

Sequence Kernel Association Tests for the Combined Ef

American Journal of Human Genetics

92, 841-853

DOI: [10.1016/j.ajhg.2013.04.015](https://doi.org/10.1016/j.ajhg.2013.04.015)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Melanoma risk loci as determinants of melanoma recurrence and survival. <i>Journal of Translational Medicine</i> , 2013, 11, 279.	4.4	30
2	The Next-Generation Sequencing Revolution and Its Impact on Genomics. <i>Cell</i> , 2013, 155, 27-38.	28.9	856
3	Quantifying Missing Heritability at Known GWAS Loci. <i>PLoS Genetics</i> , 2013, 9, e1003993.	3.5	115
4	Gene-based multiple regression association testing for combined examination of common and low frequency variants in quantitative trait analysis. <i>Frontiers in Genetics</i> , 2013, 4, 233.	2.3	9
5	Family-Based Association Test Using Both Common and Rare Variants and Accounting for Directions of Effects for Sequencing Data. <i>PLoS ONE</i> , 2014, 9, e107800.	2.5	13
6	Assessing the functional consequence of loss of function variants using electronic medical record and large-scale genomics consortium efforts. <i>Frontiers in Genetics</i> , 2014, 5, 105.	2.3	3
7	Identifying rare and common disease associated variants in genomic data using Parkinson's disease as a model. <i>Journal of Biomedical Science</i> , 2014, 21, 88.	7.0	8
8	Identification of Rare Causal Variants in Sequence-Based Studies: Methods and Applications to VPS13B, a Gene Involved in Cohen Syndrome and Autism. <i>PLoS Genetics</i> , 2014, 10, e1004729.	3.5	45
9	iCall: a genotype-calling algorithm for rare, low-frequency and common variants on the Illumina exome array. <i>Bioinformatics</i> , 2014, 30, 1714-1720.	4.1	2
10	Amerindian-specific regions under positive selection harbour new lipid variants in Latinos. <i>Nature Communications</i> , 2014, 5, 3983.	12.8	81
11	Generalized Functional Linear Models for Gene-Based Case-Control Association Studies. <i>Genetic Epidemiology</i> , 2014, 38, 622-637.	1.3	22
12	Kernel-Machine Testing Coupled with a Rank-Truncation Method for Genetic Pathway Analysis. <i>Genetic Epidemiology</i> , 2014, 38, 447-456.	1.3	12
13	Greater power and computational efficiency for kernel-based association testing of sets of genetic variants. <i>Bioinformatics</i> , 2014, 30, 3206-3214.	4.1	35
14	Common variation at PPARGC1A/B and change in body composition and metabolic traits following preventive interventions: the Diabetes Prevention Program. <i>Diabetologia</i> , 2014, 57, 485-490.	6.3	29
15	Dynamic Bayesian Testing of Sets of Variants in Complex Diseases. <i>Genetics</i> , 2014, 198, 867-878.	2.9	1
16	Combining Family- and Population-Based Imputation Data for Association Analysis of Rare and Common Variants in Large Pedigrees. <i>Genetic Epidemiology</i> , 2014, 38, 579-590.	1.3	28
17	How important are rare variants in common disease?. <i>Briefings in Functional Genomics</i> , 2014, 13, 353-361.	2.7	76
18	A Powerful and Adaptive Association Test for Rare Variants. <i>Genetics</i> , 2014, 197, 1081-1095.	2.9	150

#	ARTICLE	IF	CITATIONS
19	Advances in Genetic Discovery and Implications for Counseling of Patients and Families with Autism Spectrum Disorders. <i>Current Genetic Medicine Reports</i> , 2014, 2, 124-134.	1.9	7
20	Statistical Analysis of Next Generation Sequencing Data. , 2014, , .		20
21	Platelet Count Mediates the Contribution of a Genetic Variant in LRRC 16A to ARDS Risk. <i>Chest</i> , 2015, 147, 607-617.	0.8	46
22	Detecting association of rare and common variants by adaptive combination of P-values. <i>Genetical Research</i> , 2015, 97, e20.	0.9	3
23	Rare-Variant Kernel Machine Test for Longitudinal Data from Population and Family Samples. <i>Human Heredity</i> , 2015, 80, 126-138.	0.8	9
24	The Use of the Linear Mixed Model in Human Genetics. <i>Human Heredity</i> , 2015, 80, 196-206.	0.8	18
25	A combination of targeted enrichment methodologies for whole-exome sequencing reveals novel pathogenic mutations. <i>Scientific Reports</i> , 2015, 5, 9331.	3.3	14
26	SNP Set Association Testing for Survival Outcomes in the Presence of Intrafamilial Correlation. <i>Genetic Epidemiology</i> , 2015, 39, 406-414.	1.3	6
27	Cumulative role of rare and common putative functional genetic variants at <i>NPAS3</i> in schizophrenia susceptibility. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2015, 168, 528-535.	1.7	5
28	Statistical Selection Strategy for Risk and Protective Rare Variants Associated with Complex Traits. <i>Journal of Computational Biology</i> , 2015, 22, 1034-1043.	1.6	3
29	SPS: A Simulation Tool for Calculating Power of Set-Based Genetic Association Tests. <i>Genetic Epidemiology</i> , 2015, 39, 395-397.	1.3	3
30	Exome Analysis of Patients with Concurrent Pediatric Inflammatory Bowel Disease and Autoimmune Disease. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 1.	1.9	18
31	Association of Genes, Pathways, and Haplogroups of the Mitochondrial Genome with the Risk of Colorectal Cancer: The Multiethnic Cohort. <i>PLoS ONE</i> , 2015, 10, e0136796.	2.5	27
32	Weighted Score Tests Implementing Model-Averaging Schemes in Detection of Rare Variants in Case-Control Studies. <i>PLoS ONE</i> , 2015, 10, e0139355.	2.5	5
33	Clique-Based Clustering of Correlated SNPs in a Gene Can Improve Performance of Gene-Based Multi-Bin Linear Combination Test. <i>BioMed Research International</i> , 2015, 2015, 1-11.	1.9	9
34	Contribution of Rare and Common Genetic Variants to Plasma Lipid Levels and Carotid Stiffness and Geometry. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 628-636.	5.1	21
35	Pooled Sequencing and Rare Variant Association Tests for Identifying the Determinants of Emerging Drug Resistance in Malaria Parasites. <i>Molecular Biology and Evolution</i> , 2015, 32, 1080-1090.	8.9	34
36	Phenome-Wide Association Studies: Embracing Complexity for Discovery. <i>Human Heredity</i> , 2015, 79, 111-123.	0.8	20

