stage and optimal genotype design using multi-locus multi-allele genome-wide association analysis in a half-sib population of soybean (<i>Glycine max</i> (L.) Merr.). <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 295-306.	0.4	3
1206	Y-chromosome haplotypes are associated with variation in size and age at maturity in male Chinook salmon. <i>Evolutionary Applications</i> , 2020, 13, 2791-2806.	1.5	12

#	ARTICLE	IF	CITATIONS
1207	Evolution of the African slippery frogs (<i>Anura: Conraua</i>), including the world's largest living frog. <i>Zoologica Scripta</i> , 2020, 49, 684-696.	0.7	5
1208	Identification of quantitative trait nucleotides and candidate genes for soybean seed weight by multiple models of genome-wide association study. <i>BMC Plant Biology</i> , 2020, 20, 404.	1.6	28
1209	Testing methods and statistical models of genomic prediction for quantitative disease resistance to <i>Phytophthora sojae</i> in soybean [<i>Glycine max</i> (L.) Merr] germplasm collections. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3441-3454.	1.8	10
1210	A Novel Recurrent <i>COL5A1</i> Genetic Variant Is Associated With a Dysplasia-Associated Arterial Disease Exhibiting Dissections and Fibromuscular Dysplasia. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 40, 2686-2699.	1.1	30
1211	Bayesian copy number detection and association in large-scale studies. <i>BMC Cancer</i> , 2020, 20, 856.	1.1	0
1212	Discovery of Genomic Characteristics and Selection Signatures in Southern Chinese Local Cattle. <i>Frontiers in Genetics</i> , 2020, 11, 533052.	1.1	13
1213	Explainable Machine Learning for Early Assessment of COVID-19 Risk Prediction in Emergency Departments. <i>IEEE Access</i> , 2020, 8, 196299-196325.	2.6	55
1214	A Review of Integrative Imputation for Multi-Omics Datasets. <i>Frontiers in Genetics</i> , 2020, 11, 570255.	1.1	57
1215	Genetic Signatures of Selection for Cashmere Traits in Chinese Goats. <i>Animals</i> , 2020, 10, 1905.	1.0	21
1216	Genome wide association mapping and candidate gene mining for root architectural traits in rapeseed/canola (<i>Brassica napus</i> L.) at late growth stage. <i>Euphytica</i> , 2020, 216, 1.	0.6	5
1217	Comparing the diversity of the casein genes in the Asian mouflon and domestic sheep. <i>Animal Genetics</i> , 2020, 51, 470-475.	0.6	9
1218	A quantitative trait locus on chromosome 2 was identified that accounts for a substantial proportion of phenotypic variance of the yellow plumage color in chicken. <i>Poultry Science</i> , 2020, 99, 2902-2910.	1.5	9
1219	Genome-Wide Identification of a Regulatory Mutation in <i>BMP15</i> Controlling Prolificacy in Sheep. <i>Frontiers in Genetics</i> , 2020, 11, 585.	1.1	12
1220	Genome-wide detection of selective signatures in a Jinhua pig population. <i>Journal of Integrative Agriculture</i> , 2020, 19, 1314-1322.	1.7	7
1221	The role of <i>CAMKK2</i> polymorphisms in HIV-associated sensory neuropathy in South Africans. <i>Journal of the Neurological Sciences</i> , 2020, 416, 116987.	0.3	7
1222	Bi-Phenotypic Trait May Be Conferred by Multiple Alleles in a Germplasm Population. <i>Frontiers in Genetics</i> , 2020, 11, 559.	1.1	4
1223	Complex Data Imputation by Auto-Encoders and Convolutional Neural Networks—A Case Study on Genome Gap-Filling. <i>Computers</i> , 2020, 9, 37.	2.1	9
1224	Estimating and accounting for genotyping errors in RAD-seq experiments. <i>Molecular Ecology Resources</i> , 2020, 20, 856-870.	2.2	34

#	ARTICLE	IF	CITATIONS
1225	Genome-wide association analyses of quantitative disease resistance in diverse sets of soybean [Glycine max (L.) Merr.] plant introductions. <i>PLoS ONE</i> , 2020, 15, e0227710.	1.1	18
1226	Functional colour genes and signals of selection in colour polymorphic salamanders. <i>Molecular Ecology</i> , 2020, 29, 1284-1299.	2.0	15
1227	Assessing selection signatures within and between selected lines of dual purpose black and white and German Holstein cattle. <i>Animal Genetics</i> , 2020, 51, 391-408.	0.6	12
1228	Genome-wide analysis reveals molecular convergence underlying domestication in 7 bird and mammals. <i>BMC Genomics</i> , 2020, 21, 204.	1.2	12
1229	Registration of 11 diverse sorghum germplasm lines for grain and silage hybrid production. <i>Journal of Plant Registrations</i> , 2020, 14, 179-188.	0.4	4
1230	Toehold probe-based interrogation for haplotype phasing of long nucleic acid strands. <i>Analytical Methods</i> , 2020, 12, 4185-4190.	1.3	3
1231	Extending long-range phasing and haplotype library imputation algorithms to large and heterogeneous datasets. <i>Genetics Selection Evolution</i> , 2020, 52, 38.	1.2	3
1232	Recombination disequilibrium in ideal and natural populations. <i>Genomics</i> , 2020, 112, 3943-3950.	1.3	3
1233	Patterns of African and Asian admixture in the Afrikaner population of South Africa. <i>BMC Biology</i> , 2020, 18, 16.	1.7	12
1234	An extended model for phylogenetic maximum likelihood based on discrete morphological characters. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2020, 19, .	0.2	1
1235	Multi-resolution localization of causal variants across the genome. <i>Nature Communications</i> , 2020, 11, 1093.	5.8	37
1236	Characterization of haplotypes and single nucleotide polymorphisms associated with Gnl1a for high grain number formation in rice plant. <i>Genomics</i> , 2020, 112, 2647-2657.	1.3	11
1237	A Unifying Framework for Imputing Summary Statistics in Genome-Wide Association Studies. <i>Journal of Computational Biology</i> , 2020, 27, 418-428.	0.8	2
1238	The evolution of sexual signaling is linked to odorant receptor tuning in perfume-collecting orchid bees. <i>Nature Communications</i> , 2020, 11, 244.	5.8	35
1239	Comparative selection signature analyses identify genomic footprints in Reggiana cattle, the traditional breed of the Parmigiano-Reggiano cheese production system. <i>Animal</i> , 2020, 14, 921-932.	1.3	12
1240	TNF-Block Genotypes Influence Susceptibility to HIV-Associated Sensory Neuropathy in Indonesians and South Africans. <i>International Journal of Molecular Sciences</i> , 2020, 21, 380.	1.8	3
1241	Genetic dynamics of earlier maturity group emergence in south-to-north extension of Northeast China soybeans. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1839-1857.	1.8	12
1242	Bioinformatic Extraction of Functional Genetic Diversity from Heterogeneous Germplasm Collections for Crop Improvement. <i>Agronomy</i> , 2020, 10, 593.	1.3	6

#	ARTICLE	IF	CITATIONS
1243	Exploring the QTLâ€‘allele constitution of main stem node number and its differentiation among maturity groups in a Northeast China soybean population. <i>Crop Science</i> , 2020, 60, 1223-1238.	0.8	12
1244	Predicting heterosis in grain sorghum hybrids using sequence-based genetic similarity estimates. <i>Journal of Crop Improvement</i> , 2020, 34, 600-617.	0.9	12
1245	Genomeâ€‘wide detection of signatures of selection in three Valdostana cattle populations. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 609-621.	0.8	22
1246	The Identification of Admixture Patterns Could Refine Pharmacogenetic Counseling: Analysis of a Population-Based Sample in Mexico. <i>Frontiers in Pharmacology</i> , 2020, 11, 324.	1.6	8
1247	Polymorphisms Within the <i>RET</i> Proto-Oncogene and Risk of Sporadic Medullary Thyroid Carcinoma. <i>Thyroid</i> , 2020, 30, 1579-1588.	2.4	4
1248	BWGS: A R package for genomic selection and its application to a wheat breeding programme. <i>PLoS ONE</i> , 2020, 15, e0222733.	1.1	41
1249	Added Value of Clinical Sequencing: WGS-Based Profiling of Pharmacogenes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2308.	1.8	29
1250	A mobile sexâ€‘determining region, maleâ€‘specific haplotypes and rearing environment influence age at maturity in Chinook salmon. <i>Molecular Ecology</i> , 2021, 30, 131-147.	2.0	17
1251	Taste perception and lifestyle: insights from phenotype and genome data among Africans and Asians. <i>European Journal of Human Genetics</i> , 2021, 29, 325-337.	1.4	10
1252	Genomic regions associated with resistance to anthracnose in the Guatemalan climbing bean (<i>Phaseolus vulgaris</i> L.) germplasm collection. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1073-1083.	0.8	6
1253	Wholeâ€‘genome SNP markers reveal conservation status, signatures of selection, and introgression in Chinese Laiwu pigs. <i>Evolutionary Applications</i> , 2021, 14, 383-398.	1.5	21
1254	Historical Introgression from Wild Relatives Enhanced Climatic Adaptation and Resistance to Pneumonia in Sheep. <i>Molecular Biology and Evolution</i> , 2021, 38, 838-855.	3.5	44
1255	Ethiopian indigenous goats offer insights into past and recent demographic dynamics and local adaptation in subâ€‘Saharan African goats. <i>Evolutionary Applications</i> , 2021, 14, 1716-1731.	1.5	6
1256	Evolutionary QTL-allele changes in main stem node number among geographic and seasonal subpopulations of Chinese cultivated soybeans. <i>Molecular Genetics and Genomics</i> , 2021, 296, 313-330.	1.0	5
1257	Whole Genome Sequencing Reveals the Effects of Recent Artificial Selection on Litter Size of Bamei Mutton Sheep. <i>Animals</i> , 2021, 11, 157.	1.0	9
1258	Fine scale human genetic structure in three regions of Cameroon reveals episodic diversifying selection. <i>Scientific Reports</i> , 2021, 11, 1039.	1.6	3
1259	A Comprehensive Approach to Detect Hybridization Sheds Light on the Evolution of Earthâ€™s Largest Lizards. <i>Systematic Biology</i> , 2021, 70, 877-890.	2.7	10
1260	Sarcoglycan A mutation in miniature dachshund dogs causes limb-girdle muscular dystrophy 2D. <i>Skeletal Muscle</i> , 2021, 11, 2.	1.9	8

#	ARTICLE	IF	CITATIONS
1261	Positive selection signatures in Anqing six-end white pig population based on reduced representation genome sequencing data. <i>Animal Genetics</i> , 2021, 52, 143-154.	0.6	8
1262	Accurate Imputation of Untyped Variants from Deep Sequencing Data. <i>Methods in Molecular Biology</i> , 2021, 2243, 271-281.	0.4	6
1263	Using Breeding Populations With a Dual Purpose: Cultivar Development and Gene Mapping—A Case Study Using Resistance to Common Bacterial Blight in Dry Bean (<i>Phaseolus vulgaris</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 621097.	1.7	7
1265	Detection of selection signatures for response to Aleutian mink disease virus infection in American mink. <i>Scientific Reports</i> , 2021, 11, 2944.	1.6	16
1266	Factors Affecting Accuracy of Genotype Imputation Using Neural Networks in Deep Learning. , 2021, , .		0
1268	Genetic Diversity and Signatures of Selection for Thermal Stress in Cattle and Other Two Bos Species Adapted to Divergent Climatic Conditions. <i>Frontiers in Genetics</i> , 2021, 12, 604823.	1.1	29
1269	Tracing founder haplotypes of Japanese apple varieties: application in genomic prediction and genome-wide association study. <i>Horticulture Research</i> , 2021, 8, 49.	2.9	21
1271	A Particular SORL1 Micro-haplotype May Prevent Severe Liver Disease in a French Cohort of Alpha 1-Antitrypsin-deficient Children. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2021, 73, e68-e72.	0.9	2
1272	Pairwise linkage disequilibrium estimation for polyploids. <i>Molecular Ecology Resources</i> , 2021, 21, 1230-1242.	2.2	18
1273	Demographic History, Adaptation, and NRAP Convergent Evolution at Amino Acid Residue 100 in the World Northernmost Cattle from Siberia. <i>Molecular Biology and Evolution</i> , 2021, 38, 3093-3110.	3.5	27
1274	LEA 3: Factor models in population genetics and ecological genomics with R. <i>Molecular Ecology Resources</i> , 2021, 21, 2738-2748.	2.2	36
1275	The Genetic Variation of Lactase Persistence Alleles in Sudan and South Sudan. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	4
1276	Biologically Enhanced Genome-Wide Association Study Provides Further Evidence for Candidate Loci and Discovers Novel Loci That Influence Risk of Anterior Cruciate Ligament Rupture in a Dog Model. <i>Frontiers in Genetics</i> , 2021, 12, 593515.	1.1	7
1277	Molecular signatures of selection on the human GLI3 associated central nervous system specific enhancers. <i>Development Genes and Evolution</i> , 2021, 231, 21-32.	0.4	3
1278	ABO Genetic Variation in Neanderthals and Denisovans. <i>Molecular Biology and Evolution</i> , 2021, 38, 3373-3382.	3.5	7
1279	Identification of common predisposing loci to hematopoietic cancers in four dog breeds. <i>PLoS Genetics</i> , 2021, 17, e1009395.	1.5	16
1280	A Nonsense Variant in Hephaestin Like 1 (HEPHL1) Is Responsible for Congenital Hypotrichosis in Belted Galloway Cattle. <i>Genes</i> , 2021, 12, 643.	1.0	5
1281	Genome-Wide Analysis Reveals Selection Signatures Involved in Meat Traits and Local Adaptation in Semi-Feral Maremmana Cattle. <i>Frontiers in Genetics</i> , 2021, 12, 675569.	1.1	8