#	ARTICLE	IF	CITATIONS
37	Contribution of Large Region Joint Associations to Complex Traits Genetics. PLoS Genetics, 2015, 11, e1005103.	3.5	10
38	A review of study designs and statistical methods for genomic epidemiology studies using next generation sequencing. Frontiers in Genetics, 2015, 6, 149.	2.3	48
39	The Genetics of Neuropsychiatric Diseases: Looking In and Beyond the Exome. Annual Review of Neuroscience, 2015, 38, 47-68.	10.7	27
40	Genomic approaches for understanding the genetics of complex disease. Genome Research, 2015, 25, 1432-1441.	5.5	75
41	Empirical Bayes Scan Statistics for Detecting Clusters of Disease Risk Variants in Genetic Studies. Biometrics, 2015, 71, 1111-1120.	1.4	6
42	The role of SHANK2 rare variants in schizophrenia susceptibility. Molecular Psychiatry, 2015, 20, 1486-1486.	7.9	16
43	Sequencing rare and common APOL1 coding variants to determine kidney disease risk. Kidney International, 2015, 88, 754-763.	5.2	30
44	CWAS of longitudinal amyloid accumulation on ¹⁸ F-florbetapir PET in Alzheimer's disease implicates microglial activation gene IL1RAP. Brain, 2015, 138, 3076-3088.	7.6	117
45	The contribution of rare and common variants in 30 genes to risk nicotine dependence. Molecular Psychiatry, 2015, 20, 1467-1478.	7.9	64
46	HLA-DQA1 and PLCG2 Are Candidate Risk Loci for Childhood-Onset Steroid-Sensitive Nephrotic Syndrome. Journal of the American Society of Nephrology: JASN, 2015, 26, 1701-1710.	6.1	118
47	Kernel machine regression in neuroimaging genetics. , 2016, , 31-68.		3
48	Rare Variants Association Analysis in Large-Scale Sequencing Studies at the Single Locus Level. PLoS Computational Biology, 2016, 12, e1004993.	3.2	11
49	The MKK7 p.Glu116Lys Rare Variant Serves as a Predictor for Lung Cancer Risk and Prognosis in Chinese. PLoS Genetics, 2016, 12, e1005955.	3.5	14
50	Genetic Evaluation of Schizophrenia Using the Illumina HumanExome Chip. PLoS ONE, 2016, 11, e0150464.	2.5	12
51	A Data Fusion Approach to Enhance Association Study in Epilepsy. PLoS ONE, 2016, 11, e0164940.	2.5	4
52	Beyond Rare-Variant Association Testing: Pinpointing Rare Causal Variants in Case-Control Sequencing Study. Scientific Reports, 2016, 6, 21824.	3.3	17
53	A genome-wide analysis in cluster headache points to neprilysin and PACAP receptor gene variants. Journal of Headache and Pain, 2016, 17, 114.	6.0	38
54	Local Joint Testing Improves Power and Identifies Hidden Heritability in Association Studies. Genetics, 2016, 203, 1105-1116.	2.9	9

#	ARTICLE	IF	CITATIONS
55	Circadian gene variants influence sleep and the sleep electroencephalogram in humans. Chronobiology International, 2016, 33, 561-573.	2.0	24
56	Genetic Associationâ€“Guided Analysis of Gene Networks for the Study of Complex Traits. Circulation: Cardiovascular Genetics, 2016, 9, 179-184.	5.1	9
57	Clinical and Genetic Risk Factors for Acute Pancreatitis in Patients With Acute Lymphoblastic Leukemia. Journal of Clinical Oncology, 2016, 34, 2133-2140.	1.6	88
58	SparkScore: Leveraging Apache Spark for Distributed Genomic Inference. , 2016, , .		6
59	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. Nature Neuroscience, 2016, 19, 1433-1441.	14.8	427
60	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. Nature Neuroscience, 2016, 19, 1563-1565.	14.8	90
61	What is the probability of replicating a statistically significant association in genome-wide association studies?. Briefings in Bioinformatics, 2017, 18, bbw091.	6.5	3
62	Small Sample Kernel Association Tests for Human Genetic and Microbiome Association Studies. Genetic Epidemiology, 2016, 40, 5-19.	1.3	45
63	Test for Rare Variants by Environment Interactions in Sequencing Association Studies. Biometrics, 2016, 72, 156-164.	1.4	68
64	A Wâ€“test collapsing method for rareâ€“variant association testing in exome sequencing data. Genetic Epidemiology, 2016, 40, 591-596.	1.3	6
65	<i>genipe</i>: an automated genome-wide imputation pipeline with automatic reporting and statistical tools. Bioinformatics, 2016, 32, 3661-3663.	4.1	22
66	Poisson Approximationâ€“Based Score Test for Detecting Association of Rare Variants. Annals of Human Genetics, 2016, 80, 221-234.	0.8	1
67	A Comparison Study of Fixed and Mixed Effect Models for Gene Level Association Studies of Complex Traits. Genetic Epidemiology, 2016, 40, 702-721.	1.3	10
68	Variation of 46 Innate Immune Genes Evaluated for their Contribution in Pneumococcal Meningitis Susceptibility and Outcome. EBioMedicine, 2016, 10, 77-84.	6.1	11
69	RNF213 Is Associated with Intracranial Aneurysms in the French-Canadian Population. American Journal of Human Genetics, 2016, 99, 1072-1085.	6.2	49
70	Exome Array Analysis of Susceptibility to Pneumococcal Meningitis. Scientific Reports, 2016, 6, 29351.	3.3	7
71	Genes implicated in thiopurine-induced toxicity: Comparing TPMT enzyme activity with clinical phenotype and exome data in a paediatric IBD cohort. Scientific Reports, 2016, 6, 34658.	3.3	28
72	Powerful association test combining rare variant and gene expression using family data from Genetic Analysis Workshop 19. BMC Proceedings, 2016, 10, 251-255.	1.6	3

#	ARTICLE	IF	CITATIONS
73	Comparing strategies for combined testing of rare and common variants in whole sequence and genome-wide genotype data. BMC Proceedings, 2016, 10, 269-273.	1.6	5
74	Association of rare haplotypes on ULK4 and MAP4 genes with hypertension. BMC Proceedings, 2016, 10, 363-369.	1.6	13
76	Filtering genetic variants and placing informative priors based on putative biological function. BMC Genetics, 2016, 17, 8.	2.7	6
77	Rare Variants in the Complement Factor H-Related Protein 5 Gene Contribute to Genetic Susceptibility to IgA Nephropathy. Journal of the American Society of Nephrology: JASN, 2016, 27, 2894-2905.	6.1	56
78	GWASeq: targeted re-sequencing follow up to GWAS. BMC Genomics, 2016, 17, 176.	2.8	7
79	Genetic Epidemiology and Public Health: The Evolution From Theory to Technology. American Journal of Epidemiology, 2016, 183, 387-393.	3.4	12
80	Gene and pathway level analyses of germline DNA-repair gene variants and prostate cancer susceptibility using the iCOGS-genotyping array. British Journal of Cancer, 2016, 114, 945-952.	6.4	17
81	Comparison of haplotype-based statistical tests for disease association with rare and common variants. Briefings in Bioinformatics, 2016, 17, 657-671.	6.5	19
82	Identification of rare variants in TNNI3 with atrial fibrillation in a Chinese GenelD population. Molecular Genetics and Genomics, 2016, 291, 79-92.	2.1	13
83	Multi-marker linkage disequilibrium mapping of quantitative trait loci. Briefings in Bioinformatics, 2017, 18, 195-204.	6.5	1
84	The Generalized Higher Criticism for Testing SNP-Set Effects in Genetic Association Studies. Journal of the American Statistical Association, 2017, 112, 64-76.	3.1	72
85	Discovery and functional prioritization of Parkinson's disease candidate genes from large-scale whole exome sequencing. Genome Biology, 2017, 18, 22.	8.8	96
86	Links Between the Sequence Kernel Association and the Kernel-Based Adaptive Cluster Tests. Statistics in Biosciences, 2017, 9, 246-258.	1.2	3
87	Selection Probability for Rare Variant Association Studies. Journal of Computational Biology, 2017, 24, 400-411.	1.6	3
88	De novo and rare mutations in the HSPA1L heat shock gene associated with inflammatory bowel disease. Genome Medicine, 2017, 9, 8.	8.2	27
89	Common coding variant in <i>SERPINA1</i> increases the risk for large artery stroke. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3613-3618.	7.1	46
90	Susceptibility to type 2 diabetes may be modulated by haplotypes in G6PC2, a target of positive selection. BMC Evolutionary Biology, 2017, 17, 43.	3.2	14
91	Detecting association of rare and common variants based on cross-validation prediction error. Genetic Epidemiology, 2017, 41, 233-243.	1.3	9

#	ARTICLE	IF	CITATIONS
92	Deep Sequencing of 71 Candidate Genes to Characterize Variation Associated with Alcohol Dependence. <i>Alcoholism: Clinical and Experimental Research</i> , 2017, 41, 711-718.	2.4	13
93	Robust and rapid algorithms facilitate large-scale whole genome sequencing downstream analysis in an integrative framework. <i>Nucleic Acids Research</i> , 2017, 45, gkx019.	14.5	36
94	IGESS: a statistical approach to integrating individual-level genotype data and summary statistics in genome-wide association studies. <i>Bioinformatics</i> , 2017, 33, 2882-2889.	4.1	12
95	The Weighting is the Hardest Part: On the Behavior of the Likelihood Ratio Test and the Score Test Under a Data-Driven Weighting Scheme in Sequenced Samples. <i>Twin Research and Human Genetics</i> , 2017, 20, 108-118.	0.6	5
96	Genomic resources for the study of neuropsychiatric disorders. <i>Molecular Psychiatry</i> , 2017, 22, 1659-1663.	7.9	20
97	On the association analysis of genome-wide sequencing data: A spatial clustering approach for partitioning the entire genome into nonoverlapping windows. <i>Genetic Epidemiology</i> , 2017, 41, 332-340.	1.3	10
98	A comparison study of multivariate fixed models and Gene Association with Multiple Traits (GAMuT) for next-generation sequencing. <i>Genetic Epidemiology</i> , 2017, 41, 18-34.	1.3	3
99	Meta-analysis of quantitative pleiotropic traits for next-generation sequencing with multivariate functional linear models. <i>European Journal of Human Genetics</i> , 2017, 25, 350-359.	2.8	4
100	Evaluating Sequence-Based Genomic Prediction with an Efficient New Simulator. <i>Genetics</i> , 2017, 205, 939-953.	2.9	39
101	Multiple linear combination (MLC) regression tests for common variants adapted to linkage disequilibrium structure. <i>Genetic Epidemiology</i> , 2017, 41, 108-121.	1.3	14
102	HPV16 E7 Genetic Conservation Is Critical to Carcinogenesis. <i>Cell</i> , 2017, 170, 1164-1174.e6.	28.9	221
103	Genome-Wide Testing of Exonic Variants and Breast Cancer Risk in the California Teachers Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1462-1465.	2.5	0
104	Analysis of population-specific pharmacogenomic variants using next-generation sequencing data. <i>Scientific Reports</i> , 2017, 7, 8416.	3.3	20
105	Hepatocellular carcinoma-associated single-nucleotide variants and deletions identified by the use of genome-wide high-throughput analysis of hepatitis B virus. <i>Journal of Pathology</i> , 2017, 243, 176-192.	4.5	29
106	Genetic variants including markers from the exome chip and metabolite traits of type 2 diabetes. <i>Scientific Reports</i> , 2017, 7, 6037.	3.3	12
107	Powerful Genetic Association Analysis for Common or Rare Variants with High-Dimensional Structured Traits. <i>Genetics</i> , 2017, 206, 1779-1790.	2.9	36
108	Establishing the role of rare coding variants in known Parkinson's disease risk loci. <i>Neurobiology of Aging</i> , 2017, 59, 220.e11-220.e18.	3.1	15
109	The SNP-set based association study identifies ITGA1 as a susceptibility gene of attention-deficit/hyperactivity disorder in Han Chinese. <i>Translational Psychiatry</i> , 2017, 7, e1201-e1201.	4.8	11

#	ARTICLE	IF	CITATIONS
110	Adaptive combination of Bayes factors as a powerful method for the joint analysis of rare and common variants. <i>Scientific Reports</i> , 2017, 7, 13858.	3.3	4
111	Genetics of Spontaneous Intracerebral Hemorrhage. <i>Stroke</i> , 2017, 48, 3420-3424.	2.0	32
112	A comprehensive analysis of mitochondrial genes variants and their association with antipsychotic-induced weight gain. <i>Schizophrenia Research</i> , 2017, 187, 67-73.	2.0	18
113	Kernel-Based Measure of Variable Importance for Genetic Association Studies. <i>International Journal of Biostatistics</i> , 2017, 13, .	0.7	1
114	Burden of rare variants in ALS genes influences survival in familial and sporadic ALS. <i>Neurobiology of Aging</i> , 2017, 58, 238.e9-238.e15.	3.1	42
115	Bayesian nonparametric clustering and association studies for candidate SNP observations. <i>International Journal of Approximate Reasoning</i> , 2017, 80, 19-35.	3.3	2
116	Genome-wide association study reveals putative regulators of bioenergy traits in <i>Populus deltoides</i> . <i>New Phytologist</i> , 2017, 213, 799-811.	7.3	89
117	Genomic approaches to the assessment of human spina bifida risk. <i>Birth Defects Research</i> , 2017, 109, 120-128.	1.5	23
118	On the use of kernel machines for Mendelian randomization. <i>Quantitative Biology</i> , 2017, 5, 368-379.	0.5	4
119	Independent impacts of aging on mitochondrial DNA quantity and quality in humans. <i>BMC Genomics</i> , 2017, 18, 890.	2.8	116
120	Significance of functional disease-causal/susceptible variants identified by whole-genome analyses for the understanding of human diseases. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 2017, 93, 657-676.	3.8	5
121	Rare mutations and potentially damaging missense variants in genes encoding fibrillar collagens and proteins involved in their production are candidates for risk for preterm premature rupture of membranes. <i>PLoS ONE</i> , 2017, 12, e0174356.	2.5	14
122	Enrichment of colorectal cancer associations in functional regions: Insight for using epigenomics data in the analysis of whole genome sequence-imputed GWAS data. <i>PLoS ONE</i> , 2017, 12, e0186518.	2.5	8
123	Whole-exome sequencing in amyotrophic lateral sclerosis suggests NEK1 is a risk gene in Chinese. <i>Genome Medicine</i> , 2017, 9, 97.	8.2	23
124	Breast Cancer Clinical Trial of Chemotherapy and Trastuzumab: Potential Tool to Identify Cardiac Modifying Variants of Dilated Cardiomyopathy. <i>Journal of Cardiovascular Development and Disease</i> , 2017, 4, 6.	1.6	5
125	Patterns of Interindividual Variability in the Antibody Repertoire Targeting Proteins Across the Epstein-Barr Virus Proteome. <i>Journal of Infectious Diseases</i> , 2018, 217, 1923-1931.	4.0	13
126	Powerful and robust cross-parent phenotype association test for case-parent trios. <i>Genetic Epidemiology</i> , 2018, 42, 447-458.	1.3	4
127	Joint Analysis of Strain and Parent-of-Origin Effects for Recombinant Inbred Intercrosses Generated from Multiparent Populations with the Collaborative Cross as an Example. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 599-605.	1.8	3