#	ARTICLE	IF	CITATIONS
1282	Genome-wide identification of agronomically important genes in outcrossing crops using OutcrossSeq. <i>Molecular Plant</i> , 2021, 14, 556-570.	3.9	30
1283	Population Genomics Reveals Molecular Determinants of Specialization to Tomato in the Polyphagous Fungal Pathogen <i>Botrytis cinerea</i> in France. <i>Phytopathology</i> , 2021, 111, 2355-2366.	1.1	11
1284	Continent-wide genomic signatures of adaptation to urbanisation in a songbird across Europe. <i>Nature Communications</i> , 2021, 12, 2983.	5.8	34
1285	Determination of complete chromosomal haplotypes by bulk DNA sequencing. <i>Genome Biology</i> , 2021, 22, 139.	3.8	16
1286	Exploring the genetic features and signatures of selection in South China indigenous pigs. <i>Journal of Integrative Agriculture</i> , 2021, 20, 1359-1371.	1.7	9
1288	Contrasting demographic histories revealed in two invasive populations of the dry rot fungus <i>Serpula lacrymans</i> . <i>Molecular Ecology</i> , 2021, 30, 2772-2789.	2.0	6
1289	Prostate cancer risk variants of the HOXB genetic locus. <i>Scientific Reports</i> , 2021, 11, 11385.	1.6	6
1290	Introgression, admixture, and selection facilitate genetic adaptation to high-altitude environments in cattle. <i>Genomics</i> , 2021, 113, 1491-1503.	1.3	10
1291	Genetic dynamics of flowering date evolved from later to earlier in annual wild and cultivated soybean in China. <i>Crop Science</i> , 2021, 61, 2336-2354.	0.8	6
1292	Human-modified canids in human-modified landscapes: The evolutionary consequences of hybridization for grey wolves and free-ranging domestic dogs. <i>Evolutionary Applications</i> , 2021, 14, 2433-2456.	1.5	15
1293	Genotyping and Whole-Genome Resequencing of Welsh Sheep Breeds Reveal Candidate Genes and Variants for Adaptation to Local Environment and Socioeconomic Traits. <i>Frontiers in Genetics</i> , 2021, 12, 612492.	1.1	8
1295	Population dynamics of GC-changing mutations in humans and great apes. <i>Genetics</i> , 2021, 218, .	1.2	7
1296	Selection trends on nasal-associated SNP variants across human populations. <i>Meta Gene</i> , 2021, 28, 100872.	0.3	0
1297	Characterization of Japanese Plum (<i>Prunus salicina</i>) PsMYB10 Alleles Reveals Structural Variation and Polymorphisms Correlating With Fruit Skin Color. <i>Frontiers in Plant Science</i> , 2021, 12, 655267.	1.7	14
1298	Genome-Wide Association Mapping of bc-1 and bc-u Reveals Candidate Genes and New Adjustments to the Host-Pathogen Interaction for Resistance to Bean Common Mosaic Necrosis Virus in Common Bean. <i>Frontiers in Plant Science</i> , 2021, 12, 699569.	1.7	10
1299	An overview of current population genomics methods for the analysis of whole-genome resequencing data in eukaryotes. <i>Molecular Ecology</i> , 2021, 30, 6036-6071.	2.0	38
1300	Phase Resolution of Heterozygous Sites in Diploid Genomes is Important to Phylogenomic Analysis under the Multispecies Coalescent Model. <i>Systematic Biology</i> , 2022, 71, 334-352.	2.7	11
1301	The RING E3 ligase CLG1 targets GS3 for degradation via the endosome pathway to determine grain size in rice. <i>Molecular Plant</i> , 2021, 14, 1699-1713.	3.9	41

#	ARTICLE	IF	CITATIONS
1302	Revisiting a GWAS peak in <i>Arabidopsis thaliana</i> reveals possible confounding by genetic heterogeneity. <i>Heredity</i> , 2021, 127, 245-252.	1.2	8
1303	Development and testing of a combined species SNP array for the European seabass (<i>Dicentrarchus</i>) Tj ETQq1 1 0.784314 rgBT /Over	1.3	31
1304	Assessing the Effect of Phenotyping Scoring Systems and SNP Calling and Filtering Parameters on Detection of QTL Associated with Reaction of <i>Brassica napus</i> to <i>Sclerotinia sclerotiorum</i> . <i>PhytoFrontiers</i> , 2021, 1, 135-148.	0.8	5
1305	Search for Selection Signatures Related to Trypanosomosis Tolerance in African Goats. <i>Frontiers in Genetics</i> , 2021, 12, 715732.	1.1	8
1306	Enhanced mixture interpretation with macrohaplotypes based on long-read DNA sequencing. <i>International Journal of Legal Medicine</i> , 2021, 135, 2189-2198.	1.2	5
1307	Assessing combining abilities, genomic data, and genotype×environment interactions to predict hybrid grain sorghum performance. <i>Plant Genome</i> , 2021, 14, e20127.	1.6	12
1308	Privacy-preserving genotype imputation in a trusted execution environment. <i>Cell Systems</i> , 2021, 12, 983-993.e7.	2.9	13
1309	Genome-Wide Association Study Using Whole-Genome Sequencing Identifies a Genomic Region on Chromosome 6 Associated With Comb Traits in Nandan-Yao Chicken. <i>Frontiers in Genetics</i> , 2021, 12, 682501.	1.1	4
1311	Scalable bias-corrected linkage disequilibrium estimation under genotype uncertainty. <i>Heredity</i> , 2021, 127, 357-362.	1.2	5
1313	False discovery rate control in genome-wide association studies with population structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	33
1314	The genetic consequences of dog breed formation—Accumulation of deleterious genetic variation and fixation of mutations associated with myxomatous mitral valve disease in cavalier King Charles spaniels. <i>PLoS Genetics</i> , 2021, 17, e1009726.	1.5	12
1315	Unveiling Comparative Genomic Trajectories of Selection and Key Candidate Genes in Egg-Type Russian White and Meat-Type White Cornish Chickens. <i>Biology</i> , 2021, 10, 876.	1.3	15
1316	Associated SNPs, Heritabilities, Trait Correlations, and Genomic Breeding Values for Resistance in Snap Beans (<i>Phaseolus vulgaris</i> L.) to Root Rot Caused by <i>Fusarium solani</i> (Mart.) f. sp. <i>phaseoli</i> (Burkholder). <i>Frontiers in Plant Science</i> , 2021, 12, 697615.	1.7	2
1317	Diverse phosphate and auxin transport loci distinguish phosphate tolerant from sensitive <i>Arabidopsis</i> accessions. <i>Plant Physiology</i> , 2021, 187, 2656-2673.	2.3	9
1318	Genome-Wide Association Study to Map Genomic Regions Related to the Initiation Time of Four Growth Stage Traits in Soybean. <i>Frontiers in Genetics</i> , 2021, 12, 715529.	1.1	3
1319	A genome-wide scan to identify signatures of selection in two Iranian indigenous chicken ecotypes. <i>Genetics Selection Evolution</i> , 2021, 53, 72.	1.2	20
1320	Distinguishing genomic homogenization from parapatric speciation in an elevationally replacing pair of <i>Ramphocelus</i> tanagers. <i>Molecular Ecology</i> , 2021, 30, 5517-5529.	2.0	10
1321	Fast two-stage phasing of large-scale sequence data. <i>American Journal of Human Genetics</i> , 2021, 108, 1880-1890.	2.6	250

#	ARTICLE	IF	CITATIONS
1322	Chromosome X-wide Analysis of Positive Selection in Human Populations: Common and Private Signals of Selection and its Impact on Inactivated Genes and Enhancers. <i>Frontiers in Genetics</i> , 2021, 12, 714491.	1.1	2
1323	Genomic basis of high-altitude adaptation in Tibetan <i>Prunus</i> fruit trees. <i>Current Biology</i> , 2021, 31, 3848-3860.e8.	1.8	41
1324	Phylogeny of African Long-Fingered Frogs (Arthroleptidae: Cardioglossa) Reveals Recent Allopatric Divergences in Coloration. <i>Ichthyology and Herpetology</i> , 2021, 109, .	0.3	1
1325	Elevated diversity in loci linked to facial morphology is consistent with the hypothesis that individual facial recognition is important across hominoids. <i>American Journal of Physical Anthropology</i> , 2021, 174, 785-791.	2.1	0
1326	Genomic consequences of apple improvement. <i>Horticulture Research</i> , 2021, 8, 9.	2.9	53
1327	Genome-wide association study for resistance to the <i>Meloidogyne javanica</i> causing root-knot nematode in soybean. <i>Theoretical and Applied Genetics</i> , 2021, 134, 777-792.	1.8	15
1328	Developing SNPs and Strategies for Genomic Analysis in Alfalfa. <i>Compendium of Plant Genomes</i> , 2021, , 159-175.	0.3	0
1329	Breed Ancestry, Divergence, Admixture, and Selection Patterns of the Simbra Crossbreed. <i>Frontiers in Genetics</i> , 2020, 11, 608650.	1.1	4
1330	Genome-wide association studies revealed novel stripe rust resistance QTL in barley at seedling and adult-plant stages. <i>Euphytica</i> , 2021, 217, 1.	0.6	4
1331	Natural variation in the promoter of <i>GsERD15B</i> affects salt tolerance in soybean. <i>Plant Biotechnology Journal</i> , 2021, 19, 1155-1169.	4.1	34
1332	Lipids in Health and Disease. <i>Sub-Cellular Biochemistry</i> , 2008, , .	1.0	8
1333	The Identification of Colon Cancer Susceptibility Genes by Using Genome-Wide Scans. <i>Methods in Molecular Biology</i> , 2010, 653, 3-21.	0.4	4
1334	WhatsHap: Haplotype Assembly for Future-Generation Sequencing Reads. <i>Lecture Notes in Computer Science</i> , 2014, , 237-249.	1.0	20
1335	Variant Calling Using NGS Data in European Aspen (<i>Populus tremula</i>). , 2015, , 43-61.		5
1336	Improved Algorithms for Inferring the Minimum Mosaic of a Set of Recombinants. <i>Lecture Notes in Computer Science</i> , 2007, , 150-161.	1.0	15
1337	Integer Programming Formulations and Computations Solving Phylogenetic and Population Genetic Problems with Missing or Genotypic Data. <i>Lecture Notes in Computer Science</i> , 2007, , 51-64.	1.0	52
1338	Haplotype Inference Via Hierarchical Genotype Parsing. <i>Lecture Notes in Computer Science</i> , 2007, , 85-97.	1.0	12
1339	Imputation-Based Local Ancestry Inference in Admixed Populations. <i>Lecture Notes in Computer Science</i> , 2009, , 221-233.	1.0	11

#	ARTICLE	IF	CITATIONS
1340	An Adaptive and Memory Efficient Algorithm for Genotype Imputation. Lecture Notes in Computer Science, 2009, , 482-495.	1.0	2
1342	HLA Type Inference via Haplotypes Identical by Descent. Lecture Notes in Computer Science, 2010, , 491-505.	1.0	3
1343	Insights on Haplotype Inference on Large Genotype Datasets. Lecture Notes in Computer Science, 2010, , 47-58.	1.0	6
1344	Improved whole-chromosome phasing for disease and population genetic studies. , 0, .		1
1375	Haplotype Inference and Association Analysis in Unrelated Samples. , 2007, , 123-159.		1
1376	Scalable Statistical Introgression Mapping Using Approximate Coalescent-Based Inference. , 2019, , .		1
1377	scHaplotyper: haplotype construction and visualization for genetic diagnosis using single cell DNA sequencing data. BMC Bioinformatics, 2020, 21, 41.	1.2	9
1378	Evaluation of Haplotype Inference Using Definitive Haplotype Data Obtained from Complete Hydatidiform Moles, and Its Significance for the Analyses of Positively Selected Regions. PLoS Genetics, 2009, 5, e1000468.	1.5	18
1379	Allelic Variation at the 8q23.3 Colorectal Cancer Risk Locus Functions as a Cis-Acting Regulator of EIF3H. PLoS Genetics, 2010, 6, e1001126.	1.5	74
1380	Canine Population Structure: Assessment and Impact of Intra-Breed Stratification on SNP-Based Association Studies. PLoS ONE, 2007, 2, e1324.	1.1	66
1381	Diversity in the Glucose Transporter-4 Gene (SLC2A4) in Humans Reflects the Action of Natural Selection along the Old-World Primates Evolution. PLoS ONE, 2010, 5, e9827.	1.1	9
1382	Sequence Polymorphism in Candidate Genes for Differences in Winter Plumage between Scottish and Scandinavian Willow Grouse (<i>Lagopus lagopus</i>). PLoS ONE, 2010, 5, e10334.	1.1	18
1383	Utilizing Genotype Imputation for the Augmentation of Sequence Data. PLoS ONE, 2010, 5, e11018.	1.1	19
1384	Performance of Single Nucleotide Polymorphisms versus Haplotypes for Genome-Wide Association Analysis in Barley. PLoS ONE, 2010, 5, e14079.	1.1	118
1385	On the Origin of Tibetans and Their Genetic Basis in Adapting High-Altitude Environments. PLoS ONE, 2011, 6, e17002.	1.1	126
1386	Association Between TAS2R38 Gene Polymorphisms and Colorectal Cancer Risk: A Case-Control Study in Two Independent Populations of Caucasian Origin. PLoS ONE, 2011, 6, e20464.	1.1	77
1387	Sequence Imputation of HPV16 Genomes for Genetic Association Studies. PLoS ONE, 2011, 6, e21375.	1.1	70
1388	PanSNPdb: The Pan-Asian SNP Genotyping Database. PLoS ONE, 2011, 6, e21451.	1.1	53

#	ARTICLE	IF	CITATIONS
1389	A Targeted Association Study of Immunity Genes and Networks Suggests Novel Associations with Placental Malaria Infection. PLoS ONE, 2011, 6, e24996.	1.1	6
1390	Sample Reproducibility of Genetic Association Using Different Multimarker TDTs in Genome-Wide Association Studies: Characterization and a New Approach. PLoS ONE, 2012, 7, e29613.	1.1	5
1391	Design of a Bovine Low-Density SNP Array Optimized for Imputation. PLoS ONE, 2012, 7, e34130.	1.1	159
1392	Evolution of Outcrossing in Experimental Populations of <i>Caenorhabditis elegans</i> . PLoS ONE, 2012, 7, e35811.	1.1	94
1393	Genotype-Based Test in Mapping Cis-Regulatory Variants from Allele-Specific Expression Data. PLoS ONE, 2012, 7, e38667.	1.1	7
1394	Selection Signature Analysis Implicates the PC1/PCSK1 Region for Chicken Abdominal Fat Content. PLoS ONE, 2012, 7, e40736.	1.1	40
1395	Positive Selection on the Osteoarthritis-Risk and Decreased-Height Associated Variants at the GDF5 Gene in East Asians. PLoS ONE, 2012, 7, e42553.	1.1	24
1396	Analysis of Genome-Wide Association Studies with Multiple Outcomes Using Penalization. PLoS ONE, 2012, 7, e51198.	1.1	5
1397	An Improved Genotyping by Sequencing (GBS) Approach Offering Increased Versatility and Efficiency of SNP Discovery and Genotyping. PLoS ONE, 2013, 8, e54603.	1.1	406
1398	Assessing Methods for Assigning SNPs to Genes in Gene-Based Tests of Association Using Common Variants. PLoS ONE, 2013, 8, e62161.	1.1	38
1399	Impact of Variation at the FTO Locus on Milk Fat Yield in Holstein Dairy Cattle. PLoS ONE, 2013, 8, e63406.	1.1	23
1400	The Genetic Architecture of Maize Stalk Strength. PLoS ONE, 2013, 8, e67066.	1.1	129
1401	A Single-Nucleotide Polymorphism of Human Neuropeptide S Gene Originated from Europe Shows Decreased Bioactivity. PLoS ONE, 2013, 8, e83009.	1.1	8
1402	Sardinians Genetic Background Explained by Runs of Homozygosity and Genomic Regions under Positive Selection. PLoS ONE, 2014, 9, e91237.	1.1	37
1403	HaplotypeCN: Copy Number Haplotype Inference with Hidden Markov Model and Localized Haplotype Clustering. PLoS ONE, 2014, 9, e96841.	1.1	3
1404	fcGENE: A Versatile Tool for Processing and Transforming SNP Datasets. PLoS ONE, 2014, 9, e97589.	1.1	52
1405	A New Genotype Imputation Method with Tolerance to High Missing Rate and Rare Variants. PLoS ONE, 2014, 9, e101025.	1.1	25
1406	Genome-Wide Association Studies Identifies Seven Major Regions Responsible for Iron Deficiency Chlorosis in Soybean (<i>Glycine max</i>). PLoS ONE, 2014, 9, e107469.	1.1	92