#	ARTICLE	IF	CITATIONS
128	Exome chip analyses identify genes affecting mortality after HLA-matched unrelated-donor blood and marrow transplantation. <i>Blood</i> , 2018, 131, 2490-2499.	1.4	21
129	Next-generation sequencing of AV nodal reentrant tachycardia patients identifies broad spectrum of variants in ion channel genes. <i>European Journal of Human Genetics</i> , 2018, 26, 660-668.	2.8	12
130	Clinical, Social, and Genetic Factors Associated with Obesity at 12 Months of Age. <i>Journal of Pediatrics</i> , 2018, 196, 175-181.e7.	1.8	6
131	Kernel machine methods for integrative analysis of genome-wide methylation and genotyping studies. <i>Genetic Epidemiology</i> , 2018, 42, 156-167.	1.3	8
132	A molecule-based genetic association approach implicates a range of voltage-gated calcium channels associated with schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2018, 177, 454-467.	1.7	12
133	Insights of Acute Lymphoblastic Leukemia with Development of Genomic Investigation. <i>Methods in Molecular Biology</i> , 2018, 1754, 387-413.	0.9	1
134	Kernel machine SNP set analysis provides new insight into the association between obesity and polymorphisms located on the chromosomal 16q.12.2 region: Tehran Lipid and Glucose Study. <i>Gene</i> , 2018, 658, 146-151.	2.2	8
135	Probabilistic natural mapping of gene-level tests for genome-wide association studies. <i>Briefings in Bioinformatics</i> , 2018, 19, 545-553.	6.5	6
136	Power and sample size calculations for high-throughput sequencing-based experiments. <i>Briefings in Bioinformatics</i> , 2018, 19, 1247-1255.	6.5	32
137	Exome-Wide Association Study of Pancreatic Cancer Risk. <i>Gastroenterology</i> , 2018, 154, 719-722.e3.	1.3	38
138	Integrating expression-related SNPs into genome-wide gene- and pathway-based analyses identified novel lung cancer susceptibility genes. <i>International Journal of Cancer</i> , 2018, 142, 1602-1610.	5.1	14
139	Association detection between ordinal trait and rare variants based on adaptive combination of P values. <i>Journal of Human Genetics</i> , 2018, 63, 37-45.	2.3	10
140	Comparative study for haplotype block partitioning methods – Evidence from chromosome 6 of the North American Rheumatoid Arthritis Consortium (NARAC) dataset. <i>PLoS ONE</i> , 2018, 13, e0209603.	2.5	1
141	Exome sequencing identifies gene variants and networks associated with extreme respiratory outcomes following preterm birth. <i>BMC Genetics</i> , 2018, 19, 94.	2.7	31
142	Linear mixed models for association analysis of quantitative traits with next-generation sequencing data. <i>Genetic Epidemiology</i> , 2019, 43, 189-206.	1.3	5
144	ProxECAT: Proxy External Controls Association Test. A new case-control gene region association test using allele frequencies from public controls. <i>PLoS Genetics</i> , 2018, 14, e1007591.	3.5	23
145	Genetic variants in nuclear DNA along with environmental factors modify mitochondrial DNA copy number: a population-based exome-wide association study. <i>BMC Genomics</i> , 2018, 19, 752.	2.8	16
146	Genetic Determinants of IgA Nephropathy: Western Perspective. <i>Seminars in Nephrology</i> , 2018, 38, 443-454.	1.6	23

#	ARTICLE	IF	CITATIONS
147	A kernel machine method for detecting higher order interactions in multimodal datasets: Application to schizophrenia. <i>Journal of Neuroscience Methods</i> , 2018, 309, 161-174.	2.5	16
148	A Survey of SNP Data Analysis. <i>Big Data Mining and Analytics</i> , 2018, 1, 173-190.	8.9	12
149	Whole-Genome Sequencing in Severe Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018, 59, 614-622.	2.9	22
150	Stepwise approach to SNP-set analysis illustrated with the MetaboChip and colorectal cancer in Japanese Americans of the Multiethnic Cohort. <i>BMC Genomics</i> , 2018, 19, 524.	2.8	5
151	Frequency of Loss of Function Variants in <i>LRRK2</i> in Parkinson Disease. <i>JAMA Neurology</i> , 2018, 75, 1416.	9.0	66
152	Human genetic variants and age are the strongest predictors of humoral immune responses to common pathogens and vaccines. <i>Genome Medicine</i> , 2018, 10, 59.	8.2	113
153	A Powerful Gene-Based Test Accommodating Common and Low-Frequency Variants to Detect Both Main Effects and Gene-Gene Interaction Effects in Case-Control Studies. <i>Frontiers in Genetics</i> , 2017, 8, 228.	2.3	3
154	Associations of MAP2K3 Gene Variants With Superior Memory in SuperAgers. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 155.	3.4	22
155	Integrated analysis of human genetic association study and mouse transcriptome suggests LBH and SHF genes as novel susceptible genes for amyloid- β accumulation in Alzheimer's disease. <i>Human Genetics</i> , 2018, 137, 521-533.	3.8	22
156	<i>CHCHD10</i> variants in amyotrophic lateral sclerosis: Where is the evidence?. <i>Annals of Neurology</i> , 2018, 84, 110-116.	5.3	24
157	Germline and somatic variations influence the somatic mutational signatures of esophageal squamous cell carcinomas in a Chinese population. <i>BMC Genomics</i> , 2018, 19, 538.	2.8	19
158	Analysis of causal effect of <i>APOA5</i> variants on premature coronary artery disease. <i>Annals of Human Genetics</i> , 2018, 82, 437-447.	0.8	8
159	Variation in coagulation and fibrinolysis genes evaluated for their contribution to cerebrovascular complications in adults with bacterial meningitis in the Netherlands. <i>Journal of Infection</i> , 2018, 77, 54-59.	3.3	2
160	Mutation profiles and clinical characteristics of Chinese males with isolated hypogonadotropic hypogonadism. <i>Fertility and Sterility</i> , 2018, 110, 486-495.e5.	1.0	36
161	Genetic variation in <i>CHRNA7</i> and <i>CHRFAM7A</i> is associated with nicotine dependence and response to varenicline treatment. <i>European Journal of Human Genetics</i> , 2018, 26, 1824-1831.	2.8	13
162	Examining the role of common and rare mitochondrial variants in schizophrenia. <i>PLoS ONE</i> , 2018, 13, e0191153.	2.5	23
163	Multi-Omics Analysis Reveals a HIF Network and Hub Gene <i>EPAS1</i> Associated with Lung Adenocarcinoma. <i>EBioMedicine</i> , 2018, 32, 93-101.	6.1	35
164	Assessing Rare Variation in Complex Traits. <i>Methods in Molecular Biology</i> , 2018, 1793, 51-71.	0.9	4