#	ARTICLE	IF	CITATIONS
1407	Association of NOD2 and IL23R with Inflammatory Bowel Disease in Puerto Rico. PLoS ONE, 2014, 9, e108204.	1.1	14
1408	A Major Gene for Bovine Ovulation Rate. PLoS ONE, 2015, 10, e0129025.	1.1	28
1409	Genome-Wide Association Mapping for Resistance to Leaf and Stripe Rust in Winter-Habit Hexaploid Wheat Landraces. PLoS ONE, 2015, 10, e0129580.	1.1	120
1410	The Relationship between Runs of Homozygosity and Inbreeding in Jersey Cattle under Selection. PLoS ONE, 2015, 10, e0129967.	1.1	80
1411	Genome Scan for Selection in Structured Layer Chicken Populations Exploiting Linkage Disequilibrium Information. PLoS ONE, 2015, 10, e0130497.	1.1	19
1412	Genetic Contributions to the Development of Complications in Preterm Newborns. PLoS ONE, 2015, 10, e0131741.	1.1	40
1413	A Multi-Breed Genome-Wide Association Analysis for Canine Hypothyroidism Identifies a Shared Major Risk Locus on CFA12. PLoS ONE, 2015, 10, e0134720.	1.1	16
1414	Genomic Footprints in Selected and Unselected Beef Cattle Breeds in Korea. PLoS ONE, 2016, 11, e0151324.	1.1	9
1415	Island-Model Genomic Selection for Long-Term Genetic Improvement of Autogamous Crops. PLoS ONE, 2016, 11, e0153945.	1.1	17
1416	Single- and Bayesian Multi-Marker Genome-Wide Association for Haematological Parameters in Pigs. PLoS ONE, 2016, 11, e0159212.	1.1	22
1417	The distribution of runs of homozygosity and selection signatures in six commercial meat sheep breeds. PLoS ONE, 2017, 12, e0176780.	1.1	272
1418	Genetic diversity, breed composition and admixture of Kenyan domestic pigs. PLoS ONE, 2018, 13, e0190080.	1.1	44
1419	Parent-progeny imputation from pooled samples for cost-efficient genotyping in plant breeding. PLoS ONE, 2017, 12, e0190271.	1.1	19
1420	Signatures of positive selection in African Butana and Kenana dairy zebu cattle. PLoS ONE, 2018, 13, e0190446.	1.1	88
1421	Comparative analysis of genetic diversity and differentiation of cauliflower (<i>Brassica oleracea</i> var.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	29
1422	Selection signatures in two oldest Russian native cattle breeds revealed using high-density single nucleotide polymorphism analysis. PLoS ONE, 2020, 15, e0242200.	1.1	22
1423	Novel methods for epistasis detection in genome-wide association studies. PLoS ONE, 2020, 15, e0242927.	1.1	9
1424	Single and Multi-trait GWAS Identify Genetic Factors Associated with Production Traits in Common Bean Under Abiotic Stress Environments. G3: Genes, Genomes, Genetics, 2019, 9, 1881-1892.	0.8	76

#	ARTICLE	IF	CITATIONS
1425	Simulation-Based Evaluation of Three Methods for Local Ancestry Deconvolution of Non-model Crop Species Genomes. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 569-579.	0.8	4
1426	Species-Specific Duplication Event Associated with Elevated Levels of Nonstructural Carbohydrates in <i>Sorghum bicolor</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1511-1520.	0.8	13
1427	Admixture Mapping Links RACGAP1 Regulation to Prostate Cancer in African Americans. <i>Cancer Genomics and Proteomics</i> , 2018, 15, 185-191.	1.0	5
1429	Genome-wide association studies - A summary for the clinical gastroenterologist. <i>World Journal of Gastroenterology</i> , 2009, 15, 5377.	1.4	14
1430	Marker Imputation in Barley Association Studies. <i>Plant Genome</i> , 2009, 2, .	1.6	10
1431	A BAYESIAN GWAS METHOD UTILIZING HAPLOTYPE CLUSTERS FOR A COMPOSITE BREED POPULATION. <i>Conference on Applied Statistics in Agriculture</i> , 0, , .	0.0	2
1432	Genetic markers of body composition and carcass quality in grazing Brangus steers. <i>Genetics and Molecular Research</i> , 2011, 10, 3146-3156.	0.3	11
1433	Increasing the Power of Association Studies by Imputation-based Sparse Tag SNP Selection. <i>Communications in Information and Systems</i> , 2009, 9, 269-282.	0.3	1
1434	Practical consideration of genotype imputation: Sample size, window size, reference choice, and untyped rate. <i>Statistics and Its Interface</i> , 2011, 4, 339-351.	0.2	26
1435	An extended Tajima's D neutrality test incorporating SNP calling and imputation uncertainties. <i>Statistics and Its Interface</i> , 2015, 8, 447-456.	0.2	4
1436	Genome-wide selection signatures in Pinzgau cattle. <i>Potravinarstvo</i> , 2015, 9, 268-274.	0.5	6
1437	Accuracy of genomic breeding value prediction for intramuscular fat using different genomic relationship matrices in Hanwoo (Korean cattle). <i>Asian-Australasian Journal of Animal Sciences</i> , 2017, 30, 907-911.	2.4	12
1438	Association of SNP Haplotypes at the Myostatin Gene with Muscular Hypertrophy in Sheep. <i>Asian-Australasian Journal of Animal Sciences</i> , 2008, 21, 928-935.	2.4	24
1439	Identification of the SNP (Single Nucleotide Polymorphism) of the Stearoyl-CoA Desaturase (SCD) Associated with Unsaturated Fatty Acid in Hanwoo (Korean Cattle). <i>Asian-Australasian Journal of Animal Sciences</i> , 2011, 24, 757-765.	2.4	15
1440	Topics on Drug Metabolism. , 2012, , .		9
1441	The evolutionary history and genomics of European blackcap migration. <i>ELife</i> , 2020, 9, .	2.8	57
1442	Natural variation in teosinte at the domestication locus <i>teosinte branched1</i> . <i>PeerJ</i> , 2015, 3, e900.	0.9	13
1443	ARHap: Association Rule Haplotype Phasing. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	1

#	ARTICLE	IF	CITATIONS
1444	Is Natural Population of <i>Candida tropicalis</i> Sexual, Parasexual, and/or Asexual?. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 751676.	1.8	11
1447	Probabilistic Logic Learning from Haplotype Data. <i>Lecture Notes in Computer Science</i> , 2008, , 263-286.	1.0	0
1448	Haplotype Association Analysis. , 2008, , 205-224.		0
1449	Analysis of Population-Based Genetic Association Studies Applied to Cancer Susceptibility and Prognosis. , 2009, , 149-191.		0
1450	An Integer Programming Approach for the Selection of Tag SNPs Using Multi-allelic LD. <i>Communications in Information and Systems</i> , 2009, 9, 253-268.	0.3	1
1451	DETECTING GENOME-WIDE HAPLOTYPE POLYMORPHISM BY COMBINED USE OF MENDELIAN CONSTRAINTS AND LOCAL POPULATION STRUCTURE. , 2009, , 348-358.		5
1452	The Clark Phase-able Sample Size Problem: Long-Range Phasing and Loss of Heterozygosity in GWAS. <i>Lecture Notes in Computer Science</i> , 2010, , 158-173.	1.0	1
1453	Bounds on the Minimum Mosaic of Population Sequences under Recombination. <i>Lecture Notes in Computer Science</i> , 2010, , 152-163.	1.0	1
1454	A Review of Genetic Association Analyses in Population and Family Based Data: Methods and Software. <i>Ungyong T'onggye Yon'gu = the Korean Journal of Applied Statistics</i> , 2010, 23, 95-111.	0.0	1
1456	Prediction of Genomic Relationship Matrices using Single Nucleotide Polymorphisms in Hanwoo. <i>Journal of Animal Science and Technology</i> , 2010, 52, 357-366.	0.8	0
1457	Haplotype Inference. <i>Methods in Molecular Biology</i> , 2012, 850, 411-421.	0.4	0
1458	Renewed Interest in Haplotype: From Genetic Marker to Gene Prediction. <i>Translational Bioinformatics</i> , 2012, , 83-104.	0.0	0
1459	Statistical Methods in Genetic and Molecular Epidemiology and Their Application in Studies with Metabolic Phenotypes. , 2012, , 39-56.		0
1460	A Faster Haplotyping Algorithm Based on Block Partition, and Greedy Ligation Strategy. <i>Lecture Notes in Computer Science</i> , 2012, , 537-544.	1.0	0
1461	Associating Genotype Sequence Properties to Haplotype Inference Errors. <i>Lecture Notes in Computer Science</i> , 2012, , 132-143.	1.0	0
1462	From SNP Genotyping to Improved Pediatric Healthcare. <i>Translational Bioinformatics</i> , 2012, , 359-378.	0.0	0
1463	Homogenizing Access to Highly Time-Consuming Biomedical Applications through a Web-Based Interface. <i>Lecture Notes in Computer Science</i> , 2012, , 33-42.	1.0	0
1464	Estimation of Linkage Disequilibrium and Effective Population Size using Whole Genome Single Nucleotide Polymorphisms in Hanwoo. <i>Journal of Life Science</i> , 2012, 22, 366-372.	0.2	1

#	ARTICLE	IF	CITATIONS
1465	Forests of Latent Tree Models to Decipher Genotype-Phenotype Associations. Communications in Computer and Information Science, 2013, , 113-134.	0.4	3
1466	Machine Learning-Based Imputation of Missing SNP Genotypes in SNP Genotype Arrays. , 2013, , 193-231.		0
1467	HybHap: A Fast and Accurate Hybrid Approach for Haplotype Inference on Large Datasets. Lecture Notes in Computer Science, 2013, , 24-35.	1.0	0
1468	SNP Imputation for Association Studies. Statistics in the Health Sciences, 2014, , 213-242.	0.2	0
1469	Haplotype Imputation for Association Analysis. Statistics in the Health Sciences, 2014, , 183-211.	0.2	0
1471	Identification of Ethnically Specific Genetic Variations in Pan-Asian Ethnos. Genomics and Informatics, 2014, 12, 42.	0.4	2
1472	Accurate construction of long range haplotype In unrelated individuals. Statistica Sinica, 2014, , .	0.2	0
1473	Discovery and Characterization of Cancer Genetic Susceptibility Alleles. , 2014, , 309-321.e3.		0
1474	Identification of SNP(Single Nucleotide Polymorphism) from MC1R, MITF and TYRP1 associated with Feather Color in Chicken. Korean Journal of Poultry Science, 2014, 41, 29-37.	0.1	2
1475	Identification of Selection Signals in Chikso (Brindle Hanwoo) using Rsb Method. Journal of Agriculture & Life Science, 2014, 48, 207-216.	0.1	1
1477	Modeling Linkage Disequilibrium with Decomposable Graphical Models. , 2014, , 247-268.		0
1478	Major SNP identification for oleic acid and marbling score which are associated with Korean cattle. Journal of the Korean Data and Information Science Society, 2014, 25, 1011-1024.	0.0	3
1481	Current Study Designs, Methods, and Future Directions of Genetic Association Mapping. Advances in Bioinformatics and Biomedical Engineering Book Series, 2015, , 323-358.	0.2	0
1493	Accurate Prediction of Haplotype Inference Errors by Feature Extraction. Lecture Notes in Computer Science, 2017, , 302-313.	1.0	0
1508	Genomic scan for detection of selective sweeps in Turkmen horse population. Research on Animal Production, 2018, 9, 54-62.	0.2	3
1510	Can an Integrative SNP Approach Substitute Standard Identification in Comprehensive Case/Control Analyses?. Advances in Intelligent Systems and Computing, 2019, , 123-130.	0.5	0
1512	Genome-Wide Scan for Selection Signatures in Iranian Sarabi and Taleshi Indigenous Breed. Research on Animal Production, 2018, 9, 88-99.	0.2	2
1513	Human Genetic Factors and Resistance to Malaria. , 2019, , 1-16.		0

#	ARTICLE	IF	CITATIONS
1516	Genotyping and Statistical Analysis. , 2019, , 1-20.		0
1526	Dissection of the genetic mechanisms underlying congenital anal atresia in pigs. <i>Journal of Genetics and Genomics</i> , 2020, 47, 285-288.	1.7	0
1528	Multiparental QTL analysis: can we do it in polyploids?. <i>Acta Horticulturae</i> , 2020, , 55-64.	0.1	2
1532	Sequencing Directly from Clinical Specimens Reveals Genetic Variations in HCMV-Encoded Chemokine Receptor US28 That May Influence Antibody Levels and Interactions with Human Chemokines. <i>Microbiology Spectrum</i> , 2021, 9, e0002021.	1.2	4
1534	Method for Improving Marker Selection Efficiency through a Graphical Representation of Molecular Markers. <i>Han'guk Yukchong Hakhoe Chi</i> , 2020, 52, 374-381.	0.2	0
1536	Development of SNP markers for grain yield screening of Brazilian rice cultivars. <i>Pesquisa Agropecuaria Brasileira</i> , 0, 55, .	0.9	1
1538	Genotype Imputation with Homomorphic Encryption. , 2021, , .		2
1539	The mode of speciation during a recent radiation in open-ocean phytoplankton. <i>Current Biology</i> , 2021, 31, 5439-5449.e5.	1.8	22
1544	Genotype Error Detection Using Hidden Markov Models of Haplotype Diversity. <i>Lecture Notes in Computer Science</i> , 2007, , 73-84.	1.0	0
1545	Fast Bayesian Haplotype Inference Via Context Tree Weighting. <i>Lecture Notes in Computer Science</i> , 2008, , 259-270.	1.0	0
1549	Association of Arg194Trp, Arg280His and Arg399Gln polymorphisms in X-ray repair cross-complementing group 1 gene and risk of differentiated thyroid carcinoma in Iran. <i>Iranian Biomedical Journal</i> , 2011, 15, 73-8.	0.4	18
1550	Association of PECAM1/CD31 polymorphisms with cerebral malaria. <i>International Journal of Molecular Epidemiology and Genetics</i> , 2016, 7, 87-94.	0.4	1
1552	In Search of Complex Disease Risk through Genome Wide Association Studies. <i>Mathematics</i> , 2021, 9, 3083.	1.1	0
1553	The maintenance of standing genetic variation: Gene flow vs. selective neutrality in Atlantic stickleback fish. <i>Molecular Ecology</i> , 2022, 31, 811-821.	2.0	4
1554	Genome-wide analysis of common and rare variants via multiple knockoffs at biobank scale, with an application to Alzheimer disease genetics. <i>American Journal of Human Genetics</i> , 2021, 108, 2336-2353.	2.6	12
1555	Analysis of the Knockdown Resistance Locus (kdr) in <i>Anopheles stephensi</i> , <i>An. arabiensis</i> , and <i>Culex pipiens s.l.</i> for Insight Into the Evolution of Target-site Pyrethroid Resistance in Eastern Ethiopia. <i>American Journal of Tropical Medicine and Hygiene</i> , 2022, 106, 632-638.	0.6	6
1556	A comprehensive evaluation of factors affecting the accuracy of pig genotype imputation using a single or multi-breed reference population. <i>Journal of Integrative Agriculture</i> , 2022, 21, 486-495.	1.7	6
1557	Accuracy of genotype imputation based on reference population size and marker density in Hanwoo cattle. <i>Journal of Animal Science and Technology</i> , 2021, 63, 1232-1246.	0.8	1