#	ARTICLE	IF	CITATIONS
165	A powerful conditional gene-based association approach implicated functionally important genes for schizophrenia. <i>Bioinformatics</i> , 2019, 35, 628-635.	4.1	19
166	Targeted sequencing of candidate genes of dyslipidemia in Punjabi Sikhs: Population-specific rare variants in GCKR promote ectopic fat deposition. <i>PLoS ONE</i> , 2019, 14, e0211661.	2.5	9
167	Gene-based genome-wide association studies and meta-analyses of conotruncal heart defects. <i>PLoS ONE</i> , 2019, 14, e0219926.	2.5	15
168	Evaluation of Rare and Common Variants from Suspected Familial or Sporadic Nasopharyngeal Carcinoma (NPC) Susceptibility Genes in Sporadic NPC. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1682-1686.	2.5	5
169	Meta- ∞ MultiSKAT: Multiple phenotype meta-analysis for region-based association test. <i>Genetic Epidemiology</i> , 2019, 43, 800-814.	1.3	9
170	Set-based differential covariance testing for genomics. <i>Stat</i> , 2019, 8, e235.	0.4	1
171	NGS analysis in Marfan syndrome spectrum: Combination of rare and common genetic variants to improve genotype-phenotype correlation analysis. <i>PLoS ONE</i> , 2019, 14, e0222506.	2.5	18
172	Germline genetic host factors as predictive biomarkers in immuno-oncology. <i>Immuno-Oncology Technology</i> , 2019, 2, 14-21.	0.3	2
173	Association between mitochondrial genetic variation and breast cancer risk: The Multiethnic Cohort. <i>PLoS ONE</i> , 2019, 14, e0222284.	2.5	6
174	Efficient estimation of grouped survival models. <i>BMC Bioinformatics</i> , 2019, 20, 269.	2.6	0
175	Multiple rare and common variants in APOB gene locus associated with oxidatively modified low-density lipoprotein levels. <i>PLoS ONE</i> , 2019, 14, e0217620.	2.5	9
176	Multi-SNP mediation intersection-union test. <i>Bioinformatics</i> , 2019, 35, 4724-4729.	4.1	23
177	Genetic variation in <i>FCER1A</i> predicts peginterferon alfa-2a-induced hepatitis B surface antigen clearance in East Asian patients with chronic hepatitis B. <i>Journal of Viral Hepatitis</i> , 2019, 26, 1040-1049.	2.0	3
178	Telomere length is greater in ALS than in controls: a whole genome sequencing study. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2019, 20, 229-234.	1.7	18
179	Exonic sequencing identifies TLR1 genetic variation associated with mortality in Thais with melioidosis. <i>Emerging Microbes and Infections</i> , 2019, 8, 282-290.	6.5	3
180	Association of Genetic Variants in <i>NUDT15</i> With Thiopurine-Induced Myelosuppression in Patients With Inflammatory Bowel Disease. <i>JAMA - Journal of the American Medical Association</i> , 2019, 321, 773.	7.4	129
181	Studying the effects of haplotype partitioning methods on the RA-associated genomic results from the North American Rheumatoid Arthritis Consortium (NARAC) dataset. <i>Journal of Advanced Research</i> , 2019, 18, 113-126.	9.5	11
182	Stress-related genetic polymorphisms in association with peripartum depression symptoms and stress hormones: A longitudinal population-based study. <i>Psychoneuroendocrinology</i> , 2019, 103, 296-305.	2.7	18

#	ARTICLE	IF	CITATIONS
183	Benefits and Challenges of Rare Genetic Variation in Alzheimer's Disease. Current Genetic Medicine Reports, 2019, 7, 53-62.	1.9	9
185	CORRÂ® ORS Richard A. Brand Award: Disruption in Peroxisome Proliferator-Activated Receptor-Î³ (PPARγ) Increases Osteonecrosis Risk Through Genetic Variance and Pharmacologic Modulation. Clinical Orthopaedics and Related Research, 2019, 477, 1800-1812.	1.5	10
186	A review of kernel methods for genetic association studies. Genetic Epidemiology, 2019, 43, 122-136.	1.3	24
187	Minimal Residual Disease Testing. , 2019, , .		1
188	Identification of genetic variants associated with tacrolimus metabolism in kidney transplant recipients by extreme phenotype sampling and next generation sequencing. Pharmacogenomics Journal, 2019, 19, 375-389.	2.0	11
189	Complement C7 is a novel risk gene for Alzheimer's disease in Han Chinese. National Science Review, 2019, 6, 257-274.	9.5	55
190	Genome-wide association study of treatment-resistance in depression and meta-analysis of three independent samples. British Journal of Psychiatry, 2019, 214, 36-41.	2.8	44
191	Systematic analyses of regulatory variants in DNase I hypersensitive sites identified two novel lung cancer susceptibility loci. Carcinogenesis, 2019, 40, 432-440.	2.8	5
192	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
193	Composite Kernel Machine Regression Based on Likelihood Ratio Test for Joint Testing of Genetic and Gene-Environment Interaction Effect. Biometrics, 2019, 75, 625-637.	1.4	7
194	CoMM: a collaborative mixed model to dissecting genetic contributions to complex traits by leveraging regulatory information. Bioinformatics, 2019, 35, 1644-1652.	4.1	36
195	Exploring rare and low-frequency variants in the Saguenay-Lac-Saint-Jean population identified genes associated with asthma and allergy traits. European Journal of Human Genetics, 2019, 27, 90-101.	2.8	15
196	Targeted deep sequencing of the PEAR1 locus for platelet aggregation in European and African American families. Platelets, 2019, 30, 380-386.	2.3	19
197	Genes and variants in hematopoiesis-related pathways are associated with gemcitabine/carboplatin-induced thrombocytopenia. Pharmacogenomics Journal, 2020, 20, 179-191.	2.0	7
198	Testing the heritability and parent-of-origin hypotheses for ages at onset of psoriatic arthritis under biased sampling. Biometrics, 2020, 76, 293-303.	1.4	3
199	Distance-based analysis of variance for brain connectivity. Biometrics, 2020, 76, 257-269.	1.4	2
200	Evaluation of the antibody response to the EBV proteome in EBV-associated classical Hodgkin lymphoma. International Journal of Cancer, 2020, 147, 608-618.	5.1	15
201	Complete Sequence of the 22q11.2 Allele in 1,053 Subjects with 22q11.2 Deletion Syndrome Reveals Modifiers of Conotruncal Heart Defects. American Journal of Human Genetics, 2020, 106, 26-40.	6.2	42