#	ARTICLE	IF	CITATIONS
1558	Detecting selection using extended haplotype homozygosity (EHH)-based statistics in unphased or unpolarized data. <i>PLoS ONE</i> , 2022, 17, e0262024.	1.1	16
1559	Selective signatures and high genome-wide diversity in traditional Brazilian manioc (<i>Manihot Tj ETQq1 1 0.784314,rgBT /Overlock 10</i>	1.6	9
1560	lam hiQâ€”a novel pair of accuracy indices for imputed genotypes. <i>BMC Bioinformatics</i> , 2022, 23, 50.	1.2	2
1561	New genomic regions associated with white mold resistance in dry bean using a MAGIC population. <i>Plant Genome</i> , 2022, 15, e20190.	1.6	3
1562	Identification of important genomic footprints using eight different selection signature statistics in domestic cattle breeds. <i>Gene</i> , 2022, 816, 146165.	1.0	27
1563	Single-cell genome-wide concurrent haplotyping and copy-number profiling through genotyping-by-sequencing. <i>Nucleic Acids Research</i> , 2022, 50, e63-e63.	6.5	17
1564	Can biochemical traits bridge the gap between genomics and plant performance? A study in rice under drought. <i>Plant Physiology</i> , 2022, 189, 1139-1152.	2.3	8
1565	The genetic history of Mayotte and Madagascar cattle breeds mirrors the complex pattern of human exchanges in Western Indian Ocean. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	6
1566	Selection signatures for heat tolerance in Brazilian horse breeds. <i>Molecular Genetics and Genomics</i> , 2022, 297, 449-462.	1.0	3
1567	A comparison of single imputation and multiple imputation methods for missing data in different oncogene expression profiles. <i>Biostatistics and Epidemiology</i> , 2022, 6, 113-127.	0.4	2
1568	High male specific contribution of the X-chromosome to individual global recombination rate in dairy cattle. <i>BMC Genomics</i> , 2022, 23, 114.	1.2	0
1569	Signatures of selection in Nelore cattle revealed by whole-genome sequencing data. <i>Genomics</i> , 2022, 114, 110304.	1.3	8
1570	Genomic selection signatures in Brazilian sheep breeds reared in a tropical environment. <i>Livestock Science</i> , 2022, 258, 104865.	0.6	6
1571	Genome-Wide Local Ancestry and Direct Evidence for Mitonuclear Coadaptation in African Hybrid Cattle Populations (<i>Bos Taurus/Indicus</i>). <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
1572	Benchmarking phasing software with a whole-genome sequenced cattle pedigree. <i>BMC Genomics</i> , 2022, 23, 130.	1.2	3
1573	Runs of Homozygosity Uncover Potential Functional-Altering Mutation Associated With Body Weight and Length in Two Duroc Pig Lines. <i>Frontiers in Veterinary Science</i> , 2022, 9, 832633.	0.9	9
1574	Genome-Wide Association Studies and Haplotype-Sharing Analysis Targeting the Egg Production Traits in Shaoxing Duck. <i>Frontiers in Genetics</i> , 2022, 13, 828884.	1.1	1
1575	Introgressive hybridisation between domestic pigs (<i>Sus scrofa domesticus</i>) and endemic Corsican wild boars (<i>S. s. meridionalis</i>): effects of human-mediated interventions. <i>Heredity</i> , 2022, 128, 279-290.	1.2	3

#	ARTICLE	IF	CITATIONS
1576	An Evolutionary Insight Into the Heterogeneous Severity Pattern of the SARS-CoV-2 Infection. <i>Frontiers in Genetics</i> , 2022, 13, 859508.	1.1	3
1577	Mechanisms of pre-attachment Striga resistance in sorghum through genome-wide association studies. <i>Molecular Genetics and Genomics</i> , 2022, 297, 751-762.	1.0	12
1578	Genome-wide association study of disease resilience traits from a natural polymicrobial disease challenge model in pigs identifies the importance of the major histocompatibility complex region. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
1579	Male-biased migration from East Africa introduced pastoralism into southern Africa. <i>BMC Biology</i> , 2021, 19, 259.	1.7	4
1580	The genomic basis of high-elevation adaptation in wild house mice (<i>Mus musculus domesticus</i>) from South America. <i>Genetics</i> , 2022, 220, .	1.2	7
1581	Tracking SARS-CoV-2 Spike Protein Mutations in the United States (January 2020–March 2021) Using a Statistical Learning Strategy. <i>Viruses</i> , 2022, 14, 9.	1.5	10
1582	Long-term artificial selection of Hanwoo (Korean) cattle left genetic signatures for the breeding traits and has altered the genomic structure. <i>Scientific Reports</i> , 2022, 12, 6438.	1.6	6
1583	Phylogeography using mitogenomes: A rare Dipodidae, <i>Sicista betulina</i> , in North-western Europe. <i>Ecology and Evolution</i> , 2022, 12, e8865.	0.8	3
1584	Selection Signature Analyses Revealed Genes Associated With Adaptation, Production, and Reproduction in Selected Goat Breeds in Kenya. <i>Frontiers in Genetics</i> , 2022, 13, 858923.	1.1	4
1585	Genome-wide association studies and haplotype sharing analysis targeting the growth traits in Yandang partridge chickens. <i>Animal Biotechnology</i> , 2022, , 1-7.	0.7	0
1587	Effects of Genetic Divergence in Identifying Ancestral Origin Using HAPAA. , 2008, , 423-423.		0
1649	Genotyping, the Usefulness of Imputation to Increase SNP Density, and Imputation Methods and Tools. <i>Methods in Molecular Biology</i> , 2022, 2467, 113-138.	0.4	9
1650	METU-SNP: an integrated software system for SNP-complex disease association analysis. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 187.	1.0	3
1651	Sequencing of the Viral UL111a Gene Directly from Clinical Specimens Reveals Variants of HCMV-Encoded IL-10 That Are Associated with Altered Immune Responses to HCMV. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4644.	1.8	3
1652	A systematic analysis of gene-gene interaction in multiple sclerosis. <i>BMC Medical Genomics</i> , 2022, 15, 100.	0.7	3
1653	Revealing Genomic Footprints of Selection for Fiber and Production Traits in Three Indian Sheep Breeds. <i>Journal of Natural Fibers</i> , 2022, 19, 14963-14974.	1.7	14
1654	Capturing Genetic Diversity and Selection Signatures of the Endangered Kosovar Balusha Sheep Breed. <i>Genes</i> , 2022, 13, 866.	1.0	4
1655	The asymptotic distribution of the MLE in high-dimensional logistic models: Arbitrary covariance. <i>Bernoulli</i> , 2022, 28, .	0.7	5