#	ARTICLE	IF	CITATIONS
202	Genetic association of gemcitabine/carboplatin-induced leukopenia and neutropenia in non-small cell lung cancer patients using whole-exome sequencing. <i>Lung Cancer</i> , 2020, 147, 106-114.	2.0	5
203	A telescope GWAS analysis strategy, based on SNPs-genes-pathways ensemble and on multivariate algorithms, to characterize late onset Alzheimer's disease. <i>Scientific Reports</i> , 2020, 10, 12063.	3.3	11
204	Integration of GWAS and eQTL Analysis to Identify Risk Loci and Susceptibility Genes for Gastric Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 679.	2.3	10
205	GCH1 variants contribute to the risk and earlier age-at-onset of Parkinson's disease: a two-cohort case-control study. <i>Translational Neurodegeneration</i> , 2020, 9, 31.	8.0	30
206	Identifying genetic factors that contribute to the increased risk of congenital heart defects in infants with Down syndrome. <i>Scientific Reports</i> , 2020, 10, 18051.	3.3	14
208	Genetic modifiers of long-term survival in sickle cell anemia. <i>Clinical and Translational Medicine</i> , 2020, 10, e152.	4.0	21
209	Whole-Exome Sequencing Analysis of Alzheimer's Disease in Non-APOE*4 Carriers. <i>Journal of Alzheimer's Disease</i> , 2020, 76, 1553-1565.	2.6	18
210	Prioritizing genetic variants in GWAS with lasso using permutation-assisted tuning. <i>Bioinformatics</i> , 2020, 36, 3811-3817.	4.1	15
211	Lung Function in African American Children with Asthma Is Associated with Novel Regulatory Variants of the KIT Ligand <i>KITLG/SCF</i> and Gene-By-Air-Pollution Interaction. <i>Genetics</i> , 2020, 215, 869-886.	2.9	11
212	Differential contributions of sarcomere and mitochondria-related multigene variants to the endophenotype of hypertrophic cardiomyopathy. <i>Mitochondrion</i> , 2020, 53, 48-56.	3.4	8
213	Statistical Method Based on Bayes-Type Empirical Score Test for Assessing Genetic Association with Multilocus Genotype Data. <i>International Journal of Genomics</i> , 2020, 2020, 1-10.	1.6	2
214	Remote modulation of lncRNA <i>GCLET</i> by risk variant at 16p13 underlying genetic susceptibility to gastric cancer. <i>Science Advances</i> , 2020, 6, eaay5525.	10.3	23
215	Revisiting the complex architecture of ALS in Turkey: Expanding genotypes, shared phenotypes, molecular networks, and a public variant database. <i>Human Mutation</i> , 2020, 41, e7-e45.	2.5	10
216	Estimation of non-null SNP effect size distributions enables the detection of enriched genes underlying complex traits. <i>PLoS Genetics</i> , 2020, 16, e1008855.	3.5	9
217	Detecting rare haplotypes associated with complex diseases using both population and family data: Combined logistic Bayesian Lasso. <i>Statistical Methods in Medical Research</i> , 2020, 29, 3340-3350.	1.5	1
218	Gene-based analyses of the maternal genome implicate maternal effect genes as risk factors for conotruncal heart defects. <i>PLoS ONE</i> , 2020, 15, e0234357.	2.5	8
219	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in Patients With Osteosarcoma. <i>JAMA Oncology</i> , 2020, 6, 724.	7.1	139
220	Sequence kernel association test for survival outcomes in the presence of a non-susceptible fraction. <i>Biostatistics</i> , 2020, 21, 518-530.	1.5	3

#	ARTICLE	IF	CITATIONS
221	A Bioinformatics Crash Course for Interpreting Genomics Data. Chest, 2020, 158, S113-S123.	0.8	6
222	RAINBOW: Haplotype-based genome-wide association study using a novel SNP-set method. PLoS Computational Biology, 2020, 16, e1007663.	3.2	46
223	A polygenic predictor of treatment-resistant depression using whole exome sequencing and genome-wide genotyping. Translational Psychiatry, 2020, 10, 50.	4.8	33
224	Genetics of schizophrenia in the South African Xhosa. Science, 2020, 367, 569-573.	12.6	93
225	FAM222A encodes a protein which accumulates in plaques in Alzheimer's disease. Nature Communications, 2020, 11, 411.	12.8	16
226	Cross-Cancer Pleiotropic Analysis Reveals Novel Susceptibility Loci for Lung Cancer. Frontiers in Oncology, 2019, 9, 1492.	2.8	6
227	Statistical Methods in Genome-Wide Association Studies. Annual Review of Biomedical Data Science, 2020, 3, 265-288.	6.5	6
228	Adaptive Fisher method detects dense and sparse signals in association analysis of SNV sets. BMC Medical Genomics, 2020, 13, 46.	1.5	2
229	Large-scale identification of expression quantitative trait loci in Arabidopsis reveals novel candidate regulators of immune responses and other processes. Journal of Integrative Plant Biology, 2020, 62, 1469-1484.	8.5	7
230	Gene-Based Association Testing of Dichotomous Traits With Generalized Functional Linear Mixed Models Using Extended Pedigrees: Applications to Age-Related Macular Degeneration. Journal of the American Statistical Association, 2021, 116, 531-545.	3.1	3
231	MF-TOWMuT: Testing an optimally weighted combination of common and rare variants with multiple traits using family data. Genetic Epidemiology, 2021, 45, 64-81.	1.3	0
232	Exome Sequencing Identifies Abnormalities in Glycosylation and ANKRD36C in Patients with Immune-Mediated Thrombotic Thrombocytopenic Purpura. Thrombosis and Haemostasis, 2021, 121, 506-517.	3.4	4
233	Genomics Data Treatment in the Era of Next Generation Sequencing. , 2021, , 277-290.		0
234	The burden of rare damaging variants in hereditary atypical parkinsonism genes is increased in patients with Parkinson's disease. Neurobiology of Aging, 2021, 100, 118.e5-118.e13.	3.1	2
235	Evaluation of the MC4R gene across eMERGE network identifies many unreported obesity-associated variants. International Journal of Obesity, 2021, 45, 155-169.	3.4	19
236	Rare <i>ATG7</i> Genetic Variants Predispose to Severe Fatty Liver Disease. SSRN Electronic Journal, 0, , .	0.4	0
237	Exome-Wide Association Study Identifies <i>FN3KRP</i> and <i>PGP</i> as New Candidate Longevity Genes. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 786-795.	3.6	14
238	Status and Prospectives of Genome-Wide Association Studies in Plants. , 2021, , 413-457.		2

#	ARTICLE	IF	CITATIONS
239	The joint effect of PPARC upstream genetic variation in association with long-term persistent obesity: Tehran cardio-metabolic genetic study (TCGS). <i>Eating and Weight Disorders</i> , 2021, 26, 2325-2332.	2.5	3
240	Methods for Association Studies. , 2021, , 89-121.		1
241	Genomic data measures and methods: a primer for social scientists. , 2021, , 49-62.		2
242	Aggregating multiple expression prediction models improves the power of transcriptome-wide association studies. <i>Human Molecular Genetics</i> , 2021, 30, 939-951.	2.9	24
244	Whole-Exome Sequencing and hiPSC Cardiomyocyte Models Identify MYRIP, TRAPPC11, and SLC27A6 of Potential Importance to Left Ventricular Hypertrophy in an African Ancestry Population. <i>Frontiers in Genetics</i> , 2021, 12, 588452.	2.3	3
245	Identification of low-frequency variants of UGT1A3 associated with bladder cancer risk by next-generation sequencing. <i>Oncogene</i> , 2021, 40, 2382-2394.	5.9	8
246	Boosting GWAS using biological networks: A study on susceptibility to familial breast cancer. <i>PLoS Computational Biology</i> , 2021, 17, e1008819.	3.2	4
247	Genome-wide haplotype association study in imaging genetics using whole-brain sulcal openings of 16,304 UK Biobank subjects. <i>European Journal of Human Genetics</i> , 2021, 29, 1424-1437.	2.8	1
248	Emerging roles of rare and low-frequency genetic variants in type 1 diabetes mellitus. <i>Journal of Medical Genetics</i> , 2021, 58, 289-296.	3.2	8
249	Genome-Wide Identification of Rare and Common Variants Driving Triglyceride Levels in a Nevada Population. <i>Frontiers in Genetics</i> , 2021, 12, 639418.	2.3	7
251	Detection of Genetic Overlap Between Rheumatoid Arthritis and Systemic Lupus Erythematosus Using GWAS Summary Statistics. <i>Frontiers in Genetics</i> , 2021, 12, 656545.	2.3	9
252	Resequencing of candidate genes for Keratoconus reveals a role for Ehlers-Danlos Syndrome genes. <i>European Journal of Human Genetics</i> , 2021, 29, 1745-1755.	2.8	8
253	Family-based gene-environment interaction using sequence kernel association test (FGE-SKAT) for complex quantitative traits. <i>Scientific Reports</i> , 2021, 11, 7431.	3.3	0
254	A powerful subset-based method identifies gene set associations and improves interpretation in UK Biobank. <i>American Journal of Human Genetics</i> , 2021, 108, 669-681.	6.2	8
255	Novel Variance-Component TWAS method for studying complex human diseases with applications to Alzheimer's dementia. <i>PLoS Genetics</i> , 2021, 17, e1009482.	3.5	36
256	Comprehensive Study of Germline Mutations and Double-Hit Events in Esophageal Squamous Cell Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 637431.	2.8	5
257	MARS: leveraging allelic heterogeneity to increase power of association testing. <i>Genome Biology</i> , 2021, 22, 128.	8.8	2
258	Genome-wide association study of stage III/IV grade C periodontitis (former aggressive periodontitis) in a Spanish population. <i>Journal of Clinical Periodontology</i> , 2021, 48, 896-906.	4.9	10