#	ARTICLE	IF	CITATIONS
1656	A Genome-Wide Association Study Identifying Single-Nucleotide Polymorphisms for Iron and Zinc Biofortification in a Worldwide Barley Collection. <i>Plants</i> , 2022, 11, 1349.	1.6	9
1657	Mapping Major Disease Resistance Genes in Soybean by Genome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2022, , 313-340.	0.4	3
1658	Multiple Genomic Regions Govern Tolerance to Sulfentrazone in Snap Bean (<i>Phaseolus Vulgaris</i> L.). <i>Frontiers in Agronomy</i> , 2022, 4, .	1.5	5
1660	Gene-Based Association Tests Using New Polygenic Risk Scores and Incorporating Gene Expression Data. <i>Genes</i> , 2022, 13, 1120.	1.0	2
1661	Selection Signatures in South African Nguni and Bonsmara Cattle Populations Reveal Genes Relating to Environmental Adaptation. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
1662	Detecting Local Adaptation between North and South European Atlantic Salmon Populations. <i>Biology</i> , 2022, 11, 933.	1.3	3
1663	Genetic architecture of a composite beef cattle population. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	4
1664	An enhancer of <i>Agouti</i> contributes to parallel evolution of cryptically colored beach mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	9
1665	Genome-wide local ancestry and evidence for mitonuclear coadaptation in African hybrid cattle populations. <i>IScience</i> , 2022, 25, 104672.	1.9	8
1667	Selection signature analyses and genome-wide association reveal genomic hotspot regions that reflect differences between breeds of horse with contrasting risk of degenerative suspensory ligament desmitis. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
1668	A gain-of-function allele of a DREB transcription factor gene ameliorates drought tolerance in wheat. <i>Plant Cell</i> , 2022, 34, 4472-4494.	3.1	36
1669	Genome-wide scan for selective sweeps identifies novel loci associated with resistance to mastitis in German Holstein cattle. <i>Journal of Animal Breeding and Genetics</i> , 2023, 140, 92-105.	0.8	4
1671	Linkage Disequilibrium, Haplotype Block Structures, Effective Population Size and Genome-Wide Signatures of Selection of Two Conservation Herds of the South African Nguni Cattle. <i>Animals</i> , 2022, 12, 2133.	1.0	4
1673	An EHPB1L1 Nonsense Mutation Associated with Congenital Dyserythropoietic Anemia and Polymyopathy in Labrador Retriever Littermates. <i>Genes</i> , 2022, 13, 1427.	1.0	4
1674	The Linkage-disequilibrium and Recombinational Landscape in <i>Daphnia pulex</i> . <i>Genome Biology and Evolution</i> , 0, , .	1.1	4
1675	Genetic adaptation of skin pigmentation in highland Tibetans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	9
1677	On the way to plant data commons “ a genotyping use case. <i>Journal of Integrative Bioinformatics</i> , 2022, 19, .	1.0	1
1678	A new molecular mechanism supports that blue-greenish egg color evolved independently across chicken breeds. <i>Poultry Science</i> , 2022, 101, 102223.	1.5	3

#	ARTICLE	IF	CITATIONS
1679	A comparative analysis of current phasing and imputation software. PLoS ONE, 2022, 17, e0260177.	1.1	9
1681	Variants of HCMV UL18 Sequenced Directly from Clinical Specimens Associate with Antibody and T-Cell Responses to HCMV. International Journal of Molecular Sciences, 2022, 23, 12911.	1.8	0
1683	Assessing Genetic Diversity and Searching for Selection Signatures by Comparison between the Indigenous Livni and Duroc Breeds in Local Livestock of the Central Region of Russia. Diversity, 2022, 14, 859.	0.7	1
1684	An autoencoder-based deep learning method for genotype imputation. Frontiers in Artificial Intelligence, 0, 5, .	2.0	5
1685	Modified screening method of middle american dry bean genotypes reveals new genomic regions on Pv10 associated with anthracnose resistance. Frontiers in Plant Science, 0, 13, .	1.7	1
1686	Integrating genome-wide association studies and population genomics analysis reveals the genetic architecture of growth and backfat traits in pigs. Frontiers in Genetics, 0, 13, .	1.1	1
1687	Bayesian model and selection signature analyses reveal risk factors for canine atopic dermatitis. Communications Biology, 2022, 5, .	2.0	3
1688	A Pipeline for Phasing and Genotype Imputation on Mixed Human Data (Parents-Offspring Trios and) Tj ETQq1 1 0.784314 rgBT /Overlo 1.1 8	1.1	8
1689	Inference of gene-environment interaction from heterogeneous case-parent trios. Frontiers in Genetics, 0, 13, .	1.1	0
1690	Analytic Hierarchy Process (AHP) Based Soil Erosion Susceptibility Mapping in Northwestern Himalayas: A Case Study of Central Kashmir Province. Conservation, 2023, 3, 32-52.	0.8	6
1691	Selection signature analysis and genome-wide divergence of South African Merino breeds from their founders. Frontiers in Genetics, 0, 13, .	1.1	2
1692	Detection of QTL controlling fiber-related traits in a recombinant inbred lines population from G. hirsutum race punctatum using RTM-GWAS procedure. Industrial Crops and Products, 2023, 193, 116198.	2.5	1
1693	Genome Evolution and the Future of Phylogenomics of Non-Avian Reptiles. Animals, 2023, 13, 471.	1.0	8
1694	Selection and adaptive introgression guided the complex evolutionary history of the European common bean. Nature Communications, 2023, 14, .	5.8	8
1695	Multiple Genetic Loci Associated with Pug Dog Thoracolumbar Myelopathy. Genes, 2023, 14, 385.	1.0	1
1696	Inbred phenotypic data and non-additive effects can enhance genomic prediction models for hybrid grain sorghum. Crop Science, 2023, 63, 1183-1196.	0.8	2
1697	Discovering novel clues of natural selection on four worldwide goat breeds. Scientific Reports, 2023, 13, .	1.6	2
1698	Selective footprints and genes relevant to cold adaptation and other phenotypic traits are unscrambled in the genomes of divergently selected chicken breeds. Journal of Animal Science and Biotechnology, 2023, 14, .	2.1	2

#	ARTICLE	IF	CITATIONS
1699	Genomic diversity and signals of selection processes in wild and farm-reared red-legged partridges (<i>Alectoris rufa</i>). <i>Genomics</i> , 2023, 115, 110591.	1.3	2
1700	Whole-genome sequencing of cryopreserved resources from French Large White pigs at two distinct sampling times reveals strong signatures of convergent and divergent selection between the dam and sire lines. <i>Genetics Selection Evolution</i> , 2023, 55, .	1.2	2
1701	Genome-wide mapping of signatures of selection using a high-density array identified candidate genes for growth traits and local adaptation in chickens. <i>Genetics Selection Evolution</i> , 2023, 55, .	1.2	3
1702	A comprehensive analysis of the genetic diversity and environmental adaptability in worldwide Merino and Merino-derived sheep breeds. <i>Genetics Selection Evolution</i> , 2023, 55, .	1.2	4
1703	The systematic comparison between Gaussian mirror and Model-X knockoff models. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
1704	A VEL3 histone deacetylase complex establishes a maternal epigenetic state controlling progeny seed dormancy. <i>Nature Communications</i> , 2023, 14, .	5.8	8
1705	Transgressive Potential Prediction and Optimal Cross Design of Seed Protein Content in the Northeast China Soybean Population Based on Full Exploration of the QTL-Allele System. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3