#	ARTICLE	IF	CITATIONS
260	Whole-genome sequencing reveals new Alzheimer's disease-associated rare variants in loci related to synaptic function and neuronal development. <i>Alzheimer's and Dementia</i> , 2021, 17, 1509-1527.	0.8	50
261	Exome sequencing in high and low fetal haemoglobin Arab Indian haplotype sickle cell disease. <i>British Journal of Haematology</i> , 2021, 194, e61-e64.	2.5	2
262	Kernel machine SNP set analysis finds the association of BUD13, ZPR1, and APOA5 variants with metabolic syndrome in Tehran Cardio-metabolic Genetics Study. <i>Scientific Reports</i> , 2021, 11, 10305.	3.3	6
263	Impact of rare and common genetic variation in the interleukin-1 pathway on human cytokine responses. <i>Genome Medicine</i> , 2021, 13, 94.	8.2	5
264	A fast wavelet-based functional association analysis replicates several susceptibility loci for birth weight in a Norwegian population. <i>BMC Genomics</i> , 2021, 22, 321.	2.8	0
265	Tejaas: reverse regression increases power for detecting trans-eQTLs. <i>Genome Biology</i> , 2021, 22, 142.	8.8	4
266	Genetic Susceptibility to Periodontal Disease in Down Syndrome: A Case-Control Study. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6274.	4.1	6
267	A Constrained Generalized Functional Linear Model for Multi-Loci Genetic Mapping. <i>Stats</i> , 2021, 4, 550-576.	0.9	0
268	Scalable and Robust Regression Methods for Phenome-Wide Association Analysis on Large-Scale Biobank Data. <i>Frontiers in Genetics</i> , 2021, 12, 682638.	2.3	2
270	A two-stage testing strategy for detecting genes-environment interactions in association studies. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	0
271	IUSMMT: Survival mediation analysis of gene expression with multiple DNA methylation exposures and its application to cancers of TCGA. <i>PLoS Computational Biology</i> , 2021, 17, e1009250.	3.2	7
272	A generalized kernel machine approach to identify higher-order composite effects in multi-view datasets, with application to adolescent brain development and osteoporosis. <i>Journal of Biomedical Informatics</i> , 2021, 120, 103854.	4.3	2
274	An Integrative Co-localization (INCO) Analysis for SNV and CNV Genomic Features With an Application to Taiwan Biobank Data. <i>Frontiers in Genetics</i> , 2021, 12, 709555.	2.3	2
275	GPCR oligomerization as a target for antidepressants: Focus on GPR39. , 2021, 225, 107842.		7
276	A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimer's disease. <i>Nature Genetics</i> , 2021, 53, 1276-1282.	21.4	430
277	Statistical approaches to rare disease analyses. , 2021, , 205-213.		1
278	Germline Genetics in Immuno-oncology: From Genome-Wide to Targeted Biomarker Strategies. <i>Methods in Molecular Biology</i> , 2020, 2055, 93-117.	0.9	4
285	De Novo and Rare Variants at Multiple Loci Support the Oligogenic Origins of Atrioventricular Septal Heart Defects. <i>PLoS Genetics</i> , 2016, 12, e1005963.	3.5	92

#	ARTICLE	IF	CITATIONS
286	Identifying and exploiting trait-relevant tissues with multiple functional annotations in genome-wide association studies. PLoS Genetics, 2018, 14, e1007186.	3.5	30
287	A phenome-wide association study of 26 mendelian genes reveals phenotypic expressivity of common and rare variants within the general population. PLoS Genetics, 2020, 16, e1008802.	3.5	12
288	Using Hamming Distance as Information for SNP-Sets Clustering and Testing in Disease Association Studies. PLoS ONE, 2015, 10, e0135918.	2.5	29
289	Exome-wide association study reveals novel susceptibility genes to sporadic dilated cardiomyopathy. PLoS ONE, 2017, 12, e0172995.	2.5	92
290	Common and rare exonic MUC5B variants associated with type 2 diabetes in Han Chinese. PLoS ONE, 2017, 12, e0173784.	2.5	10
291	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. Oncotarget, 2016, 7, 72381-72394.	1.8	13
292	Pharmacogenomics, How to Deal with Different Types of Variants in Next Generation Sequencing Data in the Personalized Medicine Area. Journal of Clinical Medicine, 2021, 10, 34.	2.4	4
293	Variance component testing for identifying differentially expressed genes in RNA-seq data. PeerJ, 2017, 5, e3797.	2.0	4
294	Wavelet Screening: a novel approach to analyzing GWAS data. BMC Bioinformatics, 2021, 22, 484.	2.6	2
295	Statistical Considerations in the Analysis of Rare Variants. , 2014, , 405-422.		0
296	Single nucleotide polymorphisms in human health and disease: Towards resolution of a conundrum. Biomedical Research Journal, 2014, 1, 56.	0.5	0
297	A Robust GWSS Method to Simultaneously Detect Rare and Common Variants for Complex Disease. PLoS ONE, 2015, 10, e0120873.	2.5	0
299	Powerful Tests for Multi-Marker Association Analysis Using Ensemble Learning. PLoS ONE, 2015, 10, e0143489.	2.5	0
306	Advancements in Next-Generation Sequencing for Detecting Minimal Residual Disease. , 2019, , 159-192.		0
324	kTWAS: integrating kernel machine with transcriptome-wide association studies improves statistical power and reveals novel genes. Briefings in Bioinformatics, 2021, 22, .	6.5	30
326	Whole mitochondrial genome analysis in Chinese patients with keratoconus. Molecular Vision, 2021, 27, 270-282.	1.1	4
327	Powerful gene-based testing by integrating long-range chromatin interactions and knockoff genotypes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	5
328	Insilico Functional Analysis of Genome-Wide Dataset From 17,000 Individuals Identifies Candidate Malaria Resistance Genes Enriched in Malaria Pathogenic Pathways. Frontiers in Genetics, 2021, 12, 676960.	2.3	1

#	ARTICLE	IF	CITATIONS
329	Pharmacogenomic analysis of a genetically distinct Indigenous population. <i>Pharmacogenomics Journal</i> , 2021, , .	2.0	4
330	Stochastic Epigenetic Mutations Influence Parkinson's Disease Risk, Progression, and Mortality. <i>Journal of Parkinson's Disease</i> , 2022, 12, 545-556.	2.8	5
331	Identification of Potential Biological Factors Affecting the Treatment of Ticagrelor After Percutaneous Coronary Intervention in the Chinese Population. <i>Pharmacogenomics and Personalized Medicine</i> , 2022, Volume 15, 29-43.	0.7	2
332	Integration with systems biology approaches and -omics data to characterize risk variation. , 2022, , 289-315.		4
334	Partitioning gene-level contributions to complex-trait heritability by allele frequency identifies disease-relevant genes. <i>American Journal of Human Genetics</i> , 2022, 109, 692-709.	6.2	2
335	Deciphering Genetic Susceptibility to Tuberculous Meningitis. <i>Frontiers in Neurology</i> , 2022, 13, 820168.	2.4	2
336	Whole Exome Sequencing Identifies Genes Associated With Non-Obstructive Azoospermia. <i>Frontiers in Genetics</i> , 2022, 13, 872179.	2.3	5
350	A Comparison of Methods for Gene-Based Testing That Account for Linkage Disequilibrium. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	1
351	Gene-Based Methods for Estimating the Degree of the Skewness of X Chromosome Inactivation. <i>Genes</i> , 2022, 13, 827.	2.4	0
352	Contribution of rare whole-genome sequencing variants to plasma protein levels and the missing heritability. <i>Nature Communications</i> , 2022, 13, 2532.	12.8	9
355	Identification of a Novel Functional Non-synonymous Single Nucleotide Polymorphism in Frizzled Class Receptor 6 Gene for Involvement in Depressive Symptoms. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	2.9	1
356	Integrated Quantile RAnk Test (iQRAT) for gene-level associations. <i>Annals of Applied Statistics</i> , 2022, 16, .	1.1	3
357	Gene-Based Variant Analysis of Whole-Exome Sequencing in Relation to Eosinophil Count. <i>Frontiers in Immunology</i> , 0, 13, .	4.8	3
358	Long-Lived Individuals Show a Lower Burden of Variants Predisposing to Age-Related Diseases and a Higher Polygenic Longevity Score. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10949.	4.1	5
359	A comprehensive comparison of multilocus association methods with summary statistics in genome-wide association studies. <i>BMC Bioinformatics</i> , 2022, 23, .	2.6	4
360	Association of genetic variants in ULK4 with the age of first onset of type B aortic dissection. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	0
361	DeepPerVar: a multi-modal deep learning framework for functional interpretation of genetic variants in personal genome. <i>Bioinformatics</i> , 2022, 38, 5340-5351.	4.1	4
362	Kernel-based gene-environment interaction tests for rare variants with multiple quantitative phenotypes. <i>PLoS ONE</i> , 2022, 17, e0275929.	2.5	0

#	ARTICLE	IF	CITATIONS
363	CLIN_SKAT: an R package to conduct association analysis using functionally relevant variants. BMC Bioinformatics, 2022, 23, .	2.6	0
364	Robust Genetic Model-Based SNP-set Association Test Using CauchyGM. Bioinformatics, 0, , .	4.1	1
365	Mendelian Disorders in an Interstitial Cystitis/Bladder Pain Syndrome Cohort. Genetics & Genomics Next, 2023, 4, .	1.5	1
366	Association between ten-eleven methylcytosine dioxygenase 2 genetic variation and viral load in people with HIV. Aids, 2023, 37, 379-387.	2.2	1
368	Investigation of genetic variants and causal biomarkers associated with brain aging. Scientific Reports, 2023, 13, .	3.3	1
370	How can childhood maltreatment affect post-traumatic stress disorder in adult: Results from a composite null hypothesis perspective of mediation analysis. Frontiers in Psychiatry, 0, 14, .	2.6	0
371	Cross-cancer pleiotropic analysis identifies three novel genetic risk loci for colorectal cancer. Human Molecular Genetics, 2023, 32, 2093-2102.	2.9	3
372	Exome-wide assessment of isolated biliary atresia: A report from the <scp>National Birth Defects Prevention Study</scp> using childâ€parent trios and a caseâ€control design to identify novel rare variants. American Journal of Medical Genetics, Part A, 2023, 191, 1546-1556.	1.2	2
373	Children with Early-Onset Psychosis Have Increased Burden of Rare GRIN2A Variants. Genes, 2023, 14, 779.	2.4	2
375	Comparison of multiple imputation and other methods for the analysis of imputed genotypes. BMC Genomics, 2023, 24, .	2.8	0
376	GWAS identifies candidate genes controlling adventitious rooting in <i>Populus trichocarpa</i>. Horticulture Research, 2023, 10, .	6.3	3
377	Germline loss-of-function PAM variants are enriched in subjects with pituitary hypersecretion. Frontiers in Endocrinology, 0, 14, .	3.5	3
378	A Genome-Wide Association Study of Small Cell Lung Cancer. Archivos De Bronconeumologia, 2023, 59, 645-650.	0.8	2
379	Fast kernel-based association testing of non-linear genetic effects for biobank-scale data. Nature Communications, 2023, 14, .	12.8	1
380	Mouse and human studies support DSTYK loss of function as a low penetrance and variable expressivity risk factor for congenital urinary tract anomalies. Genetics in Medicine, 2023, , 100983.	2.4	0
381	Learning the kernel for rare variant genetic association test. Frontiers in Genetics, 0, 14, .	2.3	1
382	Excalibur: A new ensemble method based on an optimal combination of aggregation tests for rare-variant association testing for sequencing data. PLoS Computational Biology, 2023, 19, e1011488.	3.2	1
384	Weighted Selection Probability to Prioritize Susceptible Rare Variants in Multi-Phenotype Association Studies with Application to a Soybean Genetic Data Set. Journal of Computational Biology, 2023, 30, 1075-1088.	1.6	0

#	ARTICLE	IF	CITATIONS
386	HLA-DQB1*06 and Select Neighboring HLA Variants Predict Chlamydia Reinfection Risk. International Journal of Molecular Sciences, 2023, 24, 15803.	4.1	0
387	Rare variant association on unrelated individuals in caseâ€“control studies using aggregation tests: existing methods and current limitations. Briefings in Bioinformatics, 2023, 24, .	6.5	0
388	Pharmacogenomics of intravenous immunoglobulin response in Kawasaki disease. Frontiers in Immunology, 0, 14, .	4.8	1
389	Pathogenic and likely pathogenic germline variation in patients with myeloid malignancies and their unrelated HLA-matched hematopoietic stem cell donors. Journal of Translational Genetics and Genomics, 0, 8, 35-48.	0.5	0
390	GWAS supported by computer vision identifies large numbers of candidate regulators of <i>in planta</i> regeneration in <i>Populus trichocarpa</i>. G3: Genes, Genomes, Genetics, 2024, 14, .	1.8	0
392	Incorporating genetic similarity of auxiliary samples into eGene identification under the transfer learning framework. Journal of Translational Medicine, 2024, 22, .	4.4	